S.No.	Roll No.	Name	Email Address	Mobile No.	Branch	Training Start Da	Training End	Company / Institute Name	Training / Project Name	Training / Project Domain
3	151202	Shimul Garg	shimulgarg@gmail.com	8629010105	CSE	5/24/2018	07-06-2018	National Fertilizers Limited,	Coal Traffic System	Java
4	151203	Arush Kaushal	arushkaushal@gmail.com	9418981032	CSE	06-11-2018	7/19/2018	SJVN Shimla	Smart city project	Web development
6	151205	Hitesh Gupta	hitesh1205gupta@icloud.com	9501196916	CSE	06-04-2018	7/14/2018	Infowiz	Python programming	Hospital management system in pythor
7	151206	Hardik Chhabra	chhabraa009@gmail.com	9816060418	CSE	5/28/2018	07-07-2018	Ducat Gurgaon	AWS Cloud Computing	Web App using php and AWS
10	151210	Vansh Mahajan	mahajan.98.vansh@gmail.com	9459847602	CSE	06-04-2018	7/13/2018	DIT(Department of Informat	Training on Android	Android App for information storage in
11	151211	Nikita	talwarnikita1996@gmail.com		CSE	5/28/2018	07-06-2018	CS Infotech	Vitals	PHP(system for managing clinical repo
12	151212	Himank Jog	himank.juit@gmail.com	8628821312	CSE	06-04-2018	07-10-2018	Indifi Technologies	Name matching algorithm,	Web Backend (nodeJS, postgreSQL, S
13	151215	Prashant Chauhan	prashantchauhan38@gmail.com	8629010264	CSE	06-06-2018	7/17/2018	Cetpa Infotech Pvt. Ltd.	Supervised Machine Learn	Machine Learning.
15	151217	Dhruv Mohan Kapil	dhruvmkapil@gmail.com	9736360992	CSE	5/28/2018	07-07-2018	Vashisht Computer Institute	Training on Python	Python Programming
16	151218	Swastik Chugh	swastikchugh@gmail.com	8629013577	CSE	5/28/2018	07-07-2018	Neuweg Technologies	Crypto Market Advisory	Website Frontend Devolopment
17	151219	Abhishek pundir	Abhishek10pundir96@gmail.com	7807112638	CSE	5/26/2018	07-06-2018	Cetpa infotech Pvt limited	Machine learning	Apply Machine learning on different da
18	151220	Aayush Gupta	aayush.gupta1597@gmail.com	8629010334	CSE	06-04-2018	7/18/2018	Rigved TEchnologies	Automated Bot for Invoice	Robotic Process Automation, SAP
19	151221	Akhil Mittal	akhilmittal008@gmail.com	9816718191	CSE	06-04-2018	7/14/2018	INFOWIZ	Training on Python Prograr	Hospital Management System in Pytho
20	151222	Anmol Mahajan	anmol.juit@gmail.com	8627928036	CSE	5/25/2018	07-09-2018	Indian Statistical Institute, k	TMTO Attack On DES	Cryptography
23	151225	Akhil Sahota	akhilsahota96@gmail.com	-8894062518	CSE	04-06-2018	12-07-2018	DevelopTech IT Solutions P	Machine Learning	Machine Learning in Python
24	151226	Sahil Ratra	sahil07ratra@gmail.com	8629010414	CSE	06-06-2018	07-06-2018	Oil and Natural Gas Corpor	Analysis of stock data	Data mining and analysis
25	151227	Sahil Shama	sahilshama240@gmail.com	8628983716	CSE	06-04-2018	7/16/2018	Kvch	Online movie ticket booking	Python
26	151228	Jayant Rana	JAYANTRANA004@GMAIL.COM	8628952467	CSE	5/26/2018	07-05-2018	CETPA	Stock Market Trading Appl	Machine Learning
27	151229	Sameer Kumar	ksameer0001@gmail.com	9736992746	CSE	5/26/2018	07-05-2018	Cetpa Infotech pvt ltd	Stock Exchange Trading A	Machine Learning
28	151230	Arushi Rastogi	rastogi.arushi@gmail.com	8629009935	CSE	5/26/2018	07-06-2018	Cetpa Infotech Pvt Ltd	Stock market trading applic	Machine learning
29	151231	Vedika Garg	garg.vedika@gmail.com	7988078041	CSE	5/22/2018	7/18/2018	Newgen Software Technolo	Client Web Portal	Web development and Java
30	151232	Shivam Sood	shivamsood004@gmail.com	7831838710	CSE	5/26/2018	07-07-2018	CETPA INFOTECH	Machine Learning	Stock Market Prediction
33	151235	Shriya Chopra	shriyachopra47@gmail.com	8988388800	CSE	5/28/2018	07-07-2018	BSNL Kullu,HP	Wired and Wireless systen	Wired and Wireless System in Telecor
34	151236	Akshay Sharma	akshaysharma.2993@gmail.com	7018467314	CSE	06-04-2018	7/14/2018	Jaypee University of informa	Training on Course manag	Python using django framework
35	151237	Ayush Gupta	guuptaayush@gmail.com	8629010079	CSE	06-04-2018	7/14/2018	Digipodium	Online Real Estate Site	Web Application
36	151238	SHAMBHAWI PAL	shambhawipal@gmail.com		CSE	5/28/2018	07-10-2018	IIT BHU	Breast Cancer Classificatic	Machine Learning
37	151239	Ikjot Singh	singh.ikjot09@gmail.com	9816697739	CSE	06-04-2018	7/13/2018	CDAC	Big Data Technology	House Pricing Analysis using Big Data
38	151240	Samiksha Gupta	samikshagupta269@gmail.com	8629010324	CSE	06-01-2018	7/14/2018	Whiz Infotel	Training on Computer Netv	Network Security
40	151242	Saksham Thakur	sakshamthaakur@gmail.com	7833884639	CSE	5/25/2018	07-10-2018	ISI Kolkata	TMTO on DES	Cryptography
41	151244	Shubham	shubham11singh1997@gmail.com	8629009934	CSE	5/31/2018	6/27/2018	CETPA INFOTECH PRIVAT	Stock Market Trading Appl	Machine Learning
42	151245	Apoorva Agarwal	apoorva97.agarwal@gmail.com	8629010034	CSE	06-01-2018	7/14/2018	Jawaharlal Nehru University	Detection of breast cancer	Machine Learning
43	151246	Vaibhav Singh			CSE	04-06-2018	14-07-2018	JUIT	Python and cipher text	Python
44	151247	pawan palariya	pawansdpshald@gmail.com	8630788179	CSE	06-06-2018	7/17/2018	cetpa infotech private limite	supervised learning	machine learning
45	151248	Karanvir Singh Pathania	karan171097@gmail.com	8894422424	CSE	5/28/2018	07-07-2018	Bharat Sanchar Nigam Limi	Wired and Wireless Netwo	Wired and Wireless System of Telecor
46	151249	Rishav Sharma	rishav222112@gmail.com	9805675782	CSE	5/28/2018	07-07-2018	Bharat Sanchar Nigam Limi	Basic Telecom	Networking
47	151250	Shreya Gupta	gshreya132@gmail.com	9882907760	CSE	5/29/2018	07-08-2018	Edimeet	Project(internship) in creati	Web
48	151251	Jatin walia	jatwal2052@gmail.com	8683087657	CSE	06-04-2018	7/13/2018	Nielit	Crime Analysis & Analysis	Big Data
49	151252	Akanksha Sharma	akankshasharma306@gmail.com	8629010452	CSE	5/28/2018	7/13/2018	CorporateServe Solutions P	Hotel Management System	Web development
50	151253	Chirag Sharma	chirag179652@gmail.com	7833024773	CSE	5/28/2018	07-07-2018	Bharat Sanchar Nigam Ltd.	Training on Basic Telecom	Mobile Computing
51	151254	Manish Kumar Sharma	smanishkumar100@gmail.com		CSE	06-04-2018	7/16/2018	KV Computer Home Private	Hosting Drupal Website W	Cloud Computing
52	151255	Sahil Gaur	gaursahil9816238919@gmail.com	8626940919	CSE	06-04-2018	7/14/2018	Xenon DigiLabs	Training on Apache Gobbli	Big Data
53	151257	Abhishek Soni	asoni2520419@gmail.com	9877025519	CSE	5/28/2018	07-07-2018	RICCS Computer Eduation	Advanced Java	Offline Travel and Tours ticket booking
54	151258	Varnita Sachdeva	varnitasmailbox123@gmail.com	8629010075	CSE	5/28/2018	6/30/2018	HCL Infotech Ltd.	Training on Python	Video Recommendation Engine
56	151261	Lokinder Singh Mittal	lokindermittal@gmail.com	9569925290	CSE	5/28/2018	07-07-2018	Bharat Electronics Limited (	Air Traffic Management	Graphics in C++
60	151266	Kashish Taneja	kashish.220197@gmail.com	9736992610	CSE	06-01-2018	7/14/2018	MDA IT Hub Infotech Pvt.Lt	Advance java(j2ee)	Website development using advance ja
61	151267	Tushar Tayal	tayaltushar8@gmail.com	8629010101	CSE	5/26/2018	07-06-2018	F-TEC	Training on Machine Learn	Machine Learning for data mining

63	151269	Devyani Kaulas	manikaulas@gmail.com	9816668008	CSE	06-04-2018	07-04-2018	RAPS	Python(Django)	Web development
65	151271	Amit Patial	amitpatial048@gmail.com	9459102721	CSE	06-01-2018	11-07-2018	Wapcos Ltd.	Real Time GIS Tracking Sy	GIS Tracking System
66	151272	SANCHI THAREJA	sanchithareja127@gmail.com		CSE	5/28/2018	07-08-2018	ITC LIMITED	Modernised meetings	Data handling and visualisation
67	151273	Sushant	sushantvashisht41@gmail.com	9817185842	CSE	06-01-2018	07-12-2018	eBizInfosys	IASC	IASC Automation System
68	151274	Abhinav Kriti Gupta	hackriti@gmail.com	9459888422	CSE	06-05-2018	7/16/2018	HPPWD	ONLINE CONSTRUCTION	Web Development
70	151276	Archit Singh	architsingh98@gmail.com	8629010338	CSE	5/25/2018	07-10-2018	Wizard Info solutions Pvt. Lt	Online shopping Portal	Spring Boot 2.0 & Hibernate 5.0
73	151279	Ayushi Mittal	ayushimittal104@gmail.com	8629010037	CSE	5/28/2018	07-07-2018	Jaypee University of Informa	Hotel Management SAP	Web
74	151281	Dheeraj Verma	vermadheeraj317@gmail.com		CSE	06-04-2018	7/16/2018	KV Computer Home Private	Hosting Drupal Website W	CLOUD COMPUTING
75	151282	Abhinav Thakur	cl.abhinavthakur@gmail.com	9459613418	CSE	5/27/2018	07-10-2018	CDAC	IOT	Safety driving system
76	151283	Nikhil Sharma	NIKHIL.SHARMA09876543@GMAIL.C	8988038211	CSE	5/28/2018	07-09-2018	BSNL	Networking	Networking
78	151285	Rohan Gupta	rhngpt627@gmail.com	151285	CSE	06-04-2018	7/13/2018	ThinkNEXT Technologies P	Python	Library Management System
79	151286	deepanshu sharma	deepanshusharma551@gmail.com	9736992342	CSE	06-04-2018	7/16/2018	ThinkNext technologies Pvt	Python programming/librar	library management system
81	151288	Mohit Sood	mohitsoodaut@gmail.com	8219153828	CSE	06-04-2018	7/13/2018	ThinkNEXT	Python	Library Management System
82	151289	Yogesh Khurana	ykhurana1321@gmail.com	8950211182	CSE	5/28/2018	7/16/2018	NCR corporations	project on Big data	Big data
83	151290	Parv sharma	parvsharma560@gmail.com	7018184358	CSE	5/25/2018	07-06-2018	NIT Hamirpur	Training on location trackin	Realtime location tracking using androi
84	151291	Nishant Sharma	nishantsharmajp@gmail.com	7018811695	CSE	06-04-2018	7/14/2018	JUIT	course management syster	python
85	151292	Man Mayur Kaur	makaur.kaur50@gmail.com	9882159065	CSE	5/28/2018	07-07-2018	Bharat electronics limited	Air traffic management	C++
87	151294	Manika	manika.sharma1996@gmail.com	9816027755	CSE	06-04-2018	07-12-2018	IRDE (Drdo)	Anchored Mail system	python
88	151295	Devesh Kashmiri	kashmiridevesh@gmail.com	9805822369	CSE	06-06-2018	7/25/2018	Aptech Computer Educatior	Text editor using TKinter	Software development using Python
89	151296	Samarth Dixit	samarth8404@gmail.com	8629010114	CSE	5/28/2018	07-09-2018	State Bank of India	Corporate Internet Banking	Network & Security
90	151297	Sakshi Sharma	SAKSHI1996.SS@GMAIL.COM	9728267554	CSE	5/21/2018	07-05-2018	Aptron	Networking	CCNA
91	151298	siddhesh sharma	siddheshatjuit@gmail.com	9409699988	CSE	04-01-2018	6/23/2017	Jha Infotech	Website Building using Dja	Shopping website
92	151299	KARTIK SHARMA	ks.jc1995@gmail.com	9736992519	CSE	5/23/2018	07-07-2018	Learnest	K12 Ed-tech application.	Ed-Tech.
93	151300	Siddharth malik	siddharthkumarmalik@gmail.com	7838601014	CSE	06-04-2018	7/18/2018	DUCAT	Python & data science	2012 US Elections analysis
95	151302	Ashutosh Singh	ashutoshsingh24@pm.me	8629013711	CSE	5/26/2018	6/30/2018	Eckovation	Agglomerative Hierarchical	Machine Learning
97	151305	Mudit Arya	muditarya31@gmail.com	8629010035	CSE	5/27/2018	07-10-2018	MothersonSumi	Django web app	Web development
99	151308	Janvijay Singh Bisht	janvijaybisht101@gmail.com	8146146041	CSE	06-04-2018	07-11-2018	JUIT Waknaghat	Training on machine learni	Machine learning on medical images
100	151309	Shubham	kansalshubham22@gmail.com	8950299389	CSE	06-04-2018	7/13/2018	VVDN Technologies	Chat acad bot in slack	JavaScript
102	151311	Akanksha Gupta	akankshahaps97@gmail.com	9882423641	CSE	06-05-2018	7/16/2018	Thinknext private limited	Home automation	IoT
103	151312	Ishita sharma	1997ishitas@gmail.com	9882160589	CSE	5/28/2018	07-06-2018	Effectz	Android studio	Android applications
104	151313	Mayank Sharma	mayank97sml@gmail.com	8894963362	CSE	5/28/2018	07-07-2018	CBitss	Training on Android Applic	Android Mobile Operating System
105	151314	Deepanshu Singla	lakshy.9thds@gmail.com	8556069215	CSE	06-02-2018	7/18/2018	Sun Soft Technologies (Bar	Training on python and ma	Machine learning
106	151315	Sumanyu Nandwani	sumanyunandwani@gmail.com	8447653334	CSE	5/23/2018	07-06-2018	Saviance Technologies	Training on Web Designing	Training on JavaScript, HTML, CSS
108	151317	Ayushi Jayaswal	ayushijaiswal629@gmail.com	7838976336	CSE	5/28/2018	7/16/2018	Global Medical Foundation	Project on Digital Marketin	Digital Marketing and Search Engine O
110	151319	Preksha Motwani	motwani.preksha.20@gmail.com	8629010012	CSE	5/22/2018	07-12-2018	Food Safety and Standards	Refurbishing 'Diet4Life' we	Website development
111	151320	Jaipreet Chandok	jaipreetsingh01@gmail.com	9736611995	CSE	06-01-2018	7/14/2018	Himachal Futuristic Commu	Training on IC and TeleCor	Telecom
112	151322	Manik Nijhawan	manik.nijhawan@gmail.com	8629009948	CSE	06-04-2018	7/15/2018	JUIT	Job Shop Scheduling	Operating System(Python)
114	151324	Shivam Sharma	shivamjct@gmail.com	9459149422	CSE	06-07-2018	7/14/2018	BSNL	Networking	Basic Telecom
115	151325	Ritwik Tiwari	ritwiktiwari24@gmail.com	9805806088	CSE	05-01-2018	7/31/2018	Madhya Pradesh Poorv Ksh	Internship on Data Science	Collecting data and processing data to
117	151327	vaibhav sawhney	vaibhavsawhney2005@gmail.com	8629010243	CSE	06-04-2018	7/13/2018	SmartQ-Bottle Lab Technol	Web Based Technologies	Html5,CSS.JavaScript,Python,Seleniur
118	151328	Ajay Rana	ajayrana7206@gmail.com	7206120218	CSE	06-11-2018	7/20/2018	CDAC Mohali	Electricity billing system	Java
119	151330	Aashray Singal	singalaashray1996@gmail.com	7018929872	CSE	06-01-2018	07-12-2018	Shree Aanjney Electricals P	Design and Simulation of a	Networking and Security
120	151331	Aditya Baliyan	adityabaliyan08@gmail.com	8629010073	CSE	06-06-2018	7/16/2018	Cetpa Infotech	Stock market trading applic	Stock market prediction
121	151332	Vaibhav Dutta	vaibhavdutta09@gmail.com	8629857056	CSE	06-12-2018	7/21/2018	BSNL	Networking in a Station	Networking
123	151334	Vaibhav Singh	0vaibhavsingh0@gmail.com		CSE	06-01-2018	7/15/2018	Department of Computer sc	Semantic analysis of Twitte	Big data and analysis
124	151335	Neharika	neharikakhera96@gmail.com	8629010295	CSE	6/30/2018	7/16/2018	Rajasthan Cement Industrie	Java	Payroll management system
125	151336	Kunal Kumar	kunalkmr2206@gmail.com	9798892880	CSE	06-04-2018	7/13/2018	FCS Software Solutions Ltd	Employee Attendance Mar	MVC based web application in .NET Fr
126	151337	Chirag Gupta	chirag.guptaitr@gmail.com	9407400915	CSE	5/28/2018	7/14/2018	ProdSmiths Technology Sol	Web Project :- URCashbac	Python, Django, Rest Framework and F

127	151338	Uditi Taneja	udititaneja4@gmail.com	7986318063	CSE	06-07-2018	7/18/2018	Haryana Vidyut Prasaran Ni	Implementation of IT plan a	Enterprise Resource Planning (ERP)
128	151339	Kriti Khullar	kritikhullar2@gmail.com	9997825621	CSE	06-01-2018	07-12-2018	CWPS Lochbridge India Pv	Intruder Detection System	Networking (NIDS)
129	151340	Manish	manishthakur1297@gmail.com	8628829553	CSE	5/26/2018	07-05-2018	Cetpa Infotech Pvt. Ltd.	Stock Market Trading Appl	Machine Learning using Python
131	151342	Shefali Malhotra	shefalimalhotra697@gmail.com	8629010036	CSE	06-03-2018	7/18/2018	Softpro India	HRMS of Marc Laboratorie	Java
132	151343	Sunayna	sunayna.sharma1996@gmail.cm	8427207265	CSE	5/24/2018	07-06-2018	Ernst and Young	VULNERABILITY ASSESS	Cybersecurity
133	151344	Nitish Kumar	nitishtiwari505@gmail.com		CSE	06-04-2018	7/13/2018	NIELIT MOHALI	Big Data Analytics	crime analysis and prediction using big
134	151345	Sagar Garg	sagargarg97@gmail.com	9368865541	CSE	06-04-2018	7/13/2018	CRIS(Centre for railway info	Passenger Reservation Sy	C++
135	151346	Sakshi Sharma	sakshi.97.sharma@gmail.com	8629010479	CSE	5/23/2018	07-06-2018	eServ360	Workflow Automation	Web
136	151347	DANISH WADHWA	danish.wadhwa1997@gmail.com	9814525007	CSE	06-01-2018	7/17/2018	Lally Infosys, Jalandhar	J2EE TRAINING	Programming
137	151348	Brij Nandan	brijnandan9711@gmail.com	9736992560	CSE	5/25/2018	7/15/2018	F-Tec	PHP	PHP
138	151349	Priyank Agarwal	priyank.agarwal1997@gmail.com	7599325170	CSE	06-04-2018	7/13/2018	Centre for Railway Informat	Passenger Reservation Sy	C
140	151351	Harshit Bhimsaria	harshitbhimsaria@hotmail.com		CSE	5/23/2018	07-06-2018	eServ360	Workflow Editor for Whats/	Automated Campaigning
141	151352	HIMANI BANSAL	himanibansal1998@gmail.com	8629010350	CSE	5/23/2018	07-06-2018	Centric Consultancy India	HR Portal	Web Technology
142	151353	Gopal Singal	gopal2695singal@gmail.com	8629009947	CSE	06-06-2018	7/16/2018	Cetpa Infotech	Stock Market Trading Appl	Stock Market Prediction
144	151355	Utkarsh Katiyar	utkarsh_katiyar@outlook.com	9736992561	CSE	06-04-2018	7/17/2018	BSNL	Basics of Telecommunicati	Telecommunications
145	151357	Shikhar Goel	shikhar7@outlook.com	9034194941	CSE	5/28/2018	07-07-2018	AIR INDIA	CR- Alert to Planner and M	RAMCO AVIATION SYSTEM USING S
146	151358	Sourabh	SIRRADHANASOURABH@GMAIL.CO	8629010342	CSE	5/25/2018	07-05-2018	Clientside Global	Project on Web Developme	Website for restaurant
147	151359	Aditya kapoor	aditya.kapoor33@gmail.com	9896591214	CSE	5/28/2018	07-09-2018	Keysight Technologies	Web development and test	Website improvement and testing
148	151360	Sahil Thakur	sahilrd07@gmail.com	8988413260	CSE	5/28/2018	7/15/2018	Blackberry's Delhi	Sales Analysis Phase 2	Web Development
149	151361	Himanshu Kushwaha	him.kushwaha@gmail.com	8765248716	CSE	06-07-2018	7/18/2018	Bharat Sanchar Nigam Limi	Mobile Newtorking	Telephony Systems and mobile networ
150	151362	DIVAL SEHGAL	sehgaldival@gmail.com	8628049917	CSE	06-04-2018	9/15/2018	Omninos Solutions	Training on Android Applic	Mobile applications for online Doctor A
151	151363	Anirudh Sharma	anirudhsh98@gmail.com	9418957754	CSE	5/25/2018	07-07-2018	Himachal Pradesh power co	SAP-ABAP	SAP and Computer Networms
152	151364	shubham ruhela	shubhamruhela007@gmail.com	8629009938	CSE	5/28/2018	07-06-2018	HCL INFOTECH LIMITED	METRO SMART CARD SY	METRO SMART CARD SYSYTEM
153	151365	Puneet Mehta	i@puneet.cc	8295554243	CSE	5/23/2018	07-06-2018	eServ360	Data Flow Automation	Web, Automation
155	151367	Shikhar Raizada	shikharraizada96@gmail.com	7906750837	CSE	5/28/2018	6/28/2018	ONGC,Dehradun	Library Project Manageme	web
156	151368	Esha Jethi	eshajethi@gmail.com		CSE	06-01-2018	8/13/2018	HLL Infratech Services Ltd.	SAP(Material Management	Networking
157	151369	Muskan	mssidana76@gmail.com	8629010078	CSE	5/26/2018	07-05-2018	Cetpa Infotech Pvt.Ltd	Stock Market Trading Appl	Machine Learning
158	151370	Rishu Verma	rishuverma2897@gmail.com	8629010525	CSE	5/24/2018	07-11-2018	ISSA Labs (DRDO)	Scenario Generation in Tac	Web, J2EE based
159	151371	Aman Gupta	aman4.gupta.4@gmail.com	9794981005	CSE	5/28/2018	07-07-2018	Mahima Merchandizing Pvt	Human Resource Manager	Human Resource Management
160	151372	Pallavi katoch	pallavikatoch28@gmail.com	8091768017	CSE	06-04-2018	7/13/2018	ThinkNEXT technologies pri	Library management syste	Python
161	151373	Udit Goel	udit.goel2@gmail.com	8126718797	CSE	06-04-2018	7/15/2018	EMML Automation Pvt. Ltd.	Online Movie ticket booking	Python and DJango
162	151375	Deepanshu Rana	mailme.deepanshu45@gmail.com	9273800005	CSE	06-01-2018	07-12-2018	eBizInfosys	Training on Database and I	IASC Automation Systems
163	151376	Divya Ameta	rdiv.ameta@outlook.com	9079918499	CSE	06-01-2018	7/15/2018	Keen infotech	Training on web developme	Job portal
164	151377	Tejansh	tejansh.dalal@gmail.com	8077801065	CSE	06-05-2018	07-02-2018	Mosaic Technologies	Data science	Python
165	151378	Aakash Bali	aakash.bali1301@gmail.com		CSE	5/22/2018	07-02-2018	Indian Institute of Technolog	Web and Android Applicati	Web, PHP and Android
167	151380	Shivam Kartikay	shivamkartikay@gmail.com	8629010519	CSE	5/25/2018	07-10-2018	Mobiquest Mobile Technolo	CHATBOT	PHP/Web designing/Microsoft® SQL S
168	151383	Dhairya Agarwal	dhairyaagarwal1234@gmail.com	8629010507	CSE	8/25/2018	7/20/2018	Internship in Exclusife techn	traning in big data and proj	Apache hadoop and Android
169	151384	RAHUL VERMA	rahulverma5108@gmail.com	8629009993	CSE	06-04-2018	7/13/2018	National Institute Of Electro	Training on Big Data , Proje	Big Data Analytics using Hadoop
170	151385	satyam aggarwal	aggarwalsatyam425@gmail.com	9.17807E+11	CSE	8/21/2018	6/29/2018	NIELIT	IOT based Pill bottle	IOT
171	151386	Pranay pushp	ppias2019@gmail.com	7807420833	CSE	06-04-2018	7/13/2018	BSNL	Networking	Networking gsm,wifi,ngn
172	151387	Ujjwal gupta	ujjwalgupta795@gmail.com	8629010381	CSE	06-02-2018	7/22/2018	KRATIKAL TECH PRIVATE	TRAINING IN WEB APPLI	VULNERABILITY ASSESSMENT AND
173	151388	Vivek Guleria	vivekguleria717@gmail.com	8351047727	CSE	06-03-2018	7/13/2018	(Nielit) National Institute of I	Not Worked On Any Projec	No
174	151389	Anmol Kamboj	anmolkamboj97@gmail.com	8629010177	CSE	06-07-2018	7/19/2018	HPGCL	Power Plant Familiarizatior	Networking
175	151390	Yash Chowdhury	yashchowdhury01@gmail.com	8629010522	CSE	06-04-2018	7/14/2018	UPTEC Computer Consulta	Python	Python
178	151395	Simranjeet Singh Sarmota	simranjeet.rock@gmail.com	8629010084	CSE	06-01-2018	7/14/2018	Whiz Infotel	Computer Networks	Computer Networks
179	151396	Shivam Chimra	shivamchimra@gmail.com	8544711470	CSE	06-04-2018	7/14/2018	Jaypee University of Informa	Routing Protocols in WSN	Telecom
180	151397	Kanav Singla	singlaheel203@gmail.com	9815376371	CSE	5/22/2018	6/29/2018	Infowiz Software Solutions F	Python + Django	Sports News Site
181	151398	Vishal Duhan	duhan41@gmail.com	8629010029	CSE	06-12-2018	7/21/2018	BSNL	NETWORKING	NETWORKING
182	151399	Saras Gupta	saras.sherry@gmail.com	9459230616	CSE	06-04-2018	7/19/2018	Arshiya Rail Infrastructure L	Database Management	Database Management
183	151400	VAISHALI	ranavaishali507@gmail.com	8628900913	CSE	06-04-2018	7/15/2018	BSNL	Training on net numen soft	Telecommunication network(GSM)

184	151401	Bhargavi Dogra	bhargavidogra@gmail.com	8988122567	CSE	06-04-2018	7/20/2018	Microsoft Research Lab Ind	99DOTS Research Project	Data Collection and Digitization
185	151402	Sagar Gaur	sagar7307071708@gmail.com	9736977356	CSE	06-04-2018	7/14/2018	Xenon Digi Labs	Real time data analysis	Big data
187	151405	Harsh Massand	massandharsh@gmail.com	9736258484	CSE	06-01-2018	07-12-2018	Shandar events	Website development	Google engine
188	151406	Varnit Gupta	varnitgupta25@gmail.com	9736458234	CSE	5/28/2018	07-06-2018	WindowIT Technologies	Online Banking System	Advance Java
189	151407	Paras Verma	vermaparas87@gmail.com	9816850560	CSE	5/28/2018	07-06-2018	CDAC- Mohali	Event Scheduler/Reminder	IoT
190	151408	Ujwal dogra	UJWAL.DOGRA31@GMAIL.COM	9459820796	CSE	06-11-2018	7/16/2018	Nilet	Android	Blood donation app
191	151409	Anubha Chadda	chaddanubha18@gmail.com	7807195178	CSE	06-01-2018	07-12-2018	Paras Technologies	Training on Web Technolo	PHP platform
192	151411	Ayushi Dogra	shividograa@gmail.com	8894238414	CSE	06-04-2018	7/18/2018	TCIL -IT	CLOUD COMPUTING	CLOUD COMPUTING
193	151412	Himanshu Chauhan	chauhanhimanshu151412@gmail.com	9418400815	CSE	5/29/2018	6/29/2018	Indian Institute of Technolog	Deep Learning	Designing Network for Biometric Moda
194	151414	Nikesh Chauhan	nikeshchauhan1996@gmail.com	8627896801	CSE	5/29/2018	6/29/2018	Indian Institute of Technolog	Designing a deep network	Deep Learning
195	151415	Parushi Sharma	sparushi97@gmail.com	8629013576	CSE	6/13/2018	7/13/2018	Airtel Payments Bank	Centralized logging, monito	ELK Stack
196	151416	Avinash Thakur	avinash9.5thakur@gmail.com	9459283440	CSE	11-06-2018	02-07-2018	Centre for Development of A	Networking System of A Ca	Computer Networking
197	151417	Pankaj Thakur	pankajthakur151417@gmail.com	8629010144	CSE	01-06-2018	06-07-2018	CDAC mohali	IOT	IOT
198	151418	Pragya Chakshu	pragyachakshu97@gmail.com	9805443269	CSE	5/28/2018	07-11-2018	SJVN	Guest House Booking Syst	Web Designing
199	151419	Kanav Gupta	gkanav34@gmail.com	9459719225	CSE	06-04-2018	7/13/2018	NIELIT MOHALI	Crime Analysis and Predic	Big data and Hadoop
200	151420	Ayushmat B Soni	ayushmats@gmail.com	9816306110	CSE	06-04-2018	6/30/2018	Acadview Pvt Ltd	API with Instagram	Python
201	151421	Ajay Thakur	ajayt8271@gmail.com	8894667567	CSE	06-11-2018	7/21/2018	Dezign Suite	Flight management system	Big data
202	151422	Divyansh Rana								
203	151423	rajat bhushan	rjbhushan1@gmail.com	8894439681	CSE	5/26/2018	07-06-2018	cetpa	project on stock market pre	machine learning using python
204	151424	Ishu Priya	ishurangra16@gmail.com	9805460431	CSE	06-04-2018	7/18/2018	TCIL - IT	CLOUD COMPUTING	CLOUD COMPUTING
205	151425	Sagar Panwar	sagarpanwarsd@gmail.com	8629010215	CSE	06-04-2018	7/13/2018	Jaypee University of Informa	Randomization using Pytho	Random distance covered between 2 r
206	151426	Akrit Kapoor	kapoor.akrit1996@gmail.com	9805597969	CSE	06-04-2018	7/14/2018	Jaypee University of informa	Python language	Using python language to send encrypt
207	151427	aastha	aasthakashyap235@gmail.com	7807161032	CSE	5/28/2018	07-12-2018	steller edge solutions	portfolio website	website devolpment
209	151429	Riya Dhiman	rheadhiman41@gmail.com	9805588960	CSE	06-04-2018	07-04-2018	Ongc,Dehradun	Jarvis Music Player(Java)	Jarvis Music Player(Java)
210	151430	Shubham Aggarwal	agg.shubham96@gmail.com	8629010454	CSE	5/21/2018	6/29/2018	NIELIT	IOT based Pill Bottle	IOT
211	151432	vasundhra jaswal	vasundhrajaswal1308@gmail.com	8626990051	CSE	5/28/2018	07-04-2018	seimens pvt ltd	locomotives	metros in India
212	151433	sonali behal	behalsonali@gmail.com	7807011280	CSE	5/24/2018	07-06-2018	CETPA	stock market reading appli	python
213	151434	Aastha Gupta	gaastha39@gmail.com	9736165060	CSE	5/28/2018	07-06-2018	Siemens Ltd.	Data Mining	Data mining in locomotives
214	151436	Shivam Sharma	shivamsharma806@gmail.com	8988125080	CSE	5/25/2018	07-05-2018	SJVN LIMITED	Training on Web Developm	Library Management System
215	151437	Parinita kaushal	parinita.kaushal97@gmail.com	07807 067362	CSE	06-04-2018	07-11-2018	NIIT	Python in data science	Python
216	151438	Chechey	ceetshokc@gmail.com	8629010463	CSE	5/25/2018	07-05-2018	Southtech(bhutan) Pvt ltd	Library management syste	Web development
217	151439	Sonam Menda	sonammenda498@gmail.com	8629010475	CSE	5/27/2018	07-06-2018	MOIC	Ditt(Bhutan)	content management system
218	151440	Dem Zam	demzam97@gmail.com	8629010461	CSE	5/25/2018	07-05-2018	Southtech Private Limited	Training on Website develo	Website development of Library Manag
219	151441	Tshewang Dema	tee804dee@gmail.com	8629010469	CSE	5/25/2018	07-05-2018	South Tech, Thimphu TechP	Library Management Syste	Java
220	151451	ABIR	asabirso@gmail.com		IT	5/28/2018	7/13/2018	Jaypee University of Informa	99 DOTs - Microsoft Resea	Data Collection and Digitalization
222	151453	Ekesh Garg	ekesh.gargeg@gmail.com	7589436075	IT	5/22/2018	6/29/2018	Infowiz Software Solutions P	Python + Django	Yummy Tum - Food Blog
223	151455	Shivam Dhawan	shivam.dhawan26@gmail.com	9736992736	IT	5/24/2018	07-12-2018	BTR Fashion Solutions Pvt	BehindTheRamp	Web Development
224	151456	Chandan Partap Singh	cp0000@ymail.com	8629009953	IT	5/28/2018	07-06-2018	Amisoft Academy	C#.NET	Full Stack Developing
225	151457	NISHANT SEHGAL	nishantsehgalbti@gmail.com	9736992744	IT	06-04-2018	7/18/2018	Steg Technologies	PAYING GUEST	PHP
226	151458	Dikshit Sharma	dkshtsharma7@gmail.com	7807063752	IT	5/15/2018	7/27/2018	Coding Ninja's	Cifar10	Machine Learning
227	151459	Prasasti	tripathiprasasti@gmail.com	9882160594	IT	5/28/2018	7/20/2018	Arozite Technologies Pvt. L	Development and Enhance	Backend APIs for Spring based applica
228	151460	Aayush Singla	aayush.singla32@gmail.com	9464570940	IT	06-01-2018	7/15/2018	NICE Computer Center	PHP	PHP
229	151461	ritesh kumar singh	riteshsingh5667@gmail.com	8629010017	IT	06-06-2018	7/16/2018	Cetpa Infotech	Machine Learning	Machine Learning in Python
230	151462	Vinamr Mahajan	mahajan.vinamr@gmail.com	9465162515	IT	06-04-2018	07-11-2018	Jaypee Institute Of Informat	Machine Learning For Med	Machine Learning
231	151463	Siddharth Rakesh Sharma								
232	151464	Prateek Ramani	ramaniprateek@gmail.com	8629013618	IT	06-04-2018	07-03-2018	EI Systems	Data Analysis of Zomato a	Data Analytics with Machine Learning
233	151465	Ashwani Tandon	tandon.ashwani12@gmail.com	9580079855	IT	06-04-2018	7/14/2018	Reliance Power - Rosa Pow	Assets Management Portal	Web development
234	151466	Hitesh Gupta	gupta.hitesh786@gmail.com	8629010313	IT	06-08-2018	7/19/2018	CEPTAM(DRDO)	Annual Training Report Ge	JAVA(JSP) based web app for interane

235	151467	Abhishek Kumar	reach2kabhishek@gmail.com	8629010524	IT	5/29/2018	07-07-2018	BSNL Bhagalpur	Basic Telecom	Networking
236	151468	Divyansh Piplani	divyanshpiplani.juitian@gmail.com	8629010553	IT	5/28/2018	07-07-2018	Tarkuli i solutions pvt. ltd.	Competitive analysis and w	Website designing and analysis of mar
237	151469	Abhin bajaj	abhinbajaj26@gmail.com	8629010199	IT	06-01-2018	7/14/2018	HCL Technologies,Noida	Web development	Web
240	151474	Akriti goyal	akriti05g@gmail.com		IT	06-04-2018	7/13/2018	CDAC - mohali	Android application	Calories calculator
241	151475	ABHIMANYU CHAUHAN	abhimanyu21191@gmail.com	7834031904	IT	06-04-2018	07-09-2018	JUIT WAKNAGHAT	MACHINE LEARNING FOI	MACHINE LEARNING
242	151476	Yogesh Kumar	yogeshsinghal3097@gmail.com	8629009946	IT	5/25/2018	07-06-2018	eMobX(Enterprise Mobility X	iRakhwali	Android Application Development
243	151477	Shorya Sharma	sshaurya43@gmail.com	7018425882	IT	09-02-2018	9/14/2018	Bharat Sanchar Nigam Limi	Networks and communicati	Telephone Exchange
244	151478	Agrim Dogra	agrimdogra098@gmail.com		IT	5/28/2018	07-06-2018	Birla Textile Mills	handling database	Database and Python
245	151479	parth sekhri	psekhri60@gmail.com	9459821359	IT	06-01-2018	7/14/2018	Netmax Technology	cloud computing	cloud computing

Stipend Provided by Company?	Contact Person In Company	Status
No	Sh. Kulwant Singh Ponwar. 8196883629. Asstt.Manager (HRD)	Satisfactory
No	Ms Shaleeni Thakur	Satisfactory
No	Nishant goyal, 8284009795 , Associate	Satisfactory
No	Gaurav Bansal.8586956757.AWS Teacher	Satisfactory
No	Sh.Anil Semwal +91-177-2621325 Deputy Director(DIT)	Satisfactory
NO	Ms Shalini Sharma Founder CS Infotech. 9815701003	Satisfactory
11903	Mr. Subhash Sharwan	Satisfactory
No	Mr. Anirudh Kumar, Ph. No. 07428232774	Satisfactory
No	Rimpy Sharma 9814813010, Center Head	Satisfactory
No	Mr. Deepak Singh 8376032344 CMO	Satisfactory
No	Name-anirudh Kumar phone no-7428232744 designation-engineer	Satisfactory
NO	Swarnim Sudha, Manager	Satisfactory
No	Nishant Goyal.8284009795.Associate	Satisfactory
No	Dr. Subhamoy Maitra . 9830377324 . Prpfessor, Applied Statistical Unit, ISI, Kolkata	Satisfactory
No	Sahil Aggarwal. +91-8283823284. Technology Expert	Satisfactory
No.	Dibya Ranjan Barik. 9410390425. Senior programming officer	Satisfactory
No	Inderjeet Singh. 72898 72863 Faculty In charge	Satisfactory
No	Ranu Mishra. 8882146661. Marketing Head	Satisfactory
No	Mr.Ranu Mishra . Phone :+91 88821 46661	Satisfactory
No	Name: Ranu Mishra, phone : +91 8882146661, Designation: Manager	Satisfactory
No	Sanjay Mishra. 9958371963. Project Leader.	Satisfactory
NO	Anirudh Kumar(7428232774))(Engineer))	Satisfactory
No	Sh. Harbinder Lal (SDE(HR/PG) Kullu) 01902-222011 hlthakur@bsnl.co.in	Satisfactory
No	Juit	Satisfactory
No	Asit Pathak.9415082377.CEO	Satisfactory
No	Dr. S.K. Singh. 9554321133. Associate Professor, Department of Computer Science, IIT BHU	Satisfactory
No	Anil Kumar - Senior Technical Officer	Satisfactory
No	Nitin Aggarwal, 76967 69696, Manager	Satisfactory
0	9830377324	Satisfactory
No	Er. Aniruddh Kumar ,+91 7428232774, Instructor at CETPA	Satisfactory
No	Dr Ramesh k Agrawal ,phone no -9810115033,Dean Computer Science Center	Satisfactory
No		Satisfactory
No	Anirudh kumar,7428232774	Satisfactory
No	Sh. Harbinder Lal, 01902-222011, SDE(HR/PG)	Satisfactory
NO	+91 9418042440	Satisfactory
8000	Mr. Amit Jugran, founding partner,8826794809	Satisfactory
No	Name:Manish arora designtion:addl director number:tel:0172-2650121	Satisfactory
No	Hemant Kumar Sharma, 8826380516, Project Guide	Satisfactory
No	Harbinder Lal Thakur(Divisional Engineer TDM Kullu- +91 9418044300)	Satisfactory
No	(POOJA ARORA. 9266625607 Tehnical Head)	Satisfactory
No	Chandan Gaur, 8427260301, Senior Software Engineer	Satisfactory
No	Dr. Charanjit Singh , 9988299001 , Chairman	Satisfactory
No	Manjeet Singh, +919810212227, Software Consultant	Satisfactory
No	Sachin Garg. 7982605943. Mechanical Engineer	Satisfactory
No	Name:Manoj Dembla Phone No:9215212223 Designation: Managing Director	Satisfactory
No	Er. Vaneet Modi, 9814808404, HR Manager	Satisfactory

no	Pooja Seth +91 172 500 7263 incharge of training	Satisfactory
No	Arun Arora 9717740666	Satisfactory
No	Jwala Karadiya; Utilities Manager; 8392952890	Satisfactory
No	Amandeep Bhardwaj, 9876655267, Project Manager	Satisfactory
NO	Er. Kulbeer Thakur, 01792223811,Executive Engineer	Satisfactory
No	Dr B P Sharma 9810849501 Project Manager	Satisfactory
No	Akshay Seth 9999942496 Sr.Software Developer	Satisfactory
NO	(POOJA ARORA. 9266625607 Tehnical Head)	Satisfactory
NO	Harsimranjit Kaur,+91-20-2570-4100,Project manager	Satisfactory
No	Rajender Thakur(SDE NIB), 9418125025	Satisfactory
No	MunishMittal Director 9817073754	Satisfactory
No	Ramandeep Kaur.9041668822.HR Manager	Satisfactory
No	Munish Mittal,Director,7837401000	Satisfactory
NO	Monika Singh, HR manager, 8826412769	Satisfactory
No	Rajeev kumar.9418299787.Assistant professor	Satisfactory
NO	JUIT +91- 1792 -257999	Satisfactory
No	Sanjay Kumar 9467346414 R&D head	Satisfactory
no	DINESH KUTIYAL, 9412052550, scientist 'E'	Satisfactory
No	Mr. Nishant, +91 70182 37594, Instructor	Satisfactory
No	Rakesh Kumar 9919187982	Satisfactory
No	9.1875E+11	Satisfactory
No	-1452971727	Satisfactory
11000	Naren Budhwani 8879477247 co-founder	Satisfactory
No	Tanya Kishor Mishra , desig- Sr. Python and AI consultant, contact no.-0120-4646464	Satisfactory
Can't Disclose	Can't Disclose	Satisfactory
No	Surya Arya 9899614151 Manager	Satisfactory
No	Dr Ravindara Bhatt 01792 -239348 Assistant Professor(Senior Grade)	Satisfactory
No	Vivek Bansal 9810463583 Vice president	Satisfactory
No	Deepak Kumar, 7986699338 trainer	Satisfactory
No	G.D Ahuja 9815655148	Satisfactory
no	Ravi Sharma Officer Incharge of Training 9646510598	Satisfactory
No	Rajesh K. Bansal 9872246056 Sun certified java programmer, Microsoft certified specialist	Satisfactory
No	Dhruv Mehta, 9810296361, HR	Satisfactory
No	Mr. Shobhit. 9999404348. Digital Marketing Head	Satisfactory
10000	Ashok Kumar Chanana +919811318442 Head, IT (CITO)	Satisfactory
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No	01792-239348	Satisfactory
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5000	Gyaneshvar Jharbade, 9713863591, Programmer	Satisfactory
NO	Abhijeet Sawhney,9620230230,Software Developer	Satisfactory
No	Ms.Jaspinder Kaur (Training instructor) 9988025399	Satisfactory
No	Name: Mr.Vijay(Director) -9888144033	Satisfactory
No	Shivani Sharma. 9013278989. Consultant	Satisfactory
No	No.	Satisfactory
No	Manu Sood ,9418309695, Professor	Satisfactory
No	9417609386	Satisfactory
No	Mithilesh Kumar. 09911214164. Admin.	Satisfactory
NO	Vivek Dogra, 98339 82602, Founder	Satisfactory

No	Er. Sanjeev Saini. 93163 69209. XEN/IT & Consultancy	Satisfactory
No	Rakesh Puri (9811231769)	Satisfactory
No	Ranu Mishra, 8882146661 ,HR Representative	Satisfactory
No	Prathna Pandey 7080812070 HR-Manager	Satisfactory
no	Ashish Srivastava 01244434091 Assistant Manager	Satisfactory
No	Teacher Name:- Dr. Manish Arora	Satisfactory
NO	Mr.RANJIT SINGH, 8130797619,Project Manager	Satisfactory
10,000	Aditya Singh, 8373900326, Owner	Satisfactory
No	Manoj Kumar, 9463702110 ,Centre Head	Satisfactory
No	Vaneet Modi.9814808404.Manager	Satisfactory
No	Mr. Ranjeet, 8130797619, Project Manager	Satisfactory
10,000	Aditya Singh, +91 83739 00326, Owner	Satisfactory
No	Mr. Manish mehra 9810308805 vice president	Satisfactory
No	Shivani Sharma. 9013278989. Consultant	Satisfactory
No	9457705199	Satisfactory
No	MR SHAM LAL,+919971227920,Project Coordinator	Satisfactory
4000	NAME-MR. LUV KAPOOR,PHONE-9667143544,DESIGNATION-DIRECTOR	Satisfactory
No	Vikas arora. 09811407951. R & D Operating Manager	Satisfactory
No	Sharanjeet Thakur, 09717183265 , Project Manager	Satisfactory
No	Madhurendra Gupta , 05842-223000 , SDE-Switch	Satisfactory
No	Shubham Moonga Senior ,Android Developer	Satisfactory
no	Ved Prakash Sharma 9418001446 Sr.IT manager	Satisfactory
NO	8527559066	Satisfactory
10000	Aditya Vir Singh, 8373900326, Owner	Satisfactory
No	Vijay Kumar Sharma. 9410396666. GM - Programming E&D DTE ONGC	Satisfactory
No	0120-4071500	Satisfactory
NO	Name: Anirudh Kumar Phone No.: 7428232774 Designation: Employee	Satisfactory
No	Ramita Sardana, Scientist-D, 9540066878	Satisfactory
No	Kaushal Gupta 9340457557	Satisfactory
No	Munish mittal director of think next 07837 401000	Satisfactory
No	Nishul Tomar. 8265826595. Associate Manager	Satisfactory
NO	Aman Bhardwaj. 9876655267.Project Manager.	Satisfactory
No	Mr Kamlesh Vyas 09269573303 Teacher In Charge	Satisfactory
No	Aashima(HR)	Satisfactory
Rs. 5,000	Dr. Narayanan C Krishnan, 01881-242273, Assistant Professor	Satisfactory
No	Anoop Srivastava.9717049993.Head Technology	Satisfactory
No	Faiz Mohd Arif Khan.9451396824.traning teacher in rcpl	Satisfactory
No	0172 2236462	Satisfactory
NO	Dr Sarwan Singh. 0172-2236470. Deputy Director(Systems)	Satisfactory
No	NA	Satisfactory
NO	Praveen, 9870576370, Manager	Satisfactory
No	NIELIT Plot no. 925, Sector 30B, Chandigarh, 160030, India	Satisfactory
No	Simmi Arora. Xen	Satisfactory
No	Rajeev Srivastava. 8957501065 Systems Officer	Satisfactory
No	7696769696	Satisfactory
No	Ravindra Bhatt Professor	Satisfactory
No	Kamaljot Kansal . 98158-00333 . CEO	Satisfactory
NO	NO	Satisfactory
No	Sachin Garg, 7300715355, CTA to Sr. DME	Satisfactory
No	Mr.Rakesh Kumar Sharma S.D.O at BSNL Exchange ,Kangra	Satisfactory

Yes(Rs.57167)	Miss. Amy Chen (Research Fellow and Internship Supervisor) contact number:8374320582	Satisfactory
No	Chandan Gaur 8427260301 Senior Software Engineer	Satisfactory
No	Karan Bains 9418845097 Ceo	Satisfactory
No	Mr. S.K Gupta, 9815144280, CEO/Founder	Satisfactory
No	No	Satisfactory
No	Pratiyush guleria ph no. 9418056332	Satisfactory
NO	Mr. Harish ,9915090599	Satisfactory
No	Manoj Dhiman, 9876795015,Manager TCIL-IT	Satisfactory
No	Dr. Aditya Nigam (Asst. Professor)(8894607738)	Satisfactory
no	Dr. Aditya Nigam (8894607738) Asst. Prof. IIT Mandi	Satisfactory
No	Nitin Sharma +919810221611 Head of Operations	Satisfactory
NO	-8559029809	Satisfactory
NO	Harsimran Kaur	Satisfactory
N0	Er.Mahender Kumar,9418461978,Manager	Satisfactory
No	Dr. Manish Arora (Additional Director)	Satisfactory
No	Vivek Shivam,9041518874	Satisfactory
No	7307004462	Satisfactory
		Satisfactory
no	anirudh kumar ,trainer,7018144350	Satisfactory
No	Manoj Dhiman, 9876795015, Manager TCIL- IT	Satisfactory
No	Dr. Ravindara Bhatt Assistant Professor (Senior Grade) Office: First Floor, Vivekananda Bhawan, Contact No: 01792 -239348 Email: ravindara.bhatt@juit.ac.in ravibhatt2@rediffmail.com	Satisfactory
No	Juit training cell	Satisfactory
No	Deepak 8567880887 senior faculty	Satisfactory
no	9410391090	Satisfactory
No	Dr. Sarwan Singh 0172-223 6456 Deputy Director(Systems)	Satisfactory
no	7532966250	Satisfactory
No	anirudh pratap -7428232774	Satisfactory
no	Mr. Saquib Sultan, 7532966250, Assistant Marketing Manager	Satisfactory
No	Mahender Kumar 9418461978 Manager(IT)	Satisfactory
No	Dinesh Sharma. 8091045001. Head of centre	Satisfactory
Nill	Pema Tashi(CEO),ptashee@yahoo.com	Satisfactory
nill	Darshan THapa,ICT officer	Satisfactory
No	Pema Tashi(ptashee@yahoo.com), Chief Executive Officer(CEO)	Satisfactory
No	Pema Tashi, Chief Executive Officer(CEO), (975) 235-0357	Satisfactory
Yes	Ms. Amy Chen,+918374320582 ,Research Fellow, Microsoft Research Labs India	Satisfactory
No	Kamaljot Kansal. 9815800333. CEO	Satisfactory
15000	Manu Mittal - Co-founder - 8879465691	Satisfactory
No	Naveen Bansal, 9419195034, Director	Satisfactory
No	Ritika Khanna. 9888807079. HR Manager	Satisfactory
No	Ankush Singla. 1800-300-28085. Co founder	Satisfactory
25k / month	Nimish Vashisht. 9736464769. Manager	Satisfactory
No	Varun Bansal(Head Invigilator)	Satisfactory
NO	9560739748	Satisfactory
No	Mr. Ravi Raina	Satisfactory
		Satisfactory
No	Prateek Mishra ,7987968836 , Director of Techsimplus	Satisfactory
No	Sunil Ranjan Singh 8799397650 Instructor Of Training	Satisfactory
NO	Lalit Kumar 8920711384 HR	Satisfactory

No	Roma Saha, 06412422300, Junior Telecom Engineer,	Satisfactory
No	Ashutosh kukreti, director, (human resource), tarukuli enterprises pvt. Ltd.	Satisfactory
No	Er.sanjay jindal. Business project manager	Satisfactory
No	CDAC,0172 661 9000, phase 8,mohali	Satisfactory
NO	01792 -239348	Satisfactory
No	Sheetal Sharma. +91-172-4000430. HR	Satisfactory
NO	Yogesh Kumar	Satisfactory
NO	R.K Sharma, vice President(HR,Pres.,Admin. & Legal),017952444653	Satisfactory
no	HIND SHARMA,Gen. Manager (7837728450)	Satisfactory

University Requirement								Requirement for Accredation / F
S.No.	Enrollment	Name	Branch	Period of Training	Training start date	Training End Date	Status (Satisfactory / U	Institute/Company Name
214	141447	AASHISH	IT	7	30-05-2017	15-06-2017	SATISFACTORY	Network Bulls
196	141428	VAISHALI VERMA	IT	5	12-Jun-17	JULY 7 2017	SATISFACTORY	MNNIT ALLD
1	141201	SURYA DEV SINGH	CSE	6	01-06-2017	11-07-2017	SATISFACTORY	BSNL, Dehradun
2	141202	PARTH AHUJA	CSE	6	01-Jun-17	11-Jun-17	SATISFACTORY	Delhi Development Authority
3	141203	SHOBHIT KUMAR SRIVASTAVA	CSE	6	5 JUNE,2017	15 JULY,2017	SATISFACTORY	Webhobs Pvt Ltd.
5	141205	MAYANK TIWARI	CSE	6	07-06-2017	18-06-2017	SATISFACTORY	CETPA
7	141207	AKSHAT MATHUR	CSE	4	15-Jun-18	11-Jul-18	SATISFACTORY	HEWLETT-PACKARD
9	141209	NAVPREET KAUR KALER	CSE	6	Jun-17	Jul-17	SATISFACTORY	NetMAX
10	141210	ISHA	cse	6 WEEKS	5 June,2017	15 July,2017	SATISFACTORY	F-TEC
11	141213	SAURAV KUMAR	CSE	6 WEEKS	12-06-2017	20-07-2017	SATISFACTORY	JUIT
12	141214	ANKIT	cse	5 weeks	05-Jun	14-Jul	SATISFACTORY	outsourcing technologies
13	141215	RISHABH GARG	CSE	6 WEEKS	08-06-2017	10-07-2017	SATISFACTORY	CENTRE FOR RAILWAY INFORMA
14	141216	GOPAL KRISHAN AIRON	CSE	6	02-06-2017	14-07-2017	SATISFACTORY	HCL-INFOTECH
15	141217	DIKSHA MUNJAL	cse	6	01-Jun-17	15-Jul-17	SATISFACTORY	HARTRON,HISAR
16	141218	SYED ADIL ALAM	CSE	6	01-06-2017	11-07-2017	SATISFACTORY	Bank of Baroda
17	141220	MAYANK ABROL	cse	7	29-May-17	14-Jul-17	SATISFACTORY	NIC,Jammu
18	141222	ARUSHI DOGRA	C.S.E.	6	01-06-2017	15-07-2017	SATISFACTORY	Elleen Infotech Pvt. Ltd.
20	141224	SHREYA SRIVASTAVA	CSE	6 WEEKS	31-05-2017	11-07-2017	SATISFACTORY	CETPA INFOTECH
21	141225	RUDAR DAMAN	CSE	6	01-06-2017	12-07-2017	SATISFACTORY	Softinfo Systems Pvt. Ltd.
24	141228	ISHAAN VIKRAM	CSE	7 weeks	01-06-2017	13-07-2017	SATISFACTORY	national dairy research institute
25	141229	DIVYANSHOO SHARMA	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	RWX technologies pvt ltd
26	141230	SACHIN SLATHIA	cse	6 weeks	06-06-2017	15-07-2017	SATISFACTORY	regional institute of managemen
28	141233	PARASHIV SIHANIYA	CSE	6	01-06-2017	15-07-2017	SATISFACTORY	Curie Labs
30	141235	PRINCE CHAUHAN	CSE	6 WEEKS	31-05-2017	12-07-2017	SATISFACTORY	REDCARPET TECH PVT LTD
32	141237	DIVYA JAIN	CSE	6	07-06-2017	18-08-2017	SATISFACTORY	cetpa
35	141240	DEEPANSH GUPTA	CSE	6 WEEKS	05-06-2017	15-07-2017	SATISFACTORY	DUCAT
37	141242	SUNIDHI GUPTA	CSE	5	05-06-2017	09-07-2017	SATISFACTORY	Nokia Networks
39	141244	SHANU KUMAR	cse	6	31-05-2017	11-06-2017	SATISFACTORY	CETPA INFOTECH
42	141247	MANOJ KUMAR	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	Cetpa
44	141249	TEJESHWAR THAKUR	CSE	6	10-06-2017	21-07-2017	SATISFACTORY	HFCL
46	141251	MANDITYA SINGH PANWAR	CSE	5	07-06-2017	12-07-2017	SATISFACTORY	HINDUSTAN POWER
47	141252	AARON MAURICE QUADROS	CSE	6 WEEKS	06-06-2017	12-07-2017	SATISFACTORY	Sandhar Technologies Ltd.
48	141254	ILISHA KAUL	CSE	6	5th June 2017	14-Jul-17	SATISFACTORY	Tata Technologies Limited
49	141256	AKRITI JASWAL	Computer S	6 WEEKS	01-06-2017	13-07-2017	SATISFACTORY	NATIONAL INFORMATICS CENTR
50	141257	NAMAN BANSAL	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	Webhobs Pvt Ltd.
51	141258	NITIKA SHARMA	cse	6	30-05-2017	03-07-2017	SATISFACTORY	Ducat PVT. LTD.
53	141260	SHASWAT SOOD	CSE	6	30-May-17	09-Jul-17	SATISFACTORY	DUCAT
54	141261	ARPIT GARG	CSE	6	1.6.17	12.7.17	SATISFACTORY	Sai Infotech Systems Ltd.
55	141262	ADITYA NARAYAN GARG	CSE	6 WEEKS	05-06-2017	15-07-2017	SATISFACTORY	DUCAT

56	141264	LAVANYA KUMAR	CSE	6	01-06-2017	14-07-2017	SATISFACTORY	Ducat
57	141265	ABHIMANYU KAPIL	CSE	7	29.05.2017	14.07.2017	SATISFACTORY	NIC
59	141267	ARPIT MALIK	cse	6	07-06-2017	18-07-2017	SATISFACTORY	cetpa infotech pvt. Ltd.
60	141268	KSHITIJ SHARMA	CSE	6	29-05-2017	08-07-2017	SATISFACTORY	IIHT Delhi
61	141269	PRIYANJUL JOHARI	CSE	6 Weeks	29-05-2017	07-07-2017	SATISFACTORY	National Informatics Centre
63	141272	RISHIKA BAJAJ	CSE	6	5 June,2017	14 July,2017	SATISFACTORY	Aptron ,sector 2 ,noida
65	141274	CHARUL GUPTA	cse	6 weeks	05-Jun	15-Jun	SATISFACTORY	netmax
67	141276	APOORV JAIN	CSE	6	06-06-2017	15-07-2017	SATISFACTORY	Rooter Sports technologies Pvt L
68	141277	PALAK	CSE	6	01-06-2017	15-07-2017	SATISFACTORY	netmax,chandigarh
69	141278	YOGESH MITTAL	CSE	6	01-06-2017	14-07-2017	SATISFACTORY	Ducat
70	141279	AARUSH SHARMA	CSE	4	19-06-2017	17-06-2017	SATISFACTORY	Prologic First India Pvt Ltd
71	141280	AASTHA SINGH	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	APTRON
74	141283	ABHINAV GULATI	CSE	6	01-06-2017	12-07-2017	SATISFACTORY	NIC
75	141284	VIBHOR SHARMA	CSE	6	30.05.2017	10.07.2017	SATISFACTORY	NIC
76	141285	VAANI MAHESH RANA	CSE	6	05-06-2017	13-07-2017	SATISFACTORY	NeGD, Electronics Ministry
78	141289	STUTI KATNORIA	Computer S	6 weeks	01-06-2017	09-07-2017	SATISFACTORY	National Informatics Centre
79	141290	AASHRITA GOEL	cse	8 weeks	31-May-17	26-Jul-17	SATISFACTORY	SERC, Indian Institute of Science
80	141291	VIVEK SINGH	csw	6	01-Jun-17	15-Jul-17	SATISFACTORY	Kangroo Software Pvt ltd
81	141292	VEDANT OJHA	CSE	5	5 June,2017	12-Jul-17	SATISFACTORY	MIT/Naresh I technologies
82	141293	VIKRANT SINGH RANA	CSE	8	14-May-17	21-Jul-17	SATISFACTORY	E2 SOFTWARES
83	141294	ASHWANI KUMAR	CSE	6	05-06-2017	14-07-2017	SATISFACTORY	Aptron
84	141295	SARTHAK NAGPAL	CSE	5	05-Jun-17	09-Jun-17	SATISFACTORY	SLR INFOTECH
85	141296	NITIN NARANG	CSE	6	29-05-2017	12-07-2017	SATISFACTORY	DUCAT
88	141300	SHUBHAM SHARMA	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	CETPA INFOTECH
89	141316	RAJAT CHAUHAN	CSE	5	05-Jun-17	09-Jun-17	SATISFACTORY	SLR INFOTECH
90	141302	CHIRAG AHUJA	CSE	5	05-Jun-17	10-Jul-17	SATISFACTORY	SLR INFOTECH
91	141303	SAHIL KAKKAR	CSE	4	12-Jun-17	08-07-2017	SATISFACTORY	JUIT
95	141308	SHUBHAM GARG	Cse	6 weeks	01-06-2017	15-07-2017	SATISFACTORY	TENTROTRONIX INNOVATIONS P
96	141310	RISHAV SAPAHIA	CSE	6	01-06-2017	12-07-2017	SATISFACTORY	Apex Institute
98	141313	DAUGHTY SHARMA	CSE	6	01-Jun	15-Jun	SATISFACTORY	SAMYAK IT Solutions Pvt Ltd
100	141301	ROHAN SHARMA	CSE	6 WEEKS	30-May-17	09-Jul-17	SATISFACTORY	DUCAT,NOIDA
101	141317	TARUN SALUJA	CSE	8	27-05-2017	27-07-2017	SATISFACTORY	BHEL
102	141318	SAURAV MISHRA	CSE	6	29-05-2017	10-07-2017	SATISFACTORY	I.I.T kanpur
104	141320	ADITI SIRKEK	CSE	6 weeks	29-05-2017	08-07-2017	SATISFACTORY	IT Cell ,HPSEB PVT LMT
105	141321	ARKAPRAVO KAR	CSE	6 weeks	05-06-2017	15-07-2017	SATISFACTORY	Webtek Labs
106	141323	RITWIK RAJ	CSE	6	05.06.17	14.07.17	SATISFACTORY	NIELET
108	141325	AMBER SRIVASTAVA	CSE	6	01-06-2017	15-07-2017	SATISFACTORY	UPTEC, Allahabad
109	141326	AURISH GARG	CSE	6	05-06-2017	17-07-2017	SATISFACTORY	Vertex Info Solution
110	141327	HARSHIT SAINI	CSE	6	01-Jun-17	15-July,2017	Satisfactory	Global Infoways
111	141328	ADITYA JADIA	CSE	6 Weeks	07-06-2017	18-07-2017	SATISFACTORY	CETPA INFOTECH
112	141329	KHUSHBOO BANSAL	cse	5	29.05.17	4.07.2017	SATISFACTORY	Indorama Synthetics Pvt Ltd

113	141330	PULKIT AGGARWAL	CSE	6 weeks	01-Jun-17	14-Jul-17	SATISFACTORY	Apogee Tech Global Inc.
115	141332	ABHISHEK GIRI	CSE	6	05-06-2017	12-07-2017	SATISFACTORY	New Horizons
117	141334	SHAURYA RAGHUVANSHI	CSE	4	01-06-2017	30-06-2017	SATISFACTORY	Hindustan Aeronautics Limited
118	141335	SAMPADA THAKKAR	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	Bharat Heavy Electricals Limited
119	141336	MAYANK SHARMA	CSE	6	05-Jun-17	14-Jul-17	SATISFACTORY	C-DAC Mohali
120	141337	SHRIYA SHARMA		6	29-05-2017	08-07-2017	SATISFACTORY	Bharat Electronics Ltd
122	141339	PIYUSH THAKUR	CSE	6	05-06-2017	14-07-2017	SATISFACTORY	C-DAC Mohali
123	141341	CHAITANYA NEGI	CSE	6	01-06-2017	15-07-2017	SATISFACTORY	RJIL
124	141342	LOKESH CHAUDHARY	CSE	6	5 June,2017	14 July,2017	SATISFACTORY	C-DAC Mohali
125	141343	AKASH PARMAR	Computer S	6	06-06-2017	16-07-2017	SATISFACTORY	INX INFOTECH
127	141345	ESHITA SHARMA	Computer S	6 weeks	02-06-2017	07-07-2017	SATISFACTORY	INFOLOGICS IT SOLUTIONS
128	141346	SWAPNIL KHANNA	CSE	6	15.6.17	26.7.17	SATISFACTORY	Innerchef
129	141347	SHRUTI MISHRA	CSE	6	12-Jun-17	25-Jul-17	SATISFACTORY	RCPL
131	141350	ADARSH PAL	CSE	6	05-06-2017	14-07-2017	SATISFACTORY	CDAC
132	141351	TANYA GARG	CSE	6	12-06-2017	21 July,2017	SATISFACTORY	Central Scientific Instruments Or
133	141352	UJJAVAL MALHOTRA	CSE	6	05-06-2017	14-07-2017	SATISFACTORY	KASHISH TECHNOLOGIES
135	141354	ISHA PATHAK	CSE	5	12.06.2017	18.07.2017	SATISFACTORY	Infinite Computer Solutions Ltd.
136	141355	PURU BANSAL	CSE	6	01-06-2017	15-07-2017	SATISFACTORY	ALLY WIREDSOFT SOLUTIONS
137	141356	DIVJOT KAUR	CSE	5	01-06-2017	30-06-2017	SATISFACTORY	Vlink India Pvt. Ltd.
138	141357	AKHIL GOEL	CSE	6 Weeks	07-06-2017	18-07-2017	SATISFACTORY	CETPA INFOTECH
140	141359	HEMPUSHP KAUSHAL	CSE	6	05-06-2017	16-07-2017	SATISFACTORY	IIHT Delhi
142	141361	RAJA JAIN	cse	6 weeks	14-06-2017	25-07-2017	SATISFACTORY	HPSEBL
143	141362	ANIMESH PRATAP SINGH	Cse	4 weeks	29-05-2017	29-06-2017	SATISFACTORY	vertex info solution
144	141363	SANKALP JAIN	Cse	6 weeks	01-06-2017	08-07-2017	SATISFACTORY	Infomatics
145	141364	JATIN BANSAL	CSE	6 WEEKS	07-06-2017	18-07-2017	SATISFACTORY	Cetpa Infotech Pvt Ltd
146	141365	SAUNDARYA SHARMA	cse	6 weeks	01-06-2017	15-07-2017	SATISFACTORY	New Generation Stu. & Edutech
148	141367	YUKTA SHARMA	CSE	6 weeks	5th June 2017	15th july 2017	SATISFACTORY	CS Infotech
149	141368	ISHITA DEWAN	cse	6	05-06-2017	14-07-2017	SATISFACTORY	Center For Development Of Adva
150	141369	RITIKA DOGRA	CSE	6	05-06-2017	14-07-2017	SATISFACTORY	National Institute of Electronics a
151	141370	DEEPAK KUMAR	CSE	6	05-06-2017	20-07-2017	SATISFACTORY	KVCH
152	141371	RAJAT KUMAR	CSE	4 weeks	29-05-2017	29-06-2017	SATISFACTORY	Vertex Info Solution
154	141373	AMBER GOEL	cse	6 weeks	01-06-2017	01-07-2017	SATISFACTORY	Netmax Technologies Pvt Ltd
155	141374	SIDHARTH SHRIDHAR	CSE	6 WEEKS	01-06-2017	15-07-2017	SATISFACTORY	RELIANCE JIO INFOCOMM LIMIT
156	141375	AKSHIT GOEL	CSE	6WEEKS	05-06-2017	15-07-2017	SATISFACTORY	Webhobs Pvt Ltd.
157	141376	MEHAK	CSE	6	05-06-2017	15-07-2017	SATISFACTORY	Alphaltworld
158	141377	NIHARIKA	CSE	6	05.06.2017	14.07.2017	SATISFACTORY	CDAC
159	141378	AKHIL KUMAR	cs	4	29-05-2017	29-06-2017	SATISFACTORY	vertex info solution
160	141379	SHILPI KUMARI	CSE	6 weeks	29-05-2017	07-05-2017	SATISFACTORY	Centre for development of advan
161	141380	AYUSH SHARMA	CSE	6	29-05-2017	12-07-2017	SATISFACTORY	iiht,CHANDIGARH
162	143201	MANJEET CHOUDHARY	CSE	6	08-06-2017	17-07-2017	SATISFACTORY	NovioTech Pvt.Ltd.
164	144201	MRINALINI SINGH THAKUR	CSE	6	31-05-2017	06-07-2017	SATISFACTORY	DUCAT

170	141401	TANUSH CHOUDHARY	I.T	6	01-06-2017	12-06-2017	SATISFACTORY	BHARTI AIRTEL LIMITED
174	141405	RAJAT KUMAR AGGARWAL	I.T	6 WEEKS	29-06-2017	10-07-2017	SATISFACTORY	autocad
178	141409	ADITYA VIKRAM MONGA	IT	4	11-06-2017	12-07-2017	SATISFACTORY	JUIT
180	141411	AKSHITA KHURANA	IT	4	15th june 2017	11th july 2017	SATISFACTORY	Bharat Heavy Electricals Limited
181	141412	KARANDEEP SINGH CHADHA	IT	6	01-06-2017	15-07-2017	SATISFACTORY	Elleen Infotech Pvt. Ltd.
182	141413	SHRESHTH CHHABRA	IT	7	01-06-2017	15-07-2017	SATISFACTORY	ITC(Saharanpur)
183	141414	PARUL CHAWLA	IT	6	JUNE 1, 2017	JULY 12, 2017	SATISFACTORY	NIMBUS SOFTWARES, JALANDHA
185	141416	AASTHA AGARWAL	IT	6 WEEKS	01-06-2017	10-07-2017	SATISFACTORY	CONSULT PAD/JUIT
186	141417	NISHANT SINGH	IT	6	05-06-2017	15-06-2017	SATISFACTORY	CDAC
188	141420	SANCHIT JAIN	I.T.	6 WEEKS	01-06-2017	12-07-2017	SATISFACTORY	JIL IT ltd
189	141421	PUNEET SHARMA	IT	6	01-06-2017	15-07-2017	SATISFACTORY	CRIS
191	141423	AARZOO BANSAL	INFORMAT	6	06-Jun	20-Jul	SATISFACTORY	ALLSCRIPTS (INDIA) LLP
192	141450	ARPAN SHARMA	IT	6	01.06.2017	12.07.2017	SATISFACTORY	Uttrakhand Power Corporation L
193	141425	SHIVI TYAGI	it	6	01-06-2017	16-07-2017	SATISFACTORY	rcpl
194	141426	PANKHURI GOEL	IT	6 weeks	06-06-2017	13-07-2017	SATISFACTORY	DRDO (DESIDOC)
195	141427	AYOUSH TYAGI	IT	6	01-06-2017	15-07-2017	SATISFACTORY	ITC(Saharanpur)
197	141429	VIVEK GARG	it	6 weeks	05-06-2017	14-07-2017	SATISFACTORY	nielit
199	141431	PANKHURI ARORA	IT	6 weeks	1st June'17	18th june'17	SATISFACTORY	Think NEXT Technologies
200	141432	AMAN BHARADWAJ	IT	6 weeks	01-Jun-17	13-Jul-17	SATISFACTORY	IRDE
201	141434	PRACHI WADHWA	IT	6 WEEKS	01-06-2017	10-07-2017	SATISFACTORY	CONSULT PAD/JUIT
202	141435	AYUSH JAIN	IT	6	01-06-2017	13-07-2017	SATISFACTORY	IRDE-DRDO,Dehradun
203	141436	LAVANYA GARG	IT	4 Weeks	02.06.2017	01.07.2017	SATISFACTORY	ONGC
204	141437	MOHIT CHANDEL	IT	6	01-06-2017	16-07-2017	SATISFACTORY	KR Network Cloud
205	141438	RIDDHI RAJ	IT	5 weeks	05-06-2017	04-07-2017	SATISFACTORY	CMPDI
206	141439	PRAKHAR VENKTESH AGARWAL	IT	6 weeks	01-06-2017	08-07-2017	SATISFACTORY	Perpule 1Pay
207	141440	CHARUL SHARMA	IT	4	02-06-2017	04-07-2017	SATISFACTORY	Oil and natural gas corporation l
208	141441	AKSHIT SHARMA	I.T.	6	01-06-2017	15-07-2017	SATISFACTORY	MAWANA SUGAR WORKS
209	141442	VINNY MITTAL	IT	4	11-06-2017	12-07-2017	SATISFACTORY	JUIT
210	141443	RANJAN KUMAR	IT	6	01-06-2017	31-07-2017	SATISFACTORY	KR Network Cloud
211	141444	SHUBHAM DHIMAN	IT	6	01-06-2017	17-07-2017	SATISFACTORY	Vertex Info Solution
212	141445	SONAL MISHRA	IT	6	01-06-2017	14-07-2017	SATISFACTORY	junglee games india pvt ltd
213	141446	NAYANABH CHAKRAVARTY	IT	6	01-06-2017	14-06-2017	SATISFACTORY	NIC
215	141448	AKARSHIT SHARMA	IT	6 weeks	5.6.17	14.7.17	SATISFACTORY	CDAC
4	141204	PRANJAL SHARMA	CSE	6	01.06.2017	14.07.2017	SATISFACTORY	ONGC
6	141206	NANCY	CSE	6 WEEKS	06-06-2017	15-06-2017	SATISFACTORY	INDIAN INSTITUTE OF TECHNOLO
8	141208	VRINDA	C.S.E	6 WEEKS	05-06-2017	15-06-2017	SATISFACTORY	Nest Universe Solutions Pvt. Ltd.
19	141223	SHIVAM KHANNA	CSE	6	10-06-2017	22-07-2017	SATISFACTORY	ITC(Saharanpur)
29	141234	SHIVIKA AGARWAL	C.S.E	6 weeks	05-06-2017	15-06-2017	SATISFACTORY	RISL
31	141236	PRATEEK GOEL	CSE	6	june 1, 2017	july 14,2017	SATISFACTORY	PEC University of Technology
33	141238	AASTHA SHARMA	C.S.E	6 weeks	29.05.2017	08.07.2017	SATISFACTORY	CDAC
34	141239	AAYUSH BANIYAL	CSE	6	6th june 2017	14th jult 2017	SATISFACTORY	BSNL,District kullu

40	141245	UDYAN SHARMA	C.S.E.	6 weeks	05-06-2017	14-07-2017	SATISFACTORY	TCS Lucknow
45	141250	VARUN GARG	CSE	6	5.6.17	15.7.17	SATISFACTORY	CETPA Infotech
58	141266	RITVIC	C.S.E.	4 WEEKS	12-06-2017	11-07-2017	SATISFACTORY	JUIT
66	141275	SAIVYA GULATI	CSE	7	01-06-2017	15 July,2017	SATISFACTORY	Indian Institute of Technology,Rc
87	141299	RADHIKA MAHESHWARI	cse	6	03-06-2017	15-07-2017	SATISFACTORY	SOPO Internet Private ltd,Gurgac
92	141305	AMIT SINGH GULERIA	CSE	8 WEEKS	31-May-17	31-Jul-17	SATISFACTORY	KALPKRITI INC.
114	141331	AKSHITA SOOD	CSE	6	12.06.17	21.07.2017	SATISFACTORY	CSIO-CSIR
116	141333	AYUSH GOEL	C.S.E	6 weeks	29-05-2017	10-07-2017	SATISFACTORY	agicent technologies pvt ltd
126	141344	AYUSHI SINGH	CSE	6	05-06-2017	17-07-2017	SATISFACTORY	RDSO. Lucknow
147	141366	SHRITIKA BHARDWAJ	CSE	6 Weeks	05-06-2017	15-07-2017	SATISFACTORY	TCIL-IT Chandigah
153	141372	SHUBHAM ARORA	C.S.E.	6 weeks	29-05-2017	07-07-2017	SATISFACTORY	CS Soft Solutions Pvt. Ltd.
163	143202	AKANKSHA SINGH	cse	6 WEEKS	01-06-2017	14-07-2017	SATISFACTORY	HCL-INFOTECH
173	141404	PALLAVI PANJABI	IT	5	15th june 2017	15th july 2017	SATISFACTORY	Wipro Ltd.,Bangalore
175	141406	KRITI VAIDYA	I.T	6 weeks	05-06-2017	15-06-2017	SATISFACTORY	Tech Mind
176	141407	AKASH PARMAR	IT	6	03-05-2017	15-06-2017	SATISFACTORY	BSNL
179	141410	DHRITI	IT	6	JUNE 1, 2017	JULY 17,2017	SATISFACTORY	RELIANCE JIO INFOCOM LIMITED
198	141430	UJJWAL GOYAL	IT	6 weeks	JUNE 5, 2017	JULy 15, 2017	SATISFACTORY	Arena Animation
171	141402	TISTA LATHER	IT	6 weeks	11-06-2017	21-07-2017	SATISFACTORY	JUIT
130	141349	SURYANSH SINGH RAGHUVANSHI	CSE	6 weeks	01-06-2017	15-07-2017	SATISFACTORY	ALLY WIREDSOFT SOLUTIONS
121	141338	AVINASH THAKUR	CSE	4 weeks	11-Jun	09-Jul	SATISFACTORY	JUIT
99	141314	PIYUSH RAHI	CSE	6 weeks	07/06/1017	18-07-2017	SATISFACTORY	Cetpa Infotech Pvt. Ltd.
72	141281	DAVINDER SINGH	CSE	6 Weeks	04-06-2017	09-07-2017	SATISFACTORY	Cnet Technologies
62	141271	SHIVAM JINDAL	CSE	4 weeks	42897	42925	SATISFACTORY	JUIT
52	141259	KARTIK CHAUDHARY	CSE	5	08-06-2017	10-07-2017	SATISFACTORY	Delhi Development Authority
36	141241	AKSHAT GUPTA	CSE	6 weeks	01-06-2017	15-07-2017	SATISFACTORY	ALLY WIREDSOFT SOLUTIONS
27	141231	VARUN RATHOUR	CSE	4 WEEKS	11-Jun	09-Jul	SATISFACTORY	JUIT

anking Agencies			
Subject/Topic of Training	Domain/Area of Training	Stipend Rec	Aadhaar Number of Student
Routing and Switching	Routing and Switching	NA	31102497932
ETCS	NETWORKING ,IOT	NA	405179081954
Embedded Systems	BASICS	NA	600367284174
E-shopping	web development	NA	589294125503
PHP,MICRODATA		NA	968118248292
ANDROID	APP DEVELOPMENT	na	762561416937
ASP .NET WITH C#	ASP .NET WITH C#	NA	773011543563
Advanced Java	Advanced Java	NA	899135587825
ADVANCED JAVA	WEB and Database connectivit	NA	998237186121
cloud based Internet of Things	SUPPLY CHAIN MANAGEMENT	NA	959699446389
search engine optimization	search engine optimization	NA	323504903543
WEB BASED TOPXML	TUXEDO	NA	743902383324
ANALYZING	BIG DATA-HADOOP	NA	721368004189
PHP WITH MYSQL	database connectivity	na	845811282633
Connectivity configurations	Networking	none	729377772812
PHP with My SQL	Database connectivity	NA	226503237856
Web Development	Web	None	362275008858
JAVA	JAVA		533213332901
Report Generation System	ASP.NET and C#	NO	3923 4884 6573
android	android	na	530712844120
Down syndrome detection from facial images	machine learning	NA	509238072822
dictionary using binary trees	java	na	623119817402
Graphic Design	Motion Graphics and Vector Ill	10K	446196497486
COLLECTION DASHBOARD AND FRAUD DETECTION	FINTECH	INR15000	978902037613
ANDROID	APP DEVELOPMENT	NA	617186594837
EMPLOYEE PERFORMANCE & RECOGNITION PORTAL	JAVA	NA	999149602130
IOT Ecosystem for inverter	Internet of Things	NA	971925938628
warehouse management system and AWS	cloud computing		452723505491
Hadoop	BIG DATA-HADOOP	NA	435722102496
IFWT	Communication		834719220173
SAP	SAP_ERP	NA	735240730795
DLP	Information Security	3000	972667089400
Image processing	Image processing	NA	401192872001
WEB DESIGNING AND DATABASE CONNECTIVITY	WEB	N.A.	247761563180
NODEJS	WEB DEVELOPMENT	NA	658047090095
JUST shop e-commerce site	java	NA	811057292193
JAVA	JAVA	NA	335725927039
Java	Java	NA	241150487571
MultiBanking System	JAVA	NA	811186134344

CCNP	Networking	NA	437049585785
Website Development	Website Dvelopment		558251351593
warehouse management system and AWS	cloud computing	na	689979331145
Computer Networking	Networking		395134578578
App Development	Android		541842831454
cloud computing + big data hadoop	Networking	NA	778906861923
iot	iot		386575502520
DATA ANALYSIS	Web/SQL	12K + 5K	990864464947
IOT	interaction of iot with social networks		298908838321
CCNP	Networking	NA	254342283736
asp .net	full stack development		418272267414
VIRTUALIZATION	Vmware VIRTUALIZATION		698218288542
NETWORKING	NETWORKING	NA	560272075978
Website Development	Website Dvelopment		887178701673
Mobile Bill Management Portal	Android and Web Developmen	NO	7486 8329 7230
Web Desiging and databaseconnectivity	web	na	321958753811
Optimization using Parallel Programming in C and Python	Parallel Computing	20000	991446134202
Adavce Java	jdbc , Servlet	none	735771143004
Python/Advanced Java	JDBc,Servlets	None	941572269195
Web Development	WEB DEVELOPMENT	2000	464628660839
Core Java	Core Java		330210195657
Advanced Java	Advanced Java	NA	774245264755
MultiBanking System	Java Technologies		892974480584
HADOOP	BIG DATA-HADOOP	NA	635178991764
Advanced Java	Advanced Java	NA	394667372718
Python	LANGUAGE(PYTHON)	N.A.	251291254283
html,css	html,css	NA	364018235017
PHYSICAL SECURITY AND ITS IMPLEMENTATION	PHYSICAL SECURITY AND ITS IMPLEMENTA		461804590670
OOPS Programming	Computer Science	NA	481033608089
Digital Marketing(SEO)	Digital Marketing	no stipend	858744112044
JAVA	JAVA	NA	834605792914
Pert chart implementation	critical path by pert charts	NA	559419665223
Network Monitoring Tool	Networking	NA	790697114814
DATA CENTER PRACTICES,SAP ERP	NETWORKING		930162408329
Advanced Java	Advanced Java	NA	757475219099
BIG DATA-HADOOP	BIG DATA-HADOOP		277904550404
J2EE	Web		982007139153
E-Commerce Web Application	PHP	NA	832409482644
DOT NET SCHEDULER	DOT NET/ WINDOWS APP	NONE	668250472859
HADOOP	BIG DATA-HADOOP	NA	966139574771
Incident Management System	Web		764244940721

Asystguard Complete Security	Internet Security	15,000	636183125736
J2EE	Programming	NA	304681527034
HAL Summer Training	CS in Aeronautics	NA	314258828349
Web Designing	WEB		870780556189
E NOTICE APP	ANDROID	NA	622941547075
Embedded Systems	Embedded Systems	NA	379679250555
Android Technologies	Android	NULL	685311952738
4G LTE	Communication		283958703044
PHP TECHNOLOGIES	WEB DEV	NONE	264715189826
CORE AND ADVANCED JAVA	ADVANCED JAVA	NA	255260857899
Android App Development	android	na	839294257392
Web desigining	Web	7.5k	836004914484
Android	Android	NA	749191994565
ANDROID	APP DEVELOPMENT	NA	494897842902
Web crawling and Data Analysis	Python (Web crawling and Data	NA	899576068404
JAVA	JAVA	NA	758018504369
Network Services	Networks		453986802410
MACHINE LEARNING	ARTIFICIAL INTELLIGENCE	NA	582467786806
SEBI	IBM Form Designing and Andro	NA	592549163327
HADOOP	BIG DATA-HADOOP	NA	849282213710
CCNA	Networking		750010887289
Biiling Solution	SAP_ERP	na	676061380885
c, c++			486904865835
PHP , MySQL	Web	NA	467168802903
Hadoop	BIG DATA-HADOOP	NA	213482738443
Advanced Java	Database connectivity	no	711163923662
CORE JAVA	JAVA	NA	907845329694
Travel Expense Mnager App	Android	NA	213807738933
Analytics with Big Data	Analytics On Population Data		653393929540
Big data	Database connectivity		522340050539
Android App Development	APP DEVELOPMENT	NA	569390008139
CCNA	Networking	NA	483330222901
4G Long term Evolution	4G architecture	NA	794347534911
Bus Enquiry Portal	PHP	NA	798602963310
Phonebook Management system	Mean Stack Framework	No	681095372008
Android Technologies	Android Technologies		518601297018
app Development	APP DEVELOPMENT	NA	772510537230
java technologies	JAVA	NA	885991593837
MICROSOFT AZURE	CLOUD		902076217507
PHP/MYSQL	Web Development	NA	832696531891
PYTHON	WEB DEVELOPMENT	NA	833431083982

CYBER SECURITY	TELECOM	NA	723298096981
Java	Java	NA	290694375311
Data Structures in Python	Software Development	NA	418478907735
BHEL guest house management system	Web development	NA	885825504971
ANDROID	APP DEVELOPMENT	NA	964967345647
internal google system	web development	NA	374842181841
CORE JAVA	LANGUAGE(JAVA)		878374226447
C++ MINIMUN COST IN NETWORK	C++, JAVA		246595646953
ANDROID	APP DEVELOPMENT	NA	779778767191
.NET,C#	C#	NA	946589893919
Designing Homepage for Indian Railways	Web Development	NA	755355207858
HL7 FILE: HEALTHCARE INDUSTRY	JAVA	NA	710023844861
Implementation of Scada Systems	Networking, IOT		936291832746
core java with android	java application	na	615162695192
Website Change Detection	Web development using JSP	N/A	428500438406
Information system	Management Information Syat	NA	906283377569
big data hadoop	data analysis	na	996384768352
Internet of Things	IOT	NA	5882 7487 1263
FTP using socket programming	C++,MFC	NA	518827895366
JAVA BEANS	JAVA SERVELETS, JAVA		873565771949
Socket Programming & MFC	Networking	na	554687764470
PHP	Web Development	NA	230929461564
RHCSA and RHCSE v-7.0 Training	Linux and server configuration	NA	445008487120
ADF	ANDROIND	NA	968766184829
Self checkout system()	web and android		759804753379
library managemnet system	web based	NA	268928899819
DATA ANALYSIS	SALES	NA	227380774914
Data Structures in Python	Software Development	NA	506198199564
RHCSA and RHCSE v-7.0 Training	Linux and server configuration	NA	614848198655
PHP	Web Development	NA	514211837485
Create working modules using OSGI frame work, Java and Vaadin.	Java	NA	270362380406
JAVA/JSP	WEB DEVELOPMENT	na	853852794350
CyberSecurity with Python	CyberSecurity	N.A	441859289298
Reservoir Characterization-A Machine Learning Approach	Machine Learning	NA	868860405139
EXPERIMENTING WITH PYTHON	PYTHON	NA	473683075675
Quality Analysis	Software Testing	NA	834359762190
Web Designing	Java	NA	910773389929
angular Js	web	NA	338167857004
Web Crawling	Data Mining	NA	426619482533
Java	Java	NA	230790291421
Networking	Networking	NA	495702957866

Spring MVC	Spring MVC	NA	932712434752
Hadoop	BIG DATA-HADOOP	NA	257359342603
JAVA	JAVA		293550302770
Network Security	Network Security	NA	286924917659
android develepor	Android	NA	398500869337
SOFTWARE DEVELOPMENT	FULL STACK DEVELOPER (C++)	7,500	318811180417
Classification of fake and real news on the data fetched by a web crawler.	Machine Learning ,Natural Lang	NA	612132465532
java	java		740315631029
Railway Hospitality Management system	Full stack Developer	NA	591780339807
Advance Java	Web	NA	416235686365
asp .net	asp .net	NA	549418740397
Network Security	Networking	NA	603646272603
Health Care Prvider Cloud Application	Web application(HTML,PHP,JavaScript)		935707353262
Java	Java		669969183913
SWITCHING	NETWORKING		521250632968
GIS AND NETWORK PLANNING	NETWORK PLANNING		876791663535
Animation , 3d Modeling	3ds max		912049886860
Mobile Health care application development	Android Development		2416 3408 9348
MACHINE LEARNING	R and Shiny		537462742235
Text Editot	Java	NA	945396017771
big data hadoop	Big Data		966573389498
Pizzerio	Core java	NA	405985367367
JAVA search and sorting algorithms	Java	NA	8.74306E+11
Web Application			464857672712
MACHINE LEARNING	R and Shiny		236389985268
CLOUD COMPUTING + big data hadoop	CLOUD COMPUTING	NA	945451393011

University Requirement				
S.No.	Enrollmen	Name	Branch	Period of Training
214	141447	AASHISH	IT	7
196	141428	VAISHALI VERMA	IT	5
1	141201	SURYA DEV SINGH	CSE	6
2	141202	PARTH AHUJA	CSE	6
3	141203	SHOBHIT KUMAR SRIVASTAVA	CSE	6
5	141205	MAYANK TIWARI	CSE	6
7	141207	AKSHAT MATHUR	CSE	4
9	141209	NAVPREET KAUR KALER	CSE	6
10	141210	ISHA	cse	6 WEEKS
11	141213	SAURAV KUMAR	CSE	6 WEEKS
12	141214	ANKIT	cse	5 weeks
13	141215	RISHABH GARG	CSE	6 WEEKS
14	141216	GOPAL KRISHAN AIRON	CSE	6
15	141217	DIKSHA MUNJAL	cse	6
16	141218	SYED ADIL ALAM	CSE	6
17	141220	MAYANK ABROL	cse	7
18	141222	ARUSHI DOGRA	C.S.E.	6
20	141224	SHREYA SRIVASTAVA	CSE	6 WEEKS
21	141225	RUDAR DAMAN	CSE	6
23	141227	JANIT BANSAL	CSE	6 Weeks
24	141228	ISHAAN VIKRAM	CSE	7 weeks
25	141229	DIVYANSHOO SHARMA	CSE	6
26	141230	SACHIN SLATHIA	cse	6 weeks
28	141233	PARASHIV SIHANIYA	CSE	6
30	141235	PRINCE CHAUHAN	CSE	6 WEEKS
32	141237	DIVYA JAIN	CSE	6
35	141240	DEEPANSH GUPTA	CSE	6 WEEKS
37	141242	SUNIDHI GUPTA	CSE	5
39	141244	SHANU KUMAR	cse	6
42	141247	MANOJ KUMAR	CSE	6
44	141249	TEJESHWAR THAKUR	CSE	6
46	141251	MANDITYA SINGH PANWAR	CSE	5
47	141252	AARON MAURICE QUADROS	CSE	6 WEEKS
48	141254	ILISHA KAUL	CSE	6
49	141256	AKRITI JASWAL	Computer S	6 WEEKS
50	141257	NAMAN BANSAL	CSE	6
51	141258	NITIKA SHARMA	cse	6
53	141260	SHASWAT SOOD	CSE	6
54	141261	ARPIT GARG	CSE	6
55	141262	ADITYA NARAYAN GARG	CSE	6 WEEKS
56	141264	LAVANYA KUMAR	CSE	6
57	141265	ABHIMANYU KAPIL	CSE	7
59	141267	ARPIT MALIK	cse	6
60	141268	KSHITIJ SHARMA	CSE	6
61	141269	PRIYANJUL JOHARI	CSE	6 Weeks
63	141272	RISHIKA BAJAJ	CSE	6
65	141274	CHARUL GUPTA	cse	6 weeks
67	141276	APOORV JAIN	CSE	6

68	141277	PALAK	CSE	6
69	141278	YOGESH MITTAL	CSE	6
70	141279	AARUSH SHARMA	CSE	4
71	141280	AASTHA SINGH	CSE	6
73	141282	NAVDEEP SINGH	cse	6
74	141283	ABHINAV GULATI	CSE	6
75	141284	VIBHOR SHARMA	CSE	6
76	141285	VAANI MAHESH RANA	CSE	6
77	141287	BRIJESH NAND DIWAKAR	CSE	4
78	141289	STUTI KATNORIA	Computer S	6 weeks
79	141290	AASHRITA GOEL	cse	8 weeks
80	141291	VIVEK SINGH	csw	6
81	141292	VEDANT OJHA	CSE	5
82	141293	VIKRANT SINGH RANA	CSE	8
83	141294	ASHWANI KUMAR	CSE	6
84	141295	SARTHAK NAGPAL	CSE	5
85	141296	NITIN NARANG	CSE	6
88	141300	SHUBHAM SHARMA	CSE	6
89	141316	RAJAT CHAUHAN	CSE	5
90	141302	CHIRAG AHUJA	CSE	5
91	141303	SAHIL KAKKAR	CSE	4
95	141308	SHUBHAM GARG	Cse	6 weeks
96	141310	RISHAV SAPAHIA	CSE	6
97	141311	AKSHITA AWASTHI	CSE	6
98	141313	DAUGHTY SHARMA	CSE	6
100	141301	ROHAN SHARMA	CSE	6 WEEKS
101	141317	TARUN SALUJA	CSE	8
102	141318	SAURAV MISHRA	CSE	6
104	141320	ADITI SIRKEK	CSE	6 weeks
105	141321	ARKAPRAVO KAR	CSE	6 weeks
106	141323	RITWIK RAJ	CSE	6
108	141325	AMBER SRIVASTAVA	CSE	6
109	141326	AURISH GARG	CSE	6
110	141327	HARSHIT SAINI	CSE	6
111	141328	ADITYA JADIA	CSE	6 Weeks
112	141329	KHUSHBOO BANSAL	cse	5
113	141330	PULKIT AGGARWAL	CSE	6 weeks
115	141332	ABHISHEK GIRI	CSE	6
117	141334	SHAURYA RAGHUVANSHI	CSE	4
118	141335	SAMPADA THAKKAR	CSE	6
119	141336	MAYANK SHARMA	CSE	6
120	141337	SHRIYA SHARMA		6
122	141339	PIYUSH THAKUR	CSE	6
123	141341	CHAITANYA NEGI	CSE	6
124	141342	LOKESH CHAUDHARY	CSE	6
125	141343	AKASH PARMAR	Computer S	6
127	141345	ESHITA SHARMA	Computer S	6 weeks
128	141346	SWAPNIL KHANNA	CSE	6
129	141347	SHRUTI MISHRA	CSE	6
131	141350	ADARSH PAL	CSE	6

132	141351	TANYA GARG	CSE	6
133	141352	UJJAVAL MALHOTRA	CSE	6
135	141354	ISHA PATHAK	CSE	5
136	141355	PURU BANSAL	CSE	6
137	141356	DIVJOT KAUR	CSE	5
138	141357	AKHIL GOEL	CSE	6 Weeks
140	141359	HEMPUSHP KAUSHAL	CSE	6
142	141361	RAJA JAIN	cse	6 weeks
143	141362	ANIMESH PRATAP SINGH	Cse	4 weeks
144	141363	SANKALP JAIN	Cse	6 weeks
145	141364	JATIN BANSAL	CSE	6 WEEKS
146	141365	SAUNDARYA SHARMA	cse	6 weeks
148	141367	YUKTA SHARMA	CSE	6 weeks
149	141368	ISHITA DEWAN	cse	6
150	141369	RITIKA DOGRA	CSE	6
151	141370	DEEPAK KUMAR	CSE	6
152	141371	RAJAT KUMAR	CSE	4 weeks
154	141373	AMBER GOEL	cse	6 weeks
155	141374	SIDHARTH SHRIDHAR	CSE	6 WEEKS
156	141375	AKSHIT GOEL	CSE	6WEEKS
157	141376	MEHAK	CSE	6
158	141377	NIHARIKA	CSE	6
159	141378	AKHIL KUMAR	cs	4
160	141379	SHILPI KUMARI	CSE	6 weeks
161	141380	AYUSH SHARMA	CSE	6
162	143201	MANJEET CHOUDHARY	CSE	6
164	144201	MRINALINI SINGH THAKUR	CSE	6
170	141401	TANUSH CHOUDHARY	I.T	6
174	141405	RAJAT KUMAR AGGARWAL	I.T	6 WEEKS
177	141408	ROHAN KANOO	I.T	6
178	141409	ADITYA VIKRAM MONGA	IT	4
180	141411	AKSHITA KHURANA	IT	4
181	141412	KARANDEEP SINGH CHADHA	IT	6
182	141413	SHRESHTH CHHABRA	IT	7
183	141414	PARUL CHAWLA	IT	6
185	141416	AASTHA AGARWAL	IT	6 WEEKS
186	141417	NISHANT SINGH	IT	6
188	141420	SANCHIT JAIN	I.T.	6 WEEKS
189	141421	PUNEET SHARMA	IT	6
190	141422	HARSHIT SINGH	I.T	6
191	141423	AARZOO BANSAL	INFORMAT	6
192	141450	ARPAN SHARMA	IT	6
193	141425	SHIVI TYAGI	it	6
194	141426	PANKHURI GOEL	IT	6 weeks
195	141427	AYOUSH TYAGI	IT	6
197	141429	VIVEK GARG	it	6 weeks
199	141431	PANKHURI ARORA	IT	6 weeks
200	141432	AMAN BHARADWAJ	IT	6 weeks
201	141434	PRACHI WADHWA	IT	6 WEEKS
202	141435	AYUSH JAIN	IT	6

203	141436	LAVANYA GARG	IT	4 Weeks
204	141437	MOHIT CHANDEL	IT	6
205	141438	RIDDHI RAJ	IT	5 weeks
206	141439	PRAKHAR VENKTESH AGARWAL	IT	6 weeks
207	141440	CHARUL SHARMA	IT	4
208	141441	AKSHIT SHARMA	I.T.	6
209	141442	VINNY MITTAL	IT	4
210	141443	RANJAN KUMAR	IT	6
211	141444	SHUBHAM DHIMAN	IT	6
212	141445	SONAL MISHRA	IT	6
213	141446	NAYANABH CHAKRAVARTY	IT	6
215	141448	AKARSHIT SHARMA	IT	6 weeks
4	141204	PRANJAL SHARMA	CSE	6
6	141206	NANCY	CSE	6 WEEKS
8	141208	VRINDA	C.S.E	6 WEEKS
19	141223	SHIVAM KHANNA	CSE	6
29	141234	SHIVIKA AGARWAL	C.S.E	6 weeks
31	141236	PRATEEK GOEL	CSE	6
33	141238	AASTHA SHARMA	C.S.E	6 weeks
34	141239	AAYUSH BANIYAL	CSE	6
40	141245	UDYAN SHARMA	C.S.E.	6 weeks
45	141250	VARUN GARG	CSE	6
58	141266	RITVIC	C.S.E.	4 WEEKS
66	141275	SAIVYA GULATI	CSE	7
87	141299	RADHIKA MAHESHWARI	cse	6
92	141305	AMIT SINGH GULERIA	CSE	8 WEEKS
114	141331	AKSHITA SOOD	CSE	6
116	141333	AYUSH GOEL	C.S.E	6 weeks
126	141344	AYUSHI SINGH	CSE	6
147	141366	SHRITIKA BHARDWAJ	CSE	6 Weeks
153	141372	SHUBHAM ARORA	C.S.E.	6 weeks
163	143202	AKANKSHA SINGH	cse	6 WEEKS
173	141404	PALLAVI PANJABI	IT	5
175	141406	KRITI VAIDYA	I.T	6 weeks
176	141407	AKASH PARMAR	IT	6
179	141410	DHRITI	IT	6
184	141415	VAIBHAV NAGPAL		
187	141418	MUDIT BANSAL		
198	141430	UJJWAL GOYAL	IT	6 weeks
171	141402	TISTA LATHER	IT	6 weeks
172	141403	SHASHANK JAISWAL		
130	141349	SURYANSH SINGH RAGHUVANSHI	CSE	6 weeks
134	141353	RISHABH VERMA		
139	141358	SALABH AGARWAL		
141	141360	PRAKHAR GUPTA		
121	141338	AVINASH THAKUR	CSE	4 weeks
93	141306	AKSHIT BHARDWAJ		
94	141307	YASH MITTAL		
99	141314	PIYUSH RAHI	CSE	6 weeks
103	141319	VAIBHAV GUPTA		

107	141324	MOHD OSAMAH		
72	141281	DAVINDER SINGH	CSE	6 Weeks
86	141297	PRAKHAR SRIVASTAVA		
62	141271	SHIVAM JINDAL	CSE	4 weeks
64	141273	NIKUNJ GANDHI		
52	141259	KARTIK CHAUDHARY	CSE	5
36	141241	AKSHAT GUPTA	CSE	6 weeks
38	141243	ASHUTOSH BHATI		
41	141246	PORSHIYA MANGAL		
43	141248	PURU AGGARWAL		
22	141226	VINEESH SINGH		
27	141231	VARUN RATHOUR	CSE	4 WEEKS

			Requirement for Accredation /
Training start date	Training End Date	Status (Satisfactory / U	Institute/Company Name
30-05-2017	15-06-2017	SATISFACTORY	Network Bulls
12-Jun-17	JULY 7 2017	SATISFACTORY	MNNIT ALLD
01-06-2017	11-07-2017	SATISFACTORY	BSNL, Dehradun
01-Jun-17	11-Jun-17	SATISFACTORY	Delhi Development Authority
5 JUNE,2017	15 JULY,2017	SATISFACTORY	Webhobs Pvt Ltd.
07-06-2017	18-06-2017	SATISFACTORY	CETPA
15-Jun-18	11-Jul-18	SATISFACTORY	HEWLETT-PACKARD
Jun-17	Jul-17	SATISFACTORY	NetMAX
5 June,2017	15 July,2017	SATISFACTORY	F-TEC
12-06-2017	20-07-2017	SATISFACTORY	JUIT
05-Jun	14-Jul	SATISFACTORY	outsourcing technologies
08-06-2017	10-07-2017	SATISFACTORY	CENTRE FOR RAILWAY INFORMA
02-06-2017	14-07-2017	SATISFACTORY	HCL-INFOTECH
01-Jun-17	15-Jul-17	SATISFACTORY	HARTRON,HISAR
01-06-2017	11-07-2017	SATISFACTORY	Bank of Baroda
29-May-17	14-Jul-17	SATISFACTORY	NIC,Jammu
01-06-2017	15-07-2017	SATISFACTORY	Elleen Infotech Pvt. Ltd.
31-05-2017	11-07-2017	SATISFACTORY	CETPA INFOTECH
01-06-2017	12-07-2017	SATISFACTORY	Softinfo Systems Pvt. Ltd.
29-05-2017	12-07-2017	Unsatisfactory	National Informatics Centre
01-06-2017	13-07-2017	SATISFACTORY	national dairy research institute
05-06-2017	15-07-2017	SATISFACTORY	RWX technologies pvt ltd
06-06-2017	15-07-2017	SATISFACTORY	regional institute of managemer
01-06-2017	15-07-2017	SATISFACTORY	Curie Labs
31-05-2017	12-07-2017	SATISFACTORY	REDCARPET TECH PVT LTD
07-06-2017	18-08-2017	SATISFACTORY	cetpa
05-06-2017	15-07-2017	SATISFACTORY	DUCAT
05-06-2017	09-07-2017	SATISFACTORY	Nokia Networks
31-05-2017	11-06-2017	SATISFACTORY	CETPA INFOTECH
05-06-2017	15-07-2017	SATISFACTORY	Cetpa
10-06-2017	21-07-2017	SATISFACTORY	HFCL
07-06-2017	12-07-2017	SATISFACTORY	HINDUSTAN POWER
06-06-2017	12-07-2017	SATISFACTORY	Sandhar Technologies Ltd.
5th June 2017	14-Jul-17	SATISFACTORY	Tata Technologies Limited
01-06-2017	13-07-2017	SATISFACTORY	NATIONAL INFORMATICS CENTR
05-06-2017	15-07-2017	SATISFACTORY	Webhobs Pvt Ltd.
30-05-2017	03-07-2017	SATISFACTORY	Ducat PVT. LTD.
30-May-17	09-Jul-17	SATISFACTORY	DUCAT
1.6.17	12.7.17	SATISFACTORY	Sai Infotech Systems Ltd.
05-06-2017	15-07-2017	SATISFACTORY	DUCAT
01-06-2017	14-07-2017	SATISFACTORY	Ducat
29.05.2017	14.07.2017	SATISFACTORY	NIC
07-06-2017	18-07-2017	SATISFACTORY	cetpa infotech pvt. Ltd.
29-05-2017	08-07-2017	SATISFACTORY	IIHT Delhi
29-05-2017	07-07-2017	SATISFACTORY	National Informatics Centre
5 June,2017	14 July,2017	SATISFACTORY	Aptron ,sector 2 ,noida
05-Jun	15-Jun	SATISFACTORY	netmax
06-06-2017	15-07-2017	SATISFACTORY	Rooter Sports technologies Pvt L

01-06-2017	15-07-2017	SATISFACTORY	netmax,chandigarh
01-06-2017	14-07-2017	SATISFACTORY	Ducat
19-06-2017	17-06-2017	SATISFACTORY	Prologic First India Pvt Ltd
05-06-2017	15-07-2017	SATISFACTORY	APTRON
03-06-2017	15-07-2017	Unsatisfactory	curie labs
01-06-2017	12-07-2017	SATISFACTORY	NIC
30.05.2017	10.07.2017	SATISFACTORY	NIC
05-06-2017	13-07-2017	SATISFACTORY	NeGD, Electronics Ministry
24-06-2017	22-07-2017	Unsatisfactory	Orane Infosystem
01-06-2017	09-07-2017	SATISFACTORY	National Informatics Centre
31-May-17	26-Jul-17	SATISFACTORY	SERC, Indian Institute of Science
01-Jun-17	15-Jul-17	SATISFACTORY	Kangroo Software Pvt ltd
5 June,2017	12-Jul-17	SATISFACTORY	MIT/Naresh I technologies
14-May-17	21-Jul-17	SATISFACTORY	E2 SOFTWARES
05-06-2017	14-07-2017	SATISFACTORY	Aptron
05-Jun-17	09-Jun-17	SATISFACTORY	SLR INFOTECH
29-05-2017	12-07-2017	SATISFACTORY	DUCAT
05-06-2017	15-07-2017	SATISFACTORY	CETPA INFOTECH
05-Jun-17	09-Jun-17	SATISFACTORY	SLR INFOTECH
05-Jun-17	10-Jul-17	SATISFACTORY	SLR INFOTECH
12-Jun-17	08-07-2017	SATISFACTORY	JUIT
01-06-2017	15-07-2017	SATISFACTORY	TENTROTRONIX INNOVATIONS P
01-06-2017	12-07-2017	SATISFACTORY	Apex Institute
05-06-2017	15-07-2017	Unsatisfactory	Punjab National Bank
01-Jun	15-Jun	SATISFACTORY	SAMYAK IT Solutions Pvt Ltd
30-May-17	09-Jul-17	SATISFACTORY	DUCAT,NOIDA
27-05-2017	27-07-2017	SATISFACTORY	BHEL
29-05-2017	10-07-2017	SATISFACTORY	I.I.T kanpur
29-05-2017	08-07-2017	SATISFACTORY	IT Cell ,HPSEB PVT LMT
05-06-2017	15-07-2017	SATISFACTORY	Webtek Labs
05.06.17	14.07.17	SATISFACTORY	NIELET
01-06-2017	15-07-2017	SATISFACTORY	UPTEC, Allahabad
05-06-2017	17-07-2017	SATISFACTORY	Vertex Info Solution
01-Jun-17	15-July,2017	Satisfactory	Global Infoways
07-06-2017	18-07-2017	SATISFACTORY	CETPA INFOTECH
29.05.17	4.07.2017	SATISFACTORY	Indorama Synthetics Pvt Ltd
01-Jun-17	14-Jul-17	SATISFACTORY	Apogee Tech Global Inc.
05-06-2017	12-07-2017	SATISFACTORY	New Horizons
01-06-2017	30-06-2017	SATISFACTORY	Hindustan Aeronautics Limited
05-06-2017	15-07-2017	SATISFACTORY	Bharat Heavy Electricals Limited
05-Jun-17	14-Jul-17	SATISFACTORY	C-DAC Mohali
29-05-2017	08-07-2017	SATISFACTORY	Bharat Electronics Ltd
05-06-2017	14-07-2017	SATISFACTORY	C-DAC Mohali
01-06-2017	15-07-2017	SATISFACTORY	RJIL
5 June,2017	14 July,2017	SATISFACTORY	C-DAC Mohali
06-06-2017	16-07-2017	SATISFACTORY	INX INFOTECH
02-06-2017	07-07-2017	SATISFACTORY	INFOLOGICS IT SOLUTIONS
15.6.17	26.7.17	SATISFACTORY	Innerchef
12-Jun-17	25-Jul-17	SATISFACTORY	RCPL
05-06-2017	14-07-2017	SATISFACTORY	CDAC

12-06-2017	21 July,2017	SATISFACTORY	Central Scientific Instruments Or
05-06-2017	14-07-2017	SATISFACTORY	KASHISH TECHNOLOGIES
12.06.2017	18.07.2017	SATISFACTORY	Infinite Computer Solutions Ltd.
01-06-2017	15-07-2017	SATISFACTORY	ALLY WIREDSOFT SOLUTIONS
01-06-2017	30-06-2017	SATISFACTORY	Vlink India Pvt. Ltd.
07-06-2017	18-07-2017	SATISFACTORY	CETPA INFOTECH
05-06-2017	16-07-2017	SATISFACTORY	IIHT Delhi
14-06-2017	25-07-2017	SATISFACTORY	HPSEBL
29-05-2017	29-06-2017	SATISFACTORY	vertex info solution
01-06-2017	08-07-2017	SATISFACTORY	Infomatics
07-06-2017	18-07-2017	SATISFACTORY	Cetpa Infotech Pvt Ltd
01-06-2017	15-07-2017	SATISFACTORY	New Generation Stu. & Edutech
5th June 2017	15th july 2017	SATISFACTORY	CS Infotech
05-06-2017	14-07-2017	SATISFACTORY	Center For Development Of Adv
05-06-2017	14-07-2017	SATISFACTORY	National Institute of Electronics
05-06-2017	20-07-2017	SATISFACTORY	KVCH
29-05-2017	29-06-2017	SATISFACTORY	Vertex Info Solution
01-06-2017	01-07-2017	SATISFACTORY	Netmax Technologies Pvt Ltd
01-06-2017	15-07-2017	SATISFACTORY	RELIANCE JIO INFOCOMM LIMIT
05-06-2017	15-07-2017	SATISFACTORY	Webhobs Pvt Ltd.
05-06-2017	15-07-2017	SATISFACTORY	Alphaltworld
05.06.2017	14.07.2017	SATISFACTORY	CDAC
29-05-2017	29-06-2017	SATISFACTORY	vertex info solution
29-05-2017	07-05-2017	SATISFACTORY	Centre for development of adva
29-05-2017	12-07-2017	SATISFACTORY	iiht,CHANDIGARH
08-06-2017	17-07-2017	SATISFACTORY	NovioTech Pvt.Ltd.
31-05-2017	06-07-2017	SATISFACTORY	DUCAT
01-06-2017	12-06-2017	SATISFACTORY	BHARTI AIRTEL LIMITED
29-06-2017	10-07-2017	SATISFACTORY	autocad
02-06-2017	10-07-2017	Unsatisfactory	Seed
11-06-2017	12-07-2017	SATISFACTORY	JUIT
15th june 2017	11th july 2017	SATISFACTORY	Bharat Heavy Electricals Limited
01-06-2017	15-07-2017	SATISFACTORY	Elleen Infotech Pvt. Ltd.
01-06-2017	15-07-2017	SATISFACTORY	ITC(Saharanpur)
JUNE 1, 2017	JULY 12, 2017	SATISFACTORY	NIMBUS SOFTWARES, JALANDHA
01-06-2017	10-07-2017	SATISFACTORY	CONSULT PAD/JUIT
05-06-2017	15-06-2017	SATISFACTORY	CDAC
01-06-2017	12-07-2017	SATISFACTORY	JIL IT ltd
01-06-2017	15-07-2017	SATISFACTORY	CRIS
02-06-2017	10-07-2017	Unsatisfactory	Seed
06-Jun	20-Jul	SATISFACTORY	ALLSCRIPTS (INDIA) LLP
01.06.2017	12.07.2017	SATISFACTORY	Uttrakhand Power Corporation L
01-06-2017	16-07-2017	SATISFACTORY	rcpl
06-06-2017	13-07-2017	SATISFACTORY	DRDO (DESIDOC)
01-06-2017	15-07-2017	SATISFACTORY	ITC(Saharanpur)
05-06-2017	14-07-2017	SATISFACTORY	nielit
1st June'17	18th june'17	SATISFACTORY	Think NEXT Technologies
01-Jun-17	13-Jul-17	SATISFACTORY	IRDE
01-06-2017	10-07-2017	SATISFACTORY	CONSULT PAD/JUIT
01-06-2017	13-07-2017	SATISFACTORY	IRDE-DRDO,Dehradun

02.06.2017	01.07.2017	SATISFACTORY	ONGC
01-06-2017	16-07-2017	SATISFACTORY	KR Network Cloud
05-06-2017	04-07-2017	SATISFACTORY	CMPDI
01-06-2017	08-07-2017	SATISFACTORY	Perpule 1Pay
02-06-2017	04-07-2017	SATISFACTORY	Oil and natural gas corporation l
01-06-2017	15-07-2017	SATISFACTORY	MAWANA SUGAR WORKS
11-06-2017	12-07-2017	SATISFACTORY	JUIT
01-06-2017	31-07-2017	SATISFACTORY	KR Network Cloud
01-06-2017	17-07-2017	SATISFACTORY	Vertex Info Solution
01-06-2017	14-07-2017	SATISFACTORY	junglee games india pvt ltd
01-06-2017	14-06-2017	SATISFACTORY	NIC
5.6.17	14.7.17	SATISFACTORY	CDAC
01.06.2017	14.07.2017	SATISFACTORY	ONGC
06-06-2017	15-06-2017	SATISFACTORY	INDIAN INSTITUTE OF TECHNOL
05-06-2017	15-06-2017	SATISFACTORY	Nest Universe Solutions Pvt. Ltd.
10-06-2017	22-07-2017	SATISFACTORY	ITC(Saharanpur)
05-06-2017	15-06-2017	SATISFACTORY	RISL
june 1, 2017	july 14,2017	SATISFACTORY	PEC University of Technology
29.05.2017	08.07.2017	SATISFACTORY	CDAC
6th june 2017	14th jult 2017	SATISFACTORY	BSNL,District kullu
05-06-2017	14-07-2017	SATISFACTORY	TCS Lucknow
5.6.17	15.7.17	SATISFACTORY	CETPA Infotech
12-06-2017	11-07-2017	SATISFACTORY	JUIT
01-06-2017	15 July,2017	SATISFACTORY	Indian Institute of Technology,R
03-06-2017	15-07-2017	SATISFACTORY	SOPO Internet Private ltd,Gurga
31-May-17	31-Jul-17	SATISFACTORY	KALPKRITI INC.
12.06.17	21.07.2017	SATISFACTORY	CSIO-CSIR
29-05-2017	10-07-2017	SATISFACTORY	agicent technologies pvt ltd
05-06-2017	17-07-2017	SATISFACTORY	RDSO. Lucknow
05-06-2017	15-07-2017	SATISFACTORY	TCIL-IT Chandigah
29-05-2017	07-07-2017	SATISFACTORY	CS Soft Solutions Pvt. Ltd.
01-06-2017	14-07-2017	SATISFACTORY	HCL-INFOTECH
15th june 2017	15th july 2017	SATISFACTORY	Wipro Ltd.,Bangalore
05-06-2017	15-06-2017	SATISFACTORY	Tech Mind
03-05-2017	15-06-2017	SATISFACTORY	BSNL
JUNE 1, 2017	JULY 17,2017	SATISFACTORY	RELIANCE JIO INFOCOM LIMITED
		UNSATISFACTORY	
		UNSATISFACTORY	
JUNE 5, 2017	JULy 15, 2017	SATISFACTORY	Arena Animation
11-06-2017	21-07-2017	SATISFACTORY	JUIT
		UNSATISFACTORY	
01-06-2017	15-07-2017	SATISFACTORY	ALLY WIREDSOFT SOLUTIONS
		UNSATISFACTORY	
		UNSATISFACTORY	
		UNSATISFACTORY	
11-Jun	09-Jul	SATISFACTORY	JUIT
		UNSATISFACTORY	
		UNSATISFACTORY	
07/06/1017	18-07-2017	SATISFACTORY	Cetpa Infotech Pvt. Ltd.
		UNSATISFACTORY	

		UNSATISFACTORY	
04-06-2017	09-07-2017	SATISFACTORY	Cnet Technologies
		UNSATISFACTORY	
42897	42925	SATISFACTORY	JUIT
		UNSATISFACTORY	
08-06-2017	10-07-2017	SATISFACTORY	Delhi Development Authority
01-06-2017	15-07-2017	SATISFACTORY	ALLY WIREDSOFT SOLUTIONS
		UNSATISFACTORY	
		UNSATISFACTORY	
		UNSATISFACTORY	
		UNSATISFACTORY	
11-Jun	09-Jul	SATISFACTORY	JUIT

Ranking Agencies
Subject/Topic of Training
Routing and Switching
ETCS
Embedded Systems
E-shopping
PHP,MICRODATA
ANDROID
ASP .NET WITH C#
Advanced Java
ADVANCED JAVA
cloud based Internet of Things
search engine optimization
WEB BASED TOPXML
ANALYZING
PHP WITH MYSQL
Connectivity configurations
PHP with My SQL
Web Development
JAVA
Report Generation System
App Development
android
Down syndrome detection from facial images
dictionary using binary trees
Graphic Design
COLLECTION DASHBOARD AND FRAUD DETECTION
ANDROID
EMPLOYEE PERFORMANCE & RECOGNITION PORTAL
IOT Ecosystem for inverter
warehouse management system and AWS
Hadoop
IFWT
SAP
DLP
Image processing
WEB DESIGNING AND DATABASE CONNECTIVITY
NODEJS
JUST shop e-commerce site
JAVA
Java
MultiBanking System
CCNP
Website Development
warehouse management system and AWS
Computer Networking
App Development
cloud computing + big data hadoop
iot
DATA ANALYSIS

IOT
CCNP
asp .net
VIRTUALIZATION
backend web development
NETWORKING
Website Development
Mobile Bill Management Portal
Linux
Web Desiging and databaseconnectivity
Optimization using Parallel Programming in C and Python
Adavce Java
Python/Advanced Java
Web Development
Core Java
Advanced Java
MultiBanking System
HADOOP
Advanced Java
Python
html,css
PHYSICAL SECURITY AND ITS IMPLEMENTATION
OOPS Programming
Networks
Digital Marketing(SEO)
JAVA
Pert chart implementation
Network Monitoring Tool
DATA CENTER PRACTICES,SAP ERP
Advanced Java
BIG DATA-HADOOP
J2EE
E-Commerce Web Application
DOT NET SCHEDULER
HADOOP
Incident Management System
Asystguard Complete Security
J2EE
HAL Summer Training
Web Designing
E NOTICE APP
Embedded Systems
Android Technologies
4G LTE
PHP TECHNOLOGIES
CORE AND ADVANCED JAVA
Android App Development
Web desigining
Android
ANDROID

Web crawling and Data Analysis
JAVA
Network Services
MACHINE LEARNING
SEBI
HADOOP
CCNA
Biiling Solution
c, c++
PHP , MySQL
Hadoop
Advanced Java
CORE JAVA
Travel Expense Mnager App
Analytics with Big Data
Big data
Android App Development
CCNA
4G Long term Evolution
Bus Enquiry Portal
Phonebook Management system
Android Technologies
app Development
java technologies
MICROSOFT AZURE
PHP/MYSQL
PYTHON
CYBER SECURITY
Java
android develepor
Data Structures in Python
BHEL guest house management system
ANDROID
internal google system
CORE JAVA
C++ MINIMUN COST IN NETWORK
ANDROID
.NET,C#
Designing Homepage for Indian Railways
android develepor
HL7 FILE: HEALTHCARE INDUSTRY
Implementation of Scada Systems
core java with android
Website Change Detection
Information system
big data hadoop
Internet of Things
FTP using socket programming
JAVA BEANS
Socket Programming & MFC

PHP
RHCSA and RHCSE v-7.0 Training
ADF
Self checkout system()
library managemnet system
DATA ANALYSIS
Data Structures in Python
RHCSA and RHCSE v-7.0 Training
PHP
Create working modules using OSGI frame work, Java and Vaadin.
JAVA/JSP
CyberSecurity with Python
Reservoir Characterization-A Machine Learning Approach
EXPERIMENTING WITH PYTHON
Quality Analysis
Web Designing
angular Js
Web Crawling
Java
Networking
Spring MVC
Hadoop
JAVA
Network Security
android develepor
SOFTWARE DEVELOPMENT
Classification of fake and real news on the data fetched by a web crawler.
java
Railway Hospitality Management system
Advance Java
asp .net
Network Security
Health Care Prvider Cloud Application
Java
SWITCHING
GIS AND NETWORK PLANNING
Animation , 3d Modeling
Mobile Health care application development
MACHINE LEARNING
Text Editot
big data hadoop

Pizzerio
JAVA search and sorting algorithms
Web Application
MACHINE LEARNING
CLOUD COMPUTING + big data hadoop

Domain/Area of Training	Stipend Req	Aadhaar Number of Student
Routing and Switching	NA	31102497932
NETWORKING ,IOT	NA	405179081954
BASICS	NA	600367284174
web development	NA	589294125503
	NA	968118248292
APP DEVELOPMENT	na	762561416937
ASP .NET WITH C#	NA	773011543563
Advanced Java	NA	899135587825
WEB and Database connectivit	NA	998237186121
SUPPLY CHAIN MANAGEMENT	NA	959699446389
search engine optimization	NA	323504903543
TUXEDO	NA	743902383324
BIG DATA-HADOOP	NA	721368004189
database connectivity	na	845811282633
Networking	none	729377772812
Database connectivity	NA	226503237856
Web	None	362275008858
JAVA		533213332901
ASP.NET and C#	NO	3923 4884 6573
Android		311225611678
android	na	530712844120
machine learning	NA	509238072822
java	na	623119817402
Motion Graphics and Vector Ill	10K	446196497486
FINTECH	INR15000	978902037613
APP DEVELOPMENT	NA	617186594837
JAVA	NA	999149602130
Internet of Things	NA	971925938628
cloud computing		452723505491
BIG DATA-HADOOP	NA	435722102496
Communication		834719220173
SAP_ERP	NA	735240730795
Information Security	3000	972667089400
Image processing	NA	401192872001
WEB	N.A.	247761563180
WEB DEVELOPMENT	NA	658047090095
java	NA	811057292193
JAVA	NA	335725927039
Java	NA	241150487571
JAVA	NA	811186134344
Networking	NA	437049585785
Website Dvelopment		558251351593
cloud computing	na	689979331145
Networking		395134578578
Android		541842831454
Networking	NA	778906861923
iot		386575502520
Web/SQL	12K + 5K	990864464947

interaction of iot with social networks		298908838321
Networking	NA	254342283736
full stack development		418272267414
Vmware VIRTUALIZATION		698218288542
web	10k	523459582886
NETWORKING	NA	560272075978
Website Dvelopment		887178701673
Android and Web Developmen	NO	7486 8329 7230
Networking	NA	753936471536
web	na	321958753811
Parallel Computing	20000	991446134202
jdbc , Servlet	none	735771143004
JDBc,Servlets	None	941572269195
WEB DEVELOPMENT	2000	464628660839
Core Java		330210195657
Advanced Java	NA	774245264755
Java Technologies		892974480584
BIG DATA-HADOOP	NA	635178991764
Advanced Java	NA	394667372718
LANGUAGE(PYTHON)	N.A.	251291254283
html,css	NA	364018235017
PHYSICAL SECURITY AND ITS IMPLEMENTA		461804590670
Computer Science	NA	481033608089
Networking		299924539649
Digital Marketing	no stipend	858744112044
JAVA	NA	834605792914
critical path by pert charts	NA	559419665223
Networking	NA	790697114814
NETWORKING		930162408329
Advanced Java	NA	757475219099
BIG DATA-HADOOP		277904550404
Web		982007139153
PHP	NA	832409482644
DOT NET/ WINDOWS APP	NONE	668250472859
BIG DATA-HADOOP	NA	966139574771
Web		764244940721
Internet Security	15,000	636183125736
Programming	NA	304681527034
CS in Aeronautics	NA	314258828349
WEB		870780556189
ANDROID	NA	622941547075
Embedded Systems	NA	379679250555
Android	NULL	685311952738
Communication		283958703044
WEB DEV	NONE	264715189826
ADVANCED JAVA	NA	255260857899
android	na	839294257392
Web	7.5k	836004914484
Android	NA	749191994565
APP DEVELOPMENT	NA	494897842902

Python (Web crawling and Dat	NA	899576068404
JAVA	NA	758018504369
Networks		453986802410
ARTIFICIAL INTELLIGENCE	NA	582467786806
IBM Form Designing and Andro	NA	592549163327
BIG DATA-HADOOP	NA	849282213710
Networking		750010887289
SAP_ERP	na	676061380885
		486904865835
Web	NA	467168802903
BIG DATA-HADOOP	NA	213482738443
Database connectivity	no	711163923662
JAVA	NA	907845329694
Android	NA	213807738933
Analytics On Population Data		653393929540
Database connectivity		522340050539
APP DEVELOPMENT	NA	569390008139
Networking	NA	483330222901
4G architecture	NA	794347534911
PHP	NA	798602963310
Mean Stack Framework	No	681095372008
Android Technologies		518601297018
APP DEVELOPMENT	NA	772510537230
JAVA	NA	885991593837
CLOUD		902076217507
Web Development	NA	832696531891
WEB DEVELOPMENT	NA	833431083982
TELECOM	NA	723298096981
Java	NA	290694375311
android app		610627242951
Software Development	NA	418478907735
Web development	NA	885825504971
APP DEVELOPMENT	NA	964967345647
web development	NA	374842181841
LANGUAGE(JAVA)		878374226447
C++, JAVA		246595646953
APP DEVELOPMENT	NA	779778767191
C#	NA	946589893919
Web Development	NA	755355207858
android app		697441047664
JAVA	NA	710023844861
Networking, IOT		936291832746
java application	na	615162695192
Web development using JSP	N/A	428500438406
Management Information Syst	NA	906283377569
data analysis	na	996384768352
IOT	NA	5882 7487 1263
C++,MFC	NA	518827895366
JAVA SERVELETS, JAVA		873565771949
Networking	na	554687764470

Web Development	NA	230929461564
Linux and server configuration	NA	445008487120
ANDROIND	NA	968766184829
web and android		759804753379
web based	NA	268928899819
SALES	NA	227380774914
Software Development	NA	506198199564
Linux and server configuration	NA	614848198655
Web Development	NA	514211837485
Java	NA	270362380406
WEB DEVELOPMENT	na	853852794350
CyberSecurity	N.A	441859289298
Machine Learning	NA	868860405139
PYTHON	NA	473683075675
Software Testing	NA	834359762190
Java	NA	910773389929
web	NA	338167857004
Data Mining	NA	426619482533
Java	NA	230790291421
Networking	NA	495702957866
Spring MVC	NA	932712434752
BIG DATA-HADOOP	NA	257359342603
JAVA		293550302770
Network Security	NA	286924917659
Android	NA	398500869337
FULL STACK DEVELOPER (C++)	7,500	318811180417
Machine Learning ,Natural Lan	NA	612132465532
java		740315631029
Full stack Developer	NA	591780339807
Web	NA	416235686365
asp .net	NA	549418740397
Networking	NA	603646272603
Web application(HTML,PHP,JavaScript)		935707353262
Java		669969183913
NETWORKING		521250632968
NETWORK PLANNING		876791663535
3ds max		912049886860
Android Development		2416 3408 9348
R and Shiny		537462742235
Java	NA	945396017771
Big Data		966573389498

Core java	NA	405985367367
Java	NA	8.74306E+11
		464857672712
R and Shiny		236389985268
CLOUD COMPUTING	NA	945451393011

Remarks
certificate not submitted due to summer training in college
Aadhar not submitted

certi &aadhar not submitted

Diary not submitted

Certificate not submitted Summer

Certificate not submitted

adhar not submitted

cerificate not submitted

Certificate & Diary not submitted due to summer sem

Certificate & Diary not submitted due to summer sem

cerificate not submitted

Certificate & Diary not submitted due to summer sem

Certificate & Diary not submitted due to summer sem

diary and certificate not provided yet. Summer

Certificate not provided yet due to Summer training

Certificate not provided yet due to Summer training

Certificate not provided yet due to Summer training

Certificate not provided yet due to Summer training
Certificate not provided yet due to Summer training
Certificate not provided yet due to Summer training

Dept: CIVIL BATCH - 2014 - 2018

Year - 2017

(1)

University Requirement							Requirement for Accredation / Ranking Agencies				
S.No.	Enrollment No.	Branch	Period of Training (No. Of Weeks)	Training Start Date	Training End Date	Status (Satisfactory / Unsatisfactory)	Institute/Company Name	Subject/Topic of Training	Domain/Area of Training	Stipend Received (If Any)	Aadhaar Number of Student
1	141263	CE	7	29-05-2017	15-07-2017	Satisfactory	HPRDCL	Construction of roads (e PMS, RADMS, ROMDAS)	Construction, System Analysis	NO	987868746848
2	141601	CE	6	29-05-2017	08-07-2017		P K Construction Shimla	Construction of Advocate Chamber near High Court and Construction of Parking Complex at Chotta Shimla	Construction	NO	884578188153
3	141603	CE	6								
4	141604	CE	5	29-06-2017	30-06-2017	Satisfactory	HCC	Construction of NH- 34, 4 Lane (Farrakka, Raiganj Section)	Construction	NO	541252189749
5	141605	CE	6	01-06-2017	15-07-2017	Satisfactory	Indian Railways	Construction of Limited Height Subway under Railway Department	Construction	NO	253736151986
6	141606	CE	6	05-06-2017	15-07-2017	Unsatisfactory	JPHRF	Bridge Construction Pung Khadd Sujanpur Tihra (Baijnath Project)	Construction,Project Planning	NO	961362475484
7	141606	CE	6	05-06-2017	15-07-2017	Satisfactory	Syal and associates	Structural Design	Design	NO	253657634246
8	141607	CE	6	05-06-2017	10-07-2017	Satisfactory	IOCL	Construction of Oil Water Seperetor	Construction	NO	
9	141608	CE	6	05-06-2017	10-07-2017	Satisfactory	SJVNL	LUHRI Hydropower Electric Project	Construction Planning and Design	NO	470244564729
10	141609	CE	4	05-06-2017	05-07-2017		L&T	Commercial Building Construction (DLF Building in Gurugram)	Construction	NO	364358230523
11	141610	CE	6	10-06-2017	17-07-2017	Satisfactory	IIT BHU	Design and Analysisof Pitched Roof Truss Using STAAD Pro	Design and Analysis	NO	493996271823
12	141611	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	275103106040
13	141612	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Cresidential Building, Galaxy Heights	Construction	NO	911325199048
14	141613	CE	7	01-06-2017	16-07-2017	Satisfactory	PWD	Road Construction and maintenance at Mathura, UP	Construction	NO	748717944274
15	141615	CE	7	05-06-2017	17-07-2017	Satisfactory	HPPWD	Construction of Post Graduate College	Construction	NO	533592259552
16	141616	CE	6	01-06-2017	12-07-2017	Satisfactory	SJVNL	Rampur Hydro Power Station	Construction, Planning and Design	NO	642152102942
17	141617	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Sawra Kuddu Hydropower Electric Project	Construction	NO	280189613732
18	141619	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	813332527314
19	141620	CE									Pending
20	141621	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Comprehensive Development of Corridor on Outer Ring between Mukbara Chowk to Wazirabad	Construction	NO	612109067356
21	141622	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Construction of 33/220 kV Pooling Sub-Station	Construction	NO	Pending
22	141624	CE	6	02-06-2017	15-07-2017	Satisfactory	Ved Prakash Gupta	Construction of boundary wall	Construction	No	509062120363
23	141626	CE	6	05-06-2017	14-Jul	Satisfactory	DMRC	Contruction of Underground Metro	Construction and Surveying	No	725029168548
24	141627	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	867788791400
25	141630	CE	7	05-06-2017	17-07-2017	Satisfactory	M G Construction	Four Laning of Kharar-Kurali Section of NH-21 in the State of Punjab on EPC Mode	Construction	NO	958830245993
26	141633	CE	6	04-06-2017	15-07-2017	Satisfactory	HPPWD	Construction of Underground Waste Collection System at Dharamsala	Construction	NO	233964159757
27	141634	CE	6	01-06-2017	14-07-2017	Satisfactory	DrukGreen	Hydro Power Electric Project	Construction	NO	
28	141636	CE	6	05-06-2017	18-07-2017	Satisfactory	CPWD	Electrofitting	Estimation and Operation	NO	842943328993
29	141637	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Hydro Power Electric Project	Construction, Analysis and Design	NO	440663665519
30	141638	CE	6	05-06-2017	15-07-2017		NTPC	Q & A	Quality management	NO	493285031722
31	141639	CE	6	01-06-2017	15-07-2017	Satisfactory	Paharpur Cooling towers	Paharpur Cooling Tower Pvt. Ltd.	Construction and Estimation	NO	457229473693
32	141640	CE	6	08-05-2017	17-06-2017	Satisfactory	PWD	Construction tubewell	Construction and Site Investigation	NO	280438057959
33	141641	CE	5	12-06-2017	10-07-2017	Satisfactory	Renuka	Road Construction and Survey	Construction	NO	488631889287
34	141642	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Sewage Treatment Plant Operation	Site Visit and Design	NO	597153870545
35	141643	CE	6	04-06-2017	07-07-2017	Satisfactory	DMRC	Construction of Underground Metro at R K Puram and Hauz Khas Station	Construction	NO	596538281137
36	141644	CE	6	01-06-2017	12-07-2017	Satisfactory	HPPWD	Construction of multi purpose hall	Construction	NO	958282824701
37	141645	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Swara Kuddu Hydropower Project	Construction	NO	736402354843
38	141646	CE	6	01-06-2017	15-07-2017	Satisfactory	GAWAR	Road Construction of 4- Lane Panchkula and Yamuna Nagar (NH- 73)	Construction		
39	141647	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Stability analysis of Luhri HEP Stage-1	Design	NO	339213751913

40	141648	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Multiporpous Sports Stadium Ramamandir Mandi, Veterinary Hospital and College Rampur	Construction, Maintenance and Design	NO	619538309958
41	141650	CE	7	01-06-2017	15-07-2017	Satisfactory	Jaiprakash And Sons	Construction of Mega Hostel Block in NIT Hamirpur	Construction	NO	352700960035
42	141651	CE	6	01-06-2017	11-07-2017	Satisfactory	Sunrises Structures	Construction of Sun Twilight Villas and Commercials	Construction	NO	830120993663
43	141652	CE	6	01-06-2017	12-07-2017	Satisfactory	SIDCL	Road Construction	Analysis	NO	986065011649
44	141653	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Intze Tank Design	Design	NO	957707592017
45	141654	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rain Water Harvesting Tank Transportation of Exsisting Lawn Into Rain Garden	Construction	NO	873345654123
46	141655	CE	7	29-05-2017	17-07-2017	Satisfactory	UPRNNL	Building Construction	Construction	NO	584157677760
47	141656	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
48	141661	CE	7	15-06-2017	31-07-2017	Satisfactory	PWD	Residential Building Construction	Construction	NO	867213841974
49	141662	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Retaining wall construction	Construction	NO	387802984564
50	141663	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
51	141664	CE	6	29-05-2017	08-07-2017	Satisfactory	PK Construction	Car Parking Building Construction	Construction	NO	767631756894
52	141665	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rainwater Harvesting Tank	maintenance	NO	435539216442
53	141666	CE	6	05-06-2017	17-07-2017	Satisfactory	CPWD	Building Maintenance	maintenance	NO	989868620530
54	141667	CE	6	31-05-2017	11-07-2017	Satisfactory	SPCL	Construction of Bus Terminus and Parking	Construction	NO	282070765310
55	141668	CE	6	03-06-2017	14-07-2017		RED	Construction of hall	Construction	NO	892245015469
56	141669	CE	5	13-06-2017	15-07-2017	Satisfactory	PWD Dharamsala	Construction of roads	Construction	NO	774345360402
57	141670	CE	5	29-05-2017	30-06-2017	Unsatisfactory	HCC	4 Laning Farakka Raiganj Section	Construction	NO	454223208162
58	141671	CE	6	28-05-2017	14-07-2017	Satisfactory	Bansal Engineers	Building Construction	Contruction	Yes	597323298747
59	141672	CE	4	30-05-2017	30-06-2017	Satisfactory	ADRDE	Design of building	Design	NO	505348241275
60	141673	CE	6	01-06-2017	12-07-2017	Satisfactory	UPPWD	Road Contruction	Construction	NO	
61	141674	CE	6	01-06-2017	12-07-2017	Satisfactory	REASI	Water Distribution System Study	Analysis	NO	671722842063
62	141675	CE	7	01-06-2017	14-07-2017	Satisfactory	Bareilly Development Authority	Laying of Sewer Pipelines	Construction	NO	334980591932
63	141676	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Galaxy Heights Project	Construction	NO	312625902455
64	141677	CE	6	01-06-2017	11-07-2017	Satisfactory	Swastik	Underground Substation Gurugram	Construction	NO	831847743627
65	141678	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Casting of Bridge	Testing	NO	569738883949
66	141679	CE	5	30-05-2017	12-07-2017	Satisfactory	H. C. Bansal Engineers and Contractors	Building Construction	Construction	Yes	692342550589
67	141680	CE	6	01-06-2017	05-07-2017	Satisfactory	ERA	Road Construction	Construction	NO	567280282077
68	141681	CE	6	11-06-2017	16-07-2017	Satisfactory	HPPCL	Barrage division of sainj Hydro Power Electric Project	Construction	NO	346612434207
69	141682	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Construction of PG	Construction	NO	639806463361
70	141683	CE	4	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Ambuja Cement Plant Visit	Materials	NO	334214454998
71	141684	CE	6	29-05-2017	08-07-2017	Satisfactory	HPPWD	Development of New OPD at IGMC Shimla	Construction	NO	995522249985
72	141686	CE	6	01-06-2017	01-07-2017	Satisfactory		Building Construction (Mohali)	Construction	NO	411889377530
73	141687	CE	6	12-06-2017	22-07-2017	Satisfactory	HPPWD	HP State Library Building Contruction	Construction	NO	885024325960
74	141688	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Testing of materials	Testing	NO	868824583795
75	141689	CE	6	03-06-2017	17-07-2017	Unsatisfactory	Indian Railways	Construction of Railway Track	Construction	NO	409852377341
76	141690	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	691456577638
77	141691	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Highway Maintenance and PG College	Constructon	NO	
78	141692	CE	6	01-06-2017	12-07-2017	Satisfactory	DMRC	Underground Substation	Construction/ Surveying/ Geotechnical Investigation	NO	862339185428
79	141693	CE	4	05-06-2017	08-07-2017	Satisfactory	BP	Construction of new filling shed	Construction	NO	530137391222
80	141694	CE	6	30-05-2017	10-07-2017	Satisfactory	PWD	Construction of roads	Construction	NO	424523018138
81	141695	CE	6	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Concrete Mix Design	Design	NO	579641278502
82	141696	CE	4	31-05-2017	30-06-2017	Satisfactory	CPWD	Construction	Construction	NO	876016738612
83	141697	CE	4	01-06-2017	30-06-2017	Satisfactory	LMRC	Lucknow Metro Construction	Construction	NO	928844325232
84	141698	CE	7	01-06-2017	07-07-2017	Satisfactory	SJVNL	Retaining wall construction	Construction	NO	341163355226

Dept: CIVIL ENGG. BATCH : 2015-2019

Year - 2018

(2)

Summer/Industrial Training Status Summary August 2018 (Batch 2015-2019)									
S no.	**Roll No.**	**Student Name**	**Department**	**Training Dairy Submitted (Yes/No)**	**Training Report Submitted (Yes/No)**	**Training Certificate Submitted (Yes/No)**	**Viva held on (Date)**	**Viva Taken by (Faculty Name)**	**Status (Satisfactory/ Unsatisfactory)**
1	141658	Pankaj Sankhyan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Anirban Dhulia & Mr. Aakash Gupta	**Satisfactory**
2	151113	Akal Singh Gurung	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
3	151601	Divesh Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
4	151602	Puneet Pal Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
5	151604	Nikhilesh Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
6	151605	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
7	151606	Abhishek Ahluwalia	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
8	151608	Hetain Sahi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
9	151610	Kuenzang Sc Choden	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
10	151612	Shally Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
11	151613	Shivani Negi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
12	151614	Charu Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
13	151616	Harsh Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
14	151617	Ammaan Zahoor Chat	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
15	151618	Sarthak Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
16	151619	Akshay Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Rishi Rana & Mr. Kaushal Kumar	**Satisfactory**
17	151620	Rizul Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
18	151621	Abhimanyu P Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
19	151622	Arpan Chaudhary	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
20	151623	Tarun Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
21	151624	Jigyasu Khanna	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
22	151625	Harish Chander	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
23	151626	Manik Ohri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
24	151627	Ankur Jaret	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
25	151628	Ankit Tilokta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
26	151629	Sudhanshu Manikpuri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
27	151630	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
28	151631	Abhinav Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
29	151632	Gaurav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
30	151633	Divyam Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

31	151634	Dipanshu Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Niraj Parihar & Mr. Aakash Gupta	**Satisfactory**
32	151635	Ajay Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
33	151636	Himanshu Yadav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
34	151637	Aditya Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
35	151638	Prikshit Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
36	151639	Ashish Dangwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
37	151640	Akshay Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
38	151641	Vaibhav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
39	151642	Akshay Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
40	151643	Aatish Rajta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
41	151645	Puneet Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
42	151646	Pratiyush Kothari	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
43	151647	Shashi Shekhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
44	151648	Vinayak Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
45	151649	Sumit Dhankhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
46	151650	Gourav Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Abhilash Shukla & Mr. Kaushal Kumar	**Satisfactory**
47	151651	Nikhil Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
48	151652	Anirudh Pratap	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
49	151654	Nitesh Chandel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
50	151655	Arpan Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
51	151656	Shubham Soni	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
52	151657	Akhil Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
53	151658	Himanshu Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
54	151659	Parikshit Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
55	151660	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
56	151661	Amit Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
57	151662	Ashutosh Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
58	151664	Amit Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
59	151666	Deval Ashish	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
60	151667	Dikshant Agarwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

61	151668	Bhupinder Singh Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Saurabh Rawat & Mr. Abhilash Shukla	**Satisfactory**
62	151669	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
63	151670	Ahtesham Hussain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
64	151671	Nakshatra Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
65	151672	Ashish Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
66	151673	Ishan Uniyal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
67	151674	Suryabhan Singh Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
68	151675	Harshit Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
69	151676	Vedansh Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
70	151677	Gaurav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
71	151679	Maanik Vatshyayan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
72	151680	Saksham Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
73	151682	Divesh Narang	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
74	151683	Shubham Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
75	151684	Vikas Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
76	151687	Ayush Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Amardeep and Dr. Saurav	**Satisfactory**
77	151688	Kuldeep Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
78	151689	Mayank Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
79	151690	Tarun Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
80	151691	Vibhor Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
81	151692	Karan Goel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
82	151693	Saksham Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
83	151694	Ankush Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
84	151696	Saksham Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
85	151697	Sparsh N.K. Lath	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
86	151698	Kartikey	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

Kaushal Kr.

Industrial Training Coordinator

HoD CE

Dept: CIVIL BATCH - 2016-2020

Year - 2019

(3)

INDUSTRIAL TRAINING STATUS OF CIVIL ENGINEERING DEPARTMENT (2019-20)					
S. No.	Enrol. No.	Name of Student	Industrial Training Report Submitted by Student to Deptt.	Viva Held on	Status of Indutrial Training Completion
1	161659	Pranav Gupta	Submitted	08-08-2019	Satisfactory
2	161664	Vivek Kashyap	Submitted	08-08-2019	Satisfactory
3	161053	Arpit Rana	Submitted	08-08-2019	Satisfactory
4	161663	Seraj Habib	Submitted	08-08-2019	Satisfactory
5	161666	Shivam Nag	Submitted	08-08-2019	Satisfactory
6	161055	Abhinandan Thakur	Submitted	08-08-2019	Satisfactory
7	161688	Shivam Gupta	Submitted	08-08-2019	Unsatisfactory
8	161628	Sangay Zangmo	Submitted	08-08-2019	Satisfactory
9	161695	Parmila Gurung	Submitted	08-08-2019	Satisfactory
10	161693	Karma Yangzom	Submitted	08-08-2019	Satisfactory
11	161631	Sonam Tshomo	Submitted	08-08-2019	Satisfactory
12	161652	Abhinav Choudhary	Submitted	08-08-2019	Satisfactory
13	161627	Harjot Singh	Submitted	08-08-2019	Satisfactory
14	161615	Vivek Pundir	Submitted	08-08-2019	Satisfactory
15	161673	Shourabh Maanju	Submitted	08-08-2019	Satisfactory
16	161674	Aryan	Submitted	07-08-2019	Satisfactory
17	161675	Saksham Mahajan	Submitted	07-08-2019	Satisfactory
18	161625	Ajay Sharma	Submitted	07-08-2019	Satisfactory
19	161620	Piyush Pathania	Submitted	07-08-2019	Satisfactory
20	161639	Rohit Kumar	Submitted	07-08-2019	Satisfactory
21	161661	Shubang Malgotra	Submitted	07-08-2019	Satisfactory
22	161634	Yashwant Singh Rana	Submitted	07-08-2019	Satisfactory
23	161691	Ritesh Kumar Chaurasia	Submitted	07-08-2019	Satisfactory
24	161602	Harshit Bansal	Submitted	07-08-2019	Satisfactory
25	161685	Hitesh Panwar	Submitted	07-08-2019	Satisfactory
26	161655	Alakshender Singh Wazir	Submitted	07-08-2019	Satisfactory
27	161614	Himanshu Kapoor	Submitted	07-08-2019	Satisfactory
28	161612	Gaurav Chauhan	Submitted	07-08-2019	Satisfactory
29	161678	Ujjwal Nadda	Submitted	07-08-2019	Satisfactory
30	161687	Utkarsh Chauhan	Submitted	07-08-2019	Satisfactory
31	161608	Saurav Singh	Submitted	07-08-2019	Satisfactory
32	161665	Deepak Sharma	Submitted	07-08-2019	Satisfactory
33	161690	Shivam Sharma	Submitted	07-08-2019	Satisfactory
34	161637	Mayank Sharma	Submitted	07-08-2019	Satisfactory
35	161654	Samarth Sharda	Submitted	07-08-2019	Satisfactory
36	161646	Shushant Gupta	Submitted	07-08-2019	Satisfactory
37	161689	Abhishek Thakur	Submitted	07-08-2019	Satisfactory
38	161677	Keshav Singh Thakur	Submitted	07-08-2019	Satisfactory
39	161603	Abhishek Sharma	Submitted	07-08-2019	Satisfactory
40	161630	Pema Zangmo	Submitted	07-08-2019	Satisfactory
41	161694	Pema Yangden	Submitted	07-08-2019	Satisfactory
42	161629	Ngawang Dolkar	Submitted	07-08-2019	Satisfactory
43	161647	Chahat Garg	Submitted	07-08-2019	Satisfactory
44	161611	Ambuj Awasthi	Submitted	07-08-2019	Satisfactory
45	161626	Nikhil Kumar	Submitted	07-08-2019	Satisfactory
46	161649	Anish Kapil	Submitted	07-08-2019	Satisfactory
47	161686	Siddharth Verma	Submitted	07-08-2019	Satisfactory
48	161680	Deven Mahajan	Submitted	07-08-2019	Satisfactory
49	161640	Gunjan Katoch	Submitted	07-08-2019	Satisfactory
50	161671	Nitin Thakur	Submitted	07-08-2019	Satisfactory
51	161651	Nishant Thakur	Submitted	07-08-2019	Unsatisfactory
52	161636	Mukul Prashar	Submitted	07-08-2019	Unsatisfactory
53	161635	Tejas garg	Submitted	07-08-2019	Satisfactory
54	161617	Anmol Singhal	Submitted	07-08-2019	Satisfactory
55	161613	Harshit Saxena	Submitted	07-08-2019	Satisfactory
56	161696	Yash Goyal	Submitted	07-08-2019	Satisfactory
57	161698	Nagawang Dorji	Submitted	07-08-2019	Satisfactory
58	161605	Amber Soni	Submitted	07-08-2019	Satisfactory
59	161607	Sumit Kumar	Submitted	07-08-2019	Satisfactory
60	161642	Xitiz Sen	Submitted	07-08-2019	Satisfactory
61	161684	Ria Thakur	Submitted	07-08-2019	Satisfactory
62	161676	Rishav Kumar Tiwari	Submitted	07-08-2019	Satisfactory

63	161604	Amol Srivastava	Submitted	07-08-2019	Unsatisfactory
64	161601	Ritanjay ✓	Submitted	07-08-2019	Satisfactory
65	161285	Rishi Singh ✓	Submitted	07-08-2019	Satisfactory
66	161624	Ketan Mishra ✓	Submitted	07-08-2019	Satisfactory
67	151691	Vibhor Gautam ✓	Submitted	29-07-2019	Satisfactory
68	161692	Leki Wangchuk ✓	Submitted	21-08-2019	Satisfactory
69	161670	Prasanna Kumar	Not Submitted	-	Unsatisfactory
70	161644	Shankar Kumar	Not Submitted	-	Unsatisfactory
71	161001	Nikhil Sharma	Not Submitted	-	Unsatisfactory
72	161653	Pritul	Not Submitted	-	Unsatisfactory
73	161658	Aditya Vikram Singh Jamwal	Not Submitted	-	Unsatisfactory
74	161657	Anirudhu Guleria	Not Submitted	-	Unsatisfactory
75	161656	Kartikey	Not Submitted	-	Unsatisfactory
76	161668	Nikhil Negi	Not Submitted	-	Unsatisfactory
77	161632	Cheku Dorji	Not Submitted	-	Unsatisfactory
78	141658	PANKAJ SANKHYAN	Not Submitted	-	Unsatisfactory
79	151605	GAURAV SHARMA	Not Submitted	-	Unsatisfactory
80	151688	KULDEEP RANA	Not Submitted	-	Unsatisfactory
81	141625	Namit Sharma	Not Submitted	-	Unsatisfactory
82	141628	HARSH VARDHAN SINGH	Not Submitted	-	Unsatisfactory
83	141659	RAHUL VERMA	Not Submitted	-	Unsatisfactory
84	141663	ADITYA DHIMAN	Not Submitted	-	Unsatisfactory
85	151634	DIPANSHU THAKUR	Not Submitted	-	Unsatisfactory
86	151646	PRATIYUSH KOTHARI	Not Submitted	-	Unsatisfactory
87	151651	NIKHIL KUMAR SHARMA	Not Submitted	-	Unsatisfactory
88	151656	SHUBHAM SONI	Not Submitted	-	Unsatisfactory
89	151668	BHUPINDER SINGH VERMA	Not Submitted	-	Unsatisfactory
90	151677	GAURAV THAKUR	Not Submitted	-	Unsatisfactory
91	151679	MAANIK VATSHYAYAN	Not Submitted	-	Unsatisfactory
92	151689	MAYANK SINGH	Not Submitted	-	Unsatisfactory
93	151694	ANKUSH KUMAR	Not Submitted	-	Unsatisfactory
94	151616	HARSH CHAUHAN	Not Submitted	-	Unsatisfactory

Anirban Dhulia
23/08/2019

Mr. Anirban Dhulia
Mr. Aakash Gupta
Industrial Training Co-ordinator

23/8/19

Prof. Ashok Kumar Gupta
Head of the Department
Civil Engineering

HOD
CE DEPT

Received ✓ Documents
23/08/19

Dept: CIVIL ENGG. BATCH - 2017-2021

Year - 2020-2021

(4)

Summer/Industrial Training Status Summary August 2020 (Batch 2016-2020 and 2017-21)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/Unsatisfactory)
1	161001	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	22-08-2020	Mr. Anirban Dhulia	Satisfactory
2	161604	Amol Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
3	161636	Mukul Prashar	Civil Engineering	Yes	Yes	Yes	22-08-2020	Dr Aakash Gupta	Satisfactory
4	161644	Shankar Kumar	Civil Engineering	Yes	Yes	Yes	14-08-2020	Mr Anirban Dhulia and Dr Aakash Gupta	Satisfactory
5	171067	Aman Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
6	171601	Ishant Shekhri	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
7	171602	Hemant Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
8	171603	Aditya Abrol	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
9	171604	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
10	171606	Shekhar Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
11	171607	Kanishk Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
12	171608	Pawas Soni	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
13	171609	Gaurav Prakash Negi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
14	171610	Gunjan Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
15	171611	Aviral Roy	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
16	171612	Aditya Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
17	171614	Vivek Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
18	171615	Vaibhav Singh	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
19	171616	Ashish Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
20	171617	Harsh Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
21	171618	Aditya Rana	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
22	171620	Hardik Nagpal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
23	171621	Rishabh Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
24	171622	Akshit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
25	171623	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
26	171624	Saurabh Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
27	171626	Sourav Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
28	171628	Anjan Sood	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
29	171629	Sameep Aggarwal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
30	171630	Anmol Katana	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
31	171631	Manik Seth	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
32	171632	Siddhant Dubey	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
33	171633	Nikhil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
34	171634	Sukrit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
35	171635	Sahil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
36	171636	Rohit Kumar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
37	171637	Divyanshu Pandit	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory

38	171638	Anubhav Kundal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
39	171639	Mehul Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
40	171642	Saksham Kaushal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
41	171644	Saurabh Tomar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
42	171645	Kartik Verma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
43	171646	Ankit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
44	171647	Dikshant Joshi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
45	171649	Ritvik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
46	171650	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
47	171651	Suraj Chaudhary	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
48	171652	Chander Bhushan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
49	171653	Abhay	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
50	171654	Mohit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
51	171655	Aditya Shekhar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
52	171656	Rijul Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
53	171657	Tanish Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
54	171659	Akshay Pathania	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
55	171661	Himanshu Bansal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
56	171662	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
57	171664	Venus Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
58	171665	Naveen Karar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
59	171666	Nikhil Shukla	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
60	171671	Aditya Nath	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
61	171681	Abhishek Bind	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
62	171682	Sanju Kanwar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
63	171683	Manik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
64	171684	Lokesh Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory

Traning and Placement Coordinator

Head of the Department

25/8/2020

Received
29/08/2020

Dept : CIVIL ENGG. BATCH : 2018-2022

Year : 2021

(5)

Summer/Industrial Training Status Summary August 2021 (Batch 2018-22)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/ Unsatisfactory)
1	181602	Yamit Dhalaik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
2	181603	Ujjwal Kumar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
3	181604	Harshit Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
4	181605	Shubham	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
5	181606	Varun Kapil	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
6	181607	Abhay Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
7	181608	Aniket	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
8	181610	Vishal Garg	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
9	181611	Madhvender Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
10	181612	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
11	181613	Rishabh Jaswal	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
12	181614	Vishali Thapta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
13	181615	Abhay Kaith	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
14	181616	Sushant	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
15	181617	Ritik Kumar Puri	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
16	181618	Abhay Kanwar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
17	181619	Rohit Lakhera	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
18	181621	Atul Vashisht	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
19	181622	Navneet Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
20	181623	Deepak Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
21	181625	Abhay Joshi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
22	181626	Muskan Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
23	181627	Utkarsh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
24	181629	Suryansh Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
25	181630	Bhuvan Walia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
26	181631	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
27	181632	Arnav Rawat	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
28	181633	Aditya Chauhan	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
29	181634	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
30	181635	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Received
17/08/21

31	181637	Abhishek Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
32	181638	Sahil Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
33	181639	Abhinesh Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
34	181642	Yash Gupta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
35	181643	Pranav Dogra	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
36	181644	Anushka Anand	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
37	181645	Amish Kartik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
38	181647	Sonam Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
39	181648	Passang Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
40	181649	Phub Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
41	181650	Sonam Tshering	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
42	181651	Tshering Gyeltshen	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
43	181652	Kinley Zam	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
44	181653	Sonam Tshewang Dema	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
45	181654	Dechen Tshomo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
46	181655	Namgay Wangmo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
47	181656	Pema Yuden	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
48	181657	Saijal Verma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
49	181659	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
50	181660	Hemang Jandrotia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
51	181661	Deval	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
52	181662	Ayush Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
53	181663	Ritik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Kaushal Kumar

Signature of Departmental Summer Training Coordinator

4/8/21

Signature of the Head of Department

Dr. Ashish Kumar
Professor & HOD of Civil Engineering
Jaypee University of Information Technology,
Waknaghat, Distt.-Solan (HP) 173234 India

Received
17/08/21

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
131501	PREETI RANA	4 weeks	Central electronics limited	Web design & development	Web development
131502	GUNJAN GUPTA	5 weeks	JNU delhi	retrieval of inhibitor information from databases and jmol interface for known drug targets in developing Mtbdb	database development
131503	ABHINAV MISHRA	5 weeks	MIT, Indore	Network Security and Cryptography	IT/Networking and Security
131504	TANYA SINGH	5 weeks	DU, New Delhi	sturctural & functional analysis of beta lactamase families	Biophysics
131505	NANCY SINGH	6 weeks	CUHP, Dharmashala	Computational Biology	Building of network for virluent proteins
131506	KAMAKSHI BHARDWAJ	6Weeks	SO.Infotech pvt. ltd	HAdoop Technology	Big Data Analysis
131508	RAHUL DABRA	1 months	MIT, INDORE	Network security and cryptography techniques	IT/Networking and Security
131509	BHARTI SHARMA	6 weeks	Govt. Of India(NIC)	Website and android app development	Web development

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
131510	ASTHA KHANDURI	1 month	Biotech park	Structure and sequence comparison of *Japanese Encephalitis* Virus group	Bioinformatics
131511	NIMISHA ASATI	5 weeks	Delhi University South campus	Computational analysis of occurence and functional analysis of post translational modifications	Computational Bioinformatics
131512	NIKHITA SOOD	5 weeks	schrodinger	small molecule designing	drug designing
131515	ANKITA	6 weeks	Piford technologies	C++	oops
131516	TANVI KATOCH	6 wweks	CUHP,Dharamshala	Developing residue interaction networks of RNA binding proteins and searching signatures of the interface	Systems Biology
131517	SHUBHANGI KAUSHIK	6 weeks	CUHP,Dharamshala	To develop and analyze interspecoes co-evolutionary protein-protein interaction networks of E.histolytica	Systems Biology
131518	AGAM KANODIA	5 weeks	IIIT-Allahabad	Expression patterns characterizing de-regulated genes of breast tumors involved in DNA repair	Big Data analysis(Bioinformatics)
131519	VARSHA MEHTA	6 weeks	TCIL-IT(CHD)	Oracle Database	IT

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
131520	SHEENA SARSWATI	4 weeks	IBM Banglore	IT procurement	software license
131521	DEEP KSHITIZ SOOD	40 days	Times Internet	Android Development	Android Development
131522	MENCHU DANDONA	6 weeks	Encyclopaedia Britannica	web design and development	web development
131551	RIMJHIM AGARWAL	6 Weeks (June 13 - July 25)	National Reasearch Centre for Plant Biotechnology, IARI,	Learning basic techniques of Molecular Biology	Plant Biotechnology
131552	PALLAVI RAJ SHARMA	4 Weeks (June 10 - July 11)	Department of Biochemistry, AIIMS, New - Delhi	To compare different methods of RNA isolatiob and to study expression of HERV-W gene in human JEG3 cell	Biochemistry
131553	CHETNA	4 Weeks, 2 days (June 15 - July 17)	Al - Jahra Hospital, Jahra City, Kuwait	Basic techniques used in Microbiology and Serology	Microbiology and Serology
131554	SNIGDHA GHOSH	5 Weeks (June 13 - July 22)	Rajendra Memorial Research Institute of Medical Sciences	Expression of a hypothetical protein (P36) from *Leishmania donovani*	Department of Biochemistry and Cell Biology
131555	BISHAL PRASHER	8 Weeks (June 10 - August 6)	G.B. Plant National Institute of Himalayan Ecosystem and	Assessment of biochemical activity and development of propagation protocols for *Polygonatum verticillatum* for	Ecosystem Conservation

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
131556	NIKHIL SAHAI	6 Weeks (June 10 - July 23)	Institute of Genomics and Integrative Biology (IGIB), Delhi	Data mining for associations of genetic variants with Parkinson's disease	Data Mining (Bioinformatics) and Pharmacogenomics
131557	TULIKA	4 Weeks , 5 Days (June 21 - July 23)	Banaras Hindu University, Varanasi, Uttar Pradesh	Working with and handling *Drosophila melanogaster* , An experiment on bar eye mutation in *Drosophila*	Cytogenetics Laboratory , Department of Zoology
131558	PARUL SHARMA	4 Weeks (June 16 - July 15)	Central Research Institute, Kasauli, Himchal Pradesh	To get aquainted with DPT vaccine, yellow fever vaccine, packaging, production of vaccine, quality control,	Vaccine Production and Anti-sera Production
131559	PARUL MITTAL	6 Weeks (June 13 - July 23	Saichem Pharma, Solan, Himachal Pradesh	Study the characteristics and effects of the bacteria present in food samples for the use in functional food and	Department of Microbiology
131560	DEEPALI NANKANI	4 Weeks (June 20 - July 20)	CSIR-CBRI, Roorkee	Bioconcrete using microbes by calcite preipitation	Microbiology
131561	PUJA KUMARI	4 Weeks (June 13 - July 13)	Requirement for Accredation / Ranking Agencies	Processing and testing of fruit juice samples	Food Biotechnology
131562	PRERIKA MATHUR	5 Weeks, 5 days (June 10 - July 22)	Institute of Genomics and Integrative Biology (IGIB), Delhi	Elucidation of estrogen receptor protein expression in different mammalian cell lines	Pharmacogenomics
131563	SAMRITI SINGH	4 Weeks (June 15 - July 15)	Department of Horticulture, Navbahar, Shimla,	Processing of fruits and vegetables	Food Biotechnology

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
131566	ANKIT SHARMA	4 Weeks (June 15 - July 15)	State Department of Horticulture, Navbahar, Shimla ,	Processing of fruits and vegetables	Food Biotechnology
131567	SHREYA SINGH	4 Weeks, 1 day (July 1 - July 25)	Biotech Park, Lucknow, Uttar Pradesh	Bacteriological examination of selected dairy products	Microbiological Testing
131568	APOORVA BANGROO	4 Weeks , 2 days (June 20 - July 22)	Inmass DRDO, Delhi	Development of novel therapeutic modalities and various bio defense scenarios for advance training to all	CBRN Defense
131569	SHIVANI AGARWAL	5 Weeks , 4 days (June 13 - July 24)	Surya Food and Agro. Ltd. , Greater Noida, Uttar Pradesh	Quality control of the basic ingredients used in making biscuits (Priyagold)	Quality Control and Quality Assurance
131570	BRINDA SHARMA	4 Weeks, 5 days (June 15 - July 20)	National Institute of Pathology, ICMR, New Delhi	Leishmaniasis diagnosis	Molecular Biology
131571	DIVIJ CHAUHAN	4 Weeks (June 15 - July 15)	State Department of Horticulture, Navbahar, Shimla ,	Processing of fruits and vegetables	Food Biotechnology
131572	ASHWINA SINGH	5 Weeks, 2 days (June 14 - July 20)	IGMC, Shimla, Himachal Pradesh	To learn the latest detection techniques and equipments used in hospitals	Department of Microbiology and Biochemistry
131574	PASSANG LHAMO	4 Weeks (June 14 - July 14)	Jigme Dorji Wangchuck National Referral Hospital	Diagnosis of HIV-AIDS and Hb1Ac Test Analysis	Department of Pathology

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
131575	SHIVANGI GARG	4 Weeks (June 13 - July 13)	Glaciers Co. Pathankot, Punjab	Processing and testing of fruit juice samples	Food Biotechnology
131577	AKSHAY SHARMA	5 Weeks, 2 days (June 14 - July 20)	IGMC, Shimla, Himachal Pradesh	To learn the latest detection techniques and equipments used in hospitals	Department of Microbiology and Biochemistry
131578	KALPANA	4 Weeks (June 16 - July 15)	Central Research Institute, Kasauli, Himachal Pradesh	Manufacture and production of vaccines and anti - sera	Vaccine Production
131581	MAYANK GUPTA	5weeks	MRG Electrical Industries	Management of Online Inventory and Sales	Marketing and Sales
133802	KRITIKA JAGGI	4 Weeks (June 16 - July 15)	Central Research Institute, Kasauli, Himachal Pradesh	Manufacture and production of vaccines and anti - sera	Vaccine Production
133803	KINAM GUPTA	7 Weeks (June 10 - August 4)	Bose Institute, Kolkata, West Bengal	A mechanistic approach towards understanding the role of Mithramycin A in sensitizing drug resistant breast	Cancer Research
133804	ANKITA RAJTA	4 Weeks (June 15- July 15)	Department of Horticulture, Himachal Pradesh, Shimla	Quality control analysis	Food Biotechnology
133805	PARVEEN KAUR THAKUR	6 weeks	CUHP,Dharamshala	Sequence based comparitive studies on the secretory and non-secretory proteins in protists	Systems Biology

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
133809	ANKITA TRIPATHI	4 Weeks , 3 days (June 15 - July 18)	Dr. Ambedkar Institute of Technology for Handicapped, Kanpur,	Determination of laccase activity from soil sample	Molecular Biology
133812	PRIYA BHARVAL	6 weeks	CS Infotech	Development of Active Server pages using ASP.net	ASP.NET
131564	Anubhav Singh Jamwal	4 Weeks (June 15 - July 15)	State Department of Horticulture, Navbahar, Shimla ,	Processing of fruits and vegetables	Food Biotechnology
131576	Anmol Bansal	4 Weeks (June 15 - July 16)	IGMC, Shimla, Himachal Pradesh	To learn the latest detection techniques and equipments used in hospitals	Department of Microbiology and Biochemistry
131580	Gaurav Patial	8 Weeks (June 13 - August 12)	National Centre for Aquatic Animal Health, Cochin	Immobilization of bioaugumentors on a substratum for direct application in aquaculture system	Bioremediation in aquaculture system (Marine Biotechnology)
133801	Divya	5 Weeks, 3 days (June 9 - July 18)	Delhi Technological University, Shahbad, Delhi	Modulation of Natural Killer (NK) cell receptor activity by tumor cell membrane derived factors	Therapeutics
133806	Tashil Sharma	6 Weeks (June 10 - July 23)	IGMC, Shimla, Himachal Pradesh	To learn the latest detection techniques and equipments used in hospitals	Department of Microbiology and Biochemistry
133807	Natasha Thakur	6 Weeks (June 10 - July 23)	IGMC, Shimla, Himachal Pradesh	To learn the latest detection techniques and equipments used in hospitals	Department of Microbiology and Biochemistry

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2017					
Roll No.	**Student Name**	**Period of Training**	**Institute/Company Name**	**Subject/ Topic of Training**	**Domain/ Area of Training**
133808	Shagun Choudhary	4 Weeks (June 15 - July 16)	Parle Biscuits Pvt. Ltd. Industry, Neemrana, Rajasthan	Quality analysis and manufacturing of Parle biscuits	Quality and Production Department
133811	Manisha Singh	4 Weeks (June 16 - July 15)	Banaras Hindu University, Varanasi, Uttar Pradesh	Immobilizing the probiotic bacteria and checking its survivability in gastric conditions	Department of Agriculture and Dairying
133813	Sachin Sharma	6 Weeks (June 16 - July 28)	Dabur India Limited, Dabur Research Foundation, Sahidabad,	In-vitro techniques : Culture and maintenance of human cancer cell lines	Cell Biology
133815	Chetansee Khanna	5 Weeks (June 15 - July 23)	Defense Research and Development Establishment, DRDO,	Vaccine development against plague	Microbiology
131579	GORKY	4 Weeks , 4 days (June 16 - July 21	Appropriate Rural Technology Institute, Pune, Maharashtra	Bioenergy Research Project	Rural entrepreneurship (Agriculture, Energy, Environment)
131573	MEHUL SALARIA	4 Weeks (June 13 - July 13)	Glaciers Co. Pathankot, Punjab	Processing and testing of fruit juice samples	Food Biotechnology

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141501	JATIN SHARMA	06-01-2017	07-12-2017	Central University of Himachal Pradesh, School of Life Sciences	Bioinformatics	No
141503	RADHIKA ARORA	06-01-2017	07-12-2017	Motilal Nehru National Institute of Technology	Bioinformatics	No
141504	ANKITA CHAKRAVARTY	06-06-2017	13-07-2017	IIT-BHU	Growth Kinetics of Microbe	No
141506	APURVA SISONDIA	06-01-2017	14/7/2017	Oil and Natural Gas Corporation Limited	Information Consolidation for Efficiency	No
141507	NAMRATA THAKUR	06-01-2017	07-12-2017	Central University of Himachal Pradesh, School of Life Sciences	Bioinformatics	No
141508	ARUSHI SHARMA	06-01-2017	14/7/2017	Birla Institute of Scientific Research	Systems Biology	No
141509	DIKSHA SHARMA	06-05-2017	07-05-2017	Himachal Pradesh University, Bioinformatics Centre	Bionformatics	No
141510	SADHIKA BEHL	06-01-2017	14/7/2017	Birla Institute of Scientific Research	Systems Biology	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141801	SAMRITI	01-06-2017	15-07-2017	CSK-HP Palampur	Crop genetic upgradation	No
141802	TANDIN GYELTSHEN	01-06-2017	01-07-2017	Green Vally coorpation ltd	PTC	No
141803	KENCHO WANGDI	01-06-2017	01-07-2017	Green Vally coorpation ltd	PTC	No
141805	RAHUL CHAUHAN	08-06-2017	18-07-2017	indo american hybrid seed ltd	Techniques used in immunology & Rdna Technology	No
141806	AAKRITI BISHT	01-06-2017	13-07-2017	Helix Biogenesis Noida	Microbiology, Molecular Biology &	No
141807	PRATHA SOOD	12-06-2017	22-07-2017	CPRI	Fundamental of Genomics and Gene Cloning	No
141808	RAHUL PRAMJEET	01-06-2017	12-07-2017	mahavir cancer sansthan	As Concentration in breast cancer patients	No
141809	ADITI SHARMA	09-06-2017	08-07-2017	verka Milk plant Mohali	Milk Processing	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141810	SHUBHAM MITTAL	31-05-2017	07-08-2017	Hyderabad university	Anticancer Agent	No
141811	NITIN ARORA	07-06-2017	11-07-2017	AGSS research & Analytical lab delhi	Analytical technique	No
141812	RHYTHEM SHARMA	01-06-2017	17-07-2017	Indian Pharmacopoeia Commission	Analytical technique	No
141813	KSHITIZ GUPTA	03-06-2017	15-07-2017	Hero Cycle	Marketing	No
141814	SAKSHI SRIVASTAVA	30-05-2017	23-06-2017	MNIT-Allahabad	Cell Imaging	No
141815	SUSHAIN KAUL	01-06-2017	13-07-2017	GeNei Bangaluru	BioTechnique	No
141816	NILAKSH MAHAJAN	08-06-2017	18-07-2017	indo american hybrid seed ltd	Techniques used in immunology & Rdna Technology	No
141817	SHILPI MAHESHWARI	05-06-2017	14-07-2017	Cipla mumbai	Pharmaceutical technique	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141818	PALLAVI SONI	03-06-2017	17-07-2017	CSK-HP Palampur	Crop genetic upgradation	No
141819	BANDANA KUMARI	13-06-2017	08-07-2017	JUIT	Quality assessment of foods and	No
141820	ANAIDA KAD	01-06-2017	19-07-2017	BARC mumbai	Effect of Lanthanides and Actinides on	
141821	LAKSHITA SHARMA	05-06-2017	15-07-2017	AIIMS-Delhi	Basic Technique	No
141822	AKSHITA GUPTA	01-06-2017	13-07-2017	CSK-HP Palampur	Crop genetic upgradation	No
141823	NAYANIKA CHAKRAVARTY	12-06-2017	11-07-2017	NDRI	Animal cell culture	No
141824	RIMPLE CHAUDHARY	01-06-2017	15-07-2017	Nestle Una	QA	No
141826	PALLAVI GANATE	01-06-2017	16-07-2017	Minchys	Production of varous food product	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141827	KANIKA BAJPAI	01-06-2017	12-07-2017	TEVA-TAPI malanpur	Instrumental methods for drug study	No
141828	WAGEESHA SHARMA	03-06-2017	13-07-2017	Fermenta Biotech Kullu	QC	No
141829	SOMYA JAISWAL	06-05-2017	15/7/2017	Nest Universe	Computer Science	No
141830	KRITISHA THAKUR	12-06-2017	11-07-2017	NDRI karnal	Animal cell culture	No
141831	TAMANNA SONI	01-06-2017	12-07-2017	H.P State cooperative milk Producer Federation Ltd mandi	Milk and Milk Processing	No
141832	ARCHIT PUNDIR	01-06-2017	17-07-2017	ICGBE-Delhi	Effect of transcript with retained intron	yes
141833	SARITA BHAWANANI	05-06-2017	05-07-2017	NTPC- Netra	Biofuel production technology	No
141834	MOKSH TANDON	02-06-2017	15-07-2017	IGMC-Shimla	General Microbiology Technique	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141835	APOORV SHARMA	13-06-2017	08-07-2017	JUIT	Micropropogation and Hardening of Commercially	No
141836	MANSI ARORA	28/5/2017	15/7/2017	KIIT Technology Business Incubator (KIIT-TBI), School of Biotechnology	Bioinformatics	20000
141837	ATUL KUMAR	08-06-2017	18-07-2017	Indo American Hybrid seed ltd - Bangaluru	General RDT technique	No
141838	VIJAY KUMAR BHARDWAJ	08-06-2017	18-07-2017	Indo American Hybrid seed ltd - Bangaluru	General RDT technique	No
141839	ANKUSH SHARMA	01-06-2017	31-06-2017	Sentiss Pharma	Medical Biochemistry	No
141840	ABHIDEEP KAUR SIHRA	01-06-2017	14-07-2017	Pharma Instinct	General Technique	No
141841	AMIT BHANDARI	29-06-2017	17-07-2017	Amity University -Jaipur	agrobacterium rhizogenes mediated root	No
141842	SIDDHANT KALRA	06-05-2017	15/7/2017	National Jalma Institute for Leprosy and other Mycobacterial Diseases	Microbiology and Molecular Biology	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141843	SHIVANGI KAPOOR	02-06-2017	15-07-2017	IGMC-Shimla	bacteriology , mycology	No
141845	VRISH BHANU HANDA	01-06-2017	14-07-2017	Pharma Instinct	General Technique	No
141846	ARCHITA JOHARI	12-06-2017	25-07-2017	Dabur India	Analysis of Raw material & Finished Goods	No
141847	RISHABH NAUTIYAL	08-06-2017	18-07-2017	Indo American Hybrid seed ltd - Bangaluru	General RDT technique	No
141848	ARUSHI CHETTRI	13-06-2017	08-07-2017	JUIT	Quality assesment of food and Micropropogatio	No
141849	SATYAM SINGH	01-06-2017	17-07-2017	Indian Pharmacopoeia Commission	Analytical technique	No
141850	ANANDITA GOVIL	01-06-2017	13-07-2017	NBPGR-Delhi	Technique	No
141851	VEDIKA KAYASTH	01-06-2017	13-07-2017	Hindustan Unilever ltd Haridwar	Heavy Metal testing	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2018

Roll No.	Name	Traning Start date	Traning End date	Institute/Company Name	Subject/Topic of Training	Stipend Received (If Any)
141852	SAMIKSHA	13-06-2017	08-07-2017	JUIT	Micropropagation and hardening of commercially	No
143801	Kritika sharma	01-06-2017	15-07-2017	CSK Palmpur	Crop Improvement	No
143802	Kumud Razdan	05-06-2017	15-07-2017	Pragati power Corporation ltd New Delhi	Microbial Influenced Corrosion of	No

SENTISS
Clear vision of the future

Date: - 26 JUN 17

TO WHOMSOEVER IT MAY CONCERN

This is to certify that **Mr. Ankush Sharma** S/o Sh. **Khem Pal Sharma**, student of B. Tech. **Biotechnology**, from Jaypee University of Information Technology, has undergone Industrial Training for ***One month*** from 01.06.2017 to 26.06.2017 with our company.

We wish him all the best for a bright career and future.

With warm regards,

For **SENTISS PHARMA PVT. LTD.**

Meenakshi Saxena
DGM-HR&A

Sentiss Pharma Private Limited (Formerly known as Biomed Exports Private Limited)
Manufacturing Plant
Village Khera Nihla, Tehsil Nalagarh
District Solan, Himachal Pradesh-174101, India
Tel: +91-9805512822
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Tel: +91-11-26863503
Fax: +91-11-26948517
CIN No. U74899DL1994PTC059894

Central University of Himachal Pradesh

School of Life Sciences

Dr. Vikram Singh
Assistant Professor
Centre for Computational Biology and Bioinformatics

Phone: +91-9816444313, Email: vikramsingh@cuhimachal.ac.in, vikramsingh.jnu@gmail.com

To Whomsoever it may be concerned

This is to certify that Mr. Jatin Sharma, a third year B.Tech. Bioinformatics student in the Jaypee University of Information Technology bearing roll no. 141501, has worked under my guidance on the topic **"Amino-acid covariance networks in the DEATH domain containing proteins in protistal species"** for his six weeks summer internship during June-July 2017.

This is to further state that he has been very punctual during the internship duration and his efforts to complete the tasks assigned were satisfactory.

I believe, he has the right aptitude towards Bioinformatics and Computational Systems Biology based research and has a very bright future in academia as well as in industry.

Dr. Vikram Singh
(Assistant Professor)

10/8/17

Temporary Academic Block, Shahpur, District Kangra, Pin-176206, Himachal Pradesh, India

प्रशिक्षण एवं स्थानीकरण विभाग
Department of Training & Placement
मोतीलाल नेहरू राष्ट्रीय प्रौद्योगिकी संस्थान इलाहाबाद
इलाहाबाद - 211 004 (उ.प्र.) भारत
Motilal Nehru National Institute of Technology Allahabad
Allahabad - 211 004 (U.P.) INDIA

Date: July 12, 2017.

To Whom It May Concern

This is to certify that **Ms. Radhika Arora** a student of Bioinformatics from Jaypee University of Information Technology, Solan Himachal Pradesh has completed internship from 1st June 2017 to 12th July 2017 in the Biotechnology Department of this institute. She has worked under the supervision of Dr. Ashutosh Mani. During the course of internship, she has completed a project on **"Tools of Bioinformatics"** successfully.

Ashutosh Mani 12.7.17
(Ashutosh Mani)
Project Supervisor

12/7/17
(Rakesh Narain)
Professor In-charge

Radhika
10-08-17

Phone : +91-532-2545677, 2271062 Fax : +91-532-2545677, 2545341 Website : http://www.mnnit.ac.in E-mail : mnnit.placements@gmail.com

Oil and Natural Gas Corporation Limited
South Tower, Scope Minar, Laxmi Nagar, Delhi-110 092
Phone + 91 11 2240 6000 Fax + 91 11 2244 6426

14.07.2017

TO WHOMSOEVER IT MAY CONCERN

This is to certify that **Ms. APURVA SISONDIA**, a student of **'Jaypee University of Information Technology' Waknaghat, Solan** pursuing **B.Tech (Bio Informatics)** has undergone training at ONGC from **01.06.2017 to 14.07.2017.**

She has successfully completed her project work on **"Leave Management System"** in the ICE (Information Consolidation for Efficiency) department of ONGC, SCOPE Minar, New Delhi.

During the training, she took keen interest in the assigned work. We wish her all success in her academic endeavor and life.

14.7.17

(D C Jain)
DGM – I/c HR-ER

दिनेश चन्द्र जैन /Dinesh Chand Jain
उप महाप्रबन्धक (औ. आ.) – प्रभारी-मा.स.-ई.आर.
Dy. General Manager (I.E.)-I/C-HR-ER
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Asisondia
11/08/17

Central University of Himachal Pradesh

School of Life Sciences

Dr. Vikram Singh
Assistant Professor
Centre for Computational Biology and Bioinformatics

Phone: +91-9816444313, Email: vikramsingh@cuhimachal.ac.in, vikramsingh.inu@gmail.com

To Whomsoever it may be concerned

This is to certify that Ms. Namrata Thakur, a third year B.Tech. Bioinformatics student in the Jaypee University of Information Technology bearing roll no. 141507, has worked under my guidance on the topic **"Binding-site similarity network in the DEATH domain containing proteins in protistal species"** for her six weeks summer internship during June-July 2017.

This is to further state that she has been very punctual during the internship duration and her efforts to complete the tasks assigned were satisfactory.

I believe, she has the right aptitude towards Bioinformatics and Computational Systems Biology based research and has a very bright future in academia as well as in industry.

Vikram Singh.

Dr. Vikram Singh
(Assistant Professor)

Temporary Academic Block, Shahpur, District Kangra, Pin-176206, Himachal Pradesh, India

Namrata
10/08/2017

Birla Institute of Scientific Research
Statue Circle, Jaipur - 302 001, Rajasthan, India
Tel. : (0141) 2385283, 2385094, Fax : (0141) 2385121
Website : www.bisr.res.in

Jaipur

July 14, 2017

To Whom It May Concern:

Arushi Sharma worked with us as a summer trainee in Department of Biotechnology and Bioinformatics. She has proved to be one among the best trainees and delivered the project goals to the fullest with thoughts, action and debate. The work she carried out with her peers was on development of a web-resource on DNA mismatch repair proteins while annotating them from genebanks.

Arushi has a penchant for understanding the problem formulating and work meticulously on it. I am more than impressed by her workaholics even as she is considered to be a good protege.

Yours sincerely

Prashanth N Suravajhala, PhD

Scientist

10/8/17

HIMACHAL PRADESH UNIVERSITY
BIOINFORMATICS CENTRE
SUMMER HILL, SHIMLA – 171 005

Prof. S. S. Kanwar
(Coordinator)

Dated: 04 /07/ 2017

CERTIFICATE

This is to certify that the matter embodied in the project/database entitled **"NitMAP: Nitrilase Mining and Prediction"** is the result of investigations carried out by **Ms. Diksha Sharma** (B.Tech. Bioinformatics, VIth Semester) Jay Pee University of Information Technology, Waknaghat, Solan, Himachal Pradesh under my direct supervision and guidance at Sub-Distributed Information Centre (Bioinformatics Center), Himachal Pradesh University, Summer Hill, Shimla 171 005 from **5th June to 5th July 2017.**

Self attested
Diksha Sharma

(S. S. Kanwar) 4/7/2017

Dr. S. S. Kanwar, Professor
Biotechnology, H. P. University,
Shimla-171 005 (India).
Email: kanwarss2000@yahoo.com
Telefax: +91-177-2831948; 2832154

Birla Institute of Scientific Research
Statue Circle, Jaipur - 302 001, Rajasthan, India
Tel. : (0141) 2385283, 2385094, Fax : (0141) 2385121
Website : www.bisr.res.in

Jaipur

July 14, 2017

To Whom It May Concern:

Sadhika Behl worked with us as a summer trainee in Department of Biotechnology and Bioinformatics. She has proved to be one among the best trainees and delivered the project goals to the fullest with thoughts, action and debate. The work she carried out with her peers was on development of a web-resource on DNA mismatch repair proteins while annotating them from genebanks.

Sadhika worked for the project goals very well and I am more than impressed by her workaholics even as she is considered to be a good protege.

Yours sincerely

Prashanth N Suravajhala, PhD

Scientist

Sadhika
10/8/17

To whom it may concern

This is to certify that **Ms. Mansi Arora**, 3rd Year student of B.Tech Bioinformatics at Jaypee University of Information Technology, Waknaghat, Himachal Pradesh, has successfully completed her project work under my guidance at KIIT Technology Business Incubator, School of Biotechnology, KIIT University, Bhubaneswar, Odisha as an **IASc-INSA-NASI Summer Research Fellow - 2017** (LFS3990), towards the fulfilment of her national fellowship through Summer Research Fellowship Program, sponsored by **Indian Academy of Sciences, Bengaluru.**

She worked on making of **"An android application as a tool for developing Portable Medical Diagnosis"**. Her tenure was of 56 days during summer 2017, as per the fellowship guidelines. During her stay, I found her to be a self-starter, hardworking and competent girl. She was highly dedicated and significantly productive, both individually and for our team as she could punctually complete the assignments given.

I wish her all the success and strongly recommend her for any of her future endeavours.

Regards

KIIT TECHNOLOGY BUSINESS INCUBATOR (KIIT-TBI) ★ KIIT University Bhubaneswar 751024

Asst. Professor
School of Biotechnology
KIIT University, Bhubaneswar-24

Dr. Aseem Mishra
Chief Technical Officer, KIIT Technology Business Incubator
Assistant Professor, KIIT School of Biotechnology

10/08/17

SCIENCE ACADEMIES' SUMMER RESEARCH FELLOWSHIP PROGRAMME

Date: 30 March 2017

Indian Academy of Sciences
Bengaluru

Indian National Science Academy
New Delhi

The National Academy of Sciences, India
Allahabad

Ms Mansi Arora
17, Shyam Sunder
Dharamshala Deokali Road
Faizabad 224 001

Dear Ms Mansi,

This has reference to your application **LFS3990** for an IASc-INSA-NASI Summer Research Fellowship in 2017. We are happy to offer you a Fellowship to work for two months during this summer subject to verification of your marks as stated by you in the application. You will be working with Dr Aseem Mishra, Utkal University, Bhubaneswar (e-mail: Professoraseemmishra@gmail.com).

We have tried as far as practicable to assign you to a guide who works in your area of interest. **Where that has not been possible, you will work with the assigned guide in a related area that will be determined by the guide, and trust that the experience will be fruitful to you. We will not be able to make any changes in this regard.**

This Fellowship is subject to the following norms:

- The duration of the Fellowship **is eight weeks (56 days – including Sundays and General Holidays), and is not to be reduced. If you do not complete this requirement, you will not be paid the fellowship and the certificate that is usually issued on completion.**
- You will be provided second class [sleeper class] train fare from Faizabad or Solan to Utkal Univ., Bhubaneswar and back.
- If you are NOT an INSPIRE KVPY Fellowship holder, you will be paid a Fellowship of Rs. 10000 - per month towards your boarding, lodging and local transport expenses. Those who are in receipt of INSPIRE KVPY Fellowship will be covered by a separate arrangement, the details of which will be communicated later.
- As regards accommodation, please contact Dr Mishra as the Academy is not able to help you in this regard.

Please also go through carefully & comply with **all the Instructions** given in the attached sheet.

You are advised to get in touch with Dr Mishra immediately to work out the exact period of your visit. In the meantime please communicate with Mr C.S. Ravi Kumar, Coordinator, Summer Research Fellowship Programme, your acceptance of this Fellowship. We would need a joining report from you upon your arrival, and a brief report of your work at the end of four weeks so that your Fellowship for the first month can be paid. After the receipt of the final report, we shall release the remaining amount due to you along with your travel fare.

We urge you to convey your acceptance of this fellowship within 7 days by both online (the userid and password given at the bottom of the email) as well as by **returning the Form of Acceptance posted to you.** Even if you are not able to accept the fellowship, this should be communicated to the Academy immediately (both by email and in the Form of Acceptance) so that the fellowship can be awarded to another candidate in the waiting list.

With best wishes,

Yours sincerely,

Mansi Arora
10/08/17

K.L. Sebastian
Chairman, Joint Science Education Panel

Contact Address :
Indian Academy of Sciences
P.B. No. 8005
C. V. Raman Avenue
(near Mekhri Circle)
Sadashivanagar P.O.
Bengaluru 560 080

Telephone :
91-80-2266 1207
91-80-2266 1202
90-80-2266 1221
Fax : 91-80-2361 6094
Email : jointsrf@ias.ac.in
Website : www.ias.ac.in

SCIENCE ACADEMIES'
SUMMER RESEARCH FELLOWSHIPS — 2017

Instructions for the Summer Research Fellows (SRFs):

A. Acceptance of Fellowship

1. The selection letter has been sent by email (along with instruction sheet). A hard copy of the letter has also been sent by speed post (along with instruction sheet, form for conveying acceptance, and form for sending joining report).

2. At the bottom of the email, an user-id and password are also provided for each SRF which will enable them to view their online page in our website and to fill in the required details. The user-id and password should be saved and will **not be** provided a second time.

3. Your acceptance to take up this fellowship should be conveyed URGENTLY within 7 days by filling in your online page (the user-id and password provided). The Form of Acceptance to be sent by speed post should also be returned to us **by speed post or courier** within 3 days after it reaches you.

4. **Do not wait for the approval from guide to send your Acceptance form.**

5. For some reason, if you do not wish to take up the fellowship, this should be conveyed to us URGENTLY **by** (a) filling in your online page, (b) email, as well as (c) returning the Acceptance Form **all within one week of your receiving the letter of selection** so that the fellowship can be awarded without delay to another person in the waiting list.

6. After sending the acceptance, please contact your guide to fix up the exact date of joining. This exact date should then be communicated to us by email/online.

7. Two copies of your passport-size photograph should be enclosed, of which one copy to be affixed to the letter of acceptance.

8. The joining letter (in the format enclosed) should be posted to the Academy **duly countersigned by the guide** as soon as the SRF reports for work.

B. General Instructions

9. **The period of work should be NOT LESS THAN 56 days (including Sundays and holidays) under any circumstances. If the final duration turns out to be less than 56 days, the fellowship will not be deemed to have been satisfactorily completed to entitle you to the certificate and fellowship dues.**

10. If the candidate has applied for and obtained fellowship to work under any other programme during this period, the Academy fellowship will be **treated as withdrawn**.

11. If the SRF is in receipt of KVPY or INSPIRE fellowships, this should be specifically indicated in the Form of Acceptance (even if indicated in the application).

10/08/17

Website : www.jalma-icmr.org.in
e-mail : jalma@sancharnet.in

FAX : (0562) 2331755
EPABX : (0562)2331751-4
DIRECTOR : 2331756,2333595
: 2232222

राष्ट्रीय जालमा कुष्ठ एवं अन्य माइकोबैक्टीरियल रोग संस्थान,ताजगंज, आगरा
NATIONAL JALMA INSTITUTE FOR LEPROSY & OTHER MYCOBACTERIAL DISEASES
(भारतीय आयुर्विज्ञान अनुसंधान परिषद)
(Indian Council of Medical Research)
पोस्ट बॉक्स- 1101,ताजगंज, आगरा- 282 001
POST BOX-1101, TAJGANJ, AGRA-282 001

Ref: NJIL & OMD/PT/2017/ST-14

Date: 15.07.2017

CERTIFICATE

This is to certify that **Mr. Siddhant Kalra,** S/O Mr. Deepak Kalra, a bonafide student of Jaypee University of Information Technology, Solan, has completed his 6 weeks summer training from 05.06.2017 to 15.07.2017 in the department of Microbiology and Molecular Biology under supervision of Dr. Partha Sarathi Mohanty, Scientist-C, on "Database development on different tandem repeats for *M. leprae* and HIV". To the best of my knowledge and belief this is his original piece of work and has not been submitted anywhere else for award of any degree or diploma. This assistance and help receive during the course of investigation has been acknowledged.

Signature

Dr. Umesh Datta Gupta
Director-In-Charge
NJIL & OMD AGRA

DIRECTOR
National JALMA Institute for Leprosy
& Other Mycobacterial Diseases (ICMR)
Tajganj, AGRA-282 001

Website : www.jalma-icmr.org.in
e-mail : jalma@sancharnet.in

FAX : (0562) 2331755
EPABX : (0562)2331751-4
DIRECTOR : 2331756,2333595
: 2232222

राष्ट्रीय जालमा कुष्ठ एवं अन्य माइकोबैक्टीरियल रोग संस्थान,ताजगंज, आगरा
NATIONAL JALMA INSTITUTE FOR LEPROSY & OTHER MYCOBACTERIAL DISEASES
(भारतीय आयुर्विज्ञान अनुसंधान परिषद)
(Indian Council of Medical Research)
पोस्ट बॉक्स- 1101,ताजगंज, आगरा- 282 001
POST BOX-1101, TAJGANJ, AGRA-282 001

Ref: NJIL & OMD/PT/2017/ST-14 **Date: 15.07.2017**

CERTIFICATE

This is to certify that **Mr. Siddhant Kalra,** S/O Mr. Deepak Kalra, a bonafide student of Jaypee University of Information Technology, Solan, has completed his 6 weeks summer training from 05.06.2017 to 15.07.2017 in the department of Microbiology and Molecular Biology under My supervision on "Database development on different tandem repeats for *M. leprae* and HIV". To the best of my knowledge and belief this is his original piece of work and has not been submitted anywhere else for award of any degree or diploma. This assistance and help receive during the course of investigation has been acknowledged.

Signature

Dr. Partha Sarathi Mohanty
Scientist-C
NJIL & OMD AGRA

Dr. Partha Sarathi Mohanty
Scientist-C
Microbiology & Molecular Bi...
National JALMA Institute
for Leprosy and Other Mycobacterial Diseases
Tajganj, Agra

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY
WAKNAGHAT, SOLAN. H.P.

CERTIFICATE

This certificate is awarded to Mr./Ms. ...Bandana Kumari.....
Roll No. 141819.... for completing their summer training organized by Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology, Waknaghat, Solan from 9th June - 15th July, 2017.

Dr. Hemant Sood/Dr. Anil Kant
Training Co-ordinator

Dr. Sudhir Kumar
Head of Department, BT&BI

Prof. (Dr.) Samir Dev Gupta
Director & Academic Head

Bandana
8894403880

INTERNATIONAL CENTRE FOR GENETIC ENGINEERING AND BIOTECHNOLOGY

ICGEB Campus, P. O. Box :10504, Aruna Asaf Ali Marg
New Delhi - 110 067, India
http://www.icgeb.res.in

Tel: 91-11-26741358/61/
26742357; 26741680 (lab)
Fax: 91-11-26742316
Email: icgeb@icgeb.res.in

Dated: 01/09/2017

To Whom It May Concern

This is to certify that Mr. Archit Pundir, worked in my lab as the summer research fellow from the three academies during May-July 2017.

Archit was assigned to do a small task titled: "To study the effects of transcripts with retained introns upon *Mycobacterium tuberculosis* infection". The work involved some bioinformatics analysis, primer designing, PCR amplification and cloning. He was able to perform these experiments as part of his training in my lab.

His overall stay and performance in the lab was very good.

Best Wishes

Dhiraj Kumar

Dhiraj Kumar, PhD
Group Leader
Cellular Immunology Group
ICGEB, New Delhi

Archit

141832 - Archit Pundir

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY
WAKNAGHAT, SOLAN. H.P.

CERTIFICATE

This certificate is awarded to Mr./Ms. .....Apoorv Sharma.....
Roll No. 141835.... for completing their summer training organized by Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology, Waknaghat, Solan from 9th June - 15th July, 2017.

Dr. Gunjan Goel/Dr. Anil Kant
Training Co-ordinator

Dr. Sudhir Kumar
Head of Department, BT&BI

Prof. (Dr.) Samir Dev Gupta
Director & Academic Head

Apoorv

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY
WAKNAGHAT, SOLAN. H.P.

CERTIFICATE

This certificate is awarded to Mr./Ms. .....Anushi Chettri.....
Roll No. 141248... for completing their summer training organized by Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology, Waknaghat, Solan from 9th June - 15th July, 2017.

Dr. Gunjan Goel/Dr. Anil Kant
Training Co-ordinator

Dr. Sudhir Kumar
Head of Department, BT&BI

Prof. (Dr.) Samir Dev Gupta
Director & Academic Head

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY
WAKNAGHAT, SOLAN. H.P.

CERTIFICATE

Samiksha Sharma 141852

This certificate is awarded to Mr./Ms. ...Samiksha...Sharma.....
Roll No. 141852..... for completing their summer training organized by Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology, Waknaghat, Solan from 9th June - 15th July, 2017.

Dr. Hemant Sood/Dr. Anil Kant	Dr. Sudhir Kumar	Prof. (Dr.) Samir Dev Gupta
Training Co-ordinator	Head of Department, BT&BI	Director & Academic Head

Indian Academy of Sciences
Bengaluru

Indian National Science Academy
New Delhi

The National Academy of Sciences, India
Allahabad

SUMMER RESEARCH FELLOWSHIP PROGRAMME

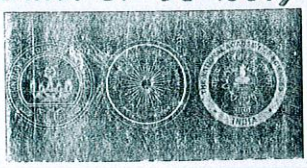
CERTIFICATE

This is to certify that Mr Amit Bhandari worked on a project entitled "Agrobacterium rhizogenes mediated hairy root induction in medicinally important Balanites aegyptiaca" during May-July 2017 as a Summer Research Fellow under the supervision of Professor S L Kothari, Amity University, Jaipur. The Summer Research Fellowship Programme is jointly sponsored by IASc (Bengaluru), INSA (New Delhi) and NASI (Allahabad).

K L Sebastian

Place: Bengaluru
Date: 31-08-2017

K.L. Sebastian
Chairman, Science Education Panel



A Bhandari.

- 9805055436.

Pharma Instinct

A++ing Value to Innovations & Systems

Certificate

This certificate is awarded to Mr./Ms. Abhideep Kaur Sehra

Son/Daughter of Mrs. Baljit Kaur and Mr. Pradeep Singh

For having successfully completed Four Weeks/Six Weeks Industrial Training in Clinical Research & Experimental Biotechnology Conducted in June 2017 at Pharma Instinct, Chandigarh.

SCO 52-53, Sector 9-D Pharma Instinct Chandigarh

Place: Chandigarh
Date : July 2017

Dr. Rajesh Sehgal
CEO

Indo-American
Hybrid Seeds (India) Pvt. Ltd.

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Rajarajeshwarinagar Post, Bengaluru - 560 098.
Tel : +91-80-28611499 Fax : +91-80-28612912
Website : **www.indamseeds.com**
CIN : U02001KA1997PTC023141

DSIR RECOGNITION NO: TU/IV-RD/1313/2016

CERTIFICATE

This is to certify that ***Mr. Atul Kumar,*** *student of B.Tech (Biotechnology), Jaypee University of Information Technology, Solan, H.P has completed training in* ***"Recombinant DNA Technology, SDS PAGE and Immunology Techniques"*** *from 8th June 2017 to 18th July 2017 in our Research and Development, Biotechnology Laboratory.*

We wish all the best for his future Endeavour's.

Dr. Devaraja Achar
Head-Biotechnology

Garden Center : 17th CROSS, II "A" MAIN K.R. ROAD, BANASHANKARI II STAGE,
BENGALURU - 560 070. INDIA

TEL : +91-080-26760111
FAX : +91-080-26761479

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Tel : +91-80-28611499 Fax : +91-80-28612912
Website : **www.indamseeds.com**
CIN : U02001KA1997PTC023141

DSIR RECOGNITION NO: TU/IV-RD/1313/2016

CERTIFICATE

This is to certify that ***Mr. Vijay Kumar Bhardwaj,*** *student of B.Tech (Biotechnology), Jaypee University of Information Technology, Solan, H.P has completed training in* ***"Recombinant DNA Technology, SDS PAGE and Immunology Techniques"*** *from 8th June 2017 to 18th July 2017 in our Research and Development, Biotechnology Laboratory.*

We wish all the best for his future Endeavour's.

Dr. Devaraja Achar
Head-Biotechnology

Self attested.

Garden Center : 17th CROSS, II "A" MAIN K.R. ROAD, BANASHANKARI II STAGE,
BENGALURU - 560 070. INDIA

TEL : +91-080-26760111
FAX : +91-080-26761479

THE H.P. STATE COOPERATIVE MILK PROPDUCERS' FEDERATION LTD.

MANDI UNIT AT CHAKKAR

HMF/MND/- Estt.-II/44/08- 1003 Dated 12.7.2017

TO WHOM IT MAY COCERN

This is to certify that Ms Tamana Soni, Roll No 141831, student of 7th semester BTech (Bio Technology), Jaypee University of Information Technology, Waknaghat, Distt Solan, HP 17324 has completed her summer training at H P Milk federation Plant at Chakkar, Distt Mandi w.e.f. 01.06.2017 to 12.07.2017 (six weeks). She was very hard working and took keen interest during the training period.

12/7/17

Manager (P&I),
Manager (P &I)
H.P. Milk Fed
Mandi Unit at Chakar

Tamana Soni

एनटीपीसी NTPC
A Maharatna Company

एन टी पी सी लिमिटेड
(भारत सरकार का उद्यम)
NTPC Limited
(A Govt. of India Enterprise)

एनटीपीसी एनर्जी टेक्नॉलाजी रिसर्च एलायंस
NTPC Energy Technology Research Alliance

01/HR/NETRA/TRG

Date: 14.07.2017

TO WHOMSOEVER IT MAY CONCERN

This is to certify that Ms. Sarita Bhawanani, a student of 3rd year B.Tech. (Biotech), from Jaypee University of Information Technology (JUIT), Waknaghat, Solan (HP) has completed her summer training from 05.06.2017 to 05.07.2017 on Area of "Bio Fuel" at NTPC Energy Technology Research Alliance (NETRA) under the guidance of Dr. H.N. Pandey, DGM (NETRA).

The hard work and sincerity with which she has carried out her training is commendable.

We wish Ms. Sarita Bhawanani, all success in her life.

(Rajan Kumar Verma)
Dy. Manager(HR)

Sarita
Self attested

प्लॉट नं. ई–3, ईकोटैक–II, उद्योग विहार, ग्रेटर नोएडा, जी बी नगर (उ.प्र.)–201306 टेली / Tel.: 0120-2356500 / 2356568 फैक्स / Fax : 0120-2356598
Plot No. E-3, Ecotech–II, Udyog Vihar, Greater Noida, G.B. Nagar (U.P.) 201306 वेबसाइट / Website : www.ntpc.co.in
पंजीकृत कार्यालय–एनटीपीसी भवन, स्कोप कम्पलैक्स, 7, इन्स्टीटयूशनल एरिया, लोधी रोड़, नई दिल्ली–110003 टेली / Tel. : +91-11-24360100, 24387000 फैक्स / Fax : +91-11-24361018
Regd. Office : NTPC Bhawan, SCOPE Complex, 7, Institutional Area, Lodhi Road, New Delhi-110003 वेबसाइट / Website : www.ntpc.co.in

INDIRA GANDHI HOSPITAL SHIMLA-171001.

No.HFW(MS)G-5/2017- 6883 Dated 27/7/17

CERTIFICATE

Certified that Ms.Moksh Tandon student of B.Tech Biotechnology from J.P. University of Information Technology Solan H.P. has completed internship training w.e.f. 02.06.2017 to 15.07.2017 in the Department of Microbiology , Indira Gandhi Medical College, Shimla.

During the above period her work and conduct was satisfactory.

Sr. Medical Superintendent,
I.G.Hospital, Shimla

Sr. Medical Superintendent
I.G. Hospital Shimla

TEVA | TAPI
Teva Active Pharmaceutical Ingredients

TEVA/MLR/HR/07/17

DATE: 15/07/ 2017

TO WHOM SO EVER IT MY CONCERN

This is certified that Ms. **Kanika Bajpai** is pursuing **B.Tech – Biotechnology** 6th Sem From **J P University of Infotech Waknaghat, Solan H.P.** has undergone successfully 45 days training in Our Organization from 01st Jun-2017 to 15th July- 2017.

During the training period we found her hard working and sincere.

We wish her all the success for her bright future.

For: - **TEVA API INDIA PVT LTD**

(Authorized Signatory)

K Bajpai

Teva API India Private Limited
CIN-U74899DL2002PTC138679
Manufacturing site: Plot No. Q1 to Q4, Ghirongi Industrial Area, Malanpur-477117, District Bhind (M.P.)
Tel : +91.7539.306199, 283151 Fax : +91.7539.283152 www.tapi.com
Head Office : 2-G, 2-H, 2-I, Ecotech-II, Udyog Vihar, Greater Noida-201306 (INDIA)
Regd. Office : M-34, Saket, New Delhi - 110017

Fermenta Biotech Limited
CIN : U99999MH1986PLC134021
Factory : Village Takoli, P.O. Nagwain, Dist. Mandi - 175 121, Himachal Pradesh, India.
Tel.: +91-1905-287249 / 048 / 246 • Fax: +91-1905-287250 • Email : info@fermentabiotech.com
Website : www.fermentabiotech.com

FBL/HR/2017 DATE : 13.07.2017

TO WHOMSOEVER IT MAY CONCERN

Name	::	Miss Wageesha Sharma
College /Institution Name	::	Jaypee University of Information Technology Waknaghat, Himachal Pradesh
Roll No.	::	141828
Stream	::	B.Tech. Biotechnology
Training Period	::	05.06.2017 to 13.07.2017
Letter Reference No. of College / Institution	::	Dr. R.S. Chauhan JUIT Dated 05.06.2017

She has successfully completed the Industrial Training for the period mentioned above in our Organisation.

Her overall performance during the training period with us is found good.

We wish her all success.

for FERMENTA BIOTECH LTD.

(H.S. Thakur)
Astt. Manager-HR/Admin.

Self Attested
Wageesha

Regd. Office : 'dil' Complex,
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Thane (W) - 400 610, Maharashtra, India.
Tel. : + 91-22-6798 0888
Fax : + 91-22-6798 0899
Email : info@fermentabiotech.com
Website : www.fermentabiotech.com

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Taluka - Vagra, Dist. Bharuch - 392 130,
Gujarat, India.
Tel. :+91-2641-291440-4
Email : info@fermentabiotech.com
Website : www.fermentabiotech.com

पशु जैव प्रौद्योगिकी केन्द्र
Animal Biotechnology Centre
भाकृअनुप–राष्ट्रीय डेरी अनुसंधान संस्थान
ICAR-National Dairy Research Institute
(मान्य विश्वविद्यालय / Deemed University)

करनाल–132 001, हरियाणा, भारत | Karnal-132 001, Haryana, India

www.ndri.res.in

भाकृअनुप
ICAR

CERTIFICATE

This is to certify that *Ms. KRITISHA THAKUR*, B. Tech (Biotechnology) student of Jaypee University of Information Technology, Waknaghat, Solan (HP) has undergone four weeks training at Animal Biotechnology Centre, ICAR- National Dairy Research Institute, Karnal. During the training, she was familiarized with the techniques of mammalian cell/ tissue culture, *in vitro* embryo production, somatic cell cloning, stem cell culture, DNA and RNA isolation, cDNA synthesis, PCR, electrophoresis, protein expression & its purification etc. She delivered a seminar on "Transhumanization" during the training. She took keen interest during the program and learned various aspects of animal biotechnology. Her performance during the training was ***very good***.

I wish her all the best in future endeavors.

Self attested
Kritisha Thakur

(Dr. M.K. Singh)
Scientist & Training Coordinator

Place: Karnal, Dated: July 11, 2017

(Dr. P. Palta)
In-charge

Minocha Industries

Minchy's
FOOD PRODUCTS

TO WHOM SO EVER IT MAY CONCERN

This is to certify that Mrs. Pallavi Ganatel has successfully completed her 6 week internship at Minocha Industries Shoghi in technical department with effect from Ist June 2017 to 12 July 2017 under the guidance and over all supervision of Mr. Ashwani Kumar.

During her tenure in our company she has shown high degree of enthusiasm & caliber and her behavior and conduct is good.

We wish her all the best in her future endeavors.

Your faithfully

For Minocha Industries

Ashwani Kumar

For Minocha Indu Partner

15/7/2017

Authorized Signature.

Self attested
Pallavi

Head Office : MINOCHA NIWAS, JAKHU, SHIMLA-171001
Adm./ Sales Office : 13, LOWER BAZAR, SHIMLA-171001
Factory : NH-22, SHOGHI, DISTT. SHIMLA-173219
E.mail : minchys@gmail.com

Tel.: +91-177-265
Tel.: +91-177-265
Tel.: +91-177-286
Fax: +91-177-265

Nestlé India Limited
VPO Nangal Kalan
Industrial Area Tahliwal
Dist. Una Himachal Pradesh- 174301

15.07.2017

Ms. Rimple Chaudhary
JAYPEE University
Waknaghat Solan.

INDUSTRIAL TRAINING

This is to inform that **Rimple Chaudhary** has successfully completed her industrial training from 1st June, 2017 to 15th July 2017.

We appreciate her for her learning in QA. She displayed good team spirit and conducted herself in a professional manner.

We wish her great success in her career.

For Nestlé India Limited
Tahliwal Factory

Human Resources Manager

भाभा परमाणु अनुसंधान केंद्र
BHABHA ATOMIC RESEARCH CENTRE

Certificate

This is to certify that Ms. Anaida Kad, an B.Tech 4th year student from Dept. of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan, H.P. had undergone research training under me on a project entitled "Effect of Lanthanides & Actinides on Heme Proteins " in Protein Crystallography Section, Radiation Biology and Health Sciences Division, B.A.R.C. during the period from 1st June, 2017 to 27th July, 2017.

Dr. Amit Das and Dr. Mukesh Kumar
Protein Crystallography Section
Radiation Biology and Health Sciences Division
B.A.R.C, Trombay, Mumbai - 400085

वैज्ञानिक अधिकारी/Scientific Officer
विकिरण जैविकी एवं स्वास्थ्य विज्ञान प्रभाग
Radiation Biology & Health Sciences Division
भारत सरकार/Government of India
भाभा परमाणु अनुसंधान केंद्र/Bhabha Atomic Research Centre
ट्रॉम्बे, मुंबई-४०००८५.भारत/Trombay, Mumbai-400085, India.

27th July, 2017

Anaida Kad

Cipla

July 14, 2017

TO WHOMSOEVER IT MAY CONCERN

This is to certify that Ms Shilpi Maheshwari has undergone training with us from June 01, 2017 to July 14, 2017. During the training she has been oriented at Vikhroli unit in Formulation R&D Department.

Gayatri Khedekar
Head Business HR – IPD

Shilpi Maheshwari

Cipla Ltd. R & D Centre, LBS Marg, Vikhroli West, Mumbai - 400 083.
Phone (022) 2576 1800, 2575 6000

Cipla Ltd. Regd. Office Cipla House, Peninsula Business Park, Ganpatrao Kadam Marg, Lower Parel, Mumbai - 400 013
Phone +91 22 24826000 Fax +91 22 24826120 E-mail contactus@cipla.com Website www.cipla.com
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VARANASI-221 005
Phone: (0542) 2307007, 2368160 Fax: 0542-2369162 Visit: iitbhu.ac.in/tpo E-mail: tpo@iitbhu.ac.in

No. 1326

TRAINING CERTIFICATE

(To be completed by the Supervisor under whom the student has taken the training)

Name of the Student ..... ANKITA CHAKRAVARTY

Father's Name ..... S.K. CHAKRAVARTY ..... Mother's Name ..... MRS. SULEKHA CHAKRAVARTY

Name of the Institute/College ..... JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

Course ..... B.tech ..... Branch ..... BIOTECHNOLOGY ..... Semester ..... 6 .....

Week / Month	Date		Actual working days put in	Remarks	Signature of the Project Supervisor
	From	To			
1st	06-06-2017	10-06-2017	5 days	Good work	
2nd	12-06-2017	17-06-2017	All days	Completed work sincerely.	
3rd	19-06-2017	24-06-2017	19-06-2017 - 21-06 23-06 - 24-06	Completed experiments on time with	
4th	26-06-2017	01-07-2017	5 days.	sincere efforts.	
5th	03-07-2017	08-07-2017	5 days	Good work	
6th	10-07-2017	13-07-2017	All days.	Excellent	
7th					
8th					

Evaluation ..... Very sincere efforts — Excellent .....

Conduct ..... Very Good .....

Other Remarks, if any ..... N.A .....

Subir Kundu
.....
Signature of the Supervisor
Name : PROF. (DR.) SUBIR KUNDU
Date : 12/07/2017.

.....
Training and Placement Officer

.....
Signature of Head of the Department
(Department Seal)

Coordinator
जैव रासायनिक अभियांत्रिकी स्कूल
School of Biochemical Engg
भारतीय प्रौद्योगिकी संस्थान
Indian Institute of Technology
(काशी हिन्दू विश्वविद्यालय)
(B.H.U.) Varanasi-221005

Molecular Cytogenetics & Tissue Culture Lab

Molecular Cytogenetics & Tissue Culture Lab
Department of Crop Improvement, CSK HP Agricultural University, Palampur-176062
INDIA
At the cutting edge of research

ISO 9001 SWISO

SWISS CERTIFICATION SCES 040

At the cutting edge of research

Department of Crop Improvement, CSK HPKV, Palampur

CERTIFICATE

Certified that **Ms Kritika Sharma** D/o Sh. P.C. Sharma, a bonafide B.Tech.(Biotechnology) student of Jaypee University of Information Technology, Solan (HP) has worked in the Molecular Cytogenetics & Tissue Culture Lab of this Department and utilized the facilities for biotechnology work w.e.f 01.06.2017 to 15.07.2017. During this period, she has acquired technical know how in respect of wide hybridization in bread wheat, application of protocols for embryo rescue approach and cytological investigations of wheat doubled haploids. She has also been familiarized with other various aspects of biotechnology, the on-going activities in the Lab and the varietal development programmes of the Department. She has more than 90 per cent attendance during her stay in this Lab.

She has been adjudged as a very sincere and hard working student. I wish all success in her career ahead.

15.07.17

Dr. H.K. Chaudhary
Programme Leader,
Mol. Cytogenet. & Tissue Culture Lab

15.07.17

Professor & Head
Department of Crop Improvement,
CSK HP Agricultural University,
Palampur-176062

Self-attested

Kritika

Hindustan Unilever Limited

Hindustan Unilever Limited
Plot No: 1, Sector 1A, IIE
Ranipur, Haridwar-249403
(Uttarakhand) INDIA

Tel: +91 (0) 1334 300200
Fax: +91 (0) 1334 300291
Web: www.hul.co.in
Cin:L15140MH1933PLC002030

14th July, 2017

This is to certify that Miss. Vedika Kayasth D/o Shri Bishwadea Srivastava has done 6 weeks Summer Training from 1st June-2017 to 10th July-2017. She has undergone the project of "Arsenic and Heavy Metal Testing by ICP-OES" in Quality Department.

During her tenure, she has performed well and has proved herself to be a good resource.

We wish her all the best for her future Endeavour.

For **HINDUSTAN UNILEVER LIMITED**

HR Executive

Head Office:-
Hindustan Unilever Limited
Unilever House,
B.D Sawant Marg,
Chakala, Andheri (E),
Mumbai 400 099

सत्यमेव जयते

Indian Pharmacopoeia Commission
Ghaziabad

IPC

Certificate of Training

This is to certify that

Dr./Mr./Ms./Mrs. Satyam Singh

has undergone training from 01st June, 2017 to 17th July, 2017 in Analytical Division of Indian Pharmacopoeia Commission (IPC), Ghaziabad.

Satyam Singh

(Dr. G. N. Singh)
Drugs Controller General (India) &
Secretary-cum-Scientific Director
IPC, Ghaziabad

Division of Genomic Resources

ICAR-National Bureau of Plant Genetic Resources

New Delhi-110 012

Dr. KV Bhat
Principal Scientist

E-mail: kvbhat2001@yahoo.com
kv.bhat@icar.gov.in

Dt. 15-07-2017

CERTIFICATE

This is to certify that Ms Anandita Govil, B. Tech student from Jaypee University of Information Technology, Waknaghat, Distt. Solan, HP has worked in ICAR-National Bureau of Plant Genetic Resources, New Delhi for her project work. She worked on "DNA Fingerprinting of mungbean varieties using simple sequence repeat markers". She has learnt the technique of DNA isolation, purification, PCR analyses of the mungbean varieties using SSR markers, statistical analysis and interpretation of results. Ms Govil was a dedicated worker and has learnt the technique earnestly. I wish her well in her future endeavors.

K V Bhat
15/7/17

(K.V. Bhat)

Dr. K.V. BHAT
Principal Scientist & Officer-In-charge
Division of Genomic Resources
National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

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Tel : +91-80-28611499 Fax : +91-80-28612912
Website : **www.indamseeds.com**
CIN : U02001KA1997PTC023141

DSIR RECOGNITION NO: TU/IV-RD/1313/2016

CERTIFICATE

This is to certify that ***Mr. Rishabh Nautiyal,*** *student of B.Tech (Biotechnology), Jaypee University of Information Technology, Solan, H.P has completed training in* ***"Recombinant DNA Technology, SDS PAGE and Immunology Techniques"*** *from 8th June 2017 to 18th July 2017 in our Research and Development, Biotechnology Laboratory.*

We wish all the best for his future Endeavour's.

Rishabh Nautiyal

Dr. Devaraja Achar
Head-Biotechnology

Garden Center : 17th CROSS, II "A" MAIN K.R. ROAD, BANASHANKARI II STAGE,
BENGALURU - 560 070. INDIA

TEL : +91-080-26760111
FAX : +91-080-26761479

Dabur
India Ltd.

SBD/HR/Genl/17
July 25th, 2017

To whom so ever it may concern

This is to certify that **Ms. Archita Johari** student of **B.Tech (Biotechnology)** from **Jaypee University Of Information Technology, Solan (H.P)** has undertaken Summer Internship Program in our organization from **June 12th, 2017 to July 25th, 2017**

During training, we found her sincere and hardworking.

We wish her all the best for her future endeavors

For **Dabur India Limited**

Pankaj Yadav
Sr. Manager – HR & Admin.

Archita Johari
10/8/17

Pharma Instinct

A++ing Value to Innovations & Systems

Certificate

This certificate is awarded to Mr./Ms. Vrish Bhanu Handa

Son/Daughter of Mrs. Mamta Handa and Mr. Sticker Handa

For having successfully completed Four Weeks/Six Weeks Industrial Training in Clinical Research & Experimental Biotechnology Conducted in June 2017 at Pharma Instinct, Chandigarh.

SCO 52-53, Sector 17-D, Pharma Instinct, Chandigarh

Vrish Bhanu Handa

Dr. Rajesh Sehgal
CEO

Place: Chandigarh
Date : July 2017

INDIRA GANDHI HOSPITAL SHIMLA-171001.

No.HFW(MS)G-5/2017- 6882 *Dated* 27/7/17

CERTIFICATE

Certified that Ms. Shivangi Kapoor student of B.Tech Biotechnology from J.P. University of Information Technology Solan H.P. has completed internship training w.e.f. 02.06.2017 to 15.07.2017 in the Department of Microbiology , Indira Gandhi Medical College, Shimla.

During the above period her work and conduct was satisfactory.

Sr. Medical Superintendent,
I.G. Hospital, Shimla

Sr. Medical Superintendent
I.G. Hospital, Shimla

INDRAPRASTHA POWER GENERATION COMPANY LTD.
&
PRAGATI POWER CORPORATION LIMITED
(GOVT. OF NCT OF DELHI UNDERTAKING)

Certificate of Training

This is to certify that Mr./Ms. KUMUD RAZDAN

Roll No. 143802 *of* JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY. *has successfully completed his/her Industrial Training in our organization from* 05-06-2017 *To* 15-07-2017

During this training his/her performance and conduct was excellent.

VWT No.: VST No.: 313
Date : 18/07/2017

आलोक कुमार
उप प्रबन्धक (प्रा. सं.)
आई.पी.जी.सी.एल. / पी.पी.सी.एल.
राजघाट पावर हाउस कम्पाउन्ड
नई दिल्ली–110002

Deputy Manager (Training)

Self-attested
Kumud Razdan

NesTiverse™ Solutions Private Limited

Universe Unites Here

CERTIFICATE OF INTERNSHIP

THIS CERTIFICATE IS PRESENTED TO

SOMYA JAISWAL

For undergoing internship in capacity of Associate Consultant in our company at NesTiverse Solutions Pvt. Ltd. - CIN: U74999DL2016PTC299676 and developing Recruitment Process Automation on Force.com Platform since Quarter 2nd 2017. Her Performance through out the internship period was good.

TECHNICAL CONSULTANT

NESTIVERSE® SOLUTIONS PVT. LTD. Est. 2016 Universe Unites Here NEW DELHI, IN CIN: U74999DL2016PTC299676 CERTIFIED

MANAGING DIRECTOR

Somya
24/8/17

Green valley

ལོག་ནམ་དང་ནགས་ཚལ་ལྷན་ཁག

Ministry of Agriculture and Forests

Royal Government of Bhutan

July 29, 2017

TO WHOM IT MAY CONCERN

This is to certify that Mr. Tandin Gyeltshen of Jaypee University of Information Technology, Solan, Himalchal Pradesh has done his internship with our company starting from 1st June,2017 and successfully completed it on the 1st July,2017 under the Green Valley Company, Haa. He visited our labs where the plant culturing and other forms of plantations were performed.

During his internship, he demonstrated punctuality and great diligence towards his work. We hope he could learn some productive things during his short internship with our company and we wish him luck for his future endeavors.

Karma Tshering

(General Manager)

Green Valley
Jyenkana Haa Bhutan

Green Valley cooperation Limited.
Haa, Bhutan. +975-17301236 Ph. +975-2-337109, email;t.thinley1917@greenvalley.com

पशु जैव प्रौद्योगिकी केन्द्र
Animal Biotechnology Centre
भाकृअनुप–राष्ट्रीय डेरी अनुसंधान संस्थान
ICAR-National Dairy Research Institute

(मान्य विश्वविद्यालय / Deemed University)

करनाल–132 001, हरियाणा, भारत | Karnal-132 001, Haryana, India

www.ndri.res.in

CERTIFICATE

This is to certify that *Ms. NAYANIKA CHAKRAVARTY,* B.Tech (Biotechnology) student of Jaypee University of Information Technology, Waknaghat, Solan (HP) has undergone four weeks training at Animal Biotechnology Centre, ICAR- National Dairy Research Institute, Karnal. During the training, she was familiarized with the techniques of mammalian cell/ tissue culture, *in vitro* embryo production, somatic cell cloning, stem cell culture, DNA and RNA isolation, cDNA synthesis, PCR, electrophoresis, protein expression & its purification etc. She delivered a seminar on "Science behind Phobias" during the training. She took keen interest during the program and learned various aspects of animal biotechnology. Her performance during the training was ***very good***.

I wish her all the best in future endeavors.

(Dr. M.K. Singh)
Scientist & Training Coordinator

self attested :
Nayanika Chakravarty

Place: Karnal, Dated: July 11, 2017

(Dr. P. Palta)
In-charge

Molecular Cytogenetics & Tissue Culture Lab

At the cutting edge of research

Department of Crop Improvement, CSK HPKV, Palampur

CERTIFICATE

Certified that **Ms Akshita Gupta** D/o Sh. Ajay Gupta, a bonafide B. Tech. (Biotechnology) student of Jaypee University of Information Technology, Solan (HP) has worked in the Molecular Cytogenetics & Tissue Culture Lab of this Department and utilized the facilities for biotechnology work w.e.f. 03.06.2017 to 17.07.2017. During this period, she has acquired technical know how in respect of wide hybridization in bread wheat, application of protocols for embryo rescue approach and cytological investigations of wheat doubled haploids. She has also been familiarized with other various aspects of biotechnology, the on-going activities in the Lab and the varietal development programmes of the Department. She has more than 90 per cent attendance during her stay in this Lab.

She has been adjudged as a very sincere and hard working student. I wish all success in her career ahead.

17.07.17

Dr. H.K. Chaudhary
Programme Leader,
Mol. Cytogenet. & Tissue Culture Lab

17.07.17

Professor & Head
Department of Crop Improvement,
CSK HP Agricultural University,
Palampur-176062

Molecular Cytogenetics & Tissue Culture Lab

At the cutting edge of research

Department of Crop Improvement, CSK HPKV, Palampur

CERTIFICATE

Certified that **Ms Pallavi Soni** D/o Sh. Vijay Soni, a bonafide B. Tech. (Biotechnology) student of Jaypee University of Information Technology, Solan (HP) has worked in the Molecular Cytogenetics & Tissue Culture Lab of this Department and utilized the facilities for biotechnology work w.e.f. 03.06.2017 to 17.07.2017. During this period, she has acquired technical know how in respect of wide hybridization in bread wheat, application of protocols for embryo rescue approach and cytological investigations of wheat doubled haploids. She has also been familiarized with other various aspects of biotechnology, the on-going activities in the Lab and the varietal development programmes of the Department. She has more than 90 per cent attendance during her stay in this Lab.

She has been adjudged as a very sincere and hard working student. I wish all success in her career ahead.

17.07.17

Dr. H.K. Chaudhary
Programme Leader,
Mol. Cytogenet. & Tissue Culture Lab

17.07.17

Professor & Head
Department of Crop Improvement,
CSK HP Agricultural University,
Palampur-176062

सत्यमेव जयते

Indian Pharmacopoeia Commission
Ghaziabad

IPC

Certificate of Training

This is to certify that

Dr./Mr./Ms./Mrs. **Rhythem Sharma**

has undergone training from 01st June, 2017 to 17th July, 2017 in Analytical Division of Indian Pharmacopoeia Commission (IPC), Ghaziabad.

Self attested

Rhythem Sharma

(Dr. G. N. Singh)
Drugs Controller General (India) &
Secretary-cum-Scientific Director
IPC, Ghaziabad

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Tel : +91-80-28611499 Fax : +91-80-28612912
Website : **www.indamseeds.com**
CIN : U02001KA1997PTC023141

DSIR RECOGNITION NO: TU/IV-RD/1313/2016

CERTIFICATE

This is to certify that ***Mr. Rahul Chauhan,*** *student of B.Tech (Biotechnology), Jaypee University of Information Technology, Solan, H.P has completed training in* ***"Recombinant DNA Technology, SDS PAGE and Immunology Techniques"*** *from 8th June 2017 to 18th July 2017 in our Research and Development, Biotechnology Laboratory.*

We wish all the best for his future Endeavour's.

Dr. Devaraja Achar
Head-Biotechnology

Rahul

Garden Center : 17th CROSS, II "A" MAIN K.R. ROAD, BANASHANKARI II STAGE,
BENGALURU - 560 070. INDIA

TEL : +91-080-26760111
FAX : +91-080-26761479

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Enroll. No. – 06/17/84

Certificate of Training

June 01, 2017 – June 30, 2017

Ms. Aakriti Bisht

This is to certify that ***Ms. Aakriti Bisht****, student of Jaypee University of Information Technology has successfully completed One Month of rigorous Hands-On Industrial Training organized by* ***Helix BioGenesis, NOIDA****. This curriculum included training on Various* ***Microbiological, Molecular biology and Biochemistry*** *Techniques- Working in Biotechnology Laboratory, Good Laboratory Practices, Basics of Calculations; Buffers and Reagent Preparation, Media preparation and sterilization, Serial Dilution Method, Culturing & Sub-Culturing Methods of Microbes, Isolation and Culturing of microbes from Soil, Water & Air, Biochemical Test for Screening of Microbes, Growth Kinetics of Microbes, Antibiotics Sensitivity Test, Culturing Techniques for E.coli./Agro bacterium or any other Microbes, Plasmid isolation, DNA isolation from microbes, DNA isolation from plant sample, Agarose Gel Electrophoresis, RNA Isolation, RNA Gel Electrophoresis, Restriction Digestion, Qualitative & Quantitative analysis of Nucleic Acid, Blotting Techniques (Transfer of DNA & RNA from Gel to membrane), Polymerase Chain Reaction (PCR), Competent Cell Preparation, cDNA Isolation and cloning, cDNA Ligation, Transformation, Blue-White selection and Colony PCR, Protein Isolation, Estimation of Protein by Bradford Method, Estimation of Protein by Biurette Method, Estimation of Protein by Lowry's Method, SDS-PAGE, Native- PAGE, Enzyme Assay – Amylase Assay and DOT ELISA.*

Ms. Aakriti Bisht *is a sincere and diligent student. We wish her every success in her career.*

Anshita.

Anshita Nagar
Director- Operations
Helix BioGenesis
NOIDA

Helix Biogenesis Pvt. Ltd. D-34, Sector-2 Noida

SELF ATTESTED

Aakriti

भा.कृ.अ.प - केंद्रीय आलू अनुसंधान संस्थान
शिमला-171001, हि.प्र. (भारत)
ICAR-Central Potato Research Institute
(Indian Council of Agricultural Research)
SHIMLA 171 001, HP

Phone: 0177-2625073(O), Fax:0177-2624460
E-mail- directorcpri@gmail.com
Website: http://cpri.ernet.in

ISO 9001:2008

No.F.PME/4-50/2017
Dated: 09.08.2017

TRAINING CERTIFICATE

This is to certify that **Ms. Pratha Sood** student of B. Tech./M. Tech. Dual Degree (Integrated), Jaypee University of Information Technology, Department of Biotechnology, Wakanaghat, Solan has undergone training in the Division of CPB & PHT, from 11th June, 2017 to 08th July, 2017 at ICAR - Central Potato Research Institute, Shimla.

Dated: 09.08.2017

(Brajesh Singh)
In-Charge, PME Cell

प्रभारी, पी.एम.ई. कक्ष
In - Charge P.M.E. Cell
केन्द्रीय आलू अनुसंधान संस्थान
Central Potato Research Institute
शिमला / **Shimla - 171001 (H.P.)**

Self Attested
Pratha

MAHAVIR
CANCER SANSTHAN
Run by Mahavir Mandir Trust
Phulwari Sharif,
Patna - 801 505 (INDIA)
Phones : (0612) 2250127, 2253956
Fax : (0612) 2253957
email : mcspatna98@gmail.com
website : www.mahavircancersansthan.com

CERTIFICATE

This is to certify that ***Mr. Rahul Pramjeet*** *student of* ***B.Tech. Biotechnology, 3rd Year*** *of* ***Department of Biotechnology & Bioinformatics, Jaypee University of Information Technology, Solan, Himachal Pradesh*** *has done project Training on* **"Assessment of Arsenic concentration in Biological Samples of Breast Cancer Patients of MCS through GF-Atomic Absorption Spectrophotometer",** *under supervision of* **Dr. Arun Kumar** *at Mahavir Cancer Sansthan and Research Centre from* ***1st June to 12th July 2017****. He has meticulously completed his research work with 98% attendance.*

He has been found sincere and dedicated with good character during the training period.

The institute wishes him success in his future endeavors.

12/07/17

Dr. Arun Kumar
Scientist - I
Mahavir Cancer Sansthan
Patna

12/07/17

Prof. Ashok Ghosh
HoD, Research
Mahavir Cancer Sansthan
Patna

Dr. Biswajit Sanyal
Director
Mahavir Cancer Sansthan
Patna

Self Attested
Rahul Pramjeet
12/8/17

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Phulo Phalo. Pure Khao Piyo.

No. RMU/Admn./ 5451 Dated: 14/7/17

TO WHOM IT MAY CONCERN

It is to certify that Miss Aditi Sharma D/o Sh. Ashwani Kumar Sharma, Roll No. 141809, student of B.Tech. (Bio-technology), 6th Semester, JAYPEE University of Inforamtion Technology, Waknaghat, District Solan (H.P.), has undergone In-plant Training in Quality Control /Production Section at Verka Mohali Dairy during the period from 09.06.2017 to 08.07.2017.

Her performance has been adjudged as **'Very Good'** during the training period.

DY. MANAGER (P & A)
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Fax : 0172-2224669 Email : gm.moh@verka.coop Website : verka.coop
TIN : 03621108325 S.T./C.S.T. No. 60196216 Dt. 01.01.88

UNIVERSITY OF HYDERABAD

SCHOOL OF LIFE SCIENCES
DEPARTMENT OF ANIMAL BIOLOGY

Dr. P. Reddanna
Professor

Gachibowli, P.O. Central University
Hyderabad - 500 046, India
Tel : (O) : +91-40 2313 4542
Fax : +91-40-23010120
e-mail : prsl@uohyd.ernet.in
preddanna@gmail.com

7th July, 2017

CERTIFICATE

This is to certify that **Mr Shubham Mittal** has done internship under my supervision during 31st May-7th July, 2017 at Department of Animal Biology, School of Life Sciences, University of Hyderabad, Hyderabad. During his internship, he worked on "*Natural Product Inhibitors of Secretory PLA_2s from Sapindustrifoliatus and Abrusprecatorious seed endosperm extracts as Anti-Inflammatory and Anticancer Agents*"

Shubham Mittal

7/7/17

Prof. P. Reddanna

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CERTIFICATE

Awarded to

Mr. Nitin Arora

B.Tech. Biotechnology, 6th Semester

of

Jaypee University of Information Technology, Solan, H.P.

For Successful Training in our

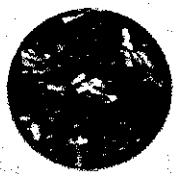
Instrumentation Department

From:- 07-06-2017 to 11-07-2017

Dr. Shivlal Singh
Director Technical

C-37/2 (Back Side) Lawrence Road Industrial Area, Delhi-110035
Ph.: 011-45022985, 9311654060, E-mail : support@agsslabs.com

Molecular Cytogenetics & Tissue Culture Lab



At the cutting edge of research

Department of Crop Improvement, CSK HPKV, Palampur

CERTIFICATE

Certified that **Ms Samriti** D/o Sh. Raj Kumar, a bonafide B. Tech. (Biotechnology) student of Jaypee University of Information Technology, Solan (HP) has worked in the Molecular Cytogenetics & Tissue Culture Lab of this Department and utilized the facilities for biotechnology work w.e.f 01.06.2017 to 15.07.2017. During this period, she has acquired technical know how in respect of wide hybridization in bread wheat, application of protocols for embryo rescue approach and cytological investigations of wheat doubled haploids. She has also been familiarized with other various aspects of biotechnology, the on-going activities in the Lab and the varietal development programmes of the Department. She has more than 90 per cent attendance during her stay in this Lab.

She has been adjudged as a very sincere and hard working student. I wish all success in her career ahead.

Chaudhary 15.07.17

Dr. H.K. Chaudhary
Programme Leader,
Mol. Cytogenet. & Tissue Culture Lab

Professor & Head
Department of Crop Improvement,
CSK HP Agricultural University,
Palampur-176062

Samriti

Molecular Cytogenetics & Tissue Culture Lab

At the cutting edge of research

Department of Crop Improvement, CSK HPKV, Palampur

CERTIFICATE

Certified that **Ms Akshita Gupta** D/o Sh. Ajay Gupta, a bonafide B. Tech. (Biotechnology) student of Jaypee University of Information Technology, Solan (HP) has worked in the Molecular Cytogenetics & Tissue Culture Lab of this Department and utilized the facilities for biotechnology work w.e.f. 03.06.2017 to 17.07.2017. During this period, she has acquired technical know how in respect of wide hybridization in bread wheat, application of protocols for embryo rescue approach and cytological investigations of wheat doubled haploids. She has also been familiarized with other various aspects of biotechnology, the on-going activities in the Lab and the varietal development programmes of the Department. She has more than 90 per cent attendance during her stay in this Lab.

She has been adjudged as a very sincere and hard working student. I wish all success in her career ahead.

17.07.17

Dr. H.K. Chaudhary
Programme Leader,
Mol. Cytogenet. & Tissue Culture Lab

Akshita

17.07.17

Professor & Head
Department of Crop Improvement,
CSK HP Agricultural University,
Palampur-176062

Department of Chemistry
रसायन विभाग
Motilal Nehru National Institute of Technology Allahabad
Allahabad-211 004, India
मोतीलाल नेहरु राष्ट्रीय प्रौद्योगिकी संस्थान इलाहाबाद
इलाहाबाद -211004, भारत
Phone: EPABX: 91-532-2445103 to 2445107 (5 Lines) Direct in Dialling: 91-532-227+Ext.No.1280
Fax: 0532-2445101, 2445077 Website:http://www.mnnit.ac.in

To Whom It May Concern

This is to certify that **Ms.Sakshi Srivastava**, Jaypee University of Information Technology, Solan, H.P. has done her **4 Week Summer Training Program in Chemical/Biochemical/Polymer Sciences and Nanotechnology 30 May -30 June, 2017** under our supervision in the Department of Chemistry at MNNIT Allahabad.

The training was given into 4 phases:

1st phase: Lecture/Tutorial/Test
2nd phase: Laboratory Practices
3rd phase: Research on Synthesis/Characterization/Evaluation
Industrial visit: M/s Dey's Medical (U.P.) Private Limited
Plot No. A-8, Industrial Area, Naini, Allahabad, U.P. 211010
4th phase: Research Project & Viva

As part of the training she has learnt various research techniques as available in our laboratory and worked on "**Colorimetry sensing of cyanide naphthalene derivative and their live cell imaging**". Her performance in the training was good. She has shown her interest and skills to learn new techniques of research.

We wish her all success for future career.

T Ghosh.
(Tamal Ghosh)
Asst.Professor
Coordinator, STPCY-2017

(P.K.Dutta)
Professor
Coordinator, STPCY-2017

Dated: 30th June, 2017

Self Attested
Sakshi

GeNei™

TRAINING CERTIFICATE

This is to certify that Mr. Sushain Kaul student of 3rd Year B.Tech. Biotechnology in Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh 173234. Has undergone hands on training from 1st June 2017 – 14th July 2017 at our facility.

Mr.Sushain has been trained on various bio techniques used in manufacturing and services related to Genomic and Proteomic products. Such as:

- RAPD application based project in detection of the DNA polymorphism.
- Labeling Antibody with Colloidal Gold
- Standardization of cultures condition in recombinant RNase inhibitor protein.
- Cesium chloride density gradient method of plasmid purification.
- Detection of polymorphic and monomorphic DNA bands Jatropha leaves samples.

During this training period Mr.Sushain has been very sincere and zealous towards his work. His conduct has been excellent.

We wish him all the best in his future endeavors.

Thanking you
Best regards
For GENEI LABORATORIES PVT.LTD

GENEI LABORATORIES PRIVATE LIMITED
BANGALORE
560 058

Authorized Signatory
Jyothi Suprajarama
Operations & HR

Sushain Kaul

Genei Laboratories Pvt Ltd.
No.6, 6th Main, College Road
Near S R S Road, Peenya
Bengaluru - 560 058, INDIA
Phone: +91 80 28396894
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Fax: +91 80 23721166
email: info@geneilabs.com
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DSIR RECOGNITION NO: TU/IV-RD/1313/2016

CERTIFICATE

This is to certify that ***Mr. Nilaksh Mahajan,*** *student of B.Tech (Biotechnology), Jaypee University of Information Technology, Solan, H.P has completed training in* ***"Recombinant DNA Technology, SDS PAGE and Immunology Techniques"*** *from 8th June 2017 to 18th July 2017 in our Research and Development, Biotechnology Laboratory.*

We wish all the best for his future Endeavour's.

Dr. Devaraja Achar
Head-Biotechnology

Garden Center : 17th CROSS, II "A" MAIN K.R. ROAD, BANASHANKARI II STAGE,
BENGALURU - 560 070. INDIA

TEL : +91-080-26760111
FAX : +91-080-26761479

HERO CYCLES

To,
Kshitiz Gupta
137 GF
Sector 3A Rachna Vaishali
Ghaziabad, Uttar Pradesh 201010

TO WHOM IT MAY CONCERN

This is to certify that Mr Kshitiz Gupta S/o Mr Rajeev Gupta and a student of Jaypee University, Solan has successfully completed his internship with Hero Cycles from 5th June 2017 to 15th July 2017 as "Intern- Corporate Communications"

I am pleased to state that he worked hard in the tasks assigned to him and has been able to present a good picture of his discipline, skills and curiousness.
I wish him all the best for his future endeavours.

HERO CYCLES LTD. DELHI

Ashish Sood
Head of NPD and Marketing - Premium Bike Segment, Hero Cycles

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University Requirement							Requirement for Accredation / Ranking Agencies				
S.No.	Enrollment No.	Branch	Period of Training (No. Of Weeks)	Training Start Date	Training End Date	Status (Satisfactory / Unsatisfactory)	Institute/Company Name	Subject/Topic of Training	Domain/Area of Training	Stipend Received (If Any)	Aadhaar Number of Student
1	141263	CE	7	29-05-2017	15-07-2017	Satisfactory	HPRDCL	Construction of roads (e PMS, RADMS, ROMDAS)	Construction, System Analysis	NO	987868746848
2	141601	CE	6	29-05-2017	08-07-2017		P K Construction Shimla	Construction of Advocate Chamber near High Court and Construction of Parking Complex at Chotta Shimla	Construction	NO	884578188153
3	141603	CE	6								
4	141604	CE	5	29-06-2017	30-06-2017	Satisfactory	HCC	Construction of NH- 34, 4 Lane (Farrakka, Raiganj Section)	Construction	NO	541252189749
5	141605	CE	6	01-06-2017	15-07-2017	Satisfactory	Indian Railways	Construction of Limited Height Subway under Railway Department	Construction	NO	253736151986
6	141606	CE	6	05-06-2017	15-07-2017	Unsatisfactory	JPHRF	Bridge Construction Pung Khadd Sujanpur Tihra (Baijnath Project)	Construction,Project Planning	NO	961362475484
7	141606	CE	6	05-06-2017	15-07-2017	Satisfactory	Syal and associates	Structural Design	Design	NO	253657634246
8	141607	CE	6	05-06-2017	10-07-2017	Satisfactory	IOCL	Construction of Oil Water Seperetor	Construction	NO	
9	141608	CE	6	05-06-2017	10-07-2017	Satisfactory	SJVNL	LUHRI Hydropower Electric Project	Construction Planning and Design	NO	470244564729
10	141609	CE	4	05-06-2017	05-07-2017		L&T	Commercial Building Construction (DLF Building in Gurugram)	Construction	NO	364358230523
11	141610	CE	6	10-06-2017	17-07-2017	Satisfactory	IIT BHU	Design and Analysisof Pitched Roof Truss Using STAAD Pro	Design and Analysis	NO	493996271823
12	141611	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	275103106040
13	141612	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Cresidential Building, Galaxy Heights	Construction	NO	911325199048
14	141613	CE	7	01-06-2017	16-07-2017	Satisfactory	PWD	Road Construction and maintenance at Mathura, UP	Construction	NO	748717944274

15	141615	CE	7	05-06-2017	17-07-2017	Satisfactory	HPPWD	Construction of Post Graduate College	Construction	NO	533592259552
16	141616	CE	6	01-06-2017	12-07-2017	Satisfactory	SJVNL	Rampur Hydro Power Station	Construction, Planning and Design	NO	642152102942
17	141617	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Sawra Kuddu Hydropower Electric Project	Construction	NO	280189613732
18	141619	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	813332527314
19	141620	CE									Pending
20	141621	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Comprehensive Development of Corridor on Outer Ring between Mukbara Chowk to Wazirabad	Construction	NO	612109067356
21	141622	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Construction of 33/220 kV Pooling Sub-Station	Construction	NO	Pending
22	141624	CE	6	02-06-2017	15-07-2017	Satisfactory	Ved Prakash Gupta	Construction of boundary wall	Construction	No	509062120363
23	141626	CE	6	05-06-2017	14-Jul	Satisfactory	DMRC	Contruction of Underground Metro	Construction and Surveying	No	725029168548
24	141627	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	867788791400
25	141630	CE	7	05-06-2017	17-07-2017	Satisfactory	M G Construction	Four Laning of Kharar-Kurali Section of NH-21 in the State of Punjab on EPC Mode	Construction	NO	958830245993
26	141633	CE	6	04-06-2017	15-07-2017	Satisfactory	HPPWD	Construction of Underground Waste Collection System at Dharamsala	Construction	NO	233964159757
27	141634	CE	6	01-06-2017	14-07-2017	Satisfactory	DrukGreen	Hydro Power Electric Project	Construction	NO	
28	141636	CE	6	05-06-2017	18-07-2017	Satisfactory	CPWD	Electrofitting	Estimation and Operation	NO	842943328993
29	141637	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Hydro Power Electric Project	Construction, Analysis and Design	NO	440663665519
30	141638	CE	6	05-06-2017	15-07-2017		NTPC	Q & A	Quality management	NO	493285031722
31	141639	CE	6	01-06-2017	15-07-2017	Satisfactory	Paharpur Cooling towers	Paharpur Cooling Tower Pvt. Ltd.	Construction and Estimation	NO	457229473693
32	141640	CE	6	08-05-2017	17-06-2017	Satisfactory	PWD	Construction tubewell	Construction and Site Investigation	NO	280438057959

33	141641	CE	5	12-06-2017	10-07-2017	Satisfactory	Renuka	Road Construction and Survey	Construction	NO	488631889287
34	141642	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Sewage Treatment Plant Operation	Site Visit and Design	NO	597153870545
35	141643	CE	6	04-06-2017	07-07-2017	Satisfactory	DMRC	Construction of Underground Metro at R K Puram and Hauz Khas Station	Construction	NO	596538281137
36	141644	CE	6	01-06-2017	12-07-2017	Satisfactory	HPPWD	Construction of multi purpose hall	Construction	NO	958282824701
37	141645	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Swara Kuddu Hydropower Project	Construction	NO	736402354843
38	141646	CE	6	01-06-2017	15-07-2017	Satisfactory	GAWAR	Road Construction of 4- Lane Panchkula and Yamuna Nagar (NH- 73)	Construction		
39	141647	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Stability analysis of Luhri HEP Stage-1	Design	NO	339213751913
40	141648	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Multiporpous Sports Stadium Ramamandir Mandi, Veterinary Hospital and College Rampur	Construction, Maintenance and Design	NO	619538309958
41	141650	CE	7	01-06-2017	15-07-2017	Satisfactory	Jaiprakash And Sons	Construction of Mega Hostel Block in NIT Hamirpur	Construction	NO	352700960035
42	141651	CE	6	01-06-2017	11-07-2017	Satisfactory	Sunrises Structures	Construction of Sun Twilight Villas and Commercials	Construction	NO	830120993663
43	141652	CE	6	01-06-2017	12-07-2017	Satisfactory	SIDCL	Road Construction	Analysis	NO	986065011649
44	141653	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Intze Tank Design	Design	NO	957707592017
45	141654	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rain Water Harvesting Tank Transportation of Exsisting Lawn into Rain Garden	Construction	NO	873345654123
46	141655	CE	7	29-05-2017	17-07-2017	Satisfactory	UPRNNL	Building Construction	Construction	NO	584157677760
47	141656	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
48	141661	CE	7	15-06-2017	31-07-2017	Satisfactory	PWD	Residential Building Construction	Construction	NO	867213841974
49	141662	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Retaining wall construction	Construction	NO	387802984564
50	141663	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
51	141664	CE	6	29-05-2017	08-07-2017	Satisfactory	PK Construction	Car Parking Building Construction	Construction	NO	767631756894

52	141665	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rainwater Harvesting Tank	maintenance	NO	435539216442
53	141666	CE	6	05-06-2017	17-07-2017	Satisfactory	CPWD	Building Maintenance	maintenance	NO	989868620530
54	141667	CE	6	31-05-2017	11-07-2017	Satisfactory	SPCL	Construction of Bus Terminus and Parking	Construction	NO	282070765310
55	141668	CE	6	03-06-2017	14-07-2017		RED	Construction of hall	Construction	NO	892245015469
56	141669	CE	5	13-06-2017	15-07-2017	Satisfactory	PWD Dharamsala	Construction of roads	Construction	NO	774345360402
57	141670	CE	5	29-05-2017	30-06-2017	Unsatisfactory	HCC	4 Laning Farakka Raiganj Section	Construction	NO	454223208162
58	141671	CE	6	28-05-2017	14-07-2017	Satisfactory	Bansal Engineers	Building Construction	Contruction	Yes	597323298747
59	141672	CE	4	30-05-2017	30-06-2017	Satisfactory	ADRDE	Design of building	Design	NO	505348241275
60	141673	CE	6	01-06-2017	12-07-2017	Satisfactory	UPPWD	Road Contruction	Construction	NO	
61	141674	CE	6	01-06-2017	12-07-2017	Satisfactory	REASI	Water Distribution System Study	Analysis	NO	671722842063
62	141675	CE	7	01-06-2017	14-07-2017	Satisfactory	Bareilly Development Authority	Laying of Sewer Pipelines	Construction	NO	334980591932
63	141676	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Galaxy Heights Project	Construction	NO	312625902455
64	141677	CE	6	01-06-2017	11-07-2017	Satisfactory	Swastik	Underground Substation Gurugram	Construction	NO	831847743627
65	141678	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Casting of Bridge	Testing	NO	569738883949
66	141679	CE	5	30-05-2017	12-07-2017	Satisfactory	H. C. Bansal Engineers and Contractors	Building Construction	Construction	Yes	692342550589
67	141680	CE	6	01-06-2017	05-07-2017	Satisfactory	ERA	Road Construction	Construction	NO	567280282077
68	141681	CE	6	11-06-2017	16-07-2017	Satisfactory	HPPCL	Barrage division of sainj Hydro Power Electric Project	Construction	NO	346612434207
69	141682	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Construction of PG	Construction	NO	639806463361
70	141683	CE	4	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Ambuja Cement Plant Visit	Materials	NO	334214454998

71	141684	CE	6	29-05-2017	08-07-2017	Satisfactory	HPPWD	Development of New OPD at IGMC Shimla	Construction	NO	995522249985
72	141686	CE	6	01-06-2017	01-07-2017	Satisfactory		Building Construction (Mohali)	Construction	NO	411889377530
73	141687	CE	6	12-06-2017	22-07-2017	Satisfactory	HPPWD	HP State Library Building Contruction	Construction	NO	885024325960
74	141688	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Testing of materials	Testing	NO	868824583795
75	141689	CE	6	03-06-2017	17-07-2017	Unsatisfactory	Indian Railways	Construction of Railway Track	Construction	NO	409852377341
76	141690	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	691456577638
77	141691	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Highway Maintenance and PG College	Constructon	NO	
78	141692	CE	6	01-06-2017	12-07-2017	Satisfactory	DMRC	Underground Substation	Construction/ Surveying/ Geotechnical Investigation	NO	862339185428
79	141693	CE	4	05-06-2017	08-07-2017	Satisfactory	BP	Construction of new filling shed	Construction	NO	530137391222
80	141694	CE	6	30-05-2017	10-07-2017	Satisfactory	PWD	Construction of roads	Construction	NO	424523018138
81	141695	CE	6	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Concrete Mix Design	Design	NO	579641278502
82	141696	CE	4	31-05-2017	30-06-2017	Satisfactory	CPWD	Construction	Construction	NO	876016738612
83	141697	CE	4	01-06-2017	30-06-2017	Satisfactory	LMRC	Lucknow Metro Construction	Construction	NO	928844325232
84	141698	CE	7	01-06-2017	07-07-2017	Satisfactory	SJVNL	Retaining wall construction	Construction	NO	341163355226

Industrial Training 2019 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	151001	SAHIL SINGLA	Numitech Solutions
2	151002	ADITYA THAKUR	PRASAR BHARATI
3	151004	MANISHA SHARMA	BSNL MSC Shimla
4	151005	ANISH VIJAN	NIELIT , Chandigarh
5	151007	ANUJ PURWAR	Semi Conductor Laboratory
6	151008	PARAS MITTAL	Newvision softcom and consultancy Pvt. Ltd.
7	151009	SAHAJ CHOPRA	BHARAT ELECTRONICS LIMITED
8	151010	KARTIK BANTA	Ericsson Global Services India Limited
9	151011	RITUL SINGH	Bharat Sanchar Nigam Limited
10	151012	JAGRITI TANDON	Jaypee University of Information Technology
11	151013	MOHIT PATEL	BSNL
12	151015	MOHIT SACHDEVA	Reliance Communications Limited
13	151016	REETIKA MITTAL	Mazagon dock shipbuilders limited
14	151017	AYUSHI AWASTHI	Bharat Sanchar Nigam Limited
15	151018	ISHITA	TCS
16	151019	MAHIMA SURI	Doordarshan, Jammu Kendra
17	151021	RICHA BHARDWAJ	Thinknext technologies pvt limited
18	151022	MAHESH KUMAR	Bsnl
19	151023	NIKHIL THAKUR	BSNL
20	151024	AKRITI GUPTA	INTEX
21	151025	KARAN AHUJA	BHEL
22	151027	AKSHAT BHATNAGAR	Siemens Technology and Services, Bangalore
23	151028	KRITIKA CHAUDHARY	DEAL
24	151030	AJAY SINGH	Maruti Suzuki
25	151031	MOHIT KUMAR GUPTA	Blue Star Limited
26	151034	PRASHANT ARYA	Reliance Jio Infocomm Ltd
27	151037	NIKHIL K SHANDELYA	BHEL
28	151039	AMOGH MISHRA	Bharat Sanchar Nigam Limited
29	151040	RHEA KUKRETI	Seceon
30	151041	BHUMIKA GARG	CDAC
31	151042	JASLEEN KAUR	CDAC Mohali
32	151043	MAHIMA PARASHAR	Cdac Mohali
33	151044	DHRUV GARG	HFCL
34	151045	RAMNEET KAUR	bsnl
35	151047	PRAFULL RAINA	CENTRE FOR DEVELOPMENT OF ADVANCED COMPUTING
36	151048	SANCHIT DANG	Bharat Electronics Limited, Panchkula
37	151049	AKHIL RANA	BSNL - Palampur
38	151052	HIMANSHU CHOUDHARY	K.C Kasliwal Thermal Training Institute
39	151053	HARSHIT JAIN	Tevetron technologies pvt. Ltd.
40	151055	SACHIN TAKYAR	HP Computer
41	151056	RUSHIL BHATNAGAR	prasar bharati
42	151057	LOVISH SINGLA	Hindustan aeronautics limited
43	151058	SIDDHARTH SHARMA	MARICO INDIA PVT.LTD
44	151059	RIYA OHRI	BSNL
45	151060	ANUBHAV TOMAR	PWD
46	151061	KAUSHIKEE	University of Information Science and Technology of Ohrid, Macedonia
47	151063	SHRUTI SABHERWAL	NTPC
48	151064	DEEPANKAR MATHUR	Purple Panda Fashions Private Limited

21/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

49	151065	PARTH DUBEY	Reliance Communications Limited
50	151066	GUNDEEP SINGH	NTPC Limited
51	151069	SMRITI THAKUR	Ambuja Cement
52	151070	MAHIMA AGARWAL	Bharat Electronics limited
53	151073	SUCHITA SINGH KANTHWAL	Think Next
54	151076	SWARIT SOOD	Macrew Technologies Pvt Ltd.
55	151077	NIKHIL VERMA	DOORDARSHAN KENDRA SHIMLA
56	151079	ABHINANDAN SHARMA	Bharat Electronics Limited, Panchkula
57	151080	SHIVAM VERMA	Bharat electronics limited
58	151081	SHAURYA MEHROTRA	Realiance Jio
59	151082	SIDDHIKA SETH	Bsnl
60	151085	KARMANYA SHARMA	C-DAC Mohali
61	151086	MANAN KASHMIRI	Rooman technologies pvt . Ltd
62	151087	KRITTIKA TEWARI	Motilal Nehru National Institute of Technology
63	151088	MANIKYA SABHARWAL	NHPC
64	151089	AADEESH JAIN	Prasar Bharati, ALL INDIA RADIO :CHHATARPUR
65	151090	ANNIE SHARMA	TCIL-IT ,
66	151091	SHIVANGI	IIT Delhi
67	151092	SHRIYA VANDITA	LG electronics (Greater Noida)
68	151093	ARPIT RITURAJ	DMRC
69	151095	AKSHIT CHANDEL	BSNL
70	151097	RISHAB UPMANYU	National Institute of Information Technology
71	151098	RISHABH KANWAR	HTIS Telecom
72	151100	KANCHAN RANI	B4S solutions pvt limited
73	151101	MEDHA GUPTA	Telecommunications Consultants India Limited-Information Technology(TCIL-IT)
74	151102	AKSHIT SHARMA	Blue Star Limited
75	151103	GOURI SHARMA	B4S solution private limited
76	151105	SIMRAN CHAUHAN	Telecommunications Consultants India Ltd-Information Technology(TCIL-IT)
77	151106	DIVYANSH KAISTHA	BSNL
78	151107	PALLVI	B4S Solutions Pvt. Ltd.
79	151108	APOORV UPADHYAY	BSNL
80	151109	SAHIL JAS	Himachal Futuristic Communications Ltd.
81	151110	SANDEEP SHARMA	Mind Grind private limited
82	151112	PARAS GUPTA	Internshala

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Dr. Rajiv Kumar
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P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Industrial Training 2020 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	161002	Tanveer singh Sodhi	AAI
2	161003	AKSHAY SOM	Doordarshan kendra , delhi
3	161005	Samson Shukla	Cetpa Infotech Pvt. Ltd.
4	161006	Sumit Thakur	Doordarshan Kendra
5	161007	Mohit Garg	Whiz Infotel
6	161009	Satyam Kumar	Bharat Electronics Limited, Ghaziabad
7	161011	Sarthak kaushik	Cetpa Infotech
8	161014	Anushka Shukla	ATC, Airport Authority of India, IGI AIRPORT, NEW DELHI
9	161015	Siddharth Singh	Aptron solutions Ltd
10	161016	Priyanshi Rastogi	National Thermal Power Corporation
11	161017	Kanika Chaudhary	Powertel, powergrid corporation of India LTD.
12	161021	Himanshi Singh	NIIT Technologies
13	161022	Lavish kumar jangir	Brain Stem Technologies
14	161023	Parthsarthi Bassi	Bharat Electronics Limited, Panchkula
15	161024	Manasvi Kashyap	Oil and Natural Gas Corporation ltd
16	161025	Shivansh Gusain	IRDE
17	161030	Himanshu Walia	Oceana Tech
18	161031	Megham Garg	Oceana Tech
19	161032	Tanya gupta	DUCAT institute ,noida
20	161033	Kushagra Srivastava	Aptron Solution Pvt. Ltd.
21	161034	Nilesh Kishor	Indian Railways, Bareilly
22	161035	Aditya Mohan	ThreatLandscape Cyber Solutions Private Limited
23	161037	Sparsh mahajan	Airmesh communications limited
24	161042	Sonia Jain	Oceana Tech
25	161043	Bahar sharma	Bharat electronics limited
26	161044	Mayank gupta	I3indya technologies
27	161045	Shailu Srivastava	BHARAT SANCHAR NIGAM LIMITED,PATNA
28	161046	Narendra Jangid	Adhoc Networks
29	161047	Suresh Arora	i3indiya technologies
30	161048	Pranav Bansal	Network Bulls
31	161051	Sanchit Garg	Advanced Tech.
32	161053	arpit rana	HP-PWD
33	161055	Abhinandan Thakur	NKC Projects pvt ltd
34	161056	Kriti Verma	BEL
35	161057	Riya Tyagi	SSDN TECHNOLOGY
36	161058	Sughosh Sharma	BSNL (Ghumarwin branch)
37	161060	Abhinav Sharma	Jetking
38	161061	Ashish Kumar	Netmax Technologies pvt. ltd.
39	161062	Abhishek Jha	LG India
40	161063	ALOK SHEKHAR BHARDWAJ	INFOSEEK TECHNOLOGIES , LUCKNOW
41	161066	Ritankshee	Kvch Oracle
42	161067	Mukul Gupta	Oceana Tech IN (Mohali)
43	161068	Inderpreet singh	Netmax Technologies Pvt. Ltd. , Chandigarh
44	161069	Mehak Beakta	Bharat Electronics Limited
45	161070	Rushmika Singh	Powertel, Powergrid corporation india Ltd.
46	161072	Akhilesh Kumar	Akvo Atmospheric Water Systems
47	161073	Surbhi Garg	NIIT
48	161074	Yashvir Singh	Bharat Electronics Limited
49	161075	Bhavya Chadha	Bharat Electronics Limited(BEL)
50	161076	Anshul Kumar	Oceanatech
51	161077	Harshita Rana	FranConnect software Pvt. Ltd.

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

52	161078	Tarun Gupta	Softechno Institute
53	161080	Ayshika Kapoor	ICT Academy - Indian Institute of Technology, Kanpur
54	161081	Utkarsh Gupta	Intercity Foundation
55	161082	Shikhar Srivastava	Volumetree
56	161083	Apurva Padiyal	CETPA Infotech Pvt Ltd
57	161084	Stakshi Sharma	Oceana Tech
58	161085	Ranjan Kumar	InterNext Engineering Solution Pvt. Ltd.
59	161086	Devashish Dimri	IRDE,DRDO,Dehradun
60	161087	Shikhar Srivastava	Railtel Corporation of India Limited
61	161088	Nupur Chaturvedi	NTPC Faridabad
62	161089	Diuman Mahajan	Edoofa
63	161090	Deepak Kumar	Niks technology
64	161091	PAYOOSNI SINGH	Maruti Suzuki
65	161092	ashish kumar verma	infoseek
66	161093	Aditya Tiwari	Niks Technology
67	161094	TANMAY CHAUDHARY	ONGC DEHRADUN
68	161095	Samyak Jain	Cloudxchange.io
69	161098	Yatharth Gautam	Cetpa Infotech Private Limited
70	161099	Somya Chaturvedi	North Western Railways
71	161100	Ajay thakur	Thinknext
72	161102	Archit Sugha	Oceana Tech
73	161104	Abhishek Koundal	Jetking
74	161107	shubham jamwal	BSNL SOLAN
75	161108	Prashant Sharma	BSNL
76	161110	Hardik sharma	Thinknext
77	161111	Abhishek sharma	Inx infotech
78	161112	Arushi verma	BSNL telecommunications
79	161113	Aayush Goyal	Oil and Natural Gas Corporation Limited
80	161114	Nitin kumar	BSNL
81	161115	Sarthak Srivastava	JIL information technology limited
82	161116	Kanwar Singh	Hughes communications
83	161117	manthan chauhan	BSNL
84	161118	Prashant kumar	BSNL

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Industrial Training 2021 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	161029	Akhilesh Sapehia	Jaypee university of information and technology
2	171001	Abhishek Bundel	Internshala Trainings
3	171002	Ayush Kumar Jaiswal	Internshala
4	171003	Mukul Bhatia	Internshala
5	171004	Diwakshu katoch	Internshala
6	171005	Akhil Chauhan	Internshala
7	171006	Prerna Kanwar	Internshala
8	171007	Sahitya bhalaik	Jaypee University of information technology
9	171008	Sanket Saxena	Internshala
10	171009	Kritik Verma	Internshala
11	171010	Sangharsh singh	Cetpa infotech Pvt ltd Noida,Uttar Pradesh
12	171012	tushar agarwal	INTERNSHALA
13	171014	ujjwal jain	INTERNSHALA
14	171015	Soham Ahuja	United Nations
15	171016	Keshav Vohra	Internshala
16	171018	rohit behl	internshala
17	171019	Shivam Sinha	Imternshala
18	171020	Sanyam	Internshala
19	171021	Archita Gupta	Internshala
20	171023	Abhishek Malik	Internshala
21	171024	pankaj	Jaypee University of information and technology
22	171025	kshitij katoch	INTERNSHALA
23	171026	Spardha Kapil	Geeks For Geeks
24	171027	sheetanshu saurabh	internshala
25	171028	Hitesh Thakur	Internshala
26	171029	Sarthak Bisht	Jaypee University of Information technology
27	171030	ALOK PANDEY	Internshala
28	171031	Shubham Kumar	INTERNSHALA
29	171032	Shivansh Suhane	JUIT
30	171033	Ritwik Sood	Jaypee University of Information Technology
31	171034	Tarun Arora	Internshala
32	171035	Ishan Goyal	Internshala
33	171036	Dhananjai Bhalaik	Internshala
34	171037	Shaurya Rajput	Jaypee University of Information Technology, Solan
35	171038	Ananya Shukla	Jaypee University of Information Technology
36	171039	Rajnikant yadav	Jaypee University Of Information Technology
37	171040	Piyush Kumar Singh	Internshala Online Training
38	171042	Ramit Bawa	Intershala
39	171043	Saurav Anand	Internshala Trainings
40	171044	Shivansh Dubey	Internshala
41	171046	Utkarsh Srivastava	Internshala
42	171047	Mehul Bandlish	Jaypee University of Information technology
43	171048	Prashant Jaiswal	Intershala
44	171049	Shachi Sharma	Internshala
45	171050	Ananya Sharma	Internshala
46	171051	Shruti Sharma	Internshala
47	171052	Shubham Singh	INTERNSHALA
48	171053	Nikita Pandey	Internshala
49	171056	Prachi Pal	internshala
50	171057	Bandana Pal	INTERNSHALA
51	171058	Ojasvi	Internshala

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

52	171059	Anushka Dixit	Internshala
53	171060	surya mahajan	internshala
54	171061	Saksham goel	Fastor
55	171062	Vishal Srivastava	EICT Academy, IIT Kanpur
56	171065	Shruti Singh	Internshala
57	171069	Anshul Deorane	Internshala
58	171070	Anupam Srivastava	Internshala Traning
59	171071	Saksham Tandon	internshala
60	171073	Saumya Jajodia	Internshala
61	171074	Akshat Gupta	Webdew
62	171075	Aadhya Bajpai	Verzeo
63	171076	Sudhanshu Mishra	Jaypee University of Information Technology, Solan
64	171078	Nikhil Tanwar	Internshala
65	171079	Kartikey Bindal	Internshala
66	171080	Nikunj	Internshala

04/08/2022

Dr. Rajiv Kumar
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P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Industrial Training 2022 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	181001	Priyank Srivastava	Internshala
2	181005	Vinayak Tiku	internshala
3	181006	Harsh mishra	EduMoon
4	181007	Aditya Kumar Jaiswal	Internshala
5	181008	Arsh Kumar	Internshala
6	181009	Gurpreet Singh	AM Tech Networks
7	181010	Surbhi kumari	Internshala
8	181011	Kartikay Kaushal	Internshala
9	181012	Nikhil Thakur	Internshala
10	181013	NIKHIL YADAV	INTERNSHALA
11	181015	Rakshit Sharma	BSNL
12	181016	Kamlesh kumar	Internshala
13	181017	Kshitij Sharma	Internshala trainings.
14	181019	Avinash Verma	INTERNSHALA
15	181020	Mudit katiyar	Internshala
16	181022	Himanshu Thakur	Internsalla
17	181023	Aditya Mishra	Internsala
18	181024	Kirti Parshionikar	Internshala
19	181025	Tavleen Singh	Internshala
20	181027	Vaibhav Rastogi	Internshala
21	181028	RAGHAV SHARMA	Internshala

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Dept: CIVIL BATCH - 2014 - 2018

Year - 2017

(1)

University Requirement							Requirement for Accredation / Ranking Agencies				
S.No.	Enrollment No.	Branch	Period of Training (No. Of Weeks)	Training Start Date	Training End Date	Status (Satisfactory / Unsatisfactory)	Institute/Company Name	Subject/Topic of Training	Domain/Area of Training	Stipend Received (If Any)	Aadhaar Number of Student
1	141263	CE	7	29-05-2017	15-07-2017	Satisfactory	HPRDCL	Construction of roads (e PMS, RADMS, ROMDAS)	Construction, System Analysis	NO	987868746848
2	141601	CE	6	29-05-2017	08-07-2017		P K Construction Shimla	Construction of Advocate Chamber near High Court and Construction of Parking Complex at Chotta Shimla	Construction	NO	884578188153
3	141603	CE	6								
4	141604	CE	5	29-06-2017	30-06-2017	Satisfactory	HCC	Construction of NH- 34, 4 Lane (Farrakka, Raiganj Section)	Construction	NO	541252189749
5	141605	CE	6	01-06-2017	15-07-2017	Satisfactory	Indian Railways	Construction of Limited Height Subway under Railway Department	Construction	NO	253736151986
6	141606	CE	6	05-06-2017	15-07-2017	Unsatisfactory	JPHRF	Bridge Construction Pung Khadd Sujanpur Tihra (Baijnath Project)	Construction,Project Planning	NO	961362475484
7	141606	CE	6	05-06-2017	15-07-2017	Satisfactory	Syal and associates	Structural Design	Design	NO	253657634246
8	141607	CE	6	05-06-2017	10-07-2017	Satisfactory	IOCL	Construction of Oil Water Seperetor	Construction	NO	
9	141608	CE	6	05-06-2017	10-07-2017	Satisfactory	SJVNL	LUHRI Hydropower Electric Project	Construction Planning and Design	NO	470244564729
10	141609	CE	4	05-06-2017	05-07-2017		L&T	Commercial Building Construction (DLF Building in Gurugram)	Construction	NO	364358230523
11	141610	CE	6	10-06-2017	17-07-2017	Satisfactory	IIT BHU	Design and Analysisof Pitched Roof Truss Using STAAD Pro	Design and Analysis	NO	493996271823
12	141611	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	275103106040
13	141612	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Cresidential Building, Galaxy Heights	Construction	NO	911325199048
14	141613	CE	7	01-06-2017	16-07-2017	Satisfactory	PWD	Road Construction and maintenance at Mathura, UP	Construction	NO	748717944274
15	141615	CE	7	05-06-2017	17-07-2017	Satisfactory	HPPWD	Construction of Post Graduate College	Construction	NO	533592259552
16	141616	CE	6	01-06-2017	12-07-2017	Satisfactory	SJVNL	Rampur Hydro Power Station	Construction, Planning and Design	NO	642152102942
17	141617	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Sawra Kuddu Hydropower Electric Project	Construction	NO	280189613732
18	141619	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	813332527314
19	141620	CE									Pending
20	141621	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Comprehensive Development of Corridor on Outer Ring between Mukbara Chowk to Wazirabad	Construction	NO	612109067356
21	141622	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Construction of 33/220 kV Pooling Sub-Station	Construction	NO	Pending
22	141624	CE	6	02-06-2017	15-07-2017	Satisfactory	Ved Prakash Gupta	Construction of boundary wall	Construction	No	509062120363
23	141626	CE	6	05-06-2017	14-Jul	Satisfactory	DMRC	Contruction of Underground Metro	Construction and Surveying	No	725029168548
24	141627	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	867788791400
25	141630	CE	7	05-06-2017	17-07-2017	Satisfactory	M G Construction	Four Laning of Kharar-Kurali Section of NH-21 in the State of Punjab on EPC Mode	Construction	NO	958830245993
26	141633	CE	6	04-06-2017	15-07-2017	Satisfactory	HPPWD	Construction of Underground Waste Collection System at Dharamsala	Construction	NO	233964159757
27	141634	CE	6	01-06-2017	14-07-2017	Satisfactory	DrukGreen	Hydro Power Electric Project	Construction	NO	
28	141636	CE	6	05-06-2017	18-07-2017	Satisfactory	CPWD	Electrofitting	Estimation and Operation	NO	842943328993
29	141637	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Hydro Power Electric Project	Construction, Analysis and Design	NO	440663665519
30	141638	CE	6	05-06-2017	15-07-2017		NTPC	Q & A	Quality management	NO	493285031722
31	141639	CE	6	01-06-2017	15-07-2017	Satisfactory	Paharpur Cooling towers	Paharpur Cooling Tower Pvt. Ltd.	Construction and Estimation	NO	457229473693
32	141640	CE	6	08-05-2017	17-06-2017	Satisfactory	PWD	Construction tubewell	Construction and Site Investigation	NO	280438057959
33	141641	CE	5	12-06-2017	10-07-2017	Satisfactory	Renuka	Road Construction and Survey	Construction	NO	488631889287
34	141642	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Sewage Treatment Plant Operation	Site Visit and Design	NO	597153870545
35	141643	CE	6	04-06-2017	07-07-2017	Satisfactory	DMRC	Construction of Underground Metro at R K Puram and Hauz Khas Station	Construction	NO	596538281137
36	141644	CE	6	01-06-2017	12-07-2017	Satisfactory	HPPWD	Construction of multi purpose hall	Construction	NO	958282824701
37	141645	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Swara Kuddu Hydropower Project	Construction	NO	736402354843
38	141646	CE	6	01-06-2017	15-07-2017	Satisfactory	GAWAR	Road Construction of 4- Lane Panchkula and Yamuna Nagar (NH- 73)	Construction		
39	141647	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Stability analysis of Luhri HEP Stage-1	Design	NO	339213751913

40	141648	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Multiporpous Sports Stadium Ramamandir Mandi, Veterinary Hospital and College Rampur	Construction, Maintenance and Design	NO	619538309958
41	141650	CE	7	01-06-2017	15-07-2017	Satisfactory	Jaiprakash And Sons	Construction of Mega Hostel Block in NIT Hamirpur	Construction	NO	352700960035
42	141651	CE	6	01-06-2017	11-07-2017	Satisfactory	Sunrises Structures	Construction of Sun Twilight Villas and Commercials	Construction	NO	830120993663
43	141652	CE	6	01-06-2017	12-07-2017	Satisfactory	SIDCL	Road Construction	Analysis	NO	986065011649
44	141653	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Intze Tank Design	Design	NO	957707592017
45	141654	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rain Water Harvesting Tank Transportation of Exsisting Lawn Into Rain Garden	Construction	NO	873345654123
46	141655	CE	7	29-05-2017	17-07-2017	Satisfactory	UPRNNL	Building Construction	Construction	NO	584157677760
47	141656	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
48	141661	CE	7	15-06-2017	31-07-2017	Satisfactory	PWD	Residential Building Construction	Construction	NO	867213841974
49	141662	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Retaining wall construction	Construction	NO	387802984564
50	141663	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
51	141664	CE	6	29-05-2017	08-07-2017	Satisfactory	PK Construction	Car Parking Building Construction	Construction	NO	767631756894
52	141665	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rainwater Harvesting Tank	maintenance	NO	435539216442
53	141666	CE	6	05-06-2017	17-07-2017	Satisfactory	CPWD	Building Maintenance	maintenance	NO	989868620530
54	141667	CE	6	31-05-2017	11-07-2017	Satisfactory	SPCL	Construction of Bus Terminus and Parking	Construction	NO	282070765310
55	141668	CE	6	03-06-2017	14-07-2017		RED	Construction of hall	Construction	NO	892245015469
56	141669	CE	5	13-06-2017	15-07-2017	Satisfactory	PWD Dharamsala	Construction of roads	Construction	NO	774345360402
57	141670	CE	5	29-05-2017	30-06-2017	Unsatisfactory	HCC	4 Laning Farakka Raiganj Section	Construction	NO	454223208162
58	141671	CE	6	28-05-2017	14-07-2017	Satisfactory	Bansal Engineers	Building Construction	Contruction	Yes	597323298747
59	141672	CE	4	30-05-2017	30-06-2017	Satisfactory	ADRDE	Design of building	Design	NO	505348241275
60	141673	CE	6	01-06-2017	12-07-2017	Satisfactory	UPPWD	Road Contruction	Construction	NO	
61	141674	CE	6	01-06-2017	12-07-2017	Satisfactory	REASI	Water Distribution System Study	Analysis	NO	671722842063
62	141675	CE	7	01-06-2017	14-07-2017	Satisfactory	Bareilly Development Authority	Laying of Sewer Pipelines	Construction	NO	334980591932
63	141676	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Galaxy Heights Project	Construction	NO	312625902455
64	141677	CE	6	01-06-2017	11-07-2017	Satisfactory	Swastik	Underground Substation Gurugram	Construction	NO	831847743627
65	141678	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Casting of Bridge	Testing	NO	569738883949
66	141679	CE	5	30-05-2017	12-07-2017	Satisfactory	H. C. Bansal Engineers and Contractors	Building Construction	Construction	Yes	692342550589
67	141680	CE	6	01-06-2017	05-07-2017	Satisfactory	ERA	Road Construction	Construction	NO	567280282077
68	141681	CE	6	11-06-2017	16-07-2017	Satisfactory	HPPCL	Barrage division of sainj Hydro Power Electric Project	Construction	NO	346612434207
69	141682	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Construction of PG	Construction	NO	639806463361
70	141683	CE	4	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Ambuja Cement Plant Visit	Materials	NO	334214454998
71	141684	CE	6	29-05-2017	08-07-2017	Satisfactory	HPPWD	Development of New OPD at IGMC Shimla	Construction	NO	995522249985
72	141686	CE	6	01-06-2017	01-07-2017	Satisfactory		Building Construction (Mohali)	Construction	NO	411889377530
73	141687	CE	6	12-06-2017	22-07-2017	Satisfactory	HPPWD	HP State Library Building Contruction	Construction	NO	885024325960
74	141688	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Testing of materials	Testing	NO	868824583795
75	141689	CE	6	03-06-2017	17-07-2017	Unsatisfactory	Indian Railways	Construction of Railway Track	Construction	NO	409852377341
76	141690	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	691456577638
77	141691	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Highway Maintenance and PG College	Constructon	NO	
78	141692	CE	6	01-06-2017	12-07-2017	Satisfactory	DMRC	Underground Substation	Construction/ Surveying/ Geotechnical Investigation	NO	862339185428
79	141693	CE	4	05-06-2017	08-07-2017	Satisfactory	BP	Construction of new filling shed	Construction	NO	530137391222
80	141694	CE	6	30-05-2017	10-07-2017	Satisfactory	PWD	Construction of roads	Construction	NO	424523018138
81	141695	CE	6	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Concrete Mix Design	Design	NO	579641278502
82	141696	CE	4	31-05-2017	30-06-2017	Satisfactory	CPWD	Construction	Construction	NO	876016738612
83	141697	CE	4	01-06-2017	30-06-2017	Satisfactory	LMRC	Lucknow Metro Construction	Construction	NO	928844325232
84	141698	CE	7	01-06-2017	07-07-2017	Satisfactory	SJVNL	Retaining wall construction	Construction	NO	341163355226

Dept: CIVIL ENGG. BATCH : 2015-2019

Year - 2018

(2)

Summer/Industrial Training Status Summary August 2018 (Batch 2015-2019)									
S no.	**Roll No.**	**Student Name**	**Department**	**Training Dairy Submitted (Yes/No)**	**Training Report Submitted (Yes/No)**	**Training Certificate Submitted (Yes/No)**	**Viva held on (Date)**	**Viva Taken by (Faculty Name)**	**Status (Satisfactory/ Unsatisfactory)**
1	141658	Pankaj Sankhyan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Anirban Dhulia & Mr. Aakash Gupta	**Satisfactory**
2	151113	Akal Singh Gurung	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
3	151601	Divesh Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
4	151602	Puneet Pal Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
5	151604	Nikhilesh Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
6	151605	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
7	151606	Abhishek Ahluwalia	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
8	151608	Hetain Sahi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
9	151610	Kuenzang Sc Choden	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
10	151612	Shally Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
11	151613	Shivani Negi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
12	151614	Charu Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
13	151616	Harsh Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
14	151617	Ammaan Zahoor Chat	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
15	151618	Sarthak Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
16	151619	Akshay Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Rishi Rana & Mr. Kaushal Kumar	**Satisfactory**
17	151620	Rizul Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
18	151621	Abhimanyu P Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
19	151622	Arpan Chaudhary	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
20	151623	Tarun Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
21	151624	Jigyasu Khanna	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
22	151625	Harish Chander	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
23	151626	Manik Ohri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
24	151627	Ankur Jaret	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
25	151628	Ankit Tilokta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
26	151629	Sudhanshu Manikpuri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
27	151630	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
28	151631	Abhinav Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
29	151632	Gaurav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
30	151633	Divyam Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

31	151634	Dipanshu Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Niraj Parihar & Mr. Aakash Gupta	**Satisfactory**
32	151635	Ajay Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
33	151636	Himanshu Yadav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
34	151637	Aditya Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
35	151638	Prikshit Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
36	151639	Ashish Dangwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
37	151640	Akshay Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
38	151641	Vaibhav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
39	151642	Akshay Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
40	151643	Aatish Rajta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
41	151645	Puneet Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
42	151646	Pratiyush Kothari	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
43	151647	Shashi Shekhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
44	151648	Vinayak Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
45	151649	Sumit Dhankhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
46	151650	Gourav Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Abhilash Shukla & Mr. Kaushal Kumar	**Satisfactory**
47	151651	Nikhil Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
48	151652	Anirudh Pratap	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
49	151654	Nitesh Chandel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
50	151655	Arpan Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
51	151656	Shubham Soni	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
52	151657	Akhil Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
53	151658	Himanshu Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
54	151659	Parikshit Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
55	151660	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
56	151661	Amit Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
57	151662	Ashutosh Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
58	151664	Amit Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
59	151666	Deval Ashish	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
60	151667	Dikshant Agarwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

61	151668	Bhupinder Singh Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Saurabh Rawat & Mr. Abhilash Shukla	**Satisfactory**
62	151669	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
63	151670	Ahtesham Hussain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
64	151671	Nakshatra Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
65	151672	Ashish Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
66	151673	Ishan Uniyal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
67	151674	Suryabhan Singh Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
68	151675	Harshit Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
69	151676	Vedansh Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
70	151677	Gaurav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
71	151679	Maanik Vatshyayan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
72	151680	Saksham Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
73	151682	Divesh Narang	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
74	151683	Shubham Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
75	151684	Vikas Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
76	151687	Ayush Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Amardeep and Dr. Saurav	**Satisfactory**
77	151688	Kuldeep Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
78	151689	Mayank Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
79	151690	Tarun Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
80	151691	Vibhor Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
81	151692	Karan Goel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
82	151693	Saksham Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
83	151694	Ankush Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
84	151696	Saksham Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
85	151697	Sparsh N.K. Lath	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
86	151698	Kartikey	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

Kaushal Kr.

Industrial Training Coordinator

HoD CE

Dept: CIVIL BATCH - 2016-2020

Year - 2019

(3)

INDUSTRIAL TRAINING STATUS OF CIVIL ENGINEERING DEPARTMENT (2019-20)					
S. No.	Enrol. No.	Name of Student	Industrial Training Report Submitted by Student to Deptt.	Viva Held on	Status of Indutrial Training Completion
1	161659	Pranav Gupta	Submitted	08-08-2019	Satisfactory
2	161664	Vivek Kashyap	Submitted	08-08-2019	Satisfactory
3	161053	Arpit Rana	Submitted	08-08-2019	Satisfactory
4	161663	Seraj Habib	Submitted	08-08-2019	Satisfactory
5	161666	Shivam Nag	Submitted	08-08-2019	Satisfactory
6	161055	Abhinandan Thakur	Submitted	08-08-2019	Satisfactory
7	161688	Shivam Gupta	Submitted	08-08-2019	Unsatisfactory
8	161628	Sangay Zangmo	Submitted	08-08-2019	Satisfactory
9	161695	Parmila Gurung	Submitted	08-08-2019	Satisfactory
10	161693	Karma Yangzom	Submitted	08-08-2019	Satisfactory
11	161631	Sonam Tshomo	Submitted	08-08-2019	Satisfactory
12	161652	Abhinav Choudhary	Submitted	08-08-2019	Satisfactory
13	161627	Harjot Singh	Submitted	08-08-2019	Satisfactory
14	161615	Vivek Pundir	Submitted	08-08-2019	Satisfactory
15	161673	Shourabh Maanju	Submitted	08-08-2019	Satisfactory
16	161674	Aryan	Submitted	07-08-2019	Satisfactory
17	161675	Saksham Mahajan	Submitted	07-08-2019	Satisfactory
18	161625	Ajay Sharma	Submitted	07-08-2019	Satisfactory
19	161620	Piyush Pathania	Submitted	07-08-2019	Satisfactory
20	161639	Rohit Kumar	Submitted	07-08-2019	Satisfactory
21	161661	Shubang Malgotra	Submitted	07-08-2019	Satisfactory
22	161634	Yashwant Singh Rana	Submitted	07-08-2019	Satisfactory
23	161691	Ritesh Kumar Chaurasia	Submitted	07-08-2019	Satisfactory
24	161602	Harshit Bansal	Submitted	07-08-2019	Satisfactory
25	161685	Hitesh Panwar	Submitted	07-08-2019	Satisfactory
26	161655	Alakshender Singh Wazir	Submitted	07-08-2019	Satisfactory
27	161614	Himanshu Kapoor	Submitted	07-08-2019	Satisfactory
28	161612	Gaurav Chauhan	Submitted	07-08-2019	Satisfactory
29	161678	Ujjwal Nadda	Submitted	07-08-2019	Satisfactory
30	161687	Utkarsh Chauhan	Submitted	07-08-2019	Satisfactory
31	161608	Saurav Singh	Submitted	07-08-2019	Satisfactory
32	161665	Deepak Sharma	Submitted	07-08-2019	Satisfactory
33	161690	Shivam Sharma	Submitted	07-08-2019	Satisfactory
34	161637	Mayank Sharma	Submitted	07-08-2019	Satisfactory
35	161654	Samarth Sharda	Submitted	07-08-2019	Satisfactory
36	161646	Shushant Gupta	Submitted	07-08-2019	Satisfactory
37	161689	Abhishek Thakur	Submitted	07-08-2019	Satisfactory
38	161677	Keshav Singh Thakur	Submitted	07-08-2019	Satisfactory
39	161603	Abhishek Sharma	Submitted	07-08-2019	Satisfactory
40	161630	Pema Zangmo	Submitted	07-08-2019	Satisfactory
41	161694	Pema Yangden	Submitted	07-08-2019	Satisfactory
42	161629	Ngawang Dolkar	Submitted	07-08-2019	Satisfactory
43	161647	Chahat Garg	Submitted	07-08-2019	Satisfactory
44	161611	Ambuj Awasthi	Submitted	07-08-2019	Satisfactory
45	161626	Nikhil Kumar	Submitted	07-08-2019	Satisfactory
46	161649	Anish Kapil	Submitted	07-08-2019	Satisfactory
47	161686	Siddharth Verma	Submitted	07-08-2019	Satisfactory
48	161680	Deven Mahajan	Submitted	07-08-2019	Satisfactory
49	161640	Gunjan Katoch	Submitted	07-08-2019	Satisfactory
50	161671	Nitin Thakur	Submitted	07-08-2019	Satisfactory
51	161651	Nishant Thakur	Submitted	07-08-2019	Unsatisfactory
52	161636	Mukul Prashar	Submitted	07-08-2019	Unsatisfactory
53	161635	Tejas garg	Submitted	07-08-2019	Satisfactory
54	161617	Anmol Singhal	Submitted	07-08-2019	Satisfactory
55	161613	Harshit Saxena	Submitted	07-08-2019	Satisfactory
56	161696	Yash Goyal	Submitted	07-08-2019	Satisfactory
57	161698	Nagawang Dorji	Submitted	07-08-2019	Satisfactory
58	161605	Amber Soni	Submitted	07-08-2019	Satisfactory
59	161607	Sumit Kumar	Submitted	07-08-2019	Satisfactory
60	161642	Xitiz Sen	Submitted	07-08-2019	Satisfactory
61	161684	Ria Thakur	Submitted	07-08-2019	Satisfactory
62	161676	Rishav Kumar Tiwari	Submitted	07-08-2019	Satisfactory

63	161604	Amol Srivastava	Submitted	07-08-2019	Unsatisfactory
64	161601	Ritanjay ✓	Submitted	07-08-2019	Satisfactory
65	161285	Rishi Singh ✓	Submitted	07-08-2019	Satisfactory
66	161624	Ketan Mishra ✓	Submitted	07-08-2019	Satisfactory
67	151691	Vibhor Gautam ✓	Submitted	29-07-2019	Satisfactory
68	161692	Leki Wangchuk ✓	Submitted	21-08-2019	Satisfactory
69	161670	Prasanna Kumar	Not Submitted	-	Unsatisfactory
70	161644	Shankar Kumar	Not Submitted	-	Unsatisfactory
71	161001	Nikhil Sharma	Not Submitted	-	Unsatisfactory
72	161653	Pritul	Not Submitted	-	Unsatisfactory
73	161658	Aditya Vikram Singh Jamwal	Not Submitted	-	Unsatisfactory
74	161657	Anirudhu Guleria	Not Submitted	-	Unsatisfactory
75	161656	Kartikey	Not Submitted	-	Unsatisfactory
76	161668	Nikhil Negi	Not Submitted	-	Unsatisfactory
77	161632	Cheku Dorji	Not Submitted	-	Unsatisfactory
78	141658	PANKAJ SANKHYAN	Not Submitted	-	Unsatisfactory
79	151605	GAURAV SHARMA	Not Submitted	-	Unsatisfactory
80	151688	KULDEEP RANA	Not Submitted	-	Unsatisfactory
81	141625	Namit Sharma	Not Submitted	-	Unsatisfactory
82	141628	HARSH VARDHAN SINGH	Not Submitted	-	Unsatisfactory
83	141659	RAHUL VERMA	Not Submitted	-	Unsatisfactory
84	141663	ADITYA DHIMAN	Not Submitted	-	Unsatisfactory
85	151634	DIPANSHU THAKUR	Not Submitted	-	Unsatisfactory
86	151646	PRATIYUSH KOTHARI	Not Submitted	-	Unsatisfactory
87	151651	NIKHIL KUMAR SHARMA	Not Submitted	-	Unsatisfactory
88	151656	SHUBHAM SONI	Not Submitted	-	Unsatisfactory
89	151668	BHUPINDER SINGH VERMA	Not Submitted	-	Unsatisfactory
90	151677	GAURAV THAKUR	Not Submitted	-	Unsatisfactory
91	151679	MAANIK VATSHYAYAN	Not Submitted	-	Unsatisfactory
92	151689	MAYANK SINGH	Not Submitted	-	Unsatisfactory
93	151694	ANKUSH KUMAR	Not Submitted	-	Unsatisfactory
94	151616	HARSH CHAUHAN	Not Submitted	-	Unsatisfactory

Anirban Dhulia
23/08/2019

Mr. Anirban Dhulia
Mr. Aakash Gupta
Industrial Training Co-ordinator

23/8/19

Prof. Ashok Kumar Gupta
Head of the Department
Civil Engineering

HOD
CE DEPT

Received ✓ Documents
23/08/19

Dept: CIVIL ENGG. BATCH - 2017-2021

Year - 2020-2021

(4)

Summer/Industrial Training Status Summary August 2020 (Batch 2016-2020 and 2017-21)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/Unsatisfactory)
1	161001	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	22-08-2020	Mr. Anirban Dhulia	Satisfactory
2	161604	Amol Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
3	161636	Mukul Prashar	Civil Engineering	Yes	Yes	Yes	22-08-2020	Dr Aakash Gupta	Satisfactory
4	161644	Shankar Kumar	Civil Engineering	Yes	Yes	Yes	14-08-2020	Mr Anirban Dhulia and Dr Aakash Gupta	Satisfactory
5	171067	Aman Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
6	171601	Ishant Shekhri	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
7	171602	Hemant Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
8	171603	Aditya Abrol	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
9	171604	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
10	171606	Shekhar Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
11	171607	Kanishk Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
12	171608	Pawas Soni	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
13	171609	Gaurav Prakash Negi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
14	171610	Gunjan Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
15	171611	Aviral Roy	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
16	171612	Aditya Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
17	171614	Vivek Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
18	171615	Vaibhav Singh	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
19	171616	Ashish Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
20	171617	Harsh Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
21	171618	Aditya Rana	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
22	171620	Hardik Nagpal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
23	171621	Rishabh Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
24	171622	Akshit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
25	171623	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
26	171624	Saurabh Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
27	171626	Sourav Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
28	171628	Anjan Sood	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
29	171629	Sameep Aggarwal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
30	171630	Anmol Katana	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
31	171631	Manik Seth	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
32	171632	Siddhant Dubey	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
33	171633	Nikhil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
34	171634	Sukrit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
35	171635	Sahil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
36	171636	Rohit Kumar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
37	171637	Divyanshu Pandit	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory

38	171638	Anubhav Kundal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
39	171639	Mehul Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
40	171642	Saksham Kaushal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
41	171644	Saurabh Tomar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
42	171645	Kartik Verma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
43	171646	Ankit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
44	171647	Dikshant Joshi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
45	171649	Ritvik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
46	171650	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
47	171651	Suraj Chaudhary	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
48	171652	Chander Bhushan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
49	171653	Abhay	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
50	171654	Mohit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
51	171655	Aditya Shekhar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
52	171656	Rijul Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
53	171657	Tanish Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
54	171659	Akshay Pathania	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
55	171661	Himanshu Bansal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
56	171662	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
57	171664	Venus Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
58	171665	Naveen Karar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
59	171666	Nikhil Shukla	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
60	171671	Aditya Nath	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
61	171681	Abhishek Bind	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
62	171682	Sanju Kanwar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
63	171683	Manik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
64	171684	Lokesh Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory

Traning and Placement Coordinator

Head of the Department

25/8/2020

Received
29/08/2020

Dept : CIVIL ENGG. BATCH : 2018-2022

Year : 2021

(5)

Summer/Industrial Training Status Summary August 2021 (Batch 2018-22)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/ Unsatisfactory)
1	181602	Yamit Dhalaik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
2	181603	Ujjwal Kumar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
3	181604	Harshit Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
4	181605	Shubham	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
5	181606	Varun Kapil	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
6	181607	Abhay Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
7	181608	Aniket	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
8	181610	Vishal Garg	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
9	181611	Madhvender Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
10	181612	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
11	181613	Rishabh Jaswal	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
12	181614	Vishali Thapta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
13	181615	Abhay Kaith	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
14	181616	Sushant	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
15	181617	Ritik Kumar Puri	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
16	181618	Abhay Kanwar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
17	181619	Rohit Lakhera	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
18	181621	Atul Vashisht	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
19	181622	Navneet Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
20	181623	Deepak Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
21	181625	Abhay Joshi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
22	181626	Muskan Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
23	181627	Utkarsh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
24	181629	Suryansh Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
25	181630	Bhuvan Walia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
26	181631	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
27	181632	Arnav Rawat	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
28	181633	Aditya Chauhan	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
29	181634	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
30	181635	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Received
17/08/21

31	181637	Abhishek Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
32	181638	Sahil Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
33	181639	Abhinesh Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
34	181642	Yash Gupta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
35	181643	Pranav Dogra	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
36	181644	Anushka Anand	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
37	181645	Amish Kartik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
38	181647	Sonam Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
39	181648	Passang Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
40	181649	Phub Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
41	181650	Sonam Tshering	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
42	181651	Tshering Gyeltshen	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
43	181652	Kinley Zam	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
44	181653	Sonam Tshewang Dema	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
45	181654	Dechen Tshomo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
46	181655	Namgay Wangmo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
47	181656	Pema Yuden	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
48	181657	Saijal Verma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
49	181659	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
50	181660	Hemang Jandrotia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
51	181661	Deval	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
52	181662	Ayush Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
53	181663	Ritik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Kaushal Kumar

Signature of Departmental Summer Training Coordinator

4/8/21

Signature of the Head of Department

Dr. Ashish Kumar
Professor & HOD of Civil Engineering
Jaypee University of Information Technology,
Waknaghat, Distt.-Solan (HP) 173234 India

Received
17/08/21

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151511	Mritunjay Singh Chandel	5/28/2018	07-09-2018	Movvel Tech solution	Web portal designing for complaints	NO
151501	Mandeep Singh	5/21/2018	07-06-2018	Window IT	ATM systems	NO
151502	Hitesh	5/23/2018	07-05-2018	International Crops Research Institute for the Semi-Arid Tropics	Developing a web server for knowledge mining of plant genes	22500.00 INR
151503	Shorya singh thakur	5/21/2018	07-04-2018	HPU	(NitMAP)	No
151505	Sanjeevani Ravi Srivastava	5/21/2018	07-02-2018	Defence Research and Development Organisation(DRDO)	Microarray Data Analysis,Functional Annotation and Relationship	no
151507	Pulkit Anupam Srivastava	5/23/2018	07-05-2018	International Crops Research Institute for the Semi-Arid Tropics	Optimization of parameters for prediction of biological processes/pathways of	22500.00 INR
151508	rashika singhal	06-05-2018	7/13/2018	ADI Biosolution	computational sequence analysis and functional annotation of GSK3 for	no
151509	Shweta Parmar	06-05-2018	7/13/2018	ADI Biosolution	Computational Sequence Analysis and Functional Annotation of QAPRTase in	NO

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151510	ARSHIYA CHAUHAN	06-01-2018	6/30/2018	VERKA MILK PLANT MOHALI	Production and quality control	No
151801	Pratibha Pandey	8/25/2018	07-07-2018	Jaypee Hospital	Different techniques and procedures in molecular laboratory	No
151802	Bhushan Kumar	06-01-2018	7/16/2018	Bayer's Crop Science	Training in plant tissue culture	No
151804	Arunima	06-01-2018	7/15/2018	Jaypee university of information technology	Protein analysis	No
151806	Priya saxena	06-01-2018	7/16/2018	Allele Life Sciences (p) Ltd. Noida	"Gene Expression Profiling Of Tumor Suppressor Gene WT1 By Real Time PCR"	No
151809	Lalit Prakash Sharma	06-01-2018	07-10-2016	VERKA MILK PLANT MOHALI	quality control	no
151810	Swati Srivastava	5/22/2018	7/22/2018	Pondicherry University	Process development for extracting energy precursor (volatile fatty acids) from	20000
151813	Vishakha Saini	6/1/0018	7/16/2018	Allele Life Sciences Pvt. Ltd	Gene expression profiling of APS gene by real time PCR	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151814	Akriti	5/22/2018	07-07-2018	Mahavir Cancer Sansthan & Research Centre	Study of synergistic toxic effect of arsenic and profenofos on Swiss albino	no
151815	Yashaswi sood	1-6-18	10-7-18	VERKA MILK PLANT MOHALI	Quality assurance	No
151816	DIKSHA SHARMA	5/21/2018	6/30/2018	VERKA MILK PLANT MOHALI	Training on Production, Quality Control and Quality Assurance	NO
151820	NISHTHA THAKUR	5/21/2018	6/30/2018	VERKA MILK PLANT MOHALI	Production and Quality Control	No
151832	Vidushi	1-6-18	10-7-18	VERKA MILK PLANT MOHALI	Production and quality control of milk products.	No
151837	Shubham Gupta	06-01-2018	07-10-2018	VERKA MILK PLANT MOHALI	Quality assurance , quality control, production	No
151838	SHAGUN AGARWAL	5/25/2018	07-12-2018	National Institute of Plant Genome Research	TA cloning and basic plant tissue culture techniques	NO
151840	Subhashree pradhan	06-01-2018	7/18/2018	Anthem Biosciences Pvt Ltd, Bengaluru	Cell culture assay,enzyme assay,molecular biology techniques and hplc	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151845	Anubhavi Singh	06-04-2018	7/16/2018	Paras Healthcare	Medical Microbiology	No
151847	Sophia Puri	5/21/2018	6/30/2018	ICAR-CIPHET	SELECTION OF ENRICHMENT MEDIA AND CULTURE	No
151851	Saesha Verma	06-11-2018	7/20/2018	Indian Institute of Technology, Mandi	Microfluidic based point of care testing device for measuring urine albumin	Yes but amount not received yet
151836	Kritika Thakur	06-07-2018	7/18/2018	State Forensic Lab, H.P.	Basic Techniques of DNA isolation in Forensic science	No
151853	Payal Thakur	06-07-2018	7/18/2018	State Forensic Lab, H.P.	Basic techniques of DNA isolation in forensic science	No
151812	Shivam Sharma	5/29/2018	07-07-2018	Fermenta Biotech Limited	Production of Penicillin	No
151824	Anwesha Chowdhury	5/28/2018	7/14/2018	Uttar Banga Krishi Viswavidyalaya	Training on Marker Analysis by SSR and RAPD	No
151825	Kashish jishtu	06-02-2018	07-09-2018	Indira Gandhi medical college shimla	Identification of strains of HIV virus and TB bacteria.	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151819	Kirti Vardhan	5/22/2018	6/30/2018	ARBRO Pharmaceutical Private Limited	Trainnig on molecular biology and microbiology.	No
151807	Tanya Kuthiala	06-12-2018	7/31/2018	DRDO- Institute of Nuclear Medicine and Allied Sciences	"Radiation induced effects on tumour spheroids"	No
151839	Kunjan Govil	5/28/2018	7/13/2018	DRDO- Institute of Nuclear Medicine and Allied Sciences	General techniques used to study effect of radiation on mice	No
151850	Vaishali Sharma	06-04-2018	08-03-2018	DRDO- Institute of Nuclear Medicine and Allied Sciences	Techniques used to study the effect of radiation on mice tissues	No
151834	Abha Sharma	06-01-2018	7/13/2018	Haldirams Co. Manufacturing Pvt. Ltd. Gurgaon	Quality check and assurance of food	no
151830	Tania sharma	5/25/2018	9-7-18	VERKA MILK PLANT MOHALI	Milk procurement and quality processing of milk	No
151843	Yash sharma	06-01-2018	7/17/2018	ICRISAT-international crops research institute for the semi arid tropics	Genomics and bioinformatics lab	No
151841	Anushka kashyap	06-04-2018	7/19/2018	Mincheys food products	Production and quality analysis	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151817	Sehaj Singh Gulati	06-01-2018	7/13/2018	Iris Edu Solutions	Molecular Biology Techniques	No
151844	SOUMYA BHATNAGAR	06-04-2018	7/14/2018	Balajee's edibles pvt. Ltd.	Manufacturing products	No
151818	Harjas Saini	01-06-2018	12-07-2018	Mankind Research Centre	Microbiology	No
151849	Shraddha Sinha	06-04-2018	7/16/2018	Accutest research laboratories Pvt Ltd	Bioequivalence studies	No
151822	Tanvi Taneja	07-01-2018	8/15/2018	Allele life sciences PVT. LTD, sector 10, Noida	Extraction of mushroom tyrosinase and partial purification	No
151827	Rashika Dhar	25-05-2018	13-07-2018	CSIR-IGIB, New delhi,110007	Green synthesis of silver nanoparticles using Terminalia Bellerica stem	No
151842	Saveena Solanki	06-01-2018	7/15/2018	Netaji Subhas Institute of Technology, New delhi,110078	Wastewater Treatment and Energy Generation Using Microbial Fuel Cell	No
151805	Siddhant Singh	6/13/2018	7/13/2018	Rapture Biotech international (p) ltd.	Advance training program	No

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2019						
Roll No.	**Name**	**Training Start Date**	**Training End Date**	**Company / Institute Name**	**Training / Project Name**	**Stipend Provided by Company?**
151846	Janhvi Chauhan	1st june 2018	15th july 2018	CITY HOSPITAL AND RESEARCH CENTREPVT.LTD	Training in Pathology Department	No
151831	Ishita Jaiswal	7th june 2018	14th july 2018	JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY	Project on Proteome Analysis	No
151808	Sakshi Gupta	6th june 2018	18th july 2018	H.P. MILK FEDERATION PLANT CHAKKAR	Quality Verification and Quality Control of milk and milk products	No
151811	Isha Srivastava	7th june 2018	14th july 2018	JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY	Project on Proteome Analysis	No
151821	JANDEEP SINGH	01\06\2018	14\07\2018	IVY HOSPITAL	Diagnotic Techniques	NO
151803	Himalya Attri	04-06-2018	7-13-18	Milestone Gears Pvt. Ltd	Quality Control and Production	

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
1	Arav Sood	151356			Unsatisfactory
2	Joshita Sharma	151442	12-08-2019	12-08-2019	Satisfactory
3	Gaurav Sahu	161004	21-08-2019	21-08-2019	Satisfactory
4	Lavish Kumar Jangir	161022	12-08-2019	12-08-2019	Satisfactory
5	Deepika Gupta	161201	12-08-2019	12-08-2019	Satisfactory
6	Pratyush Kumar	161202	12-08-2019	12-08-2019	Satisfactory
7	Rohit Garg	161203	12-08-2019	12-08-2019	Satisfactory
8	Robin Chauhan	161204	12-08-2019	12-08-2019	Satisfactory
9	Uday Gupta	161205	12-08-2019	12-08-2019	Satisfactory
10	Charchit Kapoor	161207	12-08-2019	12-08-2019	Satisfactory
11	Jyoti	161208	13-08-2019	13-08-2019	Satisfactory
12	Mukul Garg	161209	12-08-2019	12-08-2019	Satisfactory
13	Kamal Kant Thakur	161210	12-08-2019	12-08-2019	Satisfactory
14	Sachin Gupta	161211	12-08-2019	12-08-2019	Satisfactory
15	Abhishek Jain	161212	12-08-2019	12-08-2019	Satisfactory
16	Bhanu Pratap	161213	12-08-2019	12-08-2019	Satisfactory
17	Rahul Rana	161214	12-08-2019	12-08-2019	Satisfactory
18	Navneet Thakur	161215	13-08-2019	13-08-2019	Satisfactory
19	Vaishali Sharma	161216	13-08-2019	13-08-2019	Satisfactory
20	Suchetan Pathania	161217	13-08-2019	13-08-2019	Satisfactory
21	Minal Aggarwal	161218	13-08-2019	13-08-2019	Satisfactory
22	Devvrat Bhardwaj	161219	13-08-2019	13-08-2019	Satisfactory
23	Shobhit Marwaha	161220	13-08-2019	13-08-2019	Satisfactory
24	Ishita Jain	161221	13-08-2019	13-08-2019	Satisfactory
25	Ashish Gupta	161222	13-08-2019	13-08-2019	Satisfactory
26	Shagun Jindal	161224	13-08-2019	13-08-2019	Satisfactory
27	Vandit Sharma	161225	13-08-2019	13-08-2019	Satisfactory
28	Kanika Puri	161227	13-08-2019	13-08-2019	Satisfactory
29	Neha Tyagi	161229	13-08-2019	13-08-2019	Satisfactory
30	Ashish Sharma	161231	13-08-2019	13-08-2019	Satisfactory
31	Mridul Prashar	161232	13-08-2019	13-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
32	Vinamra Jain	161233	13-08-2019	13-08-2019	Satisfactory
33	Tapasya	161234	13-08-2019	13-08-2019	Satisfactory
34	Sonali Sehgal	161235	13-08-2019	13-08-2019	Satisfactory
35	Aryan Pal Singh	161236	14-08-2019	14-08-2019	Satisfactory
36	Abhishek Katoch	161237	14-08-2019	14-08-2019	Satisfactory
37	Anirudh Sharma	161238	14-08-2019	14-08-2019	Satisfactory
38	Hament Kumar Bassi	161239	14-08-2019	14-08-2019	Satisfactory
39	Robin Singh	161240	14-08-2019	14-08-2019	Satisfactory
40	Parth Verma	161241	14-08-2019	14-08-2019	Satisfactory
41	Shivam Sharma	161242	14-08-2019	14-08-2019	Satisfactory
42	Kanishk Sood	161243	14-08-2019	14-08-2019	Satisfactory
43	Amandeep Saini	161244	14-08-2019	14-08-2019	Satisfactory
44	Aruba Sood	161245	14-08-2019	14-08-2019	Satisfactory
45	Abiral Singh	161246	14-08-2019	14-08-2019	Satisfactory
46	Sahil Kaith	161247	14-08-2019	14-08-2019	Satisfactory
47	Vrinda Choudhary	161248	14-08-2019	14-08-2019	Satisfactory
48	Skund Verma	161249	14-08-2019	14-08-2019	Satisfactory
49	Akash Mahajan	161250	14-08-2019	14-08-2019	Satisfactory
50	Harshita Chauhan	161251	14-08-2019	14-08-2019	Satisfactory
51	Faiz Ali	161252	14-08-2019	14-08-2019	Satisfactory
52	Anmol Garg	161253	12-08-2019	12-08-2019	Satisfactory
53	Ankita Chauhan	161254	12-08-2019	12-08-2019	Satisfactory
54	Varan Kaushal	161255	12-08-2019	12-08-2019	Satisfactory
55	Mukul Sharma	161256	12-08-2019	12-08-2019	Satisfactory
56	Vishal Pant	161257	12-08-2019	12-08-2019	Satisfactory
57	Rishi Kumar Rai	161259			Unsatisfactory
58	Sandeep Hodkasia	161260	12-08-2019	12-08-2019	Satisfactory
59	Ishan Gupta	161261	12-08-2019	12-08-2019	Satisfactory
60	Aditya Mohan	161262	12-08-2019	12-08-2019	Satisfactory
61	Rishabh Malhotra	161263	12-08-2019	12-08-2019	Satisfactory
62	Arunish Sharma	161264	12-08-2019	12-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
63	Aditya Jain	161265	12-08-2019	12-08-2019	Satisfactory
64	Vasu Gupta	161266	12-08-2019	12-08-2019	Satisfactory
65	Manas Dubey	161267	12-08-2019	12-08-2019	Satisfactory
66	Rajat Kumar Puri	161269	12-08-2019	12-08-2019	Satisfactory
67	Paritosh Sharma	161270	12-08-2019	12-08-2019	Satisfactory
68	Varun Choudhary	161271	12-08-2019	12-08-2019	Satisfactory
69	Shiva Chandel	161272	13-08-2019	13-08-2019	Satisfactory
70	Ashish Bhardwaj	161273	26-08-2019	26-08-2019	Satisfactory
71	Aditya Thakur	161274	13-08-2019	13-08-2019	Satisfactory
72	Nishchal Kumar Garg	161275	13-08-2019	13-08-2019	Satisfactory
73	Sidhant Thakur	161276			Unsatisfactory
74	Ketan Batra	161277	13-08-2019	13-08-2019	Satisfactory
75	Laxit Rana	161278	13-08-2019	13-08-2019	Satisfactory
76	Ayush Agrawal	161279	13-08-2019	13-08-2019	Satisfactory
77	Vivek Sharma	161280	13-08-2019	13-08-2019	Satisfactory
78	Aditya Chaudhary	161281	13-08-2019	13-08-2019	Satisfactory
79	Ankit Srivastava	161284			Unsatisfactory
80	Atharvan Gupta	161286	13-08-2019	13-08-2019	Satisfactory
81	Shashank Shekhar	161287	13-08-2019	13-08-2019	Satisfactory
82	Akriti Sood	161288	13-08-2019	13-08-2019	Satisfactory
83	Sakshi Chhimpa	161289	13-08-2019	13-08-2019	Satisfactory
84	Mayank Bisht	161290			Unsatisfactory
85	Viplove Sharma	161291	13-08-2019	13-08-2019	Satisfactory
86	Sarthak Thakur	161292	14-08-2019	14-08-2019	Satisfactory
87	Sidhant Sharma	161293	14-08-2019	14-08-2019	Satisfactory
88	Kritika Sharma	161294	14-08-2019	14-08-2019	Satisfactory
89	Hritik Negi	161295	14-08-2019	14-08-2019	Satisfactory
90	Divyam Kudeshia	161296	14-08-2019	14-08-2019	Satisfactory
91	Rohit Garg	161297	14-08-2019	14-08-2019	Satisfactory
92	Shivam Garg	161298	14-08-2019	14-08-2019	Satisfactory
93	Abhiraj Srivastava	161299	14-08-2019	14-08-2019	Satisfactory
94	Ayush Saini	161300	26-08-2019	26-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
95	Anusheel Priyam	161301	14-08-2019	14-08-2019	Satisfactory
96	Anshul Sharma	161303	14-08-2019	14-08-2019	Satisfactory
97	Akshit Gupta	161304	14-08-2019	14-08-2019	Satisfactory
98	Aditi Manglesh	161305	14-08-2019	14-08-2019	Satisfactory
99	Munish Thakur	161306	14-08-2019	14-08-2019	Satisfactory
100	Nishil Pagare	161307	14-08-2019	14-08-2019	Satisfactory
101	Anand Vashistha	161308	14-08-2019	14-08-2019	Satisfactory
102	Ajay Kumar	161309	14-08-2019	14-08-2019	Satisfactory
103	Tavishi Sharma	161310	13-08-2019	13-08-2019	Satisfactory
104	Ritin Bhardwaj	161311	12-08-2011	12-08-2011	Satisfactory
105	Abhishek Bhardwaj	161312	12-08-2011	12-08-2011	Satisfactory
106	Pradyut Lohani	161313	12-08-2011	12-08-2011	Satisfactory
107	Arpit Jain	161314	12-08-2011	12-08-2011	Satisfactory
108	Piyush Taneja	161316	12-08-2011	12-08-2011	Satisfactory
109	Harshit Chrangoo	161317	12-08-2011	12-08-2011	Satisfactory
110	Manika Kansal	161318	12-08-2011	12-08-2011	Satisfactory
111	Kashish Bajaj	161319	12-08-2011	12-08-2011	Satisfactory
112	Shivang Goyal	161320	12-08-2011	12-08-2011	Satisfactory
113	Pamit Kumar Singh	161321	12-08-2011	12-08-2011	Satisfactory
114	Shubham Gupta	161322	12-08-2011	12-08-2011	Satisfactory
115	Nikhil Jangra	161323	12-08-2011	12-08-2011	Satisfactory
116	Aayushman Saraswat	161324	12-08-2011	12-08-2011	Satisfactory
117	Prashasy Ashok	161325	12-08-2011	12-08-2011	Satisfactory
118	Sankalp Singhania	161326	12-08-2011	12-08-2011	Satisfactory
119	Mayank Fulera	161327	12-08-2011	12-08-2011	Satisfactory
120	Aman Srivastav	161328	13-08-2019	13-08-2019	Satisfactory
121	Asmita Sharma	161329	13-08-2019	13-08-2019	Satisfactory
122	Satyam Aggarwal	161330	13-08-2019	13-08-2019	Satisfactory
123	Varun Saxena	161332	13-08-2019	13-08-2019	Satisfactory
124	Garvit Gupta	161333	13-08-2019	13-08-2019	Satisfactory
125	Abhishek Raj	161334			Unsatisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
126	Suyash Pandey	161335	13-08-2019	13-08-2019	Satisfactory
127	Rishabh Agarwal	161336	13-08-2019	13-08-2019	Satisfactory
128	Hemant Chauhan	161337	13-08-2019	13-08-2019	Satisfactory
129	Hima K S	161338	13-08-2019	13-08-2019	Satisfactory
130	Sanchit Thakur	161340			Unsatisfactory
131	Sanya Ahuja	161341	13-08-2019	13-08-2019	Satisfactory
132	Ankit Gera	161342	13-08-2019	13-08-2019	Satisfactory
133	Rishabh Goyal	161343	13-08-2019	13-08-2019	Satisfactory
134	Shubham Singla	161344	13-08-2019	13-08-2019	Satisfactory
135	Shivam Tyagi	161345	13-08-2019	13-08-2019	Satisfactory
136	Upasana Bhasin	161347	13-08-2019	13-08-2019	Satisfactory
137	Divyansh Kushwaha	161348			Unsatisfactory
138	Tushar Gautam	161350	14-08-2019	14-08-2019	Satisfactory
139	Rashi Gupta	161351	14-08-2019	14-08-2019	Satisfactory
140	Simran Paul	161352	14-08-2019	14-08-2019	Satisfactory
141	Bhavna Verma	161353	14-08-2019	14-08-2019	Satisfactory
142	Arpit Dogra	161355	14-08-2019	14-08-2019	Satisfactory
143	Varun Mishra	161356	14-08-2019	14-08-2019	Satisfactory
144	Naman Bangathia	161357	14-08-2019	14-08-2019	Satisfactory
145	Sparsh Bhardwaj	161358	14-08-2019	14-08-2019	Satisfactory
146	Anmol Rana	161359	14-08-2019	14-08-2019	Satisfactory
147	Tikshika Gupta	161360	14-08-2019	14-08-2019	Satisfactory
148	Vipul Kashyap	161361	14-08-2019	14-08-2019	Satisfactory
149	Ridhi Soni	161362	14-08-2019	14-08-2019	Satisfactory
150	Shobhit	161363	14-08-2019	14-08-2019	Satisfactory
151	Sakshum Kalsotra	161364	14-08-2019	14-08-2019	Satisfactory
152	Himanshu Nadda	161366	14-08-2019	14-08-2019	Satisfactory
153	Riya Sharma	161367	14-08-2019	14-08-2019	Satisfactory
154	Prag Sangha	161368	16-08-2019	16-08-2019	Satisfactory
155	Rahul Rana	161369	14-08-2019	14-08-2019	Satisfactory
156	Aabhas Kashyap	161370	16-08-2019	16-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
157	Anshul Thakur	161371	16-08-2019	16-08-2019	Satisfactory
158	Naveen Sharma	161372	16-08-2019	16-08-2019	Satisfactory
159	Piyush Thakur	161373	16-08-2019	16-08-2019	Satisfactory
160	Shivam Jagota	161375	16-08-2019	16-08-2019	Satisfactory
161	Saurav Thakur	161376	16-08-2019	16-08-2019	Satisfactory
162	Manish Sharma	161377	14-08-2019	14-08-2019	Satisfactory
163	Yashwin S Guleria	161378	16-08-2019	16-08-2019	Satisfactory
164	Prashant Gautam	161379	16-08-2019	16-08-2019	Satisfactory
165	Manu Gupta	161380			Unsatisfactory
166	Rahil Patial	161381	16-08-2019	16-08-2019	Satisfactory
167	Kartik Mahajan	161382	16-08-2019	16-08-2019	Satisfactory
168	Vanshika Chauhan	161383	13-08-2019	13-08-2019	Satisfactory
169	Gulshan Sankhyan	161384	16-08-2019	16-08-2019	Satisfactory
170	Angana Kaushal	161385	14-08-2019	14-08-2019	Satisfactory
171	Riya Singh	161386	14-08-2019	14-08-2019	Satisfactory
172	Rohit Kashyap	161387	17-08-2019	17-08-2019	Satisfactory
173	Sarthak Singh	161389	17-08-2019	17-08-2019	Satisfactory
174	Muskan Kaushal	161390	17-08-2019	17-08-2019	Satisfactory
175	Jyotir Aditya Sharma	161452	21-08-2019	21-08-2019	Satisfactory
176	Srishti Gupta	161453	13-08-2019	13-08-2019	Satisfactory
177	Himanshu Gupta	161454	14-08-2019	14-08-2019	Satisfactory
178	Naimish Awasthi	161455	17-08-2019	17-08-2019	Satisfactory
179	Shubham Garg	161456	17-08-2019	17-08-2019	Satisfactory
180	Dhruv Dhingra	161457	17-08-2019	17-08-2019	Satisfactory
181	Shailesh Mishra	161458			Unsatisfactory
182	Nidhish Manchanda	161459	17-08-2019	17-08-2019	Satisfactory
183	Rishabh Tewari	161460	17-08-2019	17-08-2019	Satisfactory
184	Sajal Lahoti	161461	17-08-2019	17-08-2019	Satisfactory
185	Dhairya Agarwal	161462	17-08-2019	17-08-2019	Satisfactory
186	Vikas Singh	161463	17-08-2019	17-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
187	Rahul Gupta	161465	17-08-2019	17-08-2019	Satisfactory
188	Kanishk Kala	161466	14-08-2019	14-08-2019	Satisfactory
189	Sachin	161467	17-08-2019	17-08-2019	Satisfactory
190	Mukul Chugh	161468	17-08-2019	17-08-2019	Satisfactory
191	Udisha Pandey	161469	17-08-2019	17-08-2019	Satisfactory
192	Hritik Agarwal	161470	23-08-2019	23-08-2019	Satisfactory
193	Prattyush S Sinha	161471	17-08-2019	17-08-2019	Satisfactory
194	Chandrashekhar Choudhary	161472	17-08-2019	17-08-2019	Satisfactory
195	Arpit Tyagi	161473	22-08-2019	22-08-2019	Satisfactory
196	Amritanshu Singh	161474	17-08-2018	17-08-2018	Satisfactory
197	Bhawna	161476	17-08-2018	17-08-2018	Satisfactory
198	Shruti Parihar	161477	17-08-2018	17-08-2018	Satisfactory
199	Ayush Patel	161478	17-08-2018	17-08-2018	Satisfactory
200	Shail Vatsal Vashist	161480	17-08-2018	17-08-2018	Satisfactory
201	Prajwal Thakur	161616	17-08-2018	17-08-2018	Satisfactory

(Signature of HOD)

Industrial Training 2019 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	151001	SAHIL SINGLA	Numitech Solutions
2	151002	ADITYA THAKUR	PRASAR BHARATI
3	151004	MANISHA SHARMA	BSNL MSC Shimla
4	151005	ANISH VIJAN	NIELIT , Chandigarh
5	151007	ANUJ PURWAR	Semi Conductor Laboratory
6	151008	PARAS MITTAL	Newvision softcom and consultancy Pvt. Ltd.
7	151009	SAHAJ CHOPRA	BHARAT ELECTRONICS LIMITED
8	151010	KARTIK BANTA	Ericsson Global Services India Limited
9	151011	RITUL SINGH	Bharat Sanchar Nigam Limited
10	151012	JAGRITI TANDON	Jaypee University of Information Technology
11	151013	MOHIT PATEL	BSNL
12	151015	MOHIT SACHDEVA	Reliance Communications Limited
13	151016	REETIKA MITTAL	Mazagon dock shipbuilders limited
14	151017	AYUSHI AWASTHI	Bharat Sanchar Nigam Limited
15	151018	ISHITA	TCS
16	151019	MAHIMA SURI	Doordarshan, Jammu Kendra
17	151021	RICHA BHARDWAJ	Thinknext technologies pvt limited
18	151022	MAHESH KUMAR	Bsnl
19	151023	NIKHIL THAKUR	BSNL
20	151024	AKRITI GUPTA	INTEX
21	151025	KARAN AHUJA	BHEL
22	151027	AKSHAT BHATNAGAR	Siemens Technology and Services, Bangalore
23	151028	KRITIKA CHAUDHARY	DEAL
24	151030	AJAY SINGH	Maruti Suzuki
25	151031	MOHIT KUMAR GUPTA	Blue Star Limited
26	151034	PRASHANT ARYA	Reliance Jio Infocomm Ltd
27	151037	NIKHIL K SHANDELYA	BHEL
28	151039	AMOGH MISHRA	Bharat Sanchar Nigam Limited
29	151040	RHEA KUKRETI	Seceon
30	151041	BHUMIKA GARG	CDAC
31	151042	JASLEEN KAUR	CDAC Mohali
32	151043	MAHIMA PARASHAR	Cdac Mohali
33	151044	DHRUV GARG	HFCL
34	151045	RAMNEET KAUR	bsnl
35	151047	PRAFULL RAINA	CENTRE FOR DEVELOPMENT OF ADVANCED COMPUTING
36	151048	SANCHIT DANG	Bharat Electronics Limited, Panchkula
37	151049	AKHIL RANA	BSNL - Palampur
38	151052	HIMANSHU CHOUDHARY	K.C Kasliwal Thermal Training Institute
39	151053	HARSHIT JAIN	Tevetron technologies pvt. Ltd.
40	151055	SACHIN TAKYAR	HP Computer
41	151056	RUSHIL BHATNAGAR	prasar bharati
42	151057	LOVISH SINGLA	Hindustan aeronautics limited
43	151058	SIDDHARTH SHARMA	MARICO INDIA PVT.LTD
44	151059	RIYA OHRI	BSNL
45	151060	ANUBHAV TOMAR	PWD
46	151061	KAUSHIKEE	University of Information Science and Technology of Ohrid, Macedonia
47	151063	SHRUTI SABHERWAL	NTPC
48	151064	DEEPANKAR MATHUR	Purple Panda Fashions Private Limited

21/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
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P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

49	151065	PARTH DUBEY	Reliance Communications Limited
50	151066	GUNDEEP SINGH	NTPC Limited
51	151069	SMRITI THAKUR	Ambuja Cement
52	151070	MAHIMA AGARWAL	Bharat Electronics limited
53	151073	SUCHITA SINGH KANTHWAL	Think Next
54	151076	SWARIT SOOD	Macrew Technologies Pvt Ltd.
55	151077	NIKHIL VERMA	DOORDARSHAN KENDRA SHIMLA
56	151079	ABHINANDAN SHARMA	Bharat Electronics Limited, Panchkula
57	151080	SHIVAM VERMA	Bharat electronics limited
58	151081	SHAURYA MEHROTRA	Realiance Jio
59	151082	SIDDHIKA SETH	Bsnl
60	151085	KARMANYA SHARMA	C-DAC Mohali
61	151086	MANAN KASHMIRI	Rooman technologies pvt . Ltd
62	151087	KRITTIKA TEWARI	Motilal Nehru National Institute of Technology
63	151088	MANIKYA SABHARWAL	NHPC
64	151089	AADEESH JAIN	Prasar Bharati, ALL INDIA RADIO :CHHATARPUR
65	151090	ANNIE SHARMA	TCIL-IT ,
66	151091	SHIVANGI	IIT Delhi
67	151092	SHRIYA VANDITA	LG electronics (Greater Noida)
68	151093	ARPIT RITURAJ	DMRC
69	151095	AKSHIT CHANDEL	BSNL
70	151097	RISHAB UPMANYU	National Institute of Information Technology
71	151098	RISHABH KANWAR	HTIS Telecom
72	151100	KANCHAN RANI	B4S solutions pvt limited
73	151101	MEDHA GUPTA	Telecommunications Consultants India Limited-Information Technology(TCIL-IT)
74	151102	AKSHIT SHARMA	Blue Star Limited
75	151103	GOURI SHARMA	B4S solution private limited
76	151105	SIMRAN CHAUHAN	Telecommunications Consultants India Ltd-Information Technology(TCIL-IT)
77	151106	DIVYANSH KAISTHA	BSNL
78	151107	PALLVI	B4S Solutions Pvt. Ltd.
79	151108	APOORV UPADHYAY	BSNL
80	151109	SAHIL JAS	Himachal Futuristic Communications Ltd.
81	151110	SANDEEP SHARMA	Mind Grind private limited
82	151112	PARAS GUPTA	Internshala

09/08/2022

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Industrial Training 2020 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	161002	Tanveer singh Sodhi	AAI
2	161003	AKSHAY SOM	Doordarshan kendra , delhi
3	161005	Samson Shukla	Cetpa Infotech Pvt. Ltd.
4	161006	Sumit Thakur	Doordarshan Kendra
5	161007	Mohit Garg	Whiz Infotel
6	161009	Satyam Kumar	Bharat Electronics Limited, Ghaziabad
7	161011	Sarthak kaushik	Cetpa Infotech
8	161014	Anushka Shukla	ATC, Airport Authority of India, IGI AIRPORT, NEW DELHI
9	161015	Siddharth Singh	Aptron solutions Ltd
10	161016	Priyanshi Rastogi	National Thermal Power Corporation
11	161017	Kanika Chaudhary	Powertel, powergrid corporation of India LTD.
12	161021	Himanshi Singh	NIIT Technologies
13	161022	Lavish kumar jangir	Brain Stem Technologies
14	161023	Parthsarthi Bassi	Bharat Electronics Limited, Panchkula
15	161024	Manasvi Kashyap	Oil and Natural Gas Corporation ltd
16	161025	Shivansh Gusain	IRDE
17	161030	Himanshu Walia	Oceana Tech
18	161031	Megham Garg	Oceana Tech
19	161032	Tanya gupta	DUCAT institute ,noida
20	161033	Kushagra Srivastava	Aptron Solution Pvt. Ltd.
21	161034	Nilesh Kishor	Indian Railways, Bareilly
22	161035	Aditya Mohan	ThreatLandscape Cyber Solutions Private Limited
23	161037	Sparsh mahajan	Airmesh communications limited
24	161042	Sonia Jain	Oceana Tech
25	161043	Bahar sharma	Bharat electronics limited
26	161044	Mayank gupta	I3indya technologies
27	161045	Shailu Srivastava	BHARAT SANCHAR NIGAM LIMITED,PATNA
28	161046	Narendra Jangid	Adhoc Networks
29	161047	Suresh Arora	i3indiya technologies
30	161048	Pranav Bansal	Network Bulls
31	161051	Sanchit Garg	Advanced Tech.
32	161053	arpit rana	HP-PWD
33	161055	Abhinandan Thakur	NKC Projects pvt ltd
34	161056	Kriti Verma	BEL
35	161057	Riya Tyagi	SSDN TECHNOLOGY
36	161058	Sughosh Sharma	BSNL (Ghumarwin branch)
37	161060	Abhinav Sharma	Jetking
38	161061	Ashish Kumar	Netmax Technologies pvt. ltd.
39	161062	Abhishek Jha	LG India
40	161063	ALOK SHEKHAR BHARDWAJ	INFOSEEK TECHNOLOGIES , LUCKNOW
41	161066	Ritankshee	Kvch Oracle
42	161067	Mukul Gupta	Oceana Tech IN (Mohali)
43	161068	Inderpreet singh	Netmax Technologies Pvt. Ltd. , Chandigarh
44	161069	Mehak Beakta	Bharat Electronics Limited
45	161070	Rushmika Singh	Powertel, Powergrid corporation india Ltd.
46	161072	Akhilesh Kumar	Akvo Atmospheric Water Systems
47	161073	Surbhi Garg	NIIT
48	161074	Yashvir Singh	Bharat Electronics Limited
49	161075	Bhavya Chadha	Bharat Electronics Limited(BEL)
50	161076	Anshul Kumar	Oceanatech
51	161077	Harshita Rana	FranConnect software Pvt. Ltd.

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52	161078	Tarun Gupta	Softechno Institute
53	161080	Ayshika Kapoor	ICT Academy - Indian Institute of Technology, Kanpur
54	161081	Utkarsh Gupta	Intercity Foundation
55	161082	Shikhar Srivastava	Volumetree
56	161083	Apurva Padiyal	CETPA Infotech Pvt Ltd
57	161084	Stakshi Sharma	Oceana Tech
58	161085	Ranjan Kumar	InterNext Engineering Solution Pvt. Ltd.
59	161086	Devashish Dimri	IRDE,DRDO,Dehradun
60	161087	Shikhar Srivastava	Railtel Corporation of India Limited
61	161088	Nupur Chaturvedi	NTPC Faridabad
62	161089	Diuman Mahajan	Edoofa
63	161090	Deepak Kumar	Niks technology
64	161091	PAYOOSNI SINGH	Maruti Suzuki
65	161092	ashish kumar verma	infoseek
66	161093	Aditya Tiwari	Niks Technology
67	161094	TANMAY CHAUDHARY	ONGC DEHRADUN
68	161095	Samyak Jain	Cloudxchange.io
69	161098	Yatharth Gautam	Cetpa Infotech Private Limited
70	161099	Somya Chaturvedi	North Western Railways
71	161100	Ajay thakur	Thinknext
72	161102	Archit Sugha	Oceana Tech
73	161104	Abhishek Koundal	Jetking
74	161107	shubham jamwal	BSNL SOLAN
75	161108	Prashant Sharma	BSNL
76	161110	Hardik sharma	Thinknext
77	161111	Abhishek sharma	Inx infotech
78	161112	Arushi verma	BSNL telecommunications
79	161113	Aayush Goyal	Oil and Natural Gas Corporation Limited
80	161114	Nitin kumar	BSNL
81	161115	Sarthak Srivastava	JIL information technology limited
82	161116	Kanwar Singh	Hughes communications
83	161117	manthan chauhan	BSNL
84	161118	Prashant kumar	BSNL

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Industrial Training 2021 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	161029	Akhilesh Sapehia	Jaypee university of information and technology
2	171001	Abhishek Bundel	Internshala Trainings
3	171002	Ayush Kumar Jaiswal	Internshala
4	171003	Mukul Bhatia	Internshala
5	171004	Diwakshu katoch	Internshala
6	171005	Akhil Chauhan	Internshala
7	171006	Prerna Kanwar	Internshala
8	171007	Sahitya bhalaik	Jaypee University of information technology
9	171008	Sanket Saxena	Internshala
10	171009	Kritik Verma	Internshala
11	171010	Sangharsh singh	Cetpa infotech Pvt ltd Noida,Uttar Pradesh
12	171012	tushar agarwal	INTERNSHALA
13	171014	ujjwal jain	INTERNSHALA
14	171015	Soham Ahuja	United Nations
15	171016	Keshav Vohra	Internshala
16	171018	rohit behl	internshala
17	171019	Shivam Sinha	Imternshala
18	171020	Sanyam	Internshala
19	171021	Archita Gupta	Internshala
20	171023	Abhishek Malik	Internshala
21	171024	pankaj	Jaypee University of information and technology
22	171025	kshitij katoch	INTERNSHALA
23	171026	Spardha Kapil	Geeks For Geeks
24	171027	sheetanshu saurabh	internshala
25	171028	Hitesh Thakur	Internshala
26	171029	Sarthak Bisht	Jaypee University of Information technology
27	171030	ALOK PANDEY	Internshala
28	171031	Shubham Kumar	INTERNSHALA
29	171032	Shivansh Suhane	JUIT
30	171033	Ritwik Sood	Jaypee University of Information Technology
31	171034	Tarun Arora	Internshala
32	171035	Ishan Goyal	Internshala
33	171036	Dhananjai Bhalaik	Internshala
34	171037	Shaurya Rajput	Jaypee University of Information Technology, Solan
35	171038	Ananya Shukla	Jaypee University of Information Technology
36	171039	Rajnikant yadav	Jaypee University Of Information Technology
37	171040	Piyush Kumar Singh	Internshala Online Training
38	171042	Ramit Bawa	Intershala
39	171043	Saurav Anand	Internshala Trainings
40	171044	Shivansh Dubey	Internshala
41	171046	Utkarsh Srivastava	Internshala
42	171047	Mehul Bandlish	Jaypee University of Information technology
43	171048	Prashant Jaiswal	Intershala
44	171049	Shachi Sharma	Internshala
45	171050	Ananya Sharma	Internshala
46	171051	Shruti Sharma	Internshala
47	171052	Shubham Singh	INTERNSHALA
48	171053	Nikita Pandey	Internshala
49	171056	Prachi Pal	internshala
50	171057	Bandana Pal	INTERNSHALA
51	171058	Ojasvi	Internshala

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

52	171059	Anushka Dixit	Internshala
53	171060	surya mahajan	internshala
54	171061	Saksham goel	Fastor
55	171062	Vishal Srivastava	EICT Academy, IIT Kanpur
56	171065	Shruti Singh	Internshala
57	171069	Anshul Deorane	Internshala
58	171070	Anupam Srivastava	Internshala Traning
59	171071	Saksham Tandon	internshala
60	171073	Saumya Jajodia	Internshala
61	171074	Akshat Gupta	Webdew
62	171075	Aadhya Bajpai	Verzeo
63	171076	Sudhanshu Mishra	Jaypee University of Information Technology, Solan
64	171078	Nikhil Tanwar	Internshala
65	171079	Kartikey Bindal	Internshala
66	171080	Nikunj	Internshala

04/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Industrial Training 2022 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	181001	Priyank Srivastava	Internshala
2	181005	Vinayak Tiku	internshala
3	181006	Harsh mishra	EduMoon
4	181007	Aditya Kumar Jaiswal	Internshala
5	181008	Arsh Kumar	Internshala
6	181009	Gurpreet Singh	AM Tech Networks
7	181010	Surbhi kumari	Internshala
8	181011	Kartikay Kaushal	Internshala
9	181012	Nikhil Thakur	Internshala
10	181013	NIKHIL YADAV	INTERNSHALA
11	181015	Rakshit Sharma	BSNL
12	181016	Kamlesh kumar	Internshala
13	181017	Kshitij Sharma	Internshala trainings.
14	181019	Avinash Verma	INTERNSHALA
15	181020	Mudit katiyar	Internshala
16	181022	Himanshu Thakur	Internsalla
17	181023	Aditya Mishra	Internsala
18	181024	Kirti Parshionikar	Internshala
19	181025	Tavleen Singh	Internshala
20	181027	Vaibhav Rastogi	Internshala
21	181028	RAGHAV SHARMA	Internshala

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Dept: CIVIL BATCH - 2014 - 2018

Year - 2017

(1)

University Requirement							Requirement for Accredation / Ranking Agencies				
S.No.	Enrollment No.	Branch	Period of Training (No. Of Weeks)	Training Start Date	Training End Date	Status (Satisfactory / Unsatisfactory)	Institute/Company Name	Subject/Topic of Training	Domain/Area of Training	Stipend Received (If Any)	Aadhaar Number of Student
1	141263	CE	7	29-05-2017	15-07-2017	Satisfactory	HPRDCL	Construction of roads (e PMS, RADMS, ROMDAS)	Construction, System Analysis	NO	987868746848
2	141601	CE	6	29-05-2017	08-07-2017		P K Construction Shimla	Construction of Advocate Chamber near High Court and Construction of Parking Complex at Chotta Shimla	Construction	NO	884578188153
3	141603	CE	6								
4	141604	CE	5	29-06-2017	30-06-2017	Satisfactory	HCC	Construction of NH- 34, 4 Lane (Farrakka, Raiganj Section)	Construction	NO	541252189749
5	141605	CE	6	01-06-2017	15-07-2017	Satisfactory	Indian Railways	Construction of Limited Height Subway under Railway Department	Construction	NO	253736151986
6	141606	CE	6	05-06-2017	15-07-2017	Unsatisfactory	JPHRF	Bridge Construction Pung Khadd Sujanpur Tihra (Baijnath Project)	Construction,Project Planning	NO	961362475484
7	141606	CE	6	05-06-2017	15-07-2017	Satisfactory	Syal and associates	Structural Design	Design	NO	253657634246
8	141607	CE	6	05-06-2017	10-07-2017	Satisfactory	IOCL	Construction of Oil Water Seperetor	Construction	NO	
9	141608	CE	6	05-06-2017	10-07-2017	Satisfactory	SJVNL	LUHRI Hydropower Electric Project	Construction Planning and Design	NO	470244564729
10	141609	CE	4	05-06-2017	05-07-2017		L&T	Commercial Building Construction (DLF Building in Gurugram)	Construction	NO	364358230523
11	141610	CE	6	10-06-2017	17-07-2017	Satisfactory	IIT BHU	Design and Analysisof Pitched Roof Truss Using STAAD Pro	Design and Analysis	NO	493996271823
12	141611	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	275103106040
13	141612	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Cresidential Building, Galaxy Heights	Construction	NO	911325199048
14	141613	CE	7	01-06-2017	16-07-2017	Satisfactory	PWD	Road Construction and maintenance at Mathura, UP	Construction	NO	748717944274
15	141615	CE	7	05-06-2017	17-07-2017	Satisfactory	HPPWD	Construction of Post Graduate College	Construction	NO	533592259552
16	141616	CE	6	01-06-2017	12-07-2017	Satisfactory	SJVNL	Rampur Hydro Power Station	Construction, Planning and Design	NO	642152102942
17	141617	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Sawra Kuddu Hydropower Electric Project	Construction	NO	280189613732
18	141619	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	813332527314
19	141620	CE									Pending
20	141621	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Comprehensive Development of Corridor on Outer Ring between Mukbara Chowk to Wazirabad	Construction	NO	612109067356
21	141622	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Construction of 33/220 kV Pooling Sub-Station	Construction	NO	Pending
22	141624	CE	6	02-06-2017	15-07-2017	Satisfactory	Ved Prakash Gupta	Construction of boundary wall	Construction	No	509062120363
23	141626	CE	6	05-06-2017	14-Jul	Satisfactory	DMRC	Contruction of Underground Metro	Construction and Surveying	No	725029168548
24	141627	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	867788791400
25	141630	CE	7	05-06-2017	17-07-2017	Satisfactory	M G Construction	Four Laning of Kharar-Kurali Section of NH-21 in the State of Punjab on EPC Mode	Construction	NO	958830245993
26	141633	CE	6	04-06-2017	15-07-2017	Satisfactory	HPPWD	Construction of Underground Waste Collection System at Dharamsala	Construction	NO	233964159757
27	141634	CE	6	01-06-2017	14-07-2017	Satisfactory	DrukGreen	Hydro Power Electric Project	Construction	NO	
28	141636	CE	6	05-06-2017	18-07-2017	Satisfactory	CPWD	Electrofitting	Estimation and Operation	NO	842943328993
29	141637	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Hydro Power Electric Project	Construction, Analysis and Design	NO	440663665519
30	141638	CE	6	05-06-2017	15-07-2017		NTPC	Q & A	Quality management	NO	493285031722
31	141639	CE	6	01-06-2017	15-07-2017	Satisfactory	Paharpur Cooling towers	Paharpur Cooling Tower Pvt. Ltd.	Construction and Estimation	NO	457229473693
32	141640	CE	6	08-05-2017	17-06-2017	Satisfactory	PWD	Construction tubewell	Construction and Site Investigation	NO	280438057959
33	141641	CE	5	12-06-2017	10-07-2017	Satisfactory	Renuka	Road Construction and Survey	Construction	NO	488631889287
34	141642	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Sewage Treatment Plant Operation	Site Visit and Design	NO	597153870545
35	141643	CE	6	04-06-2017	07-07-2017	Satisfactory	DMRC	Construction of Underground Metro at R K Puram and Hauz Khas Station	Construction	NO	596538281137
36	141644	CE	6	01-06-2017	12-07-2017	Satisfactory	HPPWD	Construction of multi purpose hall	Construction	NO	958282824701
37	141645	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Swara Kuddu Hydropower Project	Construction	NO	736402354843
38	141646	CE	6	01-06-2017	15-07-2017	Satisfactory	GAWAR	Road Construction of 4- Lane Panchkula and Yamuna Nagar (NH- 73)	Construction		
39	141647	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Stability analysis of Luhri HEP Stage-1	Design	NO	339213751913

40	141648	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Multiporpous Sports Stadium Ramamandir Mandi, Veterinary Hospital and College Rampur	Construction, Maintenance and Design	NO	619538309958
41	141650	CE	7	01-06-2017	15-07-2017	Satisfactory	Jaiprakash And Sons	Construction of Mega Hostel Block in NIT Hamirpur	Construction	NO	352700960035
42	141651	CE	6	01-06-2017	11-07-2017	Satisfactory	Sunrises Structures	Construction of Sun Twilight Villas and Commercials	Construction	NO	830120993663
43	141652	CE	6	01-06-2017	12-07-2017	Satisfactory	SIDCL	Road Construction	Analysis	NO	986065011649
44	141653	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Intze Tank Design	Design	NO	957707592017
45	141654	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rain Water Harvesting Tank Transportation of Exsisting Lawn Into Rain Garden	Construction	NO	873345654123
46	141655	CE	7	29-05-2017	17-07-2017	Satisfactory	UPRNNL	Building Construction	Construction	NO	584157677760
47	141656	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
48	141661	CE	7	15-06-2017	31-07-2017	Satisfactory	PWD	Residential Building Construction	Construction	NO	867213841974
49	141662	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Retaining wall construction	Construction	NO	387802984564
50	141663	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
51	141664	CE	6	29-05-2017	08-07-2017	Satisfactory	PK Construction	Car Parking Building Construction	Construction	NO	767631756894
52	141665	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rainwater Harvesting Tank	maintenance	NO	435539216442
53	141666	CE	6	05-06-2017	17-07-2017	Satisfactory	CPWD	Building Maintenance	maintenance	NO	989868620530
54	141667	CE	6	31-05-2017	11-07-2017	Satisfactory	SPCL	Construction of Bus Terminus and Parking	Construction	NO	282070765310
55	141668	CE	6	03-06-2017	14-07-2017		RED	Construction of hall	Construction	NO	892245015469
56	141669	CE	5	13-06-2017	15-07-2017	Satisfactory	PWD Dharamsala	Construction of roads	Construction	NO	774345360402
57	141670	CE	5	29-05-2017	30-06-2017	Unsatisfactory	HCC	4 Laning Farakka Raiganj Section	Construction	NO	454223208162
58	141671	CE	6	28-05-2017	14-07-2017	Satisfactory	Bansal Engineers	Building Construction	Contruction	Yes	597323298747
59	141672	CE	4	30-05-2017	30-06-2017	Satisfactory	ADRDE	Design of building	Design	NO	505348241275
60	141673	CE	6	01-06-2017	12-07-2017	Satisfactory	UPPWD	Road Contruction	Construction	NO	
61	141674	CE	6	01-06-2017	12-07-2017	Satisfactory	REASI	Water Distribution System Study	Analysis	NO	671722842063
62	141675	CE	7	01-06-2017	14-07-2017	Satisfactory	Bareilly Development Authority	Laying of Sewer Pipelines	Construction	NO	334980591932
63	141676	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Galaxy Heights Project	Construction	NO	312625902455
64	141677	CE	6	01-06-2017	11-07-2017	Satisfactory	Swastik	Underground Substation Gurugram	Construction	NO	831847743627
65	141678	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Casting of Bridge	Testing	NO	569738883949
66	141679	CE	5	30-05-2017	12-07-2017	Satisfactory	H. C. Bansal Engineers and Contractors	Building Construction	Construction	Yes	692342550589
67	141680	CE	6	01-06-2017	05-07-2017	Satisfactory	ERA	Road Construction	Construction	NO	567280282077
68	141681	CE	6	11-06-2017	16-07-2017	Satisfactory	HPPCL	Barrage division of sainj Hydro Power Electric Project	Construction	NO	346612434207
69	141682	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Construction of PG	Construction	NO	639806463361
70	141683	CE	4	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Ambuja Cement Plant Visit	Materials	NO	334214454998
71	141684	CE	6	29-05-2017	08-07-2017	Satisfactory	HPPWD	Development of New OPD at IGMC Shimla	Construction	NO	995522249985
72	141686	CE	6	01-06-2017	01-07-2017	Satisfactory		Building Construction (Mohali)	Construction	NO	411889377530
73	141687	CE	6	12-06-2017	22-07-2017	Satisfactory	HPPWD	HP State Library Building Contruction	Construction	NO	885024325960
74	141688	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Testing of materials	Testing	NO	868824583795
75	141689	CE	6	03-06-2017	17-07-2017	Unsatisfactory	Indian Railways	Construction of Railway Track	Construction	NO	409852377341
76	141690	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	691456577638
77	141691	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Highway Maintenance and PG College	Constructon	NO	
78	141692	CE	6	01-06-2017	12-07-2017	Satisfactory	DMRC	Underground Substation	Construction/ Surveying/ Geotechnical Investigation	NO	862339185428
79	141693	CE	4	05-06-2017	08-07-2017	Satisfactory	BP	Construction of new filling shed	Construction	NO	530137391222
80	141694	CE	6	30-05-2017	10-07-2017	Satisfactory	PWD	Construction of roads	Construction	NO	424523018138
81	141695	CE	6	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Concrete Mix Design	Design	NO	579641278502
82	141696	CE	4	31-05-2017	30-06-2017	Satisfactory	CPWD	Construction	Construction	NO	876016738612
83	141697	CE	4	01-06-2017	30-06-2017	Satisfactory	LMRC	Lucknow Metro Construction	Construction	NO	928844325232
84	141698	CE	7	01-06-2017	07-07-2017	Satisfactory	SJVNL	Retaining wall construction	Construction	NO	341163355226

Dept: CIVIL ENGG. BATCH : 2015-2019

Year - 2018

(2)

Summer/Industrial Training Status Summary August 2018 (Batch 2015-2019)									
S no.	**Roll No.**	**Student Name**	**Department**	**Training Dairy Submitted (Yes/No)**	**Training Report Submitted (Yes/No)**	**Training Certificate Submitted (Yes/No)**	**Viva held on (Date)**	**Viva Taken by (Faculty Name)**	**Status (Satisfactory/ Unsatisfactory)**
1	141658	Pankaj Sankhyan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Anirban Dhulia & Mr. Aakash Gupta	**Satisfactory**
2	151113	Akal Singh Gurung	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
3	151601	Divesh Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
4	151602	Puneet Pal Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
5	151604	Nikhilesh Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
6	151605	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
7	151606	Abhishek Ahluwalia	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
8	151608	Hetain Sahi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
9	151610	Kuenzang Sc Choden	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
10	151612	Shally Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
11	151613	Shivani Negi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
12	151614	Charu Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
13	151616	Harsh Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
14	151617	Ammaan Zahoor Chat	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
15	151618	Sarthak Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
16	151619	Akshay Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Rishi Rana & Mr. Kaushal Kumar	**Satisfactory**
17	151620	Rizul Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
18	151621	Abhimanyu P Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
19	151622	Arpan Chaudhary	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
20	151623	Tarun Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
21	151624	Jigyasu Khanna	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
22	151625	Harish Chander	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
23	151626	Manik Ohri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
24	151627	Ankur Jaret	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
25	151628	Ankit Tilokta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
26	151629	Sudhanshu Manikpuri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
27	151630	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
28	151631	Abhinav Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
29	151632	Gaurav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
30	151633	Divyam Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

31	151634	Dipanshu Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Niraj Parihar & Mr. Aakash Gupta	**Satisfactory**
32	151635	Ajay Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
33	151636	Himanshu Yadav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
34	151637	Aditya Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
35	151638	Prikshit Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
36	151639	Ashish Dangwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
37	151640	Akshay Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
38	151641	Vaibhav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
39	151642	Akshay Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
40	151643	Aatish Rajta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
41	151645	Puneet Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
42	151646	Pratiyush Kothari	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
43	151647	Shashi Shekhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
44	151648	Vinayak Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
45	151649	Sumit Dhankhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
46	151650	Gourav Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Abhilash Shukla & Mr. Kaushal Kumar	**Satisfactory**
47	151651	Nikhil Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
48	151652	Anirudh Pratap	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
49	151654	Nitesh Chandel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
50	151655	Arpan Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
51	151656	Shubham Soni	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
52	151657	Akhil Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
53	151658	Himanshu Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
54	151659	Parikshit Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
55	151660	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
56	151661	Amit Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
57	151662	Ashutosh Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
58	151664	Amit Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
59	151666	Deval Ashish	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
60	151667	Dikshant Agarwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

61	151668	Bhupinder Singh Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Saurabh Rawat & Mr. Abhilash Shukla	**Satisfactory**
62	151669	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
63	151670	Ahtesham Hussain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
64	151671	Nakshatra Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
65	151672	Ashish Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
66	151673	Ishan Uniyal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
67	151674	Suryabhan Singh Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
68	151675	Harshit Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
69	151676	Vedansh Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
70	151677	Gaurav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
71	151679	Maanik Vatshyayan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
72	151680	Saksham Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
73	151682	Divesh Narang	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
74	151683	Shubham Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
75	151684	Vikas Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
76	151687	Ayush Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Amardeep and Dr. Saurav	**Satisfactory**
77	151688	Kuldeep Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
78	151689	Mayank Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
79	151690	Tarun Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
80	151691	Vibhor Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
81	151692	Karan Goel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
82	151693	Saksham Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
83	151694	Ankush Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
84	151696	Saksham Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
85	151697	Sparsh N.K. Lath	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
86	151698	Kartikey	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

Kaushal Kr.

Industrial Training Coordinator

HoD CE

Dept: CIVIL BATCH - 2016-2020

Year - 2019

(3)

INDUSTRIAL TRAINING STATUS OF CIVIL ENGINEERING DEPARTMENT (2019-20)					
S. No.	Enrol. No.	Name of Student	Industrial Training Report Submitted by Student to Deptt.	Viva Held on	Status of Indutrial Training Completion
1	161659	Pranav Gupta	Submitted	08-08-2019	Satisfactory
2	161664	Vivek Kashyap	Submitted	08-08-2019	Satisfactory
3	161053	Arpit Rana	Submitted	08-08-2019	Satisfactory
4	161663	Seraj Habib	Submitted	08-08-2019	Satisfactory
5	161666	Shivam Nag	Submitted	08-08-2019	Satisfactory
6	161055	Abhinandan Thakur	Submitted	08-08-2019	Satisfactory
7	161688	Shivam Gupta	Submitted	08-08-2019	Unsatisfactory
8	161628	Sangay Zangmo	Submitted	08-08-2019	Satisfactory
9	161695	Parmila Gurung	Submitted	08-08-2019	Satisfactory
10	161693	Karma Yangzom	Submitted	08-08-2019	Satisfactory
11	161631	Sonam Tshomo	Submitted	08-08-2019	Satisfactory
12	161652	Abhinav Choudhary	Submitted	08-08-2019	Satisfactory
13	161627	Harjot Singh	Submitted	08-08-2019	Satisfactory
14	161615	Vivek Pundir	Submitted	08-08-2019	Satisfactory
15	161673	Shourabh Maanju	Submitted	08-08-2019	Satisfactory
16	161674	Aryan	Submitted	07-08-2019	Satisfactory
17	161675	Saksham Mahajan	Submitted	07-08-2019	Satisfactory
18	161625	Ajay Sharma	Submitted	07-08-2019	Satisfactory
19	161620	Piyush Pathania	Submitted	07-08-2019	Satisfactory
20	161639	Rohit Kumar	Submitted	07-08-2019	Satisfactory
21	161661	Shubang Malgotra	Submitted	07-08-2019	Satisfactory
22	161634	Yashwant Singh Rana	Submitted	07-08-2019	Satisfactory
23	161691	Ritesh Kumar Chaurasia	Submitted	07-08-2019	Satisfactory
24	161602	Harshit Bansal	Submitted	07-08-2019	Satisfactory
25	161685	Hitesh Panwar	Submitted	07-08-2019	Satisfactory
26	161655	Alakshender Singh Wazir	Submitted	07-08-2019	Satisfactory
27	161614	Himanshu Kapoor	Submitted	07-08-2019	Satisfactory
28	161612	Gaurav Chauhan	Submitted	07-08-2019	Satisfactory
29	161678	Ujjwal Nadda	Submitted	07-08-2019	Satisfactory
30	161687	Utkarsh Chauhan	Submitted	07-08-2019	Satisfactory
31	161608	Saurav Singh	Submitted	07-08-2019	Satisfactory
32	161665	Deepak Sharma	Submitted	07-08-2019	Satisfactory
33	161690	Shivam Sharma	Submitted	07-08-2019	Satisfactory
34	161637	Mayank Sharma	Submitted	07-08-2019	Satisfactory
35	161654	Samarth Sharda	Submitted	07-08-2019	Satisfactory
36	161646	Shushant Gupta	Submitted	07-08-2019	Satisfactory
37	161689	Abhishek Thakur	Submitted	07-08-2019	Satisfactory
38	161677	Keshav Singh Thakur	Submitted	07-08-2019	Satisfactory
39	161603	Abhishek Sharma	Submitted	07-08-2019	Satisfactory
40	161630	Pema Zangmo	Submitted	07-08-2019	Satisfactory
41	161694	Pema Yangden	Submitted	07-08-2019	Satisfactory
42	161629	Ngawang Dolkar	Submitted	07-08-2019	Satisfactory
43	161647	Chahat Garg	Submitted	07-08-2019	Satisfactory
44	161611	Ambuj Awasthi	Submitted	07-08-2019	Satisfactory
45	161626	Nikhil Kumar	Submitted	07-08-2019	Satisfactory
46	161649	Anish Kapil	Submitted	07-08-2019	Satisfactory
47	161686	Siddharth Verma	Submitted	07-08-2019	Satisfactory
48	161680	Deven Mahajan	Submitted	07-08-2019	Satisfactory
49	161640	Gunjan Katoch	Submitted	07-08-2019	Satisfactory
50	161671	Nitin Thakur	Submitted	07-08-2019	Satisfactory
51	161651	Nishant Thakur	Submitted	07-08-2019	Unsatisfactory
52	161636	Mukul Prashar	Submitted	07-08-2019	Unsatisfactory
53	161635	Tejas garg	Submitted	07-08-2019	Satisfactory
54	161617	Anmol Singhal	Submitted	07-08-2019	Satisfactory
55	161613	Harshit Saxena	Submitted	07-08-2019	Satisfactory
56	161696	Yash Goyal	Submitted	07-08-2019	Satisfactory
57	161698	Nagawang Dorji	Submitted	07-08-2019	Satisfactory
58	161605	Amber Soni	Submitted	07-08-2019	Satisfactory
59	161607	Sumit Kumar	Submitted	07-08-2019	Satisfactory
60	161642	Xitiz Sen	Submitted	07-08-2019	Satisfactory
61	161684	Ria Thakur	Submitted	07-08-2019	Satisfactory
62	161676	Rishav Kumar Tiwari	Submitted	07-08-2019	Satisfactory

63	161604	Amol Srivastava	Submitted	07-08-2019	Unsatisfactory
64	161601	Ritanjay ✓	Submitted	07-08-2019	Satisfactory
65	161285	Rishi Singh ✓	Submitted	07-08-2019	Satisfactory
66	161624	Ketan Mishra ✓	Submitted	07-08-2019	Satisfactory
67	151691	Vibhor Gautam ✓	Submitted	29-07-2019	Satisfactory
68	161692	Leki Wangchuk ✓	Submitted	21-08-2019	Satisfactory
69	161670	Prasanna Kumar	Not Submitted	-	Unsatisfactory
70	161644	Shankar Kumar	Not Submitted	-	Unsatisfactory
71	161001	Nikhil Sharma	Not Submitted	-	Unsatisfactory
72	161653	Pritul	Not Submitted	-	Unsatisfactory
73	161658	Aditya Vikram Singh Jamwal	Not Submitted	-	Unsatisfactory
74	161657	Anirudhu Guleria	Not Submitted	-	Unsatisfactory
75	161656	Kartikey	Not Submitted	-	Unsatisfactory
76	161668	Nikhil Negi	Not Submitted	-	Unsatisfactory
77	161632	Cheku Dorji	Not Submitted	-	Unsatisfactory
78	141658	PANKAJ SANKHYAN	Not Submitted	-	Unsatisfactory
79	151605	GAURAV SHARMA	Not Submitted	-	Unsatisfactory
80	151688	KULDEEP RANA	Not Submitted	-	Unsatisfactory
81	141625	Namit Sharma	Not Submitted	-	Unsatisfactory
82	141628	HARSH VARDHAN SINGH	Not Submitted	-	Unsatisfactory
83	141659	RAHUL VERMA	Not Submitted	-	Unsatisfactory
84	141663	ADITYA DHIMAN	Not Submitted	-	Unsatisfactory
85	151634	DIPANSHU THAKUR	Not Submitted	-	Unsatisfactory
86	151646	PRATIYUSH KOTHARI	Not Submitted	-	Unsatisfactory
87	151651	NIKHIL KUMAR SHARMA	Not Submitted	-	Unsatisfactory
88	151656	SHUBHAM SONI	Not Submitted	-	Unsatisfactory
89	151668	BHUPINDER SINGH VERMA	Not Submitted	-	Unsatisfactory
90	151677	GAURAV THAKUR	Not Submitted	-	Unsatisfactory
91	151679	MAANIK VATSHYAYAN	Not Submitted	-	Unsatisfactory
92	151689	MAYANK SINGH	Not Submitted	-	Unsatisfactory
93	151694	ANKUSH KUMAR	Not Submitted	-	Unsatisfactory
94	151616	HARSH CHAUHAN	Not Submitted	-	Unsatisfactory

Anirban Dhulia
23/08/2019

Mr. Anirban Dhulia
Mr. Aakash Gupta
Industrial Training Co-ordinator

23/8/19

Prof. Ashok Kumar Gupta
Head of the Department
Civil Engineering

HOD
CE DEPT

Received ✓ Documents
23/08/19

Dept: CIVIL ENGG. BATCH - 2017-2021

Year - 2020-2021

(4)

Summer/Industrial Training Status Summary August 2020 (Batch 2016-2020 and 2017-21)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/Unsatisfactory)
1	161001	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	22-08-2020	Mr. Anirban Dhulia	Satisfactory
2	161604	Amol Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
3	161636	Mukul Prashar	Civil Engineering	Yes	Yes	Yes	22-08-2020	Dr Aakash Gupta	Satisfactory
4	161644	Shankar Kumar	Civil Engineering	Yes	Yes	Yes	14-08-2020	Mr Anirban Dhulia and Dr Aakash Gupta	Satisfactory
5	171067	Aman Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
6	171601	Ishant Shekhri	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
7	171602	Hemant Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
8	171603	Aditya Abrol	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
9	171604	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
10	171606	Shekhar Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
11	171607	Kanishk Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
12	171608	Pawas Soni	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
13	171609	Gaurav Prakash Negi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
14	171610	Gunjan Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
15	171611	Aviral Roy	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
16	171612	Aditya Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
17	171614	Vivek Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
18	171615	Vaibhav Singh	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
19	171616	Ashish Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
20	171617	Harsh Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
21	171618	Aditya Rana	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
22	171620	Hardik Nagpal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
23	171621	Rishabh Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
24	171622	Akshit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
25	171623	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
26	171624	Saurabh Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
27	171626	Sourav Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
28	171628	Anjan Sood	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
29	171629	Sameep Aggarwal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
30	171630	Anmol Katana	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
31	171631	Manik Seth	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
32	171632	Siddhant Dubey	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
33	171633	Nikhil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
34	171634	Sukrit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
35	171635	Sahil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
36	171636	Rohit Kumar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
37	171637	Divyanshu Pandit	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory

38	171638	Anubhav Kundal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
39	171639	Mehul Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
40	171642	Saksham Kaushal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
41	171644	Saurabh Tomar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
42	171645	Kartik Verma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
43	171646	Ankit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
44	171647	Dikshant Joshi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
45	171649	Ritvik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
46	171650	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
47	171651	Suraj Chaudhary	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
48	171652	Chander Bhushan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
49	171653	Abhay	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
50	171654	Mohit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
51	171655	Aditya Shekhar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
52	171656	Rijul Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
53	171657	Tanish Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
54	171659	Akshay Pathania	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
55	171661	Himanshu Bansal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
56	171662	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
57	171664	Venus Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
58	171665	Naveen Karar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
59	171666	Nikhil Shukla	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
60	171671	Aditya Nath	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
61	171681	Abhishek Bind	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
62	171682	Sanju Kanwar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
63	171683	Manik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
64	171684	Lokesh Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory

Traning and Placement Coordinator

Head of the Department

25/8/2020

Received
29/08/2020

Dept : CIVIL ENGG. BATCH : 2018-2022

Year : 2021

(5)

Summer/Industrial Training Status Summary August 2021 (Batch 2018-22)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/ Unsatisfactory)
1	181602	Yamit Dhalaik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
2	181603	Ujjwal Kumar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
3	181604	Harshit Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
4	181605	Shubham	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
5	181606	Varun Kapil	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
6	181607	Abhay Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
7	181608	Aniket	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
8	181610	Vishal Garg	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
9	181611	Madhvender Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
10	181612	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
11	181613	Rishabh Jaswal	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
12	181614	Vishali Thapta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
13	181615	Abhay Kaith	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
14	181616	Sushant	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
15	181617	Ritik Kumar Puri	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
16	181618	Abhay Kanwar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
17	181619	Rohit Lakhera	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
18	181621	Atul Vashisht	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
19	181622	Navneet Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
20	181623	Deepak Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
21	181625	Abhay Joshi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
22	181626	Muskan Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
23	181627	Utkarsh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
24	181629	Suryansh Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
25	181630	Bhuvan Walia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
26	181631	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
27	181632	Arnav Rawat	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
28	181633	Aditya Chauhan	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
29	181634	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
30	181635	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Received
17/08/21

31	181637	Abhishek Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
32	181638	Sahil Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
33	181639	Abhinesh Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
34	181642	Yash Gupta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
35	181643	Pranav Dogra	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
36	181644	Anushka Anand	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
37	181645	Amish Kartik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
38	181647	Sonam Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
39	181648	Passang Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
40	181649	Phub Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
41	181650	Sonam Tshering	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
42	181651	Tshering Gyeltshen	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
43	181652	Kinley Zam	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
44	181653	Sonam Tshewang Dema	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
45	181654	Dechen Tshomo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
46	181655	Namgay Wangmo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
47	181656	Pema Yuden	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
48	181657	Saijal Verma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
49	181659	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
50	181660	Hemang Jandrotia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
51	181661	Deval	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
52	181662	Ayush Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
53	181663	Ritik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Kaushal Kumar

Signature of Departmental Summer Training Coordinator

4/8/21

Signature of the Head of Department

Dr. Ashish Kumar
Professor & HOD of Civil Engineering
Jaypee University of Information Technology,
Waknaghat, Distt.-Solan (HP) 173234 India

Received
17/08/21

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2020					
Student Roll No.	**Student Name**	**Branch**	**Internship Start Date**	**Internship End Date**	**Company/Institute Name**
161502	Tanya Singh	BI	5/29/2019	07-09-2019	Cetpa Infotech Pvt Ltd
161503	Vidushi Agnihotri	BI	06-03-2019	7/15/2019	Appin Technology Chandigarh
161504	Medhavi Pokhriyal	BI	06-03-2019	7/13/2019	Birla Institute of Scientific Research
161505	Shivani Rana	BI	5/27/2019	07-06-2019	Central University of Himachal Pradesh Dharamshala
161506	Disha Angra	BI	5/27/2019	07-04-2019	Symbiosis school of biological sciences, symbiosis international (Deemed
161509	SARTHAK UPADHYAY	BI	5/24/2019	07-10-2019	CSIR PALAMPUR
161511	Saishta Shree	BI	5/27/2019	07-04-2019	Symbiosis School of Biological Sciences,Symbiosis
161512	Himani Chauhan	BI	03-06-2019	July-16-2019	SPIC Center Of Excellence

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2020					
Student Roll No.	**Student Name**	**Branch**	**Internship Start Date**	**Internship End Date**	**Company/Institute Name**
161513	Yashaswi Singh Chauhan	BI	06-03-2019	7/13/2019	Jaypee University of information technology
161514	Naman Sharma	BI	06-03-2019	7/13/2019	Jaypee institute of information technology
161516	Sayra Sood	BI	06-03-2019	7/16/2019	Society for Promotion of IT in Chandigarh
161518	Piyus Mohanty	BI	06-05-2019	7/15/2019	Delhi University South Campus
161801	Rachit thakur	BT	06-03-2019	07-09-2019	Fermenta biotech ltd
161802	Himadri Hauta	BT	5/28/2019	07-06-2019	CPRI, Bemloi
161803	Lakshay Sharma	BT	5/23/2019	07-10-2019	CPRI shimla
161805	Vasudha Porwal	BT	5/27/2019	07-06-2019	University of Delhi South Campus

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2020					
Student Roll No.	**Student Name**	**Branch**	**Internship Start Date**	**Internship End Date**	**Company/Institute Name**
161806	Shriya Arora	BT	06-03-2019	7/15/2019	Dr BR Ambedkar Centre for Biomedical Research , Delhi University
161808	Mansi sharma	BT	5/27/2019	07-06-2019	Indira Gandhi Medical College shimla
161809	Harshita Mahajan	BT	06-03-2019	7/18/2019	Panjab University (Microbiology Department)
161811	Shivangini Singh	BT	5/27/2019	07-05-2019	Nit hamirpur
161813	vaibhav Handa	BT	06-05-2019	7/16/2019	national dairy research institute
161814	Shubhangi Ghosh	BT	06-01-2019	7/15/2019	National Institute of plant genomic and research delhi
161815	Rakshita	BT	06-03-2019	7/18/2019	Panjab University (Department of Microbiology)
161816	Srajit Saraswat	BT	5/27/2019	07-10-2019	SD Biosensor

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2020					
Student Roll No.	**Student Name**	**Branch**	**Internship Start Date**	**Internship End Date**	**Company/Institute Name**
161817	Shiuli Samaddar	BT	5/27/2019	6/26/2019	Institute of Liver and Biliary Sciences, Delhi
161818	Saniya mehta	BT	5/27/2019	07-05-2019	NIT Hamirpur
161819	Prahi gupta	BT	5/25/2019	07-10-2019	RDESCO AGRO FOODS
161821	Aditi Sharma	BT	5/25/2019	7/19/2019	University of Hyderabad
161822	VEENA KUMARI	BT	06-03-2019	7/15/2019	MAHAVIR CANCER SANSTHAN
161823	Aashina Puri	BT	5/27/2019	07-05-2019	CSIR-IHBT, Palampur
161824	Shristi Saha	BT	5/27/2019	07-05-2019	DRDO Delhi
161825	Priyanjalee Bhattacharjee	BT	06-03-2019	7/13/2019	Allele Life Sciences

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2020					
Student Roll No.	**Student Name**	**Branch**	**Internship Start Date**	**Internship End Date**	**Company/Institute Name**
161826	Palak Sharma	BT	06-03-2019	07-12-2019	CSIO
161828	sara bhinta	BT	5/27/2019	07-05-2019	Indra Gandhi Medical College(IGMC)
161829	Sambhavana	BT	06-03-2019	7/13/2019	Banaras Hindu University
161830	Tanvi Sehgal	BT	5/27/2019	07-05-2019	CSIR- IHBT
161831	RIMGIM KOUL	BT	5/24/2019	07-10-2019	Verka MILK PLANT Chandgarh
161832	Arush Kaushal	BT	5/27/2019	07-05-2019	CSIR -IHBT Palampur
161833	B.Soumya	BT	5/22/2019	07-02-2019	Institute of horticulture technology
161836	Dhruvika	BT	5/30/2019	07-12-2019	Nestle Samalkha

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2020					
Student Roll No.	**Student Name**	**Branch**	**Internship Start Date**	**Internship End Date**	**Company/Institute Name**
161837	Ayushi Khimta	BT	06-01-2019	7/13/2019	Indea Gandhi Medical College
161838	Arsh Tyagi	BT	06-01-2019	07-11-2019	Haldirams pvt ltd
161839	JASDEEP KAUR	BT	5/27/2019	07-06-2019	Indira gandhi medical college shimla
161840	Kritika Sharma	BT	6/27/2019	7/13/2019	Allele Life Sciences
161841	Shreeya Agrawal	BT	5/27/2019	07-05-2019	Defence Institute of Physiology and Allied Sciences, DRDO, DELHI
161842	Sunainy Ajrawat	BT	06-03-2019	7/14/2019	University of Jammu
161844	Abhishek Dogra	BT	06-01-2019	07-12-2019	HPMC, Jarol
161845	Bandana Thakur	BT	5/27/2019	07-06-2019	Indira Gandhi Medical College Shimla

Summer Industrial Training Evaluation - 2019

rahul.shrivastava to: jata.shankar, poonam.sharma, narendra.kumar

08/08/2019 03:53 PM

Cc: bi_bt, placementcell@mail.juit.ac.in, nafisuddin.khan, pankaj.kumar

Bcc: rahul.shrivastava@juit.ac.in

As instructed by the HoD, BTBI,

a 'Summer Industrial Training Evaluation committee' comprising of the following :

Prof. Sudhir Syal

Dr. Jata Shankar - Coordinator

Dr. Poonam Sharma

Dr. Narendra Kumar

Dr. Rahul Shrivastava - reporting to the office

has been constituted to evaluate final year students through viva-voce, related to 4-6 weeks training done by them during May-July 2019.

All evaluations are to be completed by 21 Aug'2019.

Thanks and regards,

Rahul
Dr. Rahul Shrivastava
Associate Professor, Department of Biotechnology and Bioinformatics
Jaypee University of Information Technology
Waknaghat, Solan -173 234, H.P. (India)
Mo; +91-8894-135-634, +91-8894-285-634
Off:01792-239355; Fax: 01792-245362

SUMMER RESEARCH FELLOWSHIP PROGRAMME
CERTIFICATE

This is to certify that Ms Aditi Sharma worked on a project entitled "To study the role of iron in regulation of GCN4 in yeast genome" during May - July 2019 as a Summer Research Fellow under the supervision of Professor Sepuri Naresh Babu, University of Hyderabad, Hyderabad. The Summer Research Fellowship Programme is jointly sponsored by IASc (Bengaluru), INSA (New Delhi) and NASI (Prayagraj).

M.R.N. Murthy

Place: Bengaluru
Date: 23-09-2019

M.R.N. Murthy
Chairman, Science Education Panel

16/8/21

Aditi Sharma

INDIAN ACADEMY OF SCIENCES
C.V Raman Avenue, P.B.No.8005, Raman Research Institute Campus, Sadashivanagar, Bengaluru 560 080, INDIA

To
The HOD
Biotech Department
JUIT, Solan

Subject: Regarding Summer Training

Respected Sir,

I, LAVIN SHARMA have completed my Summer Training from INBIT, Delhi. I lost my training diary due to some reason but I have submitted my Training Certificate and Training Report of the same. Kindly consider my case.

Thanking you
Yours faithfully
Lavin Sharma
151848

18/8/19

He has submitted Report of the training.

From: jata.shankar/Juit
To: somlata.sharma/Juit@juit.ac.in
Cc: rahul.shrivastava/Juit@juit.ac.in, poonam.sharma/Juit@juit.ac.in, narendra.kumar/Juit@juit.ac.in, sudhir.syal/Juit@juit.ac.in

Date: Saturday, August 10, 2019 12:41PM
Subject: INTERNSHIP VIVA

Ms. Somlata, Please email to 7th semester BI students

We will have viva for 7th semester BI following students on Monday 12/08/2019 at 4-5pm (in HOD room) for their Internship. Jata Shankar

1	161502	Tanya Singh
2	161503	Vidushi Agnihotri
3	161504	Medhavi Pokhriyal
4	161505	Shivani Rana
5	161506	Disha Angra
6	161509	SARTHAK UPADHYAY
7	161511	Saishta Shree
8	161512	Himani Chauhan
9	161513	Yashaswi Singh Chauhan
10	161514	Naman Sharma
11	161516	Sayra Sood
12	161518	Piyus Mohanty

10/8/2019

10/8/19

Internship viva

From: somlata sharma (somisharon@gmail.com)

To: jash116@gmail.com; rahul.shrivastava@juit.ac.in; e2-e3_bt_3rd-year2016-2020@googlegroups.com

Date: Tuesday, 13 August, 2019, 12:22 pm IST

We will have viva for 7th semester BT students on Wednesday 14/08/2019 at 2-3pm & on 16/08/19 at 4-5pm (in HOD room) for their Internship training. Students in the order of their roll number will appear with two copies of certificate and Internship diary (mandatory).
PS: paste a passport size on the diary. Other time slot will be given later.
Jata Shankar

--
Somlata Sharma
Sr. Lab Engineer
Jaypee University of Information Technology
Distt. Solan, Waknaghat.

13/8/19

13/8/19

Summer Industrial Training - Batch 2020					
Department of Biotechnology & Bioinformatics					
S.No.	Roll No.	NAME	Industrial Training Report Submitted By Student to Deptt.	Viva Held On	STATUS
1	151848	LAVIN SHARMA	12-Aug-19	12-Aug-19	SATISFACTORY
2	161502	TANYA SINGH	12-Aug-19	12-Aug-19	SATISFACTORY
3	161503	VIDUSHI AGNIHOTRI	12-Aug-19	12-Aug-19	SATISFACTORY
4	161504	MEDHAVI POKHRIYAL	12-Aug-19	12-Aug-19	SATISFACTORY
5	161505	SHIVANI RANA	12-Aug-19	12-Aug-19	SATISFACTORY
6	161506	DISHA ANGRA	12-Aug-19	12-Aug-19	SATISFACTORY
7	161508	DUSHYANT SHARMA	12-Aug-19	12-Aug-19	SATISFACTORY
8	161509	SARTHAK UPADHYAY	12-Aug-19	12-Aug-19	SATISFACTORY
9	161510	SUNIDHI THAKUR	12-Aug-19	12-Aug-19	SATISFACTORY
10	161511	SAISHTA SHREE	12-Aug-19	12-Aug-19	SATISFACTORY
11	161512	HIMANI CHAUHAN	12-Aug-19	12-Aug-19	SATISFACTORY
12	161513	YASHASWI SINGH	12-Aug-19	12-Aug-19	SATISFACTORY
13	161514	NAMAN SHARMA	12-Aug-19	12-Aug-19	SATISFACTORY
14	161515	SHUBHADITYA	12-Aug-19	12-Aug-19	SATISFACTORY
15	161516	SAYRA SOOD	12-Aug-19	12-Aug-19	SATISFACTORY
16	161518	PIYUS MOHANTY	12-Aug-19	12-Aug-19	SATISFACTORY
17	161801	RACHIT THAKUR	12-Aug-19	12-Aug-19	SATISFACTORY
18	161802	HIMADRI HAUTA	12-Aug-19	12-Aug-19	SATISFACTORY
19	161803	LAKSHAY SHARMA	12-Aug-19	12-Aug-19	SATISFACTORY
20	161805	VASUDHA PORWAL	12-Aug-19	12-Aug-19	SATISFACTORY
21	161806	SHRIYA ARORA	12-Aug-19	12-Aug-19	SATISFACTORY
22	161808	MANSI SHARMA	12-Aug-19	12-Aug-19	SATISFACTORY
23	161809	HARSHITA MAHAJAN	12-Aug-19	12-Aug-19	SATISFACTORY
24	161811	SHIVANGINI SINGH	12-Aug-19	12-Aug-19	SATISFACTORY
25	161813	VAIBHAV HANDA	12-Aug-19	12-Aug-19	SATISFACTORY
26	161814	SHUBHANGI GHOSH	12-Aug-19	12-Aug-19	SATISFACTORY
27	161815	RAKSHITA	12-Aug-19	12-Aug-19	SATISFACTORY
28	161816	SRAJIT SARASWAT	12-Aug-19	12-Aug-19	SATISFACTORY
29	161817	SHIULI SAMADDAR	12-Aug-19	12-Aug-19	SATISFACTORY
30	161818	SANIYA MEHTA	13-Aug-19	13-Aug-19	SATISFACTORY
31	161819	PRAHI GUPTA	13-Aug-19	13-Aug-19	SATISFACTORY
32	161822	VEENA KUMARI	13-Aug-19	13-Aug-19	SATISFACTORY
33	161823	AASHINA PURI	13-Aug-19	13-Aug-19	SATISFACTORY
34	161824	SHRISTI SAHA	13-Aug-19	13-Aug-19	SATISFACTORY
35	161825	PRIYANJALEE	13-Aug-19	13-Aug-19	SATISFACTORY
36	161826	PALAK SHARMA	13-Aug-19	13-Aug-19	SATISFACTORY
37	161828	SARA BHINTA	13-Aug-19	13-Aug-19	SATISFACTORY
38	161829	SAMBHAVANA	13-Aug-19	13-Aug-19	SATISFACTORY
39	161830	TANVI SEHGAL	13-Aug-19	13-Aug-19	SATISFACTORY

Summer Industrial Training - Batch 2020					
Department of Biotechnology & Bioinformatics					
S.No.	**Roll No.**	**NAME**	**Industrial Training Report Submitted By Student to Deptt.**	**Viva Held On**	**STATUS**
40	161831	RIMGIM KOUL	13-Aug-19	13-Aug-19	SATISFACTORY
41	161832	ARUSH KAUSHAL	13-Aug-19	13-Aug-19	SATISFACTORY
42	161833	B.SOUMYA	13-Aug-19	13-Aug-19	SATISFACTORY
43	161836	DHRUVIKA	13-Aug-19	13-Aug-19	SATISFACTORY
44	161837	AYUSHI KHIMTA	13-Aug-19	13-Aug-19	SATISFACTORY
45	161838	ARSH TYAGI	13-Aug-19	13-Aug-19	SATISFACTORY
46	161839	JASDEEP KAUR	13-Aug-19	13-Aug-19	SATISFACTORY
47	161840	KRITIKA SHARMA	13-Aug-19	13-Aug-19	SATISFACTORY
48	161841	SHREEYA AGRAWAL	13-Aug-19	13-Aug-19	SATISFACTORY
49	161842	SUNAINY AJRAWAT	13-Aug-19	13-Aug-19	SATISFACTORY
50	161844	ABHISHEK DOGRA	13-Aug-19	13-Aug-19	SATISFACTORY
51	161845	BANDANA THAKUR	13-Aug-19	13-Aug-19	SATISFACTORY
52	161821	ADITI SHARMA	Certificate Pending from Govt. Body		UNSATISFACTORY

26/8/19

Dr. Rahul Shrivastava
Industrial Training Coordinator

26/8/19

Prof. Sudhir Syal
Head, Dept. BTBI

Tanya Singh
161502

CETPA INFOTECH PRIVATE LIMITED

(An ISO 9001:2015 Certified Company)

Certificate of Training

This is to certify that

TANYA SINGH

has successfully completed Six Weeks Summer Training on
"Machine Learning"
from 29 May to 9 July, 2019
at CETPA INFOTECH PVT. LTD., Noida.

self-attested
Tanya

Anil Kumar Singh
Director-Training

CETPA®
Because Knowledge Matters
www.cetpainfotech.com

Vikas Kalra
Director

Vidushi Agnihotri
Roll No. 161503

ATL Education Foundation

ATL Education Foundation

Certificate of Participation

This is to certify that Mr. /Miss. VIDUSHI AGNIHOTRI has successfully completed 6 WEEKS Industrial Training with ATL Education Foundation, Chandigarh

Technology MACHINE LEARNING WITH PYTHON

Training Period JUN '19 - JUL '19

Project Undertaken "Essay Tone Detector"

His/Her performance during Internship was GOOD

self attested
Agnihotri

Vidushi Agnihotri
Roll No. 161503

Rajandeep
Course Co-ordinator

(3rd June - 15 July '2019)

Authorised Signatory

Birla Institute of Scientific Research

Statue Circle, Jaipur

Medhavi Pokhriyal
161504

CERTIFICATE

This is to certify that

Medhavi Pokhriyal

(B. Tech. Bioinformatics- III Year)

(Jaypee University of Information Technology, Solan, H.P.)

Has attended the summer training in Bioinformatics

for 6 weeks from June 03, 2019 to July 13, 2019

at

Birla Institute of Scientific Research, Jaipur

Sampat

(Dr. Sampat Nehra)

Training Coordinator

(Dr. R.K. Gothwal)

Training Co-Coordinator

Executive Director

Self Attested,
Medhavi

Shivani Rana
161505

Central University of Himachal Pradesh
School of Life Sciences

Dr. Vikram Singh
Assistant Professor
Centre for Computational Biology and Bioinformatics

Phone: +91-9816444313
Email: vikramsingh@cuhimachal.ac.in, vikramsingh.jnu@gmail.com

To Whomsoever it may be concerned

This is to certify that Ms. Shivani Rana, a third year B.Tech. Bioinformatics student in the Jaypee University of Information Technology, Waknaghat bearing roll no. 161505, has worked under my guidance on the topic "Developing and analyzing a miRNA-mRNA interaction network specific to Alzheimer's disease" for her six weeks summer internship during June-July 2019.

This is to further state that she is a very hard-working student having passion for science. She has been very punctual during the internship duration and her efforts to complete the tasks assigned were satisfactory.

I believe, she has the right aptitude for a research project at the interface of Bioinformatics and Computational Biology. She has a very bright future in academia as well as in industry.

17/07/19

Dr. Vikram Singh
(Assistant Professor)

Dr VIKRAM SINGH
Assistant Professor
Centre for Computational Biology & Bioinformatics
School of Life Sciences
Central University of Himachal Pradesh
Dharamshala 176215

161506
Disha Angra

॥वसुधैव कुटुम्बकम्॥

SYMBIOSIS SCHOOL OF BIOLOGICAL SCIENCES

Symbiosis International (Deemed University)

(Established under section 3 of the UGC Act, 1956)

Re-accredited by NAAC with 'A' grade (3.58/4) | Awarded Category - I by UGC

Founder : Prof. Dr. S. B. Mujumdar M.Sc. Ph.D. (Awarded Padma Bhushan and Padma Shri by President of India)

Ref : SSBS/168/02/2019

Date: 4 July 2019

CERTIFICATE

This is to certify that **Ms. Disha Angra** (B.Tech, Bioinformatics) of Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh, has undergone training at **Symbiosis School of Biological Sciences, Symbiosis International (Deemed University), Lavale, Pune, Maharashtra**, from 27th May to 4th of July 2019. During this period she has worked on "**Differential gene expression analysis in schizophrenia patients using publicly available microarray data**" under my guidance.

Ms. Disha Angra was sincere and hardworking during the training. I wish her a successful career.

Self attested
disha

Khare
04.07.2019

॥वसुधैव कुटुम्बकम्॥
SSBS

Dr. Satyajeet Khare

Assistant Professor,

Symbiosis School of Biological Sciences,

Symbiosis International (Deemed University)

Lavale, Pune 412115

भारत संचार निगम लिमिटेड
(भारत सरकार का उपक्रम)
BHARAT SANCHAR NIGAM LIMITED
(A Govt. of India Enterprise)

CERTIFICATE

Vocational/Industrial/Summer Training

No. : GMTD/SOL/Training/31

Certified that Mr. Dushyant Sharma S/o Sh. Gopal Sharma of Jaypee University of IT, Waknaghat,Solan (H.P.), has successfully completed 6 weeks industrial/vocational/summer training in BSNL, Solan w.e.f 17.06.2019 to 27.07.2019.

During the training period student acquainted of working knowledge of OCB-283 exchange lease line/broad band/WLL/GSM/Batteries/Power Plant & Transmission Systems. He has successfully completed the training.

Dated: - 08.08.2019

AGM (EB & Sales)
O/o GMTD Solan

Copy for information to:

1. The Principal Jaypee University of IT, Waknaghat, Solan (H.P.).
2. Student Concerned.
3. Office Copy

161508

सी.एस.आई.आर-हिमालय जैवसंपदा प्रौद्योगिकी संस्थान
पो॰ बॉ॰ न॰ 6 पालमपुर - 176 061 (हि.प्र.) भारत
CSIR-INSTITUTE OF HIMALAYAN BIORESOURCE TECHNOLOGY
CSIR-IHBT
Post Box No. 6 Palampur (H.P.) 176 061 INDIA

Sarthak Upadhyay
161509

Dr. Gireesh Nadda
Senior Scientist
Incharge Training Programme

10th July, 2019

TO WHOM IT MAY CONCERN

This is to certify that **Mr. Sarthak Upadhyay,** a student of B.Tech Bioinformatics, Jaypee University of Information Technology (JUIT) Solan, (Himachal Pradesh) undertook his summer training on the topic **"Basic tools and software used in Bioinformatics"** under the supervision of **Dr. Rakshak Kumar**, Scientist, Biotechnology Division w.e.f. 11th June, 2019 to 10th July, 2019 at this Institute. During the training programme, his conduct has been satisfactory.

I wish him all success in his future endeavours.

गिरीश नड्डा 10/7/19

(Gireesh Nadda)

Self Attested
Sarthak

इ-मेल/E-mail : director@ihbt.res.in
वेबसाइट/Website : http://www.ihbt.res.in
ई.पी.ए.बी.एक्स/EPABX : 91-1894-230742-43,233338-39
फैक्स/Fax : 91-1894-230433

Sarthak Upadhyay
161509

Department of Animal Nutrition
COVAS, CSKHPKV, Palampur176062,
ancovascskhpkv@gmail.com

AN/COVAS/REV/

Dated 7-6-2019

Dr Arun Sharma

Incharge Training

TO WHOM IT MAY CONCERN

This is to certify that **Mr Sarthak Upadhyay,** student of B Tech (Bioinformatics), JP University of Information Technology(JUIT) Solan (HP) undertook training on the topic " **Data Recording in Animal Nutrition lab and Data Feeding in Kiosk"** under my supervision w.e.f. 24th May,19 to7th June ,19 in this department of College of Veterinary and Animal Sciences. During the training, his conduct was found up to the satisfaction. Self Attested

Sarthak

I wish him all success in his future assignments.

Arun Sharma

(Dr Arun Sharma) 7/6/19

SUNIDHI THAKUR
161518

CETPA INFOTECH PRIVATE LIMITED

(An ISO 9001:2015 Certified Company)

Certificate of Training

This is to certify that

SUNIDHI THAKUR

has successfully completed Six Weeks Summer Training on
"Machine Learning"
from 29 May to 9 July, 2019
at CETPA INFOTECH PVT. LTD., Noida.

self attested

Anil Kumar Singh
Director-Training

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Vikas Kalra
Director

Verify this Certificate by Registration Number NSMac29520196W4[illegible]471 at http://www.cetpainfotech.com

161511
Saishta

॥वसुधैव कुटुम्बकम्॥

SYMBIOSIS SCHOOL OF BIOLOGICAL SCIENCES

Symbiosis International (Deemed University)

(Established under section 3 of the UGC Act, 1956)

Re-accredited by NAAC with 'A' grade (3.58/4) | Awarded Category -I by UGC

Founder : Prof. Dr. S. B. Mujumdar M.Sc. Ph.D. (Awarded Padma Bhushan and Padma Shri by President of India)

Ref : SSBS/167/02/2019

Date: 4 July 2019

CERTIFICATE

This is to certify that **Ms. Saishta Shree** (B.Tech, Bioinformatics) of Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh, has undergone training at **Symbiosis School of Biological Sciences, Symbiosis International (Deemed University), Lavale, Pune, Maharashtra,** from 27th May to 4th of July 2019. During this period she has worked on "**Differential gene expression analysis in schizophrenia patients using publicly available microarray data**" under my guidance.

Ms. Saishta Shree was sincere and hardworking during the training. I wish her a successful career.

04.07.2019

॥वसुधैव कुटुम्बकम्॥
SSBS

Dr. Satyajeet Khare

Assistant Professor,

Symbiosis School of Biological Sciences,

Symbiosis International (Deemed University)

Lavale, Pune 412115

Self-assessment

Himani Chauhan
161512

Society for Promotion of Information Technology, Chandigarh

REF NO : SPIC/2019/53772

DATED : 30-07-2019

TO WHOM IT MAY CONCERN

This is to certify that **Ms Himani Chauhan** d/o Sh Krishan Sawroop student of Third Year VIth Semester B.Tech. Bioinformatics from Jaypee University of Information Technology, Solan has completed her six weeks industrial training in **Python** from 03rd June 2019 till 16th July 2019 at SPIC Centre of Excellence under the supervision of Mr Parminder Singh. She worked on project "House **Price Predictor"** in **Python Technology** as front end and SQL Server as back end from 25th June 2019 till 16th July 2019.She has attended the department for required number of days. It embodies the original work and is the result of candidate's own efforts.

Chief Technical Officer
SPIC

Self attested
Himani

EDC Plot No 20, Chandigarh Technology Park
Chandigarh , 160101, Telephone : 0172- 2970450, 2970451

Under the aegis of Department of IT, Chandigarh Administration
PEC Campus, Sector 12, Chandigarh 160 012
Telefax : 0172–2744235, 2745502
Email : info@spicindia.com www.spicindia.com

Summer Training- 2019

Department of Biotechnology & Bioinformatics

Certificate of Participation

Awarded to

YASHASWI SINGH CHAUHAN

in recognition for successfully completing 6 weeks summer training program in the module "Bioinformatics" for duration 01 June - 14 July 2019 at the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan, H.P

Dr. Tiratha Raj Singh
Module Co-ordinator

Dr. Rahul Shrivastava
Training Co-ordinator

Prof. (Dr.) Sudhir Kumar
Head, Biotechnology and Bioinformatics

Jaypee University of Information Technology, Solan

Self attested
21.08.2019



160514

Summer Training- 2019

Department of Biotechnology & Bioinformatics

Certificate of Participation

Awarded to

NAMAN SHARMA

in recognition for successfully completing 6 weeks summer training program in the module "Bioinformatics" for duration 01 June - 14 July 2019 at the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat, Solan, H.P

Dr. Tiratha Raj Singh
Module Co-ordinator

Dr. Rahul Shrivastava
Training Co-ordinator

Prof. (Dr.) Sudhir Kumar
Head, Biotechnology and Bioinformatics

Jaypee University of Information Technology, Solan

16157
Shubhaditya

Birla Institute of Scientific Research

Statue Circle, Jaipur

CERTIFICATE

This is to certify that

Shubhaditya Bhattacharya

(B. Tech. Bioinformatics- III Year)

(Jaypee University of Information Technology, Waknaghat, Solan, H.P.)

Has attended the summer training in Biotechnology & Bioinformatics

for 6 weeks from June 03, 2019 to July 13, 2019

at

Birla Institute of Scientific Research, Jaipur

Self-Attest
Shubhaditya

Sampat

(Dr. Sampat Nehra)

Training Coordinator

(Dr. R.K. Gothwal)

Training Co-Coordinator

Executive Director

SAYRA SOOD
161516

Society for Promotion of Information Technology, Chandigarh

REF NO : SPIC/2019/53773

DATED : 30-07-2019

TO WHOM IT MAY CONCERN

This is to certify that **Ms Sayra Sood** d/o Sh Amit Sood student of Third Year VIIth Semester B.Tech. Bioinformatics from Jaypee University of Information Technology, Solan has completed her six weeks industrial training in Python from 03rd June 2019 till 16th July 2019 at SPIC Centre of Excellence under the supervision of Mr Parminder Singh. She worked on project "House Price Predictor" in **Python Technology** as front end and **SQL Server** as back end from 25th June 2019 till 16th July 2019.She has attended the department for required number of days. It embodies the original work and is the result of candidate's own efforts.

Chief Technical Officer
SPIC

Self Attested
-Sayra Sood

EDC Plot No 20, Chandigarh Technology Park
Chandigarh , 160101, Telephone : 0172- 2970450, 2970451

Under the aegis of Department of IT, Chandigarh Administration
PEC Campus, Sector 12, Chandigarh 160 012
Telefax : 0172-2744235, 2745502
Email : info@spicindia.com www.spicindia.com

Name - Piyus Mohanty
Roll no - 161518
Batch - E2

Dr. Manish Kumar
Assistant Professor
Department of Biophysics
University of Delhi South Campus
Benito Juarez Road, New Delhi-110021
Phone No.: +91-11-24157263
E-mail : manish.imt@gmail.com
manish@south.du.ac.in

डॉ. मनीष कुमार
सहायक प्राध्यापक
जैवभौतिकी विभाग
दिल्ली विश्वविद्यालय दक्षिण परिसर
बेनिटो हुआरेज़ मार्ग, नई दिल्ली-110021
दूरभाष : + 91-11-24157263
ईमेल : manish.imt@gmail.com
manish@south.du.ac.in

Ref: UDSC/BioPhy/MKu/Trainee/15 **Date:** 15-July -2019

CERTIFICATE

This is to certify that the project report entitled as '**Comparative Functional Analysis of Iron Metallo-proteins**' was carried out for partial fulfillment for the award of the degree of B.Tech. degree program. The work is a result of bona-fide work carried out by Mr. **Piyus Mohanty (Registration No. 161518), B.Tech. Bioinformatics student, Jaypee University of Information Technology, P.O. Waknaghat, Teh. Kandaghat, Distt. Solan (H.P.)** during the period **05th June– 15th July 2019**. The above-mentioned project is carried out in my research laboratory at University of Delhi South Campus, New Delhi. **Please note that no part of the work described in this thesis or done during the above-mentioned period, can be published without my explicit written consent.**

Manish Kumar

Manish Kumar
(Supervisor)

डॉ. मनीष कुमार
Dr. Manish Kumar
सहायक प्राध्यापक / Assistant Professor
जैव भौतिकी विभाग
Department of Biophysics
दिल्ली विश्वविद्यालय दक्षिण परिसर
University of Delhi South Campus
नई दिल्ली-११००२१/New Delhi-110021, INDIA

Fermenta Biotech Limited
CIN : U99999MH1986PLC134021
Factory : Village Takoli, P.O. Nagwain, Dist. Mandi - 175 121, Himachal Pradesh, India.
Tel. : +91-1905-287249 / 048 / 246 Fax : +91-1905-287250 E-mail : info@fermentabiotech.com
Website : www.fermentabiotech.com

Rachit Thakur
161801

FBL/HR/2019 DATE : 09.07.2019

TO WHOMSOEVER IT MAY CONCERN

Name	::	Mr Rachit Thakur.
College /Institution Name	::	Jaypee University Waknaghat, Distt. Solan (H.P).
Roll No.	::	161801.
Stream	::	B.Tech Biotechnology
Training Period	::	03.06.2019 To 09.07.2019.
Letter Reference No. of College / Institution	::	T&P/Batch2016-20/1993.

He has successfully completed the Industrial Training for the period mentioned above in our Organization.

His overall performance during the training period with us is found good.

We wish him all success.

For FERMENTA BIOTECH LTD.

(Savita Jamwal)
Sr. MANAGER-HR/ADMIN.

Regd. Office: 'dil' Complex,
Ghodbunder Road, Majiwada,
Thane (W) - 400 610, Maharashtra, India.
Tel. : +91-22-6798 0888
Fax : +91-22-6798 0899
Email : info@fermentabiotech.com
Website : www.fermentabiotech.com

Factory : Z-109 B&C, SEZ II, Dahej,
Taluka - Vagra, Dist. Bharuch - 392 130,
Gujarat, India.
Tel. : +91-2641-291440 / 4
Email : info@fermentabiotech.com
Website : www.fermentabiotech.com

161802
Himadri Hauta

भा.कृ.अ.प - केंद्रीय आलू अनुसंधान संस्थान
शिमला-171001, हि.प्र. (भारत)
ICAR-Central Potato Research Institute
(Indian Council of Agricultural Research)
SHIMLA 171 001, HP

Phone: 0177-2625073 (O), Fax: 0177-2624460 ISO 9001:2015
E-mail- directorcpri@gmail.com Website : http//cpri.icar.gov.in

Dr. Brajesh Singh
Incharge, PME Cell

No.F.PME/4-50/2019
Dated: 08.07.2019

TRAINING CERTIFICATE

This is to certify that **Ms. Himadri Hauta** student of B.Tech, Biotechnology, Jaypee University of Information Technology, Waknaghat, Solan has undergone training in the Division of Seed Technology, w.e.f. 28th May, 2019 to 06th July, 2019 at ICAR - Central Potato Research Institute, Shimla.

Dated: 08.07.2019

In-Charge, PME Cell

प्रभारी, पी.एम.ई. कक्ष
In - Charge P.M.E. Cell
केन्द्रीय आलू अनुसंधान संस्थान
Central Potato Research Institute
शिमला / Shimla - 171001 (H.P.)

Himadri Hauta

Lakshay Sharma
161803

भा.कृ.अ.प - केंद्रीय आलू अनुसंधान संस्थान
शिमला-171001, हि.प्र. (भारत)
ICAR-Central Potato Research Institute
(Indian Council of Agricultural Research)
SHIMLA 171 001, HP

Phone: 0177-2625073 (O), Fax: 0177-2624460 ISO 9001:2015
E-mail- directorcpri@gmail.com Website : http//cpri.icar.gov.in

Dr. Brajesh Singh
Incharge, PME Cell

No.F.PME/4-50/2019
Dated: 22.07.2019

TRAINING CERTIFICATE

This is to certify that **Sh. Lakshya Sharma** student of B.Tech, Biotechnology, Jaypee University of Information Technology, Waknaghat, Solan has undergone training in the Division of Crop Improvement, w.e.f. 23rd May, 2019 to 10th July, 2019 at ICAR - Central Potato Research Institute, Shimla.

Dated: 22.07.2019

In-Charge, PME Cell

प्रभारी, पी.एम.ई. कक्ष
In - Charge P.M.E. Cell
केन्द्रीय आलू अनुसंधान संस्थान
Central Potato Research Institute
शिमला / Shimla (H.P.)

Self Attested
Lakshay.

UDSC

UNIVERSITY OF DELHI – SOUTH CAMPUS

Department of Genetics
Benito Juarez Road, Dhaula Kuan
New Delhi - 110021 India

Tel: 91-11-24110866/24111955 (Ext.172)
Fax: 91-11-24112437/24112761/24115270
E-mail: rajam.mv@gmail.com

Prof. M. V. Rajam, FNA, FNASc, FNAAS, FTSAS

To Whom It May Concern:

This is to certify that Ms. Vasudha Porwal, B. Tech. (VI Semester) student from Jaypee University of Information Technology, Solan (HP) had spent six weeks in my laboratory during 27th May to 6th July 2019 to learn the common techniques in Plant Molecular Biology and Biotechnology. During this period, she has learned some important techniques such as preparation of medium for bacterial and plant tissue culture, plasmid DNA and genomic DNA, and RNA isolations, gel electrophoresis, preparation of competent cells and transformation of *E. coli* and *Agrobacterium tumefaciens* PCR, callus induction and *Agrobacterium*-mediated genetic transformaiton in rice, histochemical assay for GUS activity. She has learned these techniques with enthusiasm and dedication. She is sincere, industrious and devoted to the subject.

I wish her all success in her future endeavors.

Sincerely,

Prof. M. V. Rajam

Vasudha Porwal
161805

Dr. M. V. Rajam, FNA, FNASc, FNAAS, FAPAS
Professor, Department of Genetics
University of Delhi - South Campus
Benito Juarez Rd, New Delhi-110021
TelFax - 011 - 24112437

Shriya Arora
161806

Summer Undergraduate Research Programme -2019

Dr. B.R. Ambedkar Center for Biomedical Research
University of Delhi, Delhi-110007

Certificate of Participation

This is to certify that Mr./Ms./ Shriya Arora has Participated in the Summer Undergraduate Research Programme 2019 organised by Dr. B. R. Ambedkar Center for Biomedical Research, University of Delhi held between 3rd June, 2019 to 15th July, 2019.

Dr. Aparna Dixit
Co-ordinator

Prof. Daman Saluja
Director, ACBR

Shriya Arora
16/8/19

Indira Gandhi Medical College & Hospital Shimla, H.P.

No.HFW(MS)G-5/2019- 668 Dated 10/7/19

CERTIFICATE

Certified that Ms. Mansi Sharma D/O Sh.Sidharth Sharma student of B.Tech (Biotechnology) from Jaypee University Waknaghat Distt. Solan H.P has completed her Observer ship Training w.e.f. 27.05.2019 to 06.07.2019 in the department of Microbiology, Indira Gandhi Medical College Shimla.

During the above period her work and conduct was found satisfactory. She bears good moral character.

161808
Mansi

Sr. Medical Superintendent,
I.G. Hospital, Shimla.

Professor & Head
Department of Microbiology,
Shimla - 171001 (H.P.)

DEPARTMENT OF MICROBIOLOGY,

Panjab University, Chandigarh

SUMMER INTERNSHIP

HANDS ON TRAINING ON MICROBIOLOGICAL TECHNIQUES

JUNE 3- July 18, 2019

Certificate of Participation

This is to certify that Mr/Ms Harshita Mahajan *of* JAYPEE Univ. of Information Technology, Solan

successfully completed the 6 weeks Summer Internship / Hands on Training on " Microbiological Techniques" organised by Department of Microbiology, Panjab University, Chandigarh

Harshita Mahajan
161809

PROF. S.K. SONI
Chairperson and Internship Coordinator

राष्ट्रीय प्रौद्योगिकी संस्थान हमीरपुर
हमीरपुर (हि.प्र.)–177005 (भारत)
NATIONAL INSTITUTE OF TECHNOLOGY HAMIRPUR
HAMIRPUR (H.P.) - 177 005 (INDIA)
(An Institute of National Importance under Ministry of HRD)
{OFFICE OF TRAINING & PLACEMENT}
Faculty In charge
(Training and Placement)

Ref. No. NIT/HMR/TPO/2019/1202 Dated 04-07-2019

TO WHOM SO EVER IT MAY CONCERN

This is to certify that **Ms. Shivangini Singh** student of **JUIT, Waknaghat** has completed her internship program on the project titled **"Vermicomposting"** w.e.f. 27/05/2019 to 04/07/2019 under the guidance of Dr. Mamta Awasthi, Assistant Professor, Centre for Energy & Environmental Engineering of NIT Hamirpur (HP).

I wish her all the success in her future endeavors.

For –
04/07/19
Faculty Incharge (Training & Placement)
NIT Hamirpur (HP)

Shivangini
20/08/19

Fax No.: +91 1972 223834 www.nith.ac.in tpo@nith.ac.in

16183. Vaibhav. Handa Vaibhav.

पशु जैव प्रौद्योगिकी केन्द्र
Animal Biotechnology Centre
भाकृअनुप–राष्ट्रीय डेरी अनुसंधान संस्थान
ICAR-National Dairy Research Institute
(मान्य विश्वविद्यालय / Deemed University)
करनाल–132 001, हरियाणा, भारत | Karnal-132 001, Haryana, India
www.ndri.res.in

ndri

भाकृअनुप ICAR

CERTIFICATE

This is to certify that *Mr. VAIBHAV HANDA*, B.Tech. (Biotechnology) student of Jaypee University of Information Technology, Solan (H.P.) has successfully completed six weeks summer training programme held at Animal Biotechnology Centre, ICAR-N.D.R.I., Karnal from June 05 to July 16,2019. During the training, she was familiarized with the techniques of mammalian cell/tissue culture, *in vitro* embryo production, somatic cell cloning, stem cell culture, DNA and RNA isolation, cDNA synthesis, PCR, qPCR, electrophoresis, protein expression & its purification etc. He took keen interest during the program and learned various aspects of animal biotechnology. His performance during the training was ***good***.

I wish him all the best in future endeavors.

(Dr. M.K. Singh)
Scientist & Training Coordinator

Place: Karnal, Dated: July 16, 2019

(Dr. P. Palta)
Principal Scientist & In-charge

Vaibhav.

राष्ट्रीय पादप जीनोम अनुसंधान संस्थान

(जैव प्रौद्योगिकी विभाग, विज्ञान एवं प्रौद्योगिकी मंत्रालय, भारत सरकार का स्वायत अनुसंधान संस्थान)

NATIONAL INSTITUTE OF PLANT GENOME RESEARCH

(An Autonomous Institution of the Department of Biotechnology, Ministry of Science and Technology, Government of India)

अरूणा आसफ अली मार्ग, पो. बाक्स नं. 10531, नई दिल्ली-110067

Aruna Asaf Ali Marg, Post Box Number 10531, New Delhi-110067

डॉ. आशीष रंजन

स्टाफ वैज्ञानिक, रामालिंगास्वामी फेलो

Dr. Aashish Ranjan

Staff Scientist, Ramalingaswami Fellow

To Whom It May Concern

This is to certify that Ms. Shubhangi Ghosh worked as an undergraduate trainee in my lab for a period of six weeks from 3rd June, 2019 to 15th July, 2019. During this period, she learnt the basic microscopy and image analysis of plant samples.

Shubhangi is hard working with a motivation to learn new things. I wish her success in all her future endeavors.

Sincerely,

Aashish Ranjan

Dr. Aashish Ranjan
स्टाफ वैज्ञानिक, रामालिंगास्वामी फेलो
Staff Scientist, Ramalingaswami Fellow
राष्ट्रीय पादप जीनोम अनुसंधान संस्थान
National Institute of Plant Genome Research
अरूणा आसफ अली मार्ग, नई दिल्ली-110067
Aruna Asaf Ali Marg, New Delhi-110067

SHUBHANGI GHOSH

दूरभाष/Ph. : 91-11-26735117, ईपोबीएक्स/EPABX : 91-11-26741612/14/17, फैक्स/Fax : 91-11-26741658

ई-मेल /E-mail : aranjan@nipgr.ac.in, वेबसाइट/Website : http://www.nipgr.res.in

DEPARTMENT OF MICROBIOLOGY,

Panjab University, Chandigarh

SUMMER INTERNSHIP

HANDS ON TRAINING ON MICROBIOLOGICAL TECHNIQUES

JUNE 3- July 18, 2019

Certificate of Participation

This is to certify that Mr/Ms Rakshita *of* JAYPEE Univ. of Information Technology, Solan.

successfully completed the 6 weeks Summer Internship / Hands on Training on " Microbiological Techniques" organised by Department of Microbiology, Panjab University, Chandigarh

Rakshita Sidhu

Roll no. 161815

PROF. S.K. SONI

Srajit Saraswat
161816

SD BIOSENSOR

SD BIOSENSOR HEALTHCARE PVT. LTD.

Manufacturing Facility India : Plot 38, Sector 4, IMT Manesar, Gurugram-122052

Tel.: (+91) 124-694-3201 Toll Free No: (+91) 1800 10 23105 Website: www.sdbiosensor.com : Email: care@sdbiosensor.co.in

CIN - U33110HR2012PTC047034

Dated-10/07/2019

TO WHOMSOEVER IT MAY CONCERN

This is to certify that Mr. Srajit Saraswat student of B.tech (Biotech) bearing Roll No. 161816 of Jaypee University of Information Technology (Waknaghat) ,has undergone training on work namely **"Manufacturing process of Ultra Dot HIV Test(In Vitro Diagnostic Use)-is a visual , rapid, sensitive and accurate immunoassay to detect circulating antibody against HIV in human serum or plasma"** from 27/05/2019to10/07/2019

We found Mr. Srajit Saraswat is hardworking, passionate and sincere for work during training period.We wish him all the best for his future endeavors.

BIOSENSOR HEALTHCARE PVT. LTD. PLOT - 38, SECTOR-4, IMT MANESAR GURGAON-122052

SD Biosensor Healthcare Private Limited

Authorised Signatory

Self attested

Srajit Saraswat

INSTITUTE OF LIVER & BILIARY SCIENCE
(Deemed-to-be-University)
(An Autonomous Society Under Government Of NCT Of Delhi)
D-1 Vasant Kunj, New Delhi, India
Phone no: 46300000, Extn. 24301 Fax no. 26123504
Email: ilbs.academics@gmail.com, **website:** http://www.ilbs.in

F25/5/91/ILBS/AC/2016/10159/1132

Date:- 28/6/2019

TO WHOM SOEVER IT MAY CONCERN

This is to certify that Ms. Shiuli Samaddar Student of Biotechnology at Jaypee University of Information Technology has completed her Internship Training from 27.05.2019 to 26.06.2019 under the Supervision of Dr. Vikas Khillan, Additional Professor, the Department of Microbiology at the Institute of Liver and Biliary Sciences. D-1 Vasant Kunj New Delhi.

Vijay Kumar

(Dr. Vijay kumar)
Dean, Academics Ilbs

Dr. VIJAY KUMAR
Dean, Academics
Institute of Liver and Biliary Sciences
Sector D-1, Vasant Kunj
New Delhi-110 070

Roll. No :- 161817
Name :- Shiuli Samaddar

Shiuli

राष्ट्रीय प्रौद्योगिकी संस्थान हमीरपुर
हमीरपुर (हि.प्र.)–177005 (भारत)
NATIONAL INSTITUTE OF TECHNOLOGY HAMIRPUR
HAMIRPUR (H.P.) - 177 005 (INDIA)
(An Institute of National Importance under Ministry of HRD)
{OFFICE OF TRAINING & PLACEMENT}
Faculty In charge
(Training and Placement)

Ref. No. NIT/HMR/TPO/2019/1203 Dated 04-07-2019

TO WHOM SO EVER IT MAY CONCERN

This is to certify that **Ms. Saniya Mehta** student of JUIT, Waknaghat has completed her internship program on the project titled **"Vermicomposting"** w.e.f. 27/05/2019 to 04/07/2019 under the guidance of Dr. Mamta Awasthi, Assistant Professor, Centre for Energy & Environmental Engineering of NIT Hamirpur (HP).

I wish her all the success in her future endeavors.

Faculty Incharge (Training & Placement)
NIT Hamirpur (H.P.) - 177005

Faculty Incharge (Training & Placement)
NIT Hamirpur (HP)

Saniya Mehta
161818

R.S.S.

RDESCO AGRO FOODS

TO WHOMSOEVER IT MAY CONCERN

This is to certify that Ms. PRAHI GUPTA student of JUIT, WAKNAGHAT has completed her industrial training at our RDESCO AGRO FOODS w.e.f 25/05/19 to 10/07/19. The candidate has taken special training in quality control lab tests as well as protocols which are being followed during the refining process of edible oils and overall knowledge about the edible oil refining unit.

We have observed that the candidate is hard working and sincere towards her work. We wish her every success in the future.

FOR RDESCO AGRO FOODS

PLACE : ABOHAR

DATED : 11.07.2019

MANAGER.

161819
Prahi
16Aug19

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161822
Veena Kumari

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Phulwari Sharif,
Patna - 801 505 (INDIA)
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Fax : (0612) 2253957
email : mcspatna98@gmail.com
website : www.mahavircancersansthan.com

CERTIFICATE

This is to certify that ***Ms. Veena Kumari*** *student of* ***B.Tech Biotechnology, 3rd Year of Jaypee University of Information and Technology, Himachal Pradesh*** *has done project Training on* **"Assessment of arsenic concentration in Vegetable samples of Markets of Patna through GF- Atomic Absorption Spectrophotometer" under supervision of Dr. Arun Kumar** *at Mahavir Cancer Sansthan and Research Centre from* ***03rd June 2019 to 15th July 2019****. She has meticulously completed her work with* ***98%*** *attendance.*

She has been found sincere and dedicated during the training period.

The institute wishes her success in her future endeavors.

Dr. Arun Kumar	**Prof. Ashok Ghosh**	**Dr. Biswajit Sanyal**
Scientist - I	HoD, Research	Director
Mahavir Cancer Sansthan	Mahavir Cancer Sansthan	Mahavir Cancer Sansthan
Patna	Patna	Patna

Veena Kumari

सी.एस.आई.आर-हिमालय जैवसंपदा प्रौद्योगिकी संस्थान
पो॰ बॉ॰ न॰ 6 पालमपुर - 176 061 (हि.प्र.) भारत
CSIR-INSTITUTE OF HIMALAYAN BIORESOURCE TECHNOLOGY
CSIR-IHBT
Post Box No. 6 Palampur (H.P.) 176 061 INDIA

Dr. Gireesh Nadda
Senior Scientist
Incharge Training Programme

05th July, 2019

TO WHOM IT MAY CONCERN

This is to certify that **Ms. Aashina Puri,** a student of B.Tech Biotechnology, Jaypee University of Information Technology (JUIT) Solan, (Himachal Pradesh) undertook her summer training on the topic **"Basic techniques in Plant Biotechnology"** under the supervision of **Dr. Amita Bhattacharya,** Senior Principal Scientist, Biotechnology Division w.e.f. 27th May, 2019 to 05th July, 2019 at this Institute. During the training programme, her conduct has been satisfactory.

I wish her all success in her future endeavours.

5/7/19

(Gireesh Nadda)

Roll No - 161823

इ-मेल/E-mail : director@ihbt.res.in
वेबसाइट/Website : http://www.ihbt.res.in
ई.पी.ए.बी.एक्स/EPABX : 91-1894-230742-43,233338-39
फैक्स/Fax : 91-1894-230433

Srishti Saha
161824

Defence Institute of Physiology and Allied Sciences
रक्षा शरीरक्रिया एवं संबद्ध विज्ञान संस्थान
(An ISO 9001 : 2000 Certified Institute)

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भारत सरकार रक्षा मंत्रालय रक्षा अनुसंधान एवं विकास संगठन
Lucknow Road, Timarpur, Delhi – 110 054
लखनऊ रोड, तिमारपुर दिल्ली - 110 054

Certificate

This is to certify that Ms. Shristi Saha **B. Tech in Biotechnology,** from Jaypee University of Information Techonology, solan (H.P.) has undergone short-term training from 27th May 2019 to 5th July 2019 in this institute. During the training, the following techniques were demonstrated:

1. Protein extraction, precipitation, Bradford's Method & BCA Method.
2. SDS-PAGE, staining & western blotting.
3. Serial dilution & sample preparation.
4. Quantification of western blot using ImageJ.
5. Purification of DNA & agarose gel.
6. Determination of nucleic acid concentration.

Self Attested
Saha

Dr. Shweta Rawat
Sc 'E'
HRD Coordinator

Director : 91-11-23914774 Office : 91-11-23883111
FAX No : 91-11-23932869 E-mail : hrddipas@yahoo.com

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Awarded to

M/s. Priyanjalee Bhattacharjee

Duration

From 3' June 2019 to 13' July 2019

Sl. No. : ALS/07 - FB-18/19 Date : 13' July 2019 Place : Noida

Allele Life Sciences Pvt. Ltd.

Coordinator

Director

Director Signatory

Priyanjalee
161825

Ref. No. ALS/07-FB-18/19

Date: 13-07-2019

CERTIFICATE

This is to certify that **Ms. Priyanjalee Bhatacharjee,** B.Tech. in **Biotechnology** from Jaypee University, Solan, Himachal Pradesh has successfully completed her project on **"Detection and Characterisation of Enzyme from fish waste"** with us at Chemgeneics Research Foundation, *Noida*, (U.P.) from 3rd June, 2019 to 13th July, 2019. She had been very hard-working and sincere in the entire research project.

We wish her all the best for future.

Guided by

Allele Life Sciences Pvt. Ltd.

Mritunjay Kr. Singh
Research Associate
Allele Life Sciences Pvt. Ltd.

Director

K.B. Singh
Director,
Allele Life Sciences Pvt. Ltd.

Priyanjalee
161825

CSIR- CSIO

CSIR- Central Scientific Instruments Organisation
Sector 30-C, Chandigarh. India

Certificate of Training

This is to certify that Palak Sharma, daughter of Mr Ashwani Kumar Sharma and a student of Jaypee University Of Information Technology has trained with the Ubiquitous Analytical Techniques Division of CSIR-CSIO from June 3, 2019 to July 12, 2019 with Enrolment Number A2616.
Grade Awarded: Excellent

Coordinator, Trainee and Apprenticeship Cell
July 29, 2019

प्रशिक्षण समन्वयक
Training Coordinator
केन्द्रीय वैज्ञानिक उपकरण संगठन
Central Scientific Instruments Organisation
सैक्टर 30 - सी, / Sector 30-C, चण्डीगढ़ / Chandigarh

Palak Sharma

Indira Gandhi Medical College & Hospital Shimla, H.P.

No.HFW(MS)G-5/2019- 6651 Dated 10/7/19

CERTIFICATE

Certified that Ms. Sara Bhinta D/O Sh.Rajesh Bhinta student of B.Tech (Biotechnology) from Jaypee University Waknaghat Distt. Solan H.P has completed her Observer ship Training w.e.f. 27.05.2019 to 05.07.2019 in the department of Microbiology, Indira Gandhi Medical College Shimla.

During the above period her work and conduct was found satisfactory. She bears good moral character.

Sr. Medical Superintendent,
I.G. Hospital, Shimla

Professor & Head
Department of [illegible]gy,
I.G.M. [illegible] 1001 (H.P.)

Roll No - 161828

भारतीय प्रौद्योगिकी संस्थान
IIT INDIAN INSTITUTE OF TECHNOLOGY
BANARAS HINDU UNIVERSITY

जैव रासायनिक अभियांत्रिकी स्कूल
School of Biochemical Engineering

TO WHOM IT MAY CONCERN

This is to certify that Ms. Sambhavana a student of B.Tech 3rd year of Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh has successfully completed 6 weeks (From 3rd June, 2019 to 13th July, 2019) summer internship on Bioalgal/Biofuel Production using Waste Water. During the period of her internship programme with us, she was found punctual, hardworking and inquisitive.

We wish her every success in life.

Prof. (Dr.) Pradeep Srivastava
Coordinator
School of Biochemical Engineering,
Indian Institute of Technology (BHU)

समन्वयक
Coordinator
जैव रासायनिक अभियांत्रिकी स्कूल
School of Biochemical Engg.
भारतीय प्रौद्योगिकी संस्थान
Indian Institute of Technology
(का॰हि॰वि॰वि॰) वाराणसी-221005
(B.H.U.) Varanasi-221005

Sambhavana
16829

CSIR-IHBT

सी.एस.आई.आर-हिमालय जैवसंपदा प्रौद्योगिकी संस्थान

पो॰ बॉ॰ न॰ 6 पालमपुर - 176 061 (हि.प्र.) भारत

CSIR-INSTITUTE OF HIMALAYAN BIORESOURCE TECHNOLOGY

Post Box No. 6 Palampur (H.P.) 176 061 INDIA

Dr. Gireesh Nadda
Senior Scientist
Incharge Training Programme

05th July, 2019

TO WHOM IT MAY CONCERN

This is to certify that **Ms. Tanvi Sehgal,** a student of B.Tech Biotechnology, Jaypee University of Information Technology (JUIT) Solan, (Himachal Pradesh) undertook her summer training on the topic **"Basic in Plant Tissue Culture"** under the supervision of **Dr. Ashish Rambhau Warghat,** Scientist, Biotechnology Division w.e.f. 27th May, 2019 to 05th July, 2019 at this Institute. During the training programme, her conduct has been satisfactory.

I wish her all success in her future endeavours.

5/7/19

(Gireesh Nadda)

16/08/19.

Tanvi Sehgal
161830

इ-मेल/E-mail : director@ihbt.res.in
वेबसाइट/Website : http://www.ihbt.res.in
ई.पी.ए.बी.एक्स/EPABX : 91-1894-230742-43,233338-39
फैक्स/Fax : 91-1894-230433

verka
Phulo Phalo. Pure Khao Piyo.

No.MP/CHD/ADMN/ 2714 Dated: - 12.07.2019

TO WHOM IT MAY CONCERN

It is certified that Ms. Rimgim Koul D/o Sh. Kranti Koul a student of B.Tech (Biotechnology) from Jaypee University of Information and Technology, Solan has done "In-Plant Training" at Milk Plant, Chandigarh from 24.05.2019 to 10.07.2019.

During the period of training, her work and conduct remained 'Very Good'.

GENERAL MANAGER

161831

Rimgim Koul

THE PUNJAB STATE COOPERATIVE MILK PRODUCERS' FEDERATION LIMITED
MILK PLANT, INDUSTRIAL AREA-I, CHANDIGARH - 160002
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CSIR-IHBT
Post Box No. 6 Palampur (H.P.) 176 061 INDIA

Dr. Gireesh Nadda
Senior Scientist
Incharge Training Programme

05th July, 2019

TO WHOM IT MAY CONCERN

This is to certify that **Mr. Arush Kaushal,** a student of B.Tech Biotechnology, Jaypee University of Information Technology (JUIT) Solan, (Himachal Pradesh) undertook his summer training on the topic **"Basic of plant tissue culture and *in-vitro* propagation of *Podophyllum hexandrum* using embryo culture technique"** under the supervision of **Dr. Ashish Rambhau Warghat,** Scientist, Biotechnology Division w.e.f. 27th May, 2019 to 05th July, 2019 at this Institute. During the training programme, his conduct has been satisfactory.

I wish him all success in his future endeavours.

गिरीश नड्डा
5/7/19

(Gireesh Nadda)

161832
ARUSH KAUSHAL

इ-मेल/E-mail : director@ihbt.res.in
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वेबसाइट /Website : http://www.ihbt.res.in
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Reg.No : IHT/2019/05/03772

161833.

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Institute of Horticulture Technology

Recognised by Ministry of Agriculture & Farmers welfare, Government of India



प्रमाण–पत्र
Certificate

This is to certify that **Ms. B Soumya** D/o **Sh. B Gururaja Setty** R/o. Silver Springs Township. Phase - 1, Indore Madhya Pradesh, a student of Jaypee University of Information Technology, Himachal Pradesh participated in the internship programme on "**Hydroponics**" conducted by Institute of Horticulture Technology w.e.f. 22nd May, 2019 to 2nd July, 2019 at Greater Noida, Uttar Pradesh.

Institute of Horticulture Technology wishes her a successful career in Horticulture.

Sanjeev Kulshreshtha
कुल सचिव
Registrar

Institute of Horticulture Technology Greater Noida

K.L. Chadha
(K. L. Chadha)
अध्यक्ष
Chairman

B. Soumya

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Website : www.nestle.in

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161836

12 July 2019

TO WHOMSOEVER IT MAY CONCERN

This is to certify that **Ms. Dhruvika** D/o Mr. Chander Mohan student of B.Tech. Biotechnology from Jaypee University of Information Technology, Solan has successfully completed her internship at Nestlé Samalkha Factory from **30th May 2019 to 12th July 2019**. During her internship, she was deputed in Chilled Dairy production department under Mr. VPS Tyagi, Sr. Manager and has successfully completed her project report on "End-to-end understanding of Chilled Dairy Operations including quality monitoring scheme of process and reduction of high losses" under the guidance of Mr. Sandeep Dalal.

During the course of vocational training, her conduct & dedication was highly appreciable. She has demonstrated good level of energy, commitment & strong collaboration with stakeholders to drive assigned projects.

We wish Ms. Dhruvika every success in her future endeavours.

For Nestlé India Limited
Samalkha Factory

For Nestle India Limited
Samalkha Factory

Alok Kumar Authorised Signatory
Sr. Manager – HR

Dhruvika
16/8/19

Ayushi Khimta
161837

Indira Gandhi Medical College & Hospital Shimla, H.P.

No.HFW(MS)G-5/2019- 6797 Dated 16/07/19

CERTIFICATE

Certified that Ms. Ayushi Khimta D/O Sh.Shyam Khimta student of B.Tech (Biotechnology) from Jaypee University Waknaghat Distt. Solan H.P has completed her Observer ship Training w.e.f. 01.06.2019 to 13.07.2019 in the department of Microbiology, Indira Gandhi Medical College Shimla.

During the above period her work and conduct was found satisfactory. She bears good moral character.

Sr. Medical Superintendent,
I.G.M. Hospital, Shimla

Self Attested

HALDIRAM SNACKS PVT. LTD.

11th July 2019

To Whom So Ever It May Concern

This is to certify that Mr Arsh Tyagi Student of B.Tech (Biotechnology) Course from Jaypee University of Information Technology ,Solan (H.P) had successfully completed his Internship in our **Quality Assuranace & Process Department** during the month of June2019 & July2019.

During the period of stay with us, we found him sincere, intelligent, regular & well behaved.

We wish for him bright & successful future career.

For, Haldiram Snacks Pvt.Ltd.

Vireshwar Giri
Asst.Manager -HR

Arsh 161838

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W : www.haldiram.com I CIN No.: U74899DL1989PTC037732

Indira Gandhi Medical College & Hospital Shimla, H.P.

No.HFW(MS)G-5/2019- 6659 Dated 10/7/19

CERTIFICATE

Certified that Ms. Jasdeep Kaur D/O Sh.Ajmer Singh student of B.Tech (Biotechnology) from Jaypee University Waknaghat Distt. Solan H.P.has completed her Observer ship Training w.e.f. 27.05.2019 to 06.07.2019 in the department of Microbiology, Indira Gandhi Medical College Shimla.

During the above period her work and conduct was found satisfactory. She bears good moral character.

Sr. Medical Superintendent,
I.G. Hospital, Shimla

131839
Jasdeep

Professor & Head
Department of Microbiology,
I.G.M.C., Shimla - 171001 (H.P.)

Kritika (161840)

ChemGeneics
Research Foundation

Ref. No. ALS/07-FB-19/19

Date: 13-07-2019

CERTIFICATE

This is to certify that **Ms. Kritika Sharma,** B.Tech. in **Biotechnology** from Jaypee University, Solan, Himachal Pradesh has successfully completed her project on **"Detection and Characterisation of Enzyme from fish waste"** with us at Chemgeneics Research Foundation., *Noida*, (U.P.) from 27th May, 2019 to 13th July, 2019. She had been very hard-working and sincere in the entire research project.

We wish her all the best for future.

Guided by

Allele Life Sciences Pvt. Ltd.

Mritunjay Kr. Singh
Research Associate
Allele Life Sciences Pvt. Ltd.

K.B. Singh
Director,
Allele Life Sciences Pvt. Ltd.

Self attested
22 Aug, 19.

ChemGeneics Research Foundation
(A Non Profit Organisation)

Tel : +91-120 – 2540133
08851361238

Email : mail@chemgeneics.org
Web : www.chemgeneics.org

Research Lab : C- 59, Sector – 10 , Noida – 201301, IN
Branch : Tachla, Rishikesh Chamba Highway, NH-92, , Uttarakhand - 249175 , IN

CIN- U73100DL2016NPL29168 || Tax I.D - AAGCC3778C

Kritika (161840)

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Awarded to

M/s. Kritika Sharma

Duration

From 27 May 2019 to 13 July 2019

Sl. No. : ALS/07-FB-19/19

Date : 13 July 2019

Place : Noida

Allele Life Sciences Pvt. Ltd.

Director

Director Signatory

Coordinator

Self Attested
22 Aug, 2019

Shreeya Agrawal
161841

Defence Institute of Physiology and Allied Sciences
रक्षा शरीरक्रिया एवं संबद्ध विज्ञान संस्थान
(An ISO 9001 : 2000 Certified Institute)

Govt. of India, Ministry of Defence, Defence Research & Development Organization
भारत सरकार रक्षा मंत्रालय रक्षा अनुसंधान एवं विकास संगठन
Lucknow Road, Timarpur, Delhi – 110 054
लखनऊ रोड, तिमारपुर दिल्ली - 110 054

Certificate

This is to certify that Ms. Shreeya Agrawal **B. Tech in Biotechnology,** from Jaypee University of Information Techonology, solan (H.P.) has undergone short-term training from 27th May 2019 to 5th July 2019 in this institute. During the training, the following techniques were demonstrated:

1. Protein extraction, precipitation, Bradford's Method & BCA Method.
2. SDS-PAGE, staining & western blotting.
3. Serial dilution & sample preparation.
4. Quantification of western blot using ImageJ.
5. Purification of DNA & agarose gel.
6. Determination of nucleic acid concentration.

Shweta

Dr. Shweta Rawat
Sc 'E'
HRD Coordinator

Shreeya

Director : 91-11-23914774 Office : 91-11-23883111
FAX No : 91-11-23932869 E-mail : hrddipas@yahoo.com

SCHOOL OF BIOTECHNOLOGY
UNIVERSITY OF JAMMU

Baba Saheb Ambedkar Road, Jammu

NOL- JU/SBT/19/422

Dated :-13th July,2013

To whom it may concern

This is to certify that Ms. Sunainy Ajrawat, student of Jaypee University of Information and Technology, Solan, Himachal Pradesh has attended the School w.e.f 3rd June to 13th July, 2019. During her stay in the School she successfully completed hands-on training on various techniques. Her work and conduct remained satisfactory during the period.

Director
Director
School of Biotechnology
University of Jammu
Jammu

Sunainy Ajrawat
Sunainy
20-8-19

ABHISHEK DOGRA
161844

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SUNDERNAGAR-174401, DISTT. MANDI H.P.
Ph. : 01907-275222, Telefax : 01907-275210

REF. NO. hpmc/FPP/JRL/Industrial Training /2019-20: 472 Dated 15.07.2019

TO WHOM IT MAY CONCERN

This is to certify that Mr. Abhishek Dogra, student of B. Tech Biotechnology of Department of Biotechnology & Bioinformatics, Jaypee University of Information Technology, Waknaghat Distt Solan (HP), has completed his training at hpmc Fruit Processing Plant, Jarol Sunder Nagar, Distt. Mandi, Himachal Pradesh w.e.f. 01st June 2019 to 12th July 2019.

During training period his work and conduct has been found satisfactory.

I wish his all the success in his life.

Plant Manager
hpmc FPP Jarol
Sunder Nagar Distt. Mandi (H.P)

Self Attested
Abhishek Dogra

Indira Gandhi Medical College & Hospital Shimla, H.P.

No.HFW(MS)G-5/2019- 6653 Dated 10/7/19

CERTIFICATE

Certified that Ms. Bandana Thakur D/O Sh.Devinder Thakur student of B.Tech (Biotechnology) from Jaypee University Waknaghat Distt. Solan H.P has completed her Observer ship Training w.e.f. 27.05.2019 to 06.07.2019 in the department of Microbiology, Indira Gandhi Medical College Shimla.

During the above period her work and conduct was found satisfactory. She bears good moral character.

BANDANA THAKUR
161845
BThakur

Sr. Medical Superintendent,
I.G. Hospital, Shimla

Professor & Head
Department of Microbiology,
I.G.M.C., Shimla - 171001 (H.P.)

LAVIN SHARMA
151848

INDIAN BIOSCIENCES INSTITUTE OF TECHNOLOGY
G-2, Kailash Colony, New Delhi-110048
Email: inbit.director@gmail.com
Website: www.inbit.in

INDIAN BIOSCIENCES
DNA TESTING SIMPLIFIED

CERTIFICATE FOR TRAINING

This certificate is awarded to *Mr. Lavin Sharma*

Student of *JUIT, Solan* on

successful completion of Training Programme from *01st June'19* to *15th July'19*.

This certificate is being issued on successful completion of *Summer Training In Basic Molecular Biology Techniques*

under the supervision of *Mr. Sahil Kaushik*. The work

embodied in the Training is up to the mark and satisfactory for *B.Tech. Biotechnology Degree*.

Divya.

Director, Indian Biosciences

Dr. Divya Jaiswal

INDIAN BIOSCIENCES New Delhi INBIT

Skaushik.

Training Manager

Mr. Sahil Kaushik

Lavin

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
1	Arav Sood	151356			Unsatisfactory
2	Joshita Sharma	151442	12-08-2019	12-08-2019	Satisfactory
3	Gaurav Sahu	161004	21-08-2019	21-08-2019	Satisfactory
4	Lavish Kumar Jangir	161022	12-08-2019	12-08-2019	Satisfactory
5	Deepika Gupta	161201	12-08-2019	12-08-2019	Satisfactory
6	Pratyush Kumar	161202	12-08-2019	12-08-2019	Satisfactory
7	Rohit Garg	161203	12-08-2019	12-08-2019	Satisfactory
8	Robin Chauhan	161204	12-08-2019	12-08-2019	Satisfactory
9	Uday Gupta	161205	12-08-2019	12-08-2019	Satisfactory
10	Charchit Kapoor	161207	12-08-2019	12-08-2019	Satisfactory
11	Jyoti	161208	13-08-2019	13-08-2019	Satisfactory
12	Mukul Garg	161209	12-08-2019	12-08-2019	Satisfactory
13	Kamal Kant Thakur	161210	12-08-2019	12-08-2019	Satisfactory
14	Sachin Gupta	161211	12-08-2019	12-08-2019	Satisfactory
15	Abhishek Jain	161212	12-08-2019	12-08-2019	Satisfactory
16	Bhanu Pratap	161213	12-08-2019	12-08-2019	Satisfactory
17	Rahul Rana	161214	12-08-2019	12-08-2019	Satisfactory
18	Navneet Thakur	161215	13-08-2019	13-08-2019	Satisfactory
19	Vaishali Sharma	161216	13-08-2019	13-08-2019	Satisfactory
20	Suchetan Pathania	161217	13-08-2019	13-08-2019	Satisfactory
21	Minal Aggarwal	161218	13-08-2019	13-08-2019	Satisfactory
22	Devvrat Bhardwaj	161219	13-08-2019	13-08-2019	Satisfactory
23	Shobhit Marwaha	161220	13-08-2019	13-08-2019	Satisfactory
24	Ishita Jain	161221	13-08-2019	13-08-2019	Satisfactory
25	Ashish Gupta	161222	13-08-2019	13-08-2019	Satisfactory
26	Shagun Jindal	161224	13-08-2019	13-08-2019	Satisfactory
27	Vandit Sharma	161225	13-08-2019	13-08-2019	Satisfactory
28	Kanika Puri	161227	13-08-2019	13-08-2019	Satisfactory
29	Neha Tyagi	161229	13-08-2019	13-08-2019	Satisfactory
30	Ashish Sharma	161231	13-08-2019	13-08-2019	Satisfactory
31	Mridul Prashar	161232	13-08-2019	13-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
32	Vinamra Jain	161233	13-08-2019	13-08-2019	Satisfactory
33	Tapasya	161234	13-08-2019	13-08-2019	Satisfactory
34	Sonali Sehgal	161235	13-08-2019	13-08-2019	Satisfactory
35	Aryan Pal Singh	161236	14-08-2019	14-08-2019	Satisfactory
36	Abhishek Katoch	161237	14-08-2019	14-08-2019	Satisfactory
37	Anirudh Sharma	161238	14-08-2019	14-08-2019	Satisfactory
38	Hament Kumar Bassi	161239	14-08-2019	14-08-2019	Satisfactory
39	Robin Singh	161240	14-08-2019	14-08-2019	Satisfactory
40	Parth Verma	161241	14-08-2019	14-08-2019	Satisfactory
41	Shivam Sharma	161242	14-08-2019	14-08-2019	Satisfactory
42	Kanishk Sood	161243	14-08-2019	14-08-2019	Satisfactory
43	Amandeep Saini	161244	14-08-2019	14-08-2019	Satisfactory
44	Aruba Sood	161245	14-08-2019	14-08-2019	Satisfactory
45	Abiral Singh	161246	14-08-2019	14-08-2019	Satisfactory
46	Sahil Kaith	161247	14-08-2019	14-08-2019	Satisfactory
47	Vrinda Choudhary	161248	14-08-2019	14-08-2019	Satisfactory
48	Skund Verma	161249	14-08-2019	14-08-2019	Satisfactory
49	Akash Mahajan	161250	14-08-2019	14-08-2019	Satisfactory
50	Harshita Chauhan	161251	14-08-2019	14-08-2019	Satisfactory
51	Faiz Ali	161252	14-08-2019	14-08-2019	Satisfactory
52	Anmol Garg	161253	12-08-2019	12-08-2019	Satisfactory
53	Ankita Chauhan	161254	12-08-2019	12-08-2019	Satisfactory
54	Varan Kaushal	161255	12-08-2019	12-08-2019	Satisfactory
55	Mukul Sharma	161256	12-08-2019	12-08-2019	Satisfactory
56	Vishal Pant	161257	12-08-2019	12-08-2019	Satisfactory
57	Rishi Kumar Rai	161259			Unsatisfactory
58	Sandeep Hodkasia	161260	12-08-2019	12-08-2019	Satisfactory
59	Ishan Gupta	161261	12-08-2019	12-08-2019	Satisfactory
60	Aditya Mohan	161262	12-08-2019	12-08-2019	Satisfactory
61	Rishabh Malhotra	161263	12-08-2019	12-08-2019	Satisfactory
62	Arunish Sharma	161264	12-08-2019	12-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
63	Aditya Jain	161265	12-08-2019	12-08-2019	Satisfactory
64	Vasu Gupta	161266	12-08-2019	12-08-2019	Satisfactory
65	Manas Dubey	161267	12-08-2019	12-08-2019	Satisfactory
66	Rajat Kumar Puri	161269	12-08-2019	12-08-2019	Satisfactory
67	Paritosh Sharma	161270	12-08-2019	12-08-2019	Satisfactory
68	Varun Choudhary	161271	12-08-2019	12-08-2019	Satisfactory
69	Shiva Chandel	161272	13-08-2019	13-08-2019	Satisfactory
70	Ashish Bhardwaj	161273	26-08-2019	26-08-2019	Satisfactory
71	Aditya Thakur	161274	13-08-2019	13-08-2019	Satisfactory
72	Nishchal Kumar Garg	161275	13-08-2019	13-08-2019	Satisfactory
73	Sidhant Thakur	161276			Unsatisfactory
74	Ketan Batra	161277	13-08-2019	13-08-2019	Satisfactory
75	Laxit Rana	161278	13-08-2019	13-08-2019	Satisfactory
76	Ayush Agrawal	161279	13-08-2019	13-08-2019	Satisfactory
77	Vivek Sharma	161280	13-08-2019	13-08-2019	Satisfactory
78	Aditya Chaudhary	161281	13-08-2019	13-08-2019	Satisfactory
79	Ankit Srivastava	161284			Unsatisfactory
80	Atharvan Gupta	161286	13-08-2019	13-08-2019	Satisfactory
81	Shashank Shekhar	161287	13-08-2019	13-08-2019	Satisfactory
82	Akriti Sood	161288	13-08-2019	13-08-2019	Satisfactory
83	Sakshi Chhimpa	161289	13-08-2019	13-08-2019	Satisfactory
84	Mayank Bisht	161290			Unsatisfactory
85	Viplove Sharma	161291	13-08-2019	13-08-2019	Satisfactory
86	Sarthak Thakur	161292	14-08-2019	14-08-2019	Satisfactory
87	Sidhant Sharma	161293	14-08-2019	14-08-2019	Satisfactory
88	Kritika Sharma	161294	14-08-2019	14-08-2019	Satisfactory
89	Hritik Negi	161295	14-08-2019	14-08-2019	Satisfactory
90	Divyam Kudeshia	161296	14-08-2019	14-08-2019	Satisfactory
91	Rohit Garg	161297	14-08-2019	14-08-2019	Satisfactory
92	Shivam Garg	161298	14-08-2019	14-08-2019	Satisfactory
93	Abhiraj Srivastava	161299	14-08-2019	14-08-2019	Satisfactory
94	Ayush Saini	161300	26-08-2019	26-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
95	Anusheel Priyam	161301	14-08-2019	14-08-2019	Satisfactory
96	Anshul Sharma	161303	14-08-2019	14-08-2019	Satisfactory
97	Akshit Gupta	161304	14-08-2019	14-08-2019	Satisfactory
98	Aditi Manglesh	161305	14-08-2019	14-08-2019	Satisfactory
99	Munish Thakur	161306	14-08-2019	14-08-2019	Satisfactory
100	Nishil Pagare	161307	14-08-2019	14-08-2019	Satisfactory
101	Anand Vashistha	161308	14-08-2019	14-08-2019	Satisfactory
102	Ajay Kumar	161309	14-08-2019	14-08-2019	Satisfactory
103	Tavishi Sharma	161310	13-08-2019	13-08-2019	Satisfactory
104	Ritin Bhardwaj	161311	12-08-2011	12-08-2011	Satisfactory
105	Abhishek Bhardwaj	161312	12-08-2011	12-08-2011	Satisfactory
106	Pradyut Lohani	161313	12-08-2011	12-08-2011	Satisfactory
107	Arpit Jain	161314	12-08-2011	12-08-2011	Satisfactory
108	Piyush Taneja	161316	12-08-2011	12-08-2011	Satisfactory
109	Harshit Chrangoo	161317	12-08-2011	12-08-2011	Satisfactory
110	Manika Kansal	161318	12-08-2011	12-08-2011	Satisfactory
111	Kashish Bajaj	161319	12-08-2011	12-08-2011	Satisfactory
112	Shivang Goyal	161320	12-08-2011	12-08-2011	Satisfactory
113	Pamit Kumar Singh	161321	12-08-2011	12-08-2011	Satisfactory
114	Shubham Gupta	161322	12-08-2011	12-08-2011	Satisfactory
115	Nikhil Jangra	161323	12-08-2011	12-08-2011	Satisfactory
116	Aayushman Saraswat	161324	12-08-2011	12-08-2011	Satisfactory
117	Prashasy Ashok	161325	12-08-2011	12-08-2011	Satisfactory
118	Sankalp Singhania	161326	12-08-2011	12-08-2011	Satisfactory
119	Mayank Fulera	161327	12-08-2011	12-08-2011	Satisfactory
120	Aman Srivastav	161328	13-08-2019	13-08-2019	Satisfactory
121	Asmita Sharma	161329	13-08-2019	13-08-2019	Satisfactory
122	Satyam Aggarwal	161330	13-08-2019	13-08-2019	Satisfactory
123	Varun Saxena	161332	13-08-2019	13-08-2019	Satisfactory
124	Garvit Gupta	161333	13-08-2019	13-08-2019	Satisfactory
125	Abhishek Raj	161334			Unsatisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
126	Suyash Pandey	161335	13-08-2019	13-08-2019	Satisfactory
127	Rishabh Agarwal	161336	13-08-2019	13-08-2019	Satisfactory
128	Hemant Chauhan	161337	13-08-2019	13-08-2019	Satisfactory
129	Hima K S	161338	13-08-2019	13-08-2019	Satisfactory
130	Sanchit Thakur	161340			Unsatisfactory
131	Sanya Ahuja	161341	13-08-2019	13-08-2019	Satisfactory
132	Ankit Gera	161342	13-08-2019	13-08-2019	Satisfactory
133	Rishabh Goyal	161343	13-08-2019	13-08-2019	Satisfactory
134	Shubham Singla	161344	13-08-2019	13-08-2019	Satisfactory
135	Shivam Tyagi	161345	13-08-2019	13-08-2019	Satisfactory
136	Upasana Bhasin	161347	13-08-2019	13-08-2019	Satisfactory
137	Divyansh Kushwaha	161348			Unsatisfactory
138	Tushar Gautam	161350	14-08-2019	14-08-2019	Satisfactory
139	Rashi Gupta	161351	14-08-2019	14-08-2019	Satisfactory
140	Simran Paul	161352	14-08-2019	14-08-2019	Satisfactory
141	Bhavna Verma	161353	14-08-2019	14-08-2019	Satisfactory
142	Arpit Dogra	161355	14-08-2019	14-08-2019	Satisfactory
143	Varun Mishra	161356	14-08-2019	14-08-2019	Satisfactory
144	Naman Bangathia	161357	14-08-2019	14-08-2019	Satisfactory
145	Sparsh Bhardwaj	161358	14-08-2019	14-08-2019	Satisfactory
146	Anmol Rana	161359	14-08-2019	14-08-2019	Satisfactory
147	Tikshika Gupta	161360	14-08-2019	14-08-2019	Satisfactory
148	Vipul Kashyap	161361	14-08-2019	14-08-2019	Satisfactory
149	Ridhi Soni	161362	14-08-2019	14-08-2019	Satisfactory
150	Shobhit	161363	14-08-2019	14-08-2019	Satisfactory
151	Sakshum Kalsotra	161364	14-08-2019	14-08-2019	Satisfactory
152	Himanshu Nadda	161366	14-08-2019	14-08-2019	Satisfactory
153	Riya Sharma	161367	14-08-2019	14-08-2019	Satisfactory
154	Prag Sangha	161368	16-08-2019	16-08-2019	Satisfactory
155	Rahul Rana	161369	14-08-2019	14-08-2019	Satisfactory
156	Aabhas Kashyap	161370	16-08-2019	16-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
157	Anshul Thakur	161371	16-08-2019	16-08-2019	Satisfactory
158	Naveen Sharma	161372	16-08-2019	16-08-2019	Satisfactory
159	Piyush Thakur	161373	16-08-2019	16-08-2019	Satisfactory
160	Shivam Jagota	161375	16-08-2019	16-08-2019	Satisfactory
161	Saurav Thakur	161376	16-08-2019	16-08-2019	Satisfactory
162	Manish Sharma	161377	14-08-2019	14-08-2019	Satisfactory
163	Yashwin S Guleria	161378	16-08-2019	16-08-2019	Satisfactory
164	Prashant Gautam	161379	16-08-2019	16-08-2019	Satisfactory
165	Manu Gupta	161380			Unsatisfactory
166	Rahil Patial	161381	16-08-2019	16-08-2019	Satisfactory
167	Kartik Mahajan	161382	16-08-2019	16-08-2019	Satisfactory
168	Vanshika Chauhan	161383	13-08-2019	13-08-2019	Satisfactory
169	Gulshan Sankhyan	161384	16-08-2019	16-08-2019	Satisfactory
170	Angana Kaushal	161385	14-08-2019	14-08-2019	Satisfactory
171	Riya Singh	161386	14-08-2019	14-08-2019	Satisfactory
172	Rohit Kashyap	161387	17-08-2019	17-08-2019	Satisfactory
173	Sarthak Singh	161389	17-08-2019	17-08-2019	Satisfactory
174	Muskan Kaushal	161390	17-08-2019	17-08-2019	Satisfactory
175	Jyotir Aditya Sharma	161452	21-08-2019	21-08-2019	Satisfactory
176	Srishti Gupta	161453	13-08-2019	13-08-2019	Satisfactory
177	Himanshu Gupta	161454	14-08-2019	14-08-2019	Satisfactory
178	Naimish Awasthi	161455	17-08-2019	17-08-2019	Satisfactory
179	Shubham Garg	161456	17-08-2019	17-08-2019	Satisfactory
180	Dhruv Dhingra	161457	17-08-2019	17-08-2019	Satisfactory
181	Shailesh Mishra	161458			Unsatisfactory
182	Nidhish Manchanda	161459	17-08-2019	17-08-2019	Satisfactory
183	Rishabh Tewari	161460	17-08-2019	17-08-2019	Satisfactory
184	Sajal Lahoti	161461	17-08-2019	17-08-2019	Satisfactory
185	Dhairya Agarwal	161462	17-08-2019	17-08-2019	Satisfactory
186	Vikas Singh	161463	17-08-2019	17-08-2019	Satisfactory

INDUSTRIAL TRAINING STATUS OF BATCH 2016 - 2020 CSE & IT DEPARTMENT

S. No.	E. NO	Name of Student	Industrial Training report submitted by student to department	Viva held on	Status of Industrial Training Completion
187	Rahul Gupta	161465	17-08-2019	17-08-2019	Satisfactory
188	Kanishk Kala	161466	14-08-2019	14-08-2019	Satisfactory
189	Sachin	161467	17-08-2019	17-08-2019	Satisfactory
190	Mukul Chugh	161468	17-08-2019	17-08-2019	Satisfactory
191	Udisha Pandey	161469	17-08-2019	17-08-2019	Satisfactory
192	Hritik Agarwal	161470	23-08-2019	23-08-2019	Satisfactory
193	Prattyush S Sinha	161471	17-08-2019	17-08-2019	Satisfactory
194	Chandrashekhar Choudhary	161472	17-08-2019	17-08-2019	Satisfactory
195	Arpit Tyagi	161473	22-08-2019	22-08-2019	Satisfactory
196	Amritanshu Singh	161474	17-08-2018	17-08-2018	Satisfactory
197	Bhawna	161476	17-08-2018	17-08-2018	Satisfactory
198	Shruti Parihar	161477	17-08-2018	17-08-2018	Satisfactory
199	Ayush Patel	161478	17-08-2018	17-08-2018	Satisfactory
200	Shail Vatsal Vashist	161480	17-08-2018	17-08-2018	Satisfactory
201	Prajwal Thakur	161616	17-08-2018	17-08-2018	Satisfactory

(Signature of HOD)

Industrial Training 2019 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	151001	SAHIL SINGLA	Numitech Solutions
2	151002	ADITYA THAKUR	PRASAR BHARATI
3	151004	MANISHA SHARMA	BSNL MSC Shimla
4	151005	ANISH VIJAN	NIELIT , Chandigarh
5	151007	ANUJ PURWAR	Semi Conductor Laboratory
6	151008	PARAS MITTAL	Newvision softcom and consultancy Pvt. Ltd.
7	151009	SAHAJ CHOPRA	BHARAT ELECTRONICS LIMITED
8	151010	KARTIK BANTA	Ericsson Global Services India Limited
9	151011	RITUL SINGH	Bharat Sanchar Nigam Limited
10	151012	JAGRITI TANDON	Jaypee University of Information Technology
11	151013	MOHIT PATEL	BSNL
12	151015	MOHIT SACHDEVA	Reliance Communications Limited
13	151016	REETIKA MITTAL	Mazagon dock shipbuilders limited
14	151017	AYUSHI AWASTHI	Bharat Sanchar Nigam Limited
15	151018	ISHITA	TCS
16	151019	MAHIMA SURI	Doordarshan, Jammu Kendra
17	151021	RICHA BHARDWAJ	Thinknext technologies pvt limited
18	151022	MAHESH KUMAR	Bsnl
19	151023	NIKHIL THAKUR	BSNL
20	151024	AKRITI GUPTA	INTEX
21	151025	KARAN AHUJA	BHEL
22	151027	AKSHAT BHATNAGAR	Siemens Technology and Services, Bangalore
23	151028	KRITIKA CHAUDHARY	DEAL
24	151030	AJAY SINGH	Maruti Suzuki
25	151031	MOHIT KUMAR GUPTA	Blue Star Limited
26	151034	PRASHANT ARYA	Reliance Jio Infocomm Ltd
27	151037	NIKHIL K SHANDELYA	BHEL
28	151039	AMOGH MISHRA	Bharat Sanchar Nigam Limited
29	151040	RHEA KUKRETI	Seceon
30	151041	BHUMIKA GARG	CDAC
31	151042	JASLEEN KAUR	CDAC Mohali
32	151043	MAHIMA PARASHAR	Cdac Mohali
33	151044	DHRUV GARG	HFCL
34	151045	RAMNEET KAUR	bsnl
35	151047	PRAFULL RAINA	CENTRE FOR DEVELOPMENT OF ADVANCED COMPUTING
36	151048	SANCHIT DANG	Bharat Electronics Limited, Panchkula
37	151049	AKHIL RANA	BSNL - Palampur
38	151052	HIMANSHU CHOUDHARY	K.C Kasliwal Thermal Training Institute
39	151053	HARSHIT JAIN	Tevetron technologies pvt. Ltd.
40	151055	SACHIN TAKYAR	HP Computer
41	151056	RUSHIL BHATNAGAR	prasar bharati
42	151057	LOVISH SINGLA	Hindustan aeronautics limited
43	151058	SIDDHARTH SHARMA	MARICO INDIA PVT.LTD
44	151059	RIYA OHRI	BSNL
45	151060	ANUBHAV TOMAR	PWD
46	151061	KAUSHIKEE	University of Information Science and Technology of Ohrid, Macedonia
47	151063	SHRUTI SABHERWAL	NTPC
48	151064	DEEPANKAR MATHUR	Purple Panda Fashions Private Limited

21/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

49	151065	PARTH DUBEY	Reliance Communications Limited
50	151066	GUNDEEP SINGH	NTPC Limited
51	151069	SMRITI THAKUR	Ambuja Cement
52	151070	MAHIMA AGARWAL	Bharat Electronics limited
53	151073	SUCHITA SINGH KANTHWAL	Think Next
54	151076	SWARIT SOOD	Macrew Technologies Pvt Ltd.
55	151077	NIKHIL VERMA	DOORDARSHAN KENDRA SHIMLA
56	151079	ABHINANDAN SHARMA	Bharat Electronics Limited, Panchkula
57	151080	SHIVAM VERMA	Bharat electronics limited
58	151081	SHAURYA MEHROTRA	Realiance Jio
59	151082	SIDDHIKA SETH	Bsnl
60	151085	KARMANYA SHARMA	C-DAC Mohali
61	151086	MANAN KASHMIRI	Rooman technologies pvt . Ltd
62	151087	KRITTIKA TEWARI	Motilal Nehru National Institute of Technology
63	151088	MANIKYA SABHARWAL	NHPC
64	151089	AADEESH JAIN	Prasar Bharati, ALL INDIA RADIO :CHHATARPUR
65	151090	ANNIE SHARMA	TCIL-IT ,
66	151091	SHIVANGI	IIT Delhi
67	151092	SHRIYA VANDITA	LG electronics (Greater Noida)
68	151093	ARPIT RITURAJ	DMRC
69	151095	AKSHIT CHANDEL	BSNL
70	151097	RISHAB UPMANYU	National Institute of Information Technology
71	151098	RISHABH KANWAR	HTIS Telecom
72	151100	KANCHAN RANI	B4S solutions pvt limited
73	151101	MEDHA GUPTA	Telecommunications Consultants India Limited-Information Technology(TCIL-IT)
74	151102	AKSHIT SHARMA	Blue Star Limited
75	151103	GOURI SHARMA	B4S solution private limited
76	151105	SIMRAN CHAUHAN	Telecommunications Consultants India Ltd-Information Technology(TCIL-IT)
77	151106	DIVYANSH KAISTHA	BSNL
78	151107	PALLVI	B4S Solutions Pvt. Ltd.
79	151108	APOORV UPADHYAY	BSNL
80	151109	SAHIL JAS	Himachal Futuristic Communications Ltd.
81	151110	SANDEEP SHARMA	Mind Grind private limited
82	151112	PARAS GUPTA	Internshala

09/08/2022

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg.
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Dr. Rajiv Kumar
Head, Department of Electronics and Comm. Engg
Jaypee University of Information Technology,
P.O.-Waknaghat, Distt. Solan (H.P.) Pin-173 234

Industrial Training 2020 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	161002	Tanveer singh Sodhi	AAI
2	161003	AKSHAY SOM	Doordarshan kendra , delhi
3	161005	Samson Shukla	Cetpa Infotech Pvt. Ltd.
4	161006	Sumit Thakur	Doordarshan Kendra
5	161007	Mohit Garg	Whiz Infotel
6	161009	Satyam Kumar	Bharat Electronics Limited, Ghaziabad
7	161011	Sarthak kaushik	Cetpa Infotech
8	161014	Anushka Shukla	ATC, Airport Authority of India, IGI AIRPORT, NEW DELHI
9	161015	Siddharth Singh	Aptron solutions Ltd
10	161016	Priyanshi Rastogi	National Thermal Power Corporation
11	161017	Kanika Chaudhary	Powertel, powergrid corporation of India LTD.
12	161021	Himanshi Singh	NIIT Technologies
13	161022	Lavish kumar jangir	Brain Stem Technologies
14	161023	Parthsarthi Bassi	Bharat Electronics Limited, Panchkula
15	161024	Manasvi Kashyap	Oil and Natural Gas Corporation ltd
16	161025	Shivansh Gusain	IRDE
17	161030	Himanshu Walia	Oceana Tech
18	161031	Megham Garg	Oceana Tech
19	161032	Tanya gupta	DUCAT institute ,noida
20	161033	Kushagra Srivastava	Aptron Solution Pvt. Ltd.
21	161034	Nilesh Kishor	Indian Railways, Bareilly
22	161035	Aditya Mohan	ThreatLandscape Cyber Solutions Private Limited
23	161037	Sparsh mahajan	Airmesh communications limited
24	161042	Sonia Jain	Oceana Tech
25	161043	Bahar sharma	Bharat electronics limited
26	161044	Mayank gupta	I3indya technologies
27	161045	Shailu Srivastava	BHARAT SANCHAR NIGAM LIMITED,PATNA
28	161046	Narendra Jangid	Adhoc Networks
29	161047	Suresh Arora	i3indiya technologies
30	161048	Pranav Bansal	Network Bulls
31	161051	Sanchit Garg	Advanced Tech.
32	161053	arpit rana	HP-PWD
33	161055	Abhinandan Thakur	NKC Projects pvt ltd
34	161056	Kriti Verma	BEL
35	161057	Riya Tyagi	SSDN TECHNOLOGY
36	161058	Sughosh Sharma	BSNL (Ghumarwin branch)
37	161060	Abhinav Sharma	Jetking
38	161061	Ashish Kumar	Netmax Technologies pvt. ltd.
39	161062	Abhishek Jha	LG India
40	161063	ALOK SHEKHAR BHARDWAJ	INFOSEEK TECHNOLOGIES , LUCKNOW
41	161066	Ritankshee	Kvch Oracle
42	161067	Mukul Gupta	Oceana Tech IN (Mohali)
43	161068	Inderpreet singh	Netmax Technologies Pvt. Ltd. , Chandigarh
44	161069	Mehak Beakta	Bharat Electronics Limited
45	161070	Rushmika Singh	Powertel, Powergrid corporation india Ltd.
46	161072	Akhilesh Kumar	Akvo Atmospheric Water Systems
47	161073	Surbhi Garg	NIIT
48	161074	Yashvir Singh	Bharat Electronics Limited
49	161075	Bhavya Chadha	Bharat Electronics Limited(BEL)
50	161076	Anshul Kumar	Oceanatech
51	161077	Harshita Rana	FranConnect software Pvt. Ltd.

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52	161078	Tarun Gupta	Softechno Institute
53	161080	Ayshika Kapoor	ICT Academy - Indian Institute of Technology, Kanpur
54	161081	Utkarsh Gupta	Intercity Foundation
55	161082	Shikhar Srivastava	Volumetree
56	161083	Apurva Padiyal	CETPA Infotech Pvt Ltd
57	161084	Stakshi Sharma	Oceana Tech
58	161085	Ranjan Kumar	InterNext Engineering Solution Pvt. Ltd.
59	161086	Devashish Dimri	IRDE,DRDO,Dehradun
60	161087	Shikhar Srivastava	Railtel Corporation of India Limited
61	161088	Nupur Chaturvedi	NTPC Faridabad
62	161089	Diuman Mahajan	Edoofa
63	161090	Deepak Kumar	Niks technology
64	161091	PAYOOSNI SINGH	Maruti Suzuki
65	161092	ashish kumar verma	infoseek
66	161093	Aditya Tiwari	Niks Technology
67	161094	TANMAY CHAUDHARY	ONGC DEHRADUN
68	161095	Samyak Jain	Cloudxchange.io
69	161098	Yatharth Gautam	Cetpa Infotech Private Limited
70	161099	Somya Chaturvedi	North Western Railways
71	161100	Ajay thakur	Thinknext
72	161102	Archit Sugha	Oceana Tech
73	161104	Abhishek Koundal	Jetking
74	161107	shubham jamwal	BSNL SOLAN
75	161108	Prashant Sharma	BSNL
76	161110	Hardik sharma	Thinknext
77	161111	Abhishek sharma	Inx infotech
78	161112	Arushi verma	BSNL telecommunications
79	161113	Aayush Goyal	Oil and Natural Gas Corporation Limited
80	161114	Nitin kumar	BSNL
81	161115	Sarthak Srivastava	JIL information technology limited
82	161116	Kanwar Singh	Hughes communications
83	161117	manthan chauhan	BSNL
84	161118	Prashant kumar	BSNL

09/08/2022

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Industrial Training 2021 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	161029	Akhilesh Sapehia	Jaypee university of information and technology
2	171001	Abhishek Bundel	Internshala Trainings
3	171002	Ayush Kumar Jaiswal	Internshala
4	171003	Mukul Bhatia	Internshala
5	171004	Diwakshu katoch	Internshala
6	171005	Akhil Chauhan	Internshala
7	171006	Prerna Kanwar	Internshala
8	171007	Sahitya bhalaik	Jaypee University of information technology
9	171008	Sanket Saxena	Internshala
10	171009	Kritik Verma	Internshala
11	171010	Sangharsh singh	Cetpa infotech Pvt ltd Noida,Uttar Pradesh
12	171012	tushar agarwal	INTERNSHALA
13	171014	ujjwal jain	INTERNSHALA
14	171015	Soham Ahuja	United Nations
15	171016	Keshav Vohra	Internshala
16	171018	rohit behl	internshala
17	171019	Shivam Sinha	Imternshala
18	171020	Sanyam	Internshala
19	171021	Archita Gupta	Internshala
20	171023	Abhishek Malik	Internshala
21	171024	pankaj	Jaypee University of information and technology
22	171025	kshitij katoch	INTERNSHALA
23	171026	Spardha Kapil	Geeks For Geeks
24	171027	sheetanshu saurabh	internshala
25	171028	Hitesh Thakur	Internshala
26	171029	Sarthak Bisht	Jaypee University of Information technology
27	171030	ALOK PANDEY	Internshala
28	171031	Shubham Kumar	INTERNSHALA
29	171032	Shivansh Suhane	JUIT
30	171033	Ritwik Sood	Jaypee University of Information Technology
31	171034	Tarun Arora	Internshala
32	171035	Ishan Goyal	Internshala
33	171036	Dhananjai Bhalaik	Internshala
34	171037	Shaurya Rajput	Jaypee University of Information Technology, Solan
35	171038	Ananya Shukla	Jaypee University of Information Technology
36	171039	Rajnikant yadav	Jaypee University Of Information Technology
37	171040	Piyush Kumar Singh	Internshala Online Training
38	171042	Ramit Bawa	Intershala
39	171043	Saurav Anand	Internshala Trainings
40	171044	Shivansh Dubey	Internshala
41	171046	Utkarsh Srivastava	Internshala
42	171047	Mehul Bandlish	Jaypee University of Information technology
43	171048	Prashant Jaiswal	Intershala
44	171049	Shachi Sharma	Internshala
45	171050	Ananya Sharma	Internshala
46	171051	Shruti Sharma	Internshala
47	171052	Shubham Singh	INTERNSHALA
48	171053	Nikita Pandey	Internshala
49	171056	Prachi Pal	internshala
50	171057	Bandana Pal	INTERNSHALA
51	171058	Ojasvi	Internshala

09/08/2022

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52	171059	Anushka Dixit	Internshala
53	171060	surya mahajan	internshala
54	171061	Saksham goel	Fastor
55	171062	Vishal Srivastava	EICT Academy, IIT Kanpur
56	171065	Shruti Singh	Internshala
57	171069	Anshul Deorane	Internshala
58	171070	Anupam Srivastava	Internshala Traning
59	171071	Saksham Tandon	internshala
60	171073	Saumya Jajodia	Internshala
61	171074	Akshat Gupta	Webdew
62	171075	Aadhya Bajpai	Verzeo
63	171076	Sudhanshu Mishra	Jaypee University of Information Technology, Solan
64	171078	Nikhil Tanwar	Internshala
65	171079	Kartikey Bindal	Internshala
66	171080	Nikunj	Internshala

04/08/2022

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Industrial Training 2022 Passing Batch

S. No.	E. No.	Name of the Students	Internship Details
1	181001	Priyank Srivastava	Internshala
2	181005	Vinayak Tiku	internshala
3	181006	Harsh mishra	EduMoon
4	181007	Aditya Kumar Jaiswal	Internshala
5	181008	Arsh Kumar	Internshala
6	181009	Gurpreet Singh	AM Tech Networks
7	181010	Surbhi kumari	Internshala
8	181011	Kartikay Kaushal	Internshala
9	181012	Nikhil Thakur	Internshala
10	181013	NIKHIL YADAV	INTERNSHALA
11	181015	Rakshit Sharma	BSNL
12	181016	Kamlesh kumar	Internshala
13	181017	Kshitij Sharma	Internshala trainings.
14	181019	Avinash Verma	INTERNSHALA
15	181020	Mudit katiyar	Internshala
16	181022	Himanshu Thakur	Internsalla
17	181023	Aditya Mishra	Internsala
18	181024	Kirti Parshionikar	Internshala
19	181025	Tavleen Singh	Internshala
20	181027	Vaibhav Rastogi	Internshala
21	181028	RAGHAV SHARMA	Internshala

09/08/2022

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Dept: CIVIL BATCH - 2014 - 2018

Year - 2017

(1)

University Requirement							Requirement for Accredation / Ranking Agencies				
S.No.	Enrollment No.	Branch	Period of Training (No. Of Weeks)	Training Start Date	Training End Date	Status (Satisfactory / Unsatisfactory)	Institute/Company Name	Subject/Topic of Training	Domain/Area of Training	Stipend Received (If Any)	Aadhaar Number of Student
1	141263	CE	7	29-05-2017	15-07-2017	Satisfactory	HPRDCL	Construction of roads (e PMS, RADMS, ROMDAS)	Construction, System Analysis	NO	987868746848
2	141601	CE	6	29-05-2017	08-07-2017		P K Construction Shimla	Construction of Advocate Chamber near High Court and Construction of Parking Complex at Chotta Shimla	Construction	NO	884578188153
3	141603	CE	6								
4	141604	CE	5	29-06-2017	30-06-2017	Satisfactory	HCC	Construction of NH- 34, 4 Lane (Farrakka, Raiganj Section)	Construction	NO	541252189749
5	141605	CE	6	01-06-2017	15-07-2017	Satisfactory	Indian Railways	Construction of Limited Height Subway under Railway Department	Construction	NO	253736151986
6	141606	CE	6	05-06-2017	15-07-2017	Unsatisfactory	JPHRF	Bridge Construction Pung Khadd Sujanpur Tihra (Baijnath Project)	Construction,Project Planning	NO	961362475484
7	141606	CE	6	05-06-2017	15-07-2017	Satisfactory	Syal and associates	Structural Design	Design	NO	253657634246
8	141607	CE	6	05-06-2017	10-07-2017	Satisfactory	IOCL	Construction of Oil Water Seperetor	Construction	NO	
9	141608	CE	6	05-06-2017	10-07-2017	Satisfactory	SJVNL	LUHRI Hydropower Electric Project	Construction Planning and Design	NO	470244564729
10	141609	CE	4	05-06-2017	05-07-2017		L&T	Commercial Building Construction (DLF Building in Gurugram)	Construction	NO	364358230523
11	141610	CE	6	10-06-2017	17-07-2017	Satisfactory	IIT BHU	Design and Analysisof Pitched Roof Truss Using STAAD Pro	Design and Analysis	NO	493996271823
12	141611	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	275103106040
13	141612	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Cresidential Building, Galaxy Heights	Construction	NO	911325199048
14	141613	CE	7	01-06-2017	16-07-2017	Satisfactory	PWD	Road Construction and maintenance at Mathura, UP	Construction	NO	748717944274
15	141615	CE	7	05-06-2017	17-07-2017	Satisfactory	HPPWD	Construction of Post Graduate College	Construction	NO	533592259552
16	141616	CE	6	01-06-2017	12-07-2017	Satisfactory	SJVNL	Rampur Hydro Power Station	Construction, Planning and Design	NO	642152102942
17	141617	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Sawra Kuddu Hydropower Electric Project	Construction	NO	280189613732
18	141619	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	813332527314
19	141620	CE									Pending
20	141621	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Comprehensive Development of Corridor on Outer Ring between Mukbara Chowk to Wazirabad	Construction	NO	612109067356
21	141622	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Construction of 33/220 kV Pooling Sub-Station	Construction	NO	Pending
22	141624	CE	6	02-06-2017	15-07-2017	Satisfactory	Ved Prakash Gupta	Construction of boundary wall	Construction	No	509062120363
23	141626	CE	6	05-06-2017	14-Jul	Satisfactory	DMRC	Contruction of Underground Metro	Construction and Surveying	No	725029168548
24	141627	CE	6	29-05-2017	08-07-2017	Satisfactory	Naresh Bhandari	Construction of Multipurpose Ground and Stadium for Sports Facilities in Kandaghat	Construction	NO	867788791400
25	141630	CE	7	05-06-2017	17-07-2017	Satisfactory	M G Construction	Four Laning of Kharar-Kurali Section of NH-21 in the State of Punjab on EPC Mode	Construction	NO	958830245993
26	141633	CE	6	04-06-2017	15-07-2017	Satisfactory	HPPWD	Construction of Underground Waste Collection System at Dharamsala	Construction	NO	233964159757
27	141634	CE	6	01-06-2017	14-07-2017	Satisfactory	DrukGreen	Hydro Power Electric Project	Construction	NO	
28	141636	CE	6	05-06-2017	18-07-2017	Satisfactory	CPWD	Electrofitting	Estimation and Operation	NO	842943328993
29	141637	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Hydro Power Electric Project	Construction, Analysis and Design	NO	440663665519
30	141638	CE	6	05-06-2017	15-07-2017		NTPC	Q & A	Quality management	NO	493285031722
31	141639	CE	6	01-06-2017	15-07-2017	Satisfactory	Paharpur Cooling towers	Paharpur Cooling Tower Pvt. Ltd.	Construction and Estimation	NO	457229473693
32	141640	CE	6	08-05-2017	17-06-2017	Satisfactory	PWD	Construction tubewell	Construction and Site Investigation	NO	280438057959
33	141641	CE	5	12-06-2017	10-07-2017	Satisfactory	Renuka	Road Construction and Survey	Construction	NO	488631889287
34	141642	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Sewage Treatment Plant Operation	Site Visit and Design	NO	597153870545
35	141643	CE	6	04-06-2017	07-07-2017	Satisfactory	DMRC	Construction of Underground Metro at R K Puram and Hauz Khas Station	Construction	NO	596538281137
36	141644	CE	6	01-06-2017	12-07-2017	Satisfactory	HPPWD	Construction of multi purpose hall	Construction	NO	958282824701
37	141645	CE	6	01-06-2017	15-07-2017	Satisfactory	HPPCL	Swara Kuddu Hydropower Project	Construction	NO	736402354843
38	141646	CE	6	01-06-2017	15-07-2017	Satisfactory	GAWAR	Road Construction of 4- Lane Panchkula and Yamuna Nagar (NH- 73)	Construction		
39	141647	CE	6	05-06-2017	15-07-2017	Satisfactory	SJVNL	Stability analysis of Luhri HEP Stage-1	Design	NO	339213751913

40	141648	CE	6	29-05-2017	08-07-2017	Satisfactory	PWD	Multiporpous Sports Stadium Ramamandir Mandi, Veterinary Hospital and College Rampur	Construction, Maintenance and Design	NO	619538309958
41	141650	CE	7	01-06-2017	15-07-2017	Satisfactory	Jaiprakash And Sons	Construction of Mega Hostel Block in NIT Hamirpur	Construction	NO	352700960035
42	141651	CE	6	01-06-2017	11-07-2017	Satisfactory	Sunrises Structures	Construction of Sun Twilight Villas and Commercials	Construction	NO	830120993663
43	141652	CE	6	01-06-2017	12-07-2017	Satisfactory	SIDCL	Road Construction	Analysis	NO	986065011649
44	141653	CE	7	05-06-2017	18-07-2017	Satisfactory	INPH	Intze Tank Design	Design	NO	957707592017
45	141654	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rain Water Harvesting Tank Transportation of Exsisting Lawn Into Rain Garden	Construction	NO	873345654123
46	141655	CE	7	29-05-2017	17-07-2017	Satisfactory	UPRNNL	Building Construction	Construction	NO	584157677760
47	141656	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
48	141661	CE	7	15-06-2017	31-07-2017	Satisfactory	PWD	Residential Building Construction	Construction	NO	867213841974
49	141662	CE	6	01-06-2017	06-07-2017	Satisfactory	HPPTC	Retaining wall construction	Construction	NO	387802984564
50	141663	CE	7	29-05-2017	15-07-2017		HPRDCL	Construction of roads	Construction	NO	
51	141664	CE	6	29-05-2017	08-07-2017	Satisfactory	PK Construction	Car Parking Building Construction	Construction	NO	767631756894
52	141665	CE	7	01-06-2017	15-07-2017	Satisfactory	Whizkids	Rainwater Harvesting Tank	maintenance	NO	435539216442
53	141666	CE	6	05-06-2017	17-07-2017	Satisfactory	CPWD	Building Maintenance	maintenance	NO	989868620530
54	141667	CE	6	31-05-2017	11-07-2017	Satisfactory	SPCL	Construction of Bus Terminus and Parking	Construction	NO	282070765310
55	141668	CE	6	03-06-2017	14-07-2017		RED	Construction of hall	Construction	NO	892245015469
56	141669	CE	5	13-06-2017	15-07-2017	Satisfactory	PWD Dharamsala	Construction of roads	Construction	NO	774345360402
57	141670	CE	5	29-05-2017	30-06-2017	Unsatisfactory	HCC	4 Laning Farakka Raiganj Section	Construction	NO	454223208162
58	141671	CE	6	28-05-2017	14-07-2017	Satisfactory	Bansal Engineers	Building Construction	Contruction	Yes	597323298747
59	141672	CE	4	30-05-2017	30-06-2017	Satisfactory	ADRDE	Design of building	Design	NO	505348241275
60	141673	CE	6	01-06-2017	12-07-2017	Satisfactory	UPPWD	Road Contruction	Construction	NO	
61	141674	CE	6	01-06-2017	12-07-2017	Satisfactory	REASI	Water Distribution System Study	Analysis	NO	671722842063
62	141675	CE	7	01-06-2017	14-07-2017	Satisfactory	Bareilly Development Authority	Laying of Sewer Pipelines	Construction	NO	334980591932
63	141676	CE	6	05-06-2017	15-07-2017	Satisfactory	JLPL	Construction of Galaxy Heights Project	Construction	NO	312625902455
64	141677	CE	6	01-06-2017	11-07-2017	Satisfactory	Swastik	Underground Substation Gurugram	Construction	NO	831847743627
65	141678	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Casting of Bridge	Testing	NO	569738883949
66	141679	CE	5	30-05-2017	12-07-2017	Satisfactory	H. C. Bansal Engineers and Contractors	Building Construction	Construction	Yes	692342550589
67	141680	CE	6	01-06-2017	05-07-2017	Satisfactory	ERA	Road Construction	Construction	NO	567280282077
68	141681	CE	6	11-06-2017	16-07-2017	Satisfactory	HPPCL	Barrage division of sainj Hydro Power Electric Project	Construction	NO	346612434207
69	141682	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Construction of PG	Construction	NO	639806463361
70	141683	CE	4	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Ambuja Cement Plant Visit	Materials	NO	334214454998
71	141684	CE	6	29-05-2017	08-07-2017	Satisfactory	HPPWD	Development of New OPD at IGMC Shimla	Construction	NO	995522249985
72	141686	CE	6	01-06-2017	01-07-2017	Satisfactory		Building Construction (Mohali)	Construction	NO	411889377530
73	141687	CE	6	12-06-2017	22-07-2017	Satisfactory	HPPWD	HP State Library Building Contruction	Construction	NO	885024325960
74	141688	CE	6	31-05-2017	11-07-2017	Satisfactory	DMRC	Testing of materials	Testing	NO	868824583795
75	141689	CE	6	03-06-2017	17-07-2017	Unsatisfactory	Indian Railways	Construction of Railway Track	Construction	NO	409852377341
76	141690	CE	6	31-05-2017	10-07-2017	Satisfactory	Sub division Engg office	G+5 Multi tier Parking and Commercial Complex Project at General Bus Stand	Construction	NO	691456577638
77	141691	CE	6	29-05-2017	05-07-2017	Satisfactory	HPPWD	Highway Maintenance and PG College	Constructon	NO	
78	141692	CE	6	01-06-2017	12-07-2017	Satisfactory	DMRC	Underground Substation	Construction/ Surveying/ Geotechnical Investigation	NO	862339185428
79	141693	CE	4	05-06-2017	08-07-2017	Satisfactory	BP	Construction of new filling shed	Construction	NO	530137391222
80	141694	CE	6	30-05-2017	10-07-2017	Satisfactory	PWD	Construction of roads	Construction	NO	424523018138
81	141695	CE	6	05-06-2017	15-07-2017	Satisfactory	Ambuja Cement	Concrete Mix Design	Design	NO	579641278502
82	141696	CE	4	31-05-2017	30-06-2017	Satisfactory	CPWD	Construction	Construction	NO	876016738612
83	141697	CE	4	01-06-2017	30-06-2017	Satisfactory	LMRC	Lucknow Metro Construction	Construction	NO	928844325232
84	141698	CE	7	01-06-2017	07-07-2017	Satisfactory	SJVNL	Retaining wall construction	Construction	NO	341163355226

Dept: CIVIL ENGG. BATCH : 2015-2019

Year - 2018

(2)

Summer/Industrial Training Status Summary August 2018 (Batch 2015-2019)									
S no.	**Roll No.**	**Student Name**	**Department**	**Training Dairy Submitted (Yes/No)**	**Training Report Submitted (Yes/No)**	**Training Certificate Submitted (Yes/No)**	**Viva held on (Date)**	**Viva Taken by (Faculty Name)**	**Status (Satisfactory/ Unsatisfactory)**
1	141658	Pankaj Sankhyan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Anirban Dhulia & Mr. Aakash Gupta	**Satisfactory**
2	151113	Akal Singh Gurung	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
3	151601	Divesh Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
4	151602	Puneet Pal Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
5	151604	Nikhilesh Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
6	151605	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
7	151606	Abhishek Ahluwalia	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
8	151608	Hetain Sahi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
9	151610	Kuenzang Sc Choden	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
10	151612	Shally Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
11	151613	Shivani Negi	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
12	151614	Charu Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
13	151616	Harsh Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
14	151617	Ammaan Zahoor Chat	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
15	151618	Sarthak Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
16	151619	Akshay Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Rishi Rana & Mr. Kaushal Kumar	**Satisfactory**
17	151620	Rizul Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
18	151621	Abhimanyu P Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
19	151622	Arpan Chaudhary	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
20	151623	Tarun Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
21	151624	Jigyasu Khanna	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
22	151625	Harish Chander	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
23	151626	Manik Ohri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
24	151627	Ankur Jaret	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
25	151628	Ankit Tilokta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
26	151629	Sudhanshu Manikpuri	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
27	151630	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
28	151631	Abhinav Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
29	151632	Gaurav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
30	151633	Divyam Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

31	151634	Dipanshu Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Niraj Parihar & Mr. Aakash Gupta	**Satisfactory**
32	151635	Ajay Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
33	151636	Himanshu Yadav	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
34	151637	Aditya Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
35	151638	Prikshit Gupta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
36	151639	Ashish Dangwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
37	151640	Akshay Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
38	151641	Vaibhav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
39	151642	Akshay Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
40	151643	Aatish Rajta	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
41	151645	Puneet Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
42	151646	Pratiyush Kothari	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
43	151647	Shashi Shekhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
44	151648	Vinayak Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
45	151649	Sumit Dhankhar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
46	151650	Gourav Mahajan	Civil Engineering	Yes	Yes	Yes	06-08-2018	Mr. Abhilash Shukla & Mr. Kaushal Kumar	**Satisfactory**
47	151651	Nikhil Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
48	151652	Anirudh Pratap	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
49	151654	Nitesh Chandel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
50	151655	Arpan Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
51	151656	Shubham Soni	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
52	151657	Akhil Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
53	151658	Himanshu Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
54	151659	Parikshit Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
55	151660	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
56	151661	Amit Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
57	151662	Ashutosh Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
58	151664	Amit Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
59	151666	Deval Ashish	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
60	151667	Dikshant Agarwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

61	151668	Bhupinder Singh Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Saurabh Rawat & Mr. Abhilash Shukla	**Satisfactory**
62	151669	Aayush Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
63	151670	Ahtesham Hussain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
64	151671	Nakshatra Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
65	151672	Ashish Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
66	151673	Ishan Uniyal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
67	151674	Suryabhan Singh Jamwal	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
68	151675	Harshit Chauhan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
69	151676	Vedansh Garg	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
70	151677	Gaurav Thakur	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
71	151679	Maanik Vatshyayan	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
72	151680	Saksham Jain	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
73	151682	Divesh Narang	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
74	151683	Shubham Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
75	151684	Vikas Verma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
76	151687	Ayush Bhardwaj	Civil Engineering	Yes	Yes	Yes	06-08-2018	Dr. Amardeep and Dr. Saurav	**Satisfactory**
77	151688	Kuldeep Rana	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
78	151689	Mayank Singh	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
79	151690	Tarun Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
80	151691	Vibhor Gautam	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
81	151692	Karan Goel	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
82	151693	Saksham Kumar Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
83	151694	Ankush Kumar	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
84	151696	Saksham Sharma	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
85	151697	Sparsh N.K. Lath	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**
86	151698	Kartikey	Civil Engineering	Yes	Yes	Yes	06-08-2018		**Satisfactory**

Kaushal Kr.

Industrial Training Coordinator

HoD CE

Dept: CIVIL BATCH - 2016-2020

Year - 2019

(3)

INDUSTRIAL TRAINING STATUS OF CIVIL ENGINEERING DEPARTMENT (2019-20)					
S. No.	Enrol. No.	Name of Student	Industrial Training Report Submitted by Student to Deptt.	Viva Held on	Status of Indutrial Training Completion
1	161659	Pranav Gupta	Submitted	08-08-2019	Satisfactory
2	161664	Vivek Kashyap	Submitted	08-08-2019	Satisfactory
3	161053	Arpit Rana	Submitted	08-08-2019	Satisfactory
4	161663	Seraj Habib	Submitted	08-08-2019	Satisfactory
5	161666	Shivam Nag	Submitted	08-08-2019	Satisfactory
6	161055	Abhinandan Thakur	Submitted	08-08-2019	Satisfactory
7	161688	Shivam Gupta	Submitted	08-08-2019	Unsatisfactory
8	161628	Sangay Zangmo	Submitted	08-08-2019	Satisfactory
9	161695	Parmila Gurung	Submitted	08-08-2019	Satisfactory
10	161693	Karma Yangzom	Submitted	08-08-2019	Satisfactory
11	161631	Sonam Tshomo	Submitted	08-08-2019	Satisfactory
12	161652	Abhinav Choudhary	Submitted	08-08-2019	Satisfactory
13	161627	Harjot Singh	Submitted	08-08-2019	Satisfactory
14	161615	Vivek Pundir	Submitted	08-08-2019	Satisfactory
15	161673	Shourabh Maanju	Submitted	08-08-2019	Satisfactory
16	161674	Aryan	Submitted	07-08-2019	Satisfactory
17	161675	Saksham Mahajan	Submitted	07-08-2019	Satisfactory
18	161625	Ajay Sharma	Submitted	07-08-2019	Satisfactory
19	161620	Piyush Pathania	Submitted	07-08-2019	Satisfactory
20	161639	Rohit Kumar	Submitted	07-08-2019	Satisfactory
21	161661	Shubang Malgotra	Submitted	07-08-2019	Satisfactory
22	161634	Yashwant Singh Rana	Submitted	07-08-2019	Satisfactory
23	161691	Ritesh Kumar Chaurasia	Submitted	07-08-2019	Satisfactory
24	161602	Harshit Bansal	Submitted	07-08-2019	Satisfactory
25	161685	Hitesh Panwar	Submitted	07-08-2019	Satisfactory
26	161655	Alakshender Singh Wazir	Submitted	07-08-2019	Satisfactory
27	161614	Himanshu Kapoor	Submitted	07-08-2019	Satisfactory
28	161612	Gaurav Chauhan	Submitted	07-08-2019	Satisfactory
29	161678	Ujjwal Nadda	Submitted	07-08-2019	Satisfactory
30	161687	Utkarsh Chauhan	Submitted	07-08-2019	Satisfactory
31	161608	Saurav Singh	Submitted	07-08-2019	Satisfactory
32	161665	Deepak Sharma	Submitted	07-08-2019	Satisfactory
33	161690	Shivam Sharma	Submitted	07-08-2019	Satisfactory
34	161637	Mayank Sharma	Submitted	07-08-2019	Satisfactory
35	161654	Samarth Sharda	Submitted	07-08-2019	Satisfactory
36	161646	Shushant Gupta	Submitted	07-08-2019	Satisfactory
37	161689	Abhishek Thakur	Submitted	07-08-2019	Satisfactory
38	161677	Keshav Singh Thakur	Submitted	07-08-2019	Satisfactory
39	161603	Abhishek Sharma	Submitted	07-08-2019	Satisfactory
40	161630	Pema Zangmo	Submitted	07-08-2019	Satisfactory
41	161694	Pema Yangden	Submitted	07-08-2019	Satisfactory
42	161629	Ngawang Dolkar	Submitted	07-08-2019	Satisfactory
43	161647	Chahat Garg	Submitted	07-08-2019	Satisfactory
44	161611	Ambuj Awasthi	Submitted	07-08-2019	Satisfactory
45	161626	Nikhil Kumar	Submitted	07-08-2019	Satisfactory
46	161649	Anish Kapil	Submitted	07-08-2019	Satisfactory
47	161686	Siddharth Verma	Submitted	07-08-2019	Satisfactory
48	161680	Deven Mahajan	Submitted	07-08-2019	Satisfactory
49	161640	Gunjan Katoch	Submitted	07-08-2019	Satisfactory
50	161671	Nitin Thakur	Submitted	07-08-2019	Satisfactory
51	161651	Nishant Thakur	Submitted	07-08-2019	Unsatisfactory
52	161636	Mukul Prashar	Submitted	07-08-2019	Unsatisfactory
53	161635	Tejas garg	Submitted	07-08-2019	Satisfactory
54	161617	Anmol Singhal	Submitted	07-08-2019	Satisfactory
55	161613	Harshit Saxena	Submitted	07-08-2019	Satisfactory
56	161696	Yash Goyal	Submitted	07-08-2019	Satisfactory
57	161698	Nagawang Dorji	Submitted	07-08-2019	Satisfactory
58	161605	Amber Soni	Submitted	07-08-2019	Satisfactory
59	161607	Sumit Kumar	Submitted	07-08-2019	Satisfactory
60	161642	Xitiz Sen	Submitted	07-08-2019	Satisfactory
61	161684	Ria Thakur	Submitted	07-08-2019	Satisfactory
62	161676	Rishav Kumar Tiwari	Submitted	07-08-2019	Satisfactory

63	161604	Amol Srivastava	Submitted	07-08-2019	Unsatisfactory
64	161601	Ritanjay ✓	Submitted	07-08-2019	Satisfactory
65	161285	Rishi Singh ✓	Submitted	07-08-2019	Satisfactory
66	161624	Ketan Mishra ✓	Submitted	07-08-2019	Satisfactory
67	151691	Vibhor Gautam ✓	Submitted	29-07-2019	Satisfactory
68	161692	Leki Wangchuk ✓	Submitted	21-08-2019	Satisfactory
69	161670	Prasanna Kumar	Not Submitted	-	Unsatisfactory
70	161644	Shankar Kumar	Not Submitted	-	Unsatisfactory
71	161001	Nikhil Sharma	Not Submitted	-	Unsatisfactory
72	161653	Pritul	Not Submitted	-	Unsatisfactory
73	161658	Aditya Vikram Singh Jamwal	Not Submitted	-	Unsatisfactory
74	161657	Anirudhu Guleria	Not Submitted	-	Unsatisfactory
75	161656	Kartikey	Not Submitted	-	Unsatisfactory
76	161668	Nikhil Negi	Not Submitted	-	Unsatisfactory
77	161632	Cheku Dorji	Not Submitted	-	Unsatisfactory
78	141658	PANKAJ SANKHYAN	Not Submitted	-	Unsatisfactory
79	151605	GAURAV SHARMA	Not Submitted	-	Unsatisfactory
80	151688	KULDEEP RANA	Not Submitted	-	Unsatisfactory
81	141625	Namit Sharma	Not Submitted	-	Unsatisfactory
82	141628	HARSH VARDHAN SINGH	Not Submitted	-	Unsatisfactory
83	141659	RAHUL VERMA	Not Submitted	-	Unsatisfactory
84	141663	ADITYA DHIMAN	Not Submitted	-	Unsatisfactory
85	151634	DIPANSHU THAKUR	Not Submitted	-	Unsatisfactory
86	151646	PRATIYUSH KOTHARI	Not Submitted	-	Unsatisfactory
87	151651	NIKHIL KUMAR SHARMA	Not Submitted	-	Unsatisfactory
88	151656	SHUBHAM SONI	Not Submitted	-	Unsatisfactory
89	151668	BHUPINDER SINGH VERMA	Not Submitted	-	Unsatisfactory
90	151677	GAURAV THAKUR	Not Submitted	-	Unsatisfactory
91	151679	MAANIK VATSHYAYAN	Not Submitted	-	Unsatisfactory
92	151689	MAYANK SINGH	Not Submitted	-	Unsatisfactory
93	151694	ANKUSH KUMAR	Not Submitted	-	Unsatisfactory
94	151616	HARSH CHAUHAN	Not Submitted	-	Unsatisfactory

Anirban Dhulia
23/08/2019

Mr. Anirban Dhulia
Mr. Aakash Gupta
Industrial Training Co-ordinator

23/8/19

Prof. Ashok Kumar Gupta
Head of the Department
Civil Engineering

HOD
CE DEPT

Received ✓ Documents
23/08/19

Dept: CIVIL ENGG. BATCH - 2017-2021

Year - 2020-2021

(4)

Summer/Industrial Training Status Summary August 2020 (Batch 2016-2020 and 2017-21)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/Unsatisfactory)
1	161001	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	22-08-2020	Mr. Anirban Dhulia	Satisfactory
2	161604	Amol Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
3	161636	Mukul Prashar	Civil Engineering	Yes	Yes	Yes	22-08-2020	Dr Aakash Gupta	Satisfactory
4	161644	Shankar Kumar	Civil Engineering	Yes	Yes	Yes	14-08-2020	Mr Anirban Dhulia and Dr Aakash Gupta	Satisfactory
5	171067	Aman Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
6	171601	Ishant Shekhri	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
7	171602	Hemant Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
8	171603	Aditya Abrol	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
9	171604	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
10	171606	Shekhar Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
11	171607	Kanishk Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
12	171608	Pawas Soni	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
13	171609	Gaurav Prakash Negi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
14	171610	Gunjan Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
15	171611	Aviral Roy	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
16	171612	Aditya Srivastava	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
17	171614	Vivek Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
18	171615	Vaibhav Singh	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
19	171616	Ashish Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
20	171617	Harsh Goel	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
21	171618	Aditya Rana	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
22	171620	Hardik Nagpal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
23	171621	Rishabh Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
24	171622	Akshit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
25	171623	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
26	171624	Saurabh Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
27	171626	Sourav Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
28	171628	Anjan Sood	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
29	171629	Sameep Aggarwal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
30	171630	Anmol Katana	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
31	171631	Manik Seth	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
32	171632	Siddhant Dubey	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
33	171633	Nikhil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
34	171634	Sukrit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
35	171635	Sahil Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
36	171636	Rohit Kumar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
37	171637	Divyanshu Pandit	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory

38	171638	Anubhav Kundal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
39	171639	Mehul Kumar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
40	171642	Saksham Kaushal	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
41	171644	Saurabh Tomar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
42	171645	Kartik Verma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
43	171646	Ankit Thakur	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
44	171647	Dikshant Joshi	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
45	171649	Ritvik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
46	171650	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
47	171651	Suraj Chaudhary	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
48	171652	Chander Bhushan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
49	171653	Abhay	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
50	171654	Mohit Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
51	171655	Aditya Shekhar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
52	171656	Rijul Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Chandrapal Gautam	Satisfactory
53	171657	Tanish Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
54	171659	Akshay Pathania	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurabh Rawat and Dr Abhilash Shukla	Satisfactory
55	171661	Himanshu Bansal	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Saurav and Dr Amardeep	Satisfactory
56	171662	Shubham Thakur	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
57	171664	Venus Chauhan	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
58	171665	Naveen Karar	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
59	171666	Nikhil Shukla	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory
60	171671	Aditya Nath	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Tanmay Gupta and Mr Akash Bhardwaj	Satisfactory
61	171681	Abhishek Bind	Civil Engineering	Yes	Yes	Yes	20-08-2020	Prof Ashish Kumar	Satisfactory
62	171682	Sanju Kanwar	Civil Engineering	Yes	Yes	Yes	20-08-2020	Mr. Anirban Dhulia	Satisfactory
63	171683	Manik Sharma	Civil Engineering	Yes	Yes	Yes	17-08-2020	Dr Rishi Rana Mr Kaushal Kumar	Satisfactory
64	171684	Lokesh Sharma	Civil Engineering	Yes	Yes	Yes	20-08-2020	Dr. Rajiv Ganguly	Satisfactory

Traning and Placement Coordinator

Head of the Department

25/8/2020

Received
29/08/2020

Dept : CIVIL ENGG. BATCH : 2018-2022

Year : 2021

(5)

Summer/Industrial Training Status Summary August 2021 (Batch 2018-22)

S. No.	Student Roll No.	Student Name	Department	Training Diary Submitted (Yes/No)	Training Report Submitted (Yes/No)	Training Certificate Submitted (Yes/No)	Viva held on (Date)	Viva Taken by (Faculty Name)	Status (Satisfactory/ Unsatisfactory)
1	181602	Yamit Dhalaik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
2	181603	Ujjwal Kumar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
3	181604	Harshit Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
4	181605	Shubham	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
5	181606	Varun Kapil	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
6	181607	Abhay Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
7	181608	Aniket	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
8	181610	Vishal Garg	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
9	181611	Madhvender Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
10	181612	Gaurav Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
11	181613	Rishabh Jaswal	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
12	181614	Vishali Thapta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
13	181615	Abhay Kaith	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
14	181616	Sushant	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
15	181617	Ritik Kumar Puri	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
16	181618	Abhay Kanwar	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
17	181619	Rohit Lakhera	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
18	181621	Atul Vashisht	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
19	181622	Navneet Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
20	181623	Deepak Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
21	181625	Abhay Joshi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
22	181626	Muskan Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
23	181627	Utkarsh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
24	181629	Suryansh Singh	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
25	181630	Bhuvan Walia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
26	181631	Ayush Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
27	181632	Arnav Rawat	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
28	181633	Aditya Chauhan	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
29	181634	Priyanshu Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
30	181635	Rakshit Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Received
17/08/21

31	181637	Abhishek Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
32	181638	Sahil Negi	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
33	181639	Abhinesh Thakur	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
34	181642	Yash Gupta	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
35	181643	Pranav Dogra	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
36	181644	Anushka Anand	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
37	181645	Amish Kartik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
38	181647	Sonam Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
39	181648	Passang Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
40	181649	Phub Dorji	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
41	181650	Sonam Tshering	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
42	181651	Tshering Gyeltshen	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
43	181652	Kinley Zam	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
44	181653	Sonam Tshewang Dema	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
45	181654	Dechen Tshomo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
46	181655	Namgay Wangmo	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
47	181656	Pema Yuden	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
48	181657	Saijal Verma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
49	181659	Nikhil Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
50	181660	Hemang Jandrotia	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
51	181661	Deval	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
52	181662	Ayush Sharma	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory
53	181663	Ritik	Civil Engineering	Yes	Yes	Yes	31-07-2021	Mr. Kaushal Kumar	Satisfactory

Kaushal Kumar

Signature of Departmental Summer Training Coordinator

4/8/21

Signature of the Head of Department

Dr. Ashish Kumar
Professor & HOD of Civil Engineering
Jaypee University of Information Technology,
Waknaghat, Distt.-Solan (HP) 173234 India

Received
17/08/21

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171501	MUSKAN KAPOOR	TARGETING SARS-CoV-2 MAIN PROTEASE	Dr. Raj Kumar	15-05-2020	30-06-2020	06-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171503	AAKRITI CHAUHAN	Analysis of various articles on Epigenetic of Alzheimer's	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171504	GARIMA SHARMA	MACHINE LEARNING WITH PYTHON	Mr. Aqib Ahmed	05-06-2020	10-08-2020	31-08-2020	VERZEO	No. 675, 3rd floor, 9th main sector 7, HSR Layout, BANGALORE,
171505	ANJALI SHARMA	ANALYSIS OF VARIOUS ARTICLES ON EPIGENETICS	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171506	VAIBHAV GANGTA	Data Mining in Biomedical Literature	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	01-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171507	PURVANSHI SHARMA	Programming with Python(Creating a Fantasy cricket	INTERNSHALA	22-05-2020	03-07-2020	28-08-2020	Internshala	B-610, Unitech Business Zone Golf Course Extension Road, Nirvana
171508	MAHARISHI KALLA	Structural Analysis of SARS-CoV-2	Dr. Narendra Kumar	15-05-2020	30-06-2020	02-05-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171509	AAGAM MISHRA	Summer Training on HealthCare Monitoring System Based	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171510	GARIMA SINGH	Website Development	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171511	PRERNA TIWARI	Programming with python	Sarvesh agrawal	15-05-2020	26-06-2020	30-06-2020	Internshala	Internshala
171512	RIYA DHIMAN	Exploring Human Metabolome Database(HMDB) and DrugBank	Dr. Narendra Kumar	15-05-2020	30-06-2020	02-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171514	APURVA GARG	Text Mining in Biomedical Literature	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171515	SARVJEET KAUR	IMGT Database	Dr. Narendra Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171516	SRISHTI THAKUR	IMGT database	Dr. Narendra Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171517	AAKANKSHA GAUTAM	Automated Personality Classification using Data	Dr. Tiratha Raj Singh	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171518	CHHAVI THAKUR	TARGETING SARS-CoV-2 MAIN PROTEASE	Dr. Raj Kumar	15-05-2020	30-06-2020	06-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171519	MEHAK KAPOOR	TARGETING SARS-COV-2 MAIN PROTEASE	Dr. Raj Kumar	15-05-2020	30-06-2020	06-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171801	ANANYAA KAUL	PHYSICO-CHEMICAL EVALUATION OF	Dr. Poonam Sharma	15-05-2020	30-06-2020	03-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171802	VASUDEV SINGH	Fermentation Technology	Dr. Garlapati Vijay Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171804	HARMEET SINGH	PCR TECHNIQUES	Dr. Jata Shankar	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171806	DEVASHISH VERMA	Embryo Culture For In-vitro Micropropagation of New Cicer	Dr. Hemant Sood	15-05-2020	30-06-2020	01-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171807	AAKANKSHA PANDEY	Physicochemical Evaluation of Biosurfactants For Their	Dr. Poonam Sharma	15-05-2020	30-06-2020	03-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171809	REVA BHARDWAJ	Immobilization of enzymes onto the nanoparticles and their	Dr. Ashok Kumar	15-05-2020	30-06-2020	05-09-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171810	DIVYANSH RANA	Immobilization of enzymes onto the nanoparticles and their	Dr. Ashok Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171811	SOUMI BISWAS	Proteomics: Technologies and Application	Dr. Jitendraa Vashistt	15-05-2020	30-06-2020	06-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171812	SUGAM SINGH	Fermentation Technology	Dr. Garlapati Vijay Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171813	UMANG MAHESHWARI	Molecular Circuits Using Synthetic Biology	Dr. Narendra Kumar	15-05-2020	30-06-2020	03-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171814	DIWAKAR PALIWAL	PHYSICO-CHEMICAL EVALUATION OF	Dr. Poonam Sharma	15-05-2020	30-06-2020	03-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171815	ISHITA KAWAR	MICROPROPAGATION OF RHODODENDRON	Dr. Hemant Sood	15-05-2020	30-06-2020	05-06-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171816	EKTA CHOUDHARY	Animal cell culture techniques	Dr. Udayabanu, M	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171817	CHARU THAKUR	Fermentation Technology	Dr. Garlapati Vijay Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171818	RACHITA GUPTA	Animal Cell Culture Techniques	Dr. Udayabanu, M	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171819	VITASTA JALALI	Study on ATCC	Dr. Sudhir syal	15-05-2020	30-06-2020	26-08-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171820	NAVEETA KARAR	PROTEOMIC TECHNOLOGY, TECHNIQUES AND USAGE	Dr. Jitendraa Vashistt	15-05-2020	30-06-2020	06-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171821	JIGYASA	Animal Cell Culture Technologies	Dr. Udayabanu, M	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171823	KIRTI ARORA	INNOVATIONS MADE SO FAR IN COVID-19 VACCINES	Dr. Rahul Shrivastava	15-05-2020	30-06-2020	07-05-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171824	AYUSH TYAGI	Genotyping of single nucleotide polymorphisms by applying	Dr. Harish Changotra	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171825	NEHA VERMA	Introduction to Chemical Pharmacology	Dr. Rahul Shrivastava	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171826	YUKTI	Production of Disease-free potatoes via Mericloning	Dr. Hemant Sood	15-05-2020	30-06-2020	02-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171827	YASHKIRTI GARG	Chromatographic Techniques Used For Arginase	Dr. Saurabh Bansal	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171828	ISHITA	Antibody engineering	Dr. Rahul Shrivastava	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171829	KHUSHI MAHESHWARI	Quantitative Analysis of Traditional Indian Sweets and	Mr. Navdeep Soryan	01-06-2020	15-07-2020	22-08-2020	M/s Sanwaria Sweets Pvt. Ltd. (KANHA)	F-837-838, RIICO Industrial Area, Phase III, Sitapura, Tonk Road, Jaipur,

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
171830	MEGHA SHARMA	PHYTASE AND DIFFERENT CHROMATOGRAPHY	Dr. Saurabh Bansal	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171831	AMANJOT SINGH MALHOTRA	GENOTYPING OF SINGLE NUCLEOTIDE POLYMORPHIS	Dr. Harish Changotra	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171832	RISHAB ROY	Study on ATCC(American Type Culture Collection)	Dr. Sudhir Syal	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171834	MANVHI RASTOGI	VACCINATION	Dr. Rahul Shrivastava	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171835	NAYANIKA SHARMA	Animal Cell Culture Techniques	Dr. Udayabanu, M	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171837	SHIVANI CHATURVEDI	Genotyping Single Nucleotide Polymorphism	Dr. Harish Changotra	15-05-2020	30-06-2020	04-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)
171840	DIVYANSHU BHURAITA	IMMOBLISATION OF ENZYMES, ECONOMICAL AND	Dr. Ashok Kumar	15-05-2020	30-06-2020	05-07-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer Industrial Training - Biotechnology and Bioinformatics - Batch 2021

JUIT Roll no.	Full Name	Title of Summer Training Report . in Title Case	Name of Guide / Supervisor	Training Start Date	Training End Date	Viva Date	Training Institute / Company	Training Institute / Company Address (City and State)
141505	SHAURYA MEHTA	Next generation sequencing	Dr Tiratha Raj Singh	23-07-2020	04-09-2020	07-09-2020	Jaypee University of Information Technology	Wakanaghat, Solan (Himachal Pradesh)

Summer/Industrial Training Status Summary August 2020 (Batch 2017-21)									
S. No.	**Roll No.**	**Student Name**	**Depart**	**Training Diary Submitted (Yes/No)**	**Training Report Submitted (Yes/No)**	**Training Certificate Submitted (Yes/No)**	**Viva held on (Date)**	**Viva Taken by (Faculty Name)**	**Status (Satisfactory/Unsatisfactory)**
1	151208	Shivam Rai	CSE/IT	No	No	No			Unsatisfactory
2	151356	Arav Sood	CSE/IT	No	No	No			Unsatisfactory
3	151428	Itish Dhiman	CSE/IT	Yes	Yes	Yes	07-08-2020	Dr. Ruchi Verma & Dr. Ravindra Bhatt	Satisfactory
4	161226	PRIKSHIT DOGRA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Himanshu Jindal & Dr. Amit Kumar	Satisfactory
5	161334	Abhishek Raj	CSE/IT	Yes	Yes	Yes	22-09-2020	Dr. Ravindara Bhatt	Satisfactory
6	161458	SHAILESH MISHRA	CSE/IT	Yes	Yes	Yes	07-08-2020	Dr. Ruchi Verma & Dr. Ravindra Bhatt	Satisfactory
7	171044	SHIVANSH DUBEY	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
8	171061	SAKSHAM GOEL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
9	171071	SAKSHAM TANDON	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
10	171201	SEENAM	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
11	171202	PRANJAL GANGWAR	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Pardeep Kumar & Dr.Pradeep Kumar Gupta	Satisfactory
12	171204	PANKAJ PATEL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
13	171205	TANISH GUPTA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
14	171206	JAI GANGWAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
15	171207	RAHUL KRIPLANI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
16	171208	RAVI BHUSHAN SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Mr. Arvind Kumar & Dr.Vivek Sehgal	Satisfactory
17	171209	JATIN MUTNEJA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
18	171211	DWAIPAYAN VIDYANTA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
19	171212	ABHISHEK AGARWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
20	171214	DIVYANSHU SINHA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
21	171215	SUGAKSHI VIJ	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
22	171217	Ekansh Kakkar	CSE/IT	Yes	Yes	Yes	07-08-2020	Dr. Ruchi Verma & Dr. Ravindra Bhatt	Satisfactory
23	171218	AJAY SINGH	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Pardeep Kumar & Dr.Pradeep Kumar Gupta	Satisfactory
24	171219	NIKHIL SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory

25	171220	ARYAN NEGI	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
26	171221	ANANYA BAJPAI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
27	171222	ARNAV SHARMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
28	171224	NIKHIL NAGPAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
29	171225	MOLIK AGGARWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
30	171226	PRANJAL SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
31	171228	VESUWALA R C KUMAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
32	171229	SAHIL SARDANA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
33	171231	UJWAL GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
34	171232	AVISHA SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
35	171233	ADHI SHREE BANSAL	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
36	171234	TANVI SANKHYAN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
37	171235	LOKESH	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Rajni Mohna & Dr.Ekta	Satisfactory
38	171236	MOHIT MRINAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
39	171237	SHIVESH SHARMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
40	171238	MOHD SAMAD KHAN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
41	171239	GAGAN AJEET SINGH	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
42	171240	PRATIMAAN PRIYAM	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
43	171241	MOHIT UPADHYAY	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
44	171242	AMITESH SRIVASTAVA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Rajni Mohna & Dr.Ekta	Satisfactory
45	171243	FALAQ SHAHRAJ KHAN	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
46	171244	PRATYUSH THAKUR	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Mrityunjay Singh & Dr. Rakesh Kanji	Satisfactory
47	171245	AMAN PRASAD GUPTA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
48	171246	SHIVAM SHARMA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
49	171247	BHASKAR SEN	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
50	171248	OJUSVA KUMAR GOEL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
51	171250	PRADYUMN AGARWAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
52	171251	VINEET AGGARWAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
53	171252	SANJAY KUMAR	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
54	171253	HARSHAK BIR SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
55	171254	PRANJAL SAXENA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
56	171255	ABHINANDAN DHATWALIA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
57	171256	PARVESH SHARMA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Rajni Mohna & Dr.Ekta	Satisfactory

58	171257	BHAVYA SENGAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
59	171258	ADITYA NEEKHRA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
60	171259	AAYUSH VERMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
61	171260	AARUSHI BHARDWAJ	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
62	171261	GURUPDESH SINGH	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Mrityunjay Singh & Dr. Rakesh Kanji	Satisfactory
63	171262	SHUBHRA PUNDIR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
64	171263	HIMANSHU JAIN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
65	171264	RITIK AGARWAL	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Himanshu Jindal & Dr. Amit Kumar	Satisfactory
66	171265	ARNAV SHARMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
67	171266	MALAY PANDEY	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Himanshu Jindal & Dr. Amit Kumar	Satisfactory
68	171267	ASMITA PRAJAPATI	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
69	171268	DIVIJ GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
70	171269	VEDANT PUNEET SINGH	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Rajni Mohna & Dr.Ekta	Satisfactory
71	171270	KARAMJIT VERMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
72	171271	AKSHIT	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Himanshu Jindal & Dr. Amit Kumar	Satisfactory
73	171273	CHIRAG ARORA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
74	171274	SONALI GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
75	171275	ANAND AMAN	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
76	171276	SHIVAM MITTAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
77	171277	AKARSH GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
78	171278	AABHAS SINGLA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
79	171279	DEEPESH MITTAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
80	171280	UTKARSH RAJPUT	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
81	171281	AKSHAY JAIN	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
82	171282	SURAJ GUPTA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Himanshu Jindal & Dr. Amit Kumar	Satisfactory
83	171283	SARTHAK SHARMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Hemraj saini & Dr.Geetanjali	Satisfactory
84	171284	PRIYANSHU SHUKLA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
85	171285	YUKTI KATIYAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
86	171286	PRIYANSHU MITTAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
87	171287	RAKSHIT AWASTHI	CSE/IT	Yes	Yes	Yes	05-08-2020	Mr. Arvind Kumar & Dr.Vivek Sehgal	Satisfactory
88	171288	SHEEL BHARDWAJ	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
89	171289	ADITYA KUMAR SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
90	171290	RISHABH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory

91	171291	ANCHAL SHARMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
92	171292	AWANTIKA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr. Rajinder Sandhu & Dr. Ruchi Verma	Satisfactory
93	171293	SHIVANSH SHEKHAR	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Himmanshu Jindal & Dr.Jagpreet Sidhu	Satisfactory
94	171294	AKSHIT AGGARWAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
95	171295	RAHUL TOMAR	CSE/IT	Yes	Yes	Yes	05-08-2020	Mr. Arvind Kumar & Dr.Vivek Sehgal	Satisfactory
96	171296	SHASHANK SHUKLA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
97	171297	ABHINAV SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
98	171298	SAUMYA PRAKHAR SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Mr. Arvind Kumar & Dr.Vivek Sehgal	Satisfactory
99	171299	PRAKHAR AWASTHI	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
100	171300	SHIKHAR AGARWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
101	171301	SHANTANU BHARGAVA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
102	171302	SACHIN CHHONKAR	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
103	171303	PRAKHAR BHARDWAJ	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
104	171304	AAKANKSHA JAISWAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
105	171305	SHUBHAM SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
106	171306	SINGH S RAKESH KUMAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
107	171307	HIMANSHU MUTNEJA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
108	171308	SARTHAK PACHAURI	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
109	171309	VISHRUT THAKUR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
110	171310	SHUBHAM TYAGI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
111	171311	ANKUSH KHANDELWAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
112	171312	SUDHANSH SHARMA	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
113	171313	JAVED ALAM	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
114	171314	PARTH MALIK	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
115	171316	ADHIRAJ SINGH JASROTIA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
116	171317	SAGEET YADAV	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
117	171318	AJAY VERMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
118	171319	RADHESH BHATIA	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
119	171320	HARSH PANWAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
120	171321	RAHUL SONI	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
121	171322	TUSHAR THAKUR	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
122	171323	GAURAV DHIMAN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
123	171324	RITVIK CHAUHAN	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory

124	171325	TARUN KUMAR SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
125	171326	PRATIKSHA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Vivek Sehgal & Dr.Hemraj Saini	Satisfactory
126	171328	KUNAL PHOGAT	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
127	171329	PRANAV AGARWAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
128	171330	UTKARSH AGRAWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
129	171331	ACHINTYE SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
130	171332	SHIVAM BHARGAVA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
131	171334	AVI NARAYAN	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
132	171335	AYUSH SINGH	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
133	171336	ASHISH GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
134	171338	RISHABH BHANOT	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
135	171339	RAUNAK BURROWS	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
136	171340	YASH MEHROTRA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
137	171341	AAMOD DIXIT	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
138	171342	SAURABH JAIN	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
139	171343	NEERAJ GUPTA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
140	171344	PRANJAL BANSAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
141	171345	PRANSHU	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
142	171346	NISHANT BHANDARI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
143	171348	AKASH MARWAH	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
144	171350	ADITYA SINGH GANGWAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
145	171351	AKANKSHA CHOUDHARY	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
146	171352	ASHMIT GALAV	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
147	171353	ANIRUDH CHANDEL	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
148	171354	FALAQ SHAHRAJ KHAN	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
149	171355	VASUNDHARA TRIPATHI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
150	171356	MAYANK GULERIA	CSE/IT	Yes	Yes	Yes	04-08-2020	Mr. Prateek Thakral & Mr. RizWan	Satisfactory
151	171357	RAHUL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
152	171358	ISHA GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
153	171359	KRITI VARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
154	171360	MAYANK AGGARWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
155	171361	DEWESHA SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
156	171362	HIRDYANSH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory

157	171364	DEVENDRA KUMAR MISHRA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
158	171365	MAINAK PANDIT	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
159	171366	ANUBHA BHAIK	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
160	171368	SARTHAK VINAYAKA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
161	171369	DEVESH RATTAN SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
162	171370	PRINCE HARSHVARDHAN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
163	171371	PARTH MAHESHWARI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
164	171372	MANORANJAN PANDEY	CSE/IT	No	No	No			Unsatisfactory
165	171373	MAHIMA GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Rajinder Sandhu & Dr. Pardeep Kumar	Satisfactory
166	171376	SHUBHAM SHARMA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Rajni Mohna & Mr.Rizwan ur Rehman	Satisfactory
167	171378	TARINI THAKUR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Aman Sharma & Mr. Arvind Kumar	Satisfactory
168	171380	DEEPESH YADAV	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
169	171381	ROHIT RANJAN	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Kapil Sharma & Dr. Ekta Gupta	Satisfactory
170	171382	TARUN GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Geetanjali & Dr.Hari Singh	Satisfactory
171	171383	YUKTA PURI	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
172	171385	VIKRANT KUMAR	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
173	171386	GARIMA SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
174	171387	RAHUL SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Mr. Arvind Kumar & Dr.Vivek Sehgal	Satisfactory
175	171388	DAWA TENZIN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
176	171451	SHREENATH BARAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
177	171452	DIYA VERMA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Mrityunjay Singh & Dr. Rakesh Kanji	Satisfactory
178	171453	VAIBHAV JINDAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Ruchi Verma & Dr. Rajni Mohana	Satisfactory
179	171454	AMIT VERMA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Vivek Sehgal & Dr.Hemraj Saini	Satisfactory
180	171456	GARIMA KATIYAR	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory
181	171457	ARYAN AGRAWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
182	171458	LAKSHYA JAIN	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
183	171459	ANKIT PATHAK	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory
184	171460	ABHINAV MISHRA	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
185	171461	AMAN PRAJAPATI	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
186	171462	PRASHASTI DWIVEDI	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Mrityunjay Singh & Dr. Rakesh Kanji	Satisfactory
187	171463	ROHAN TYAGI	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
188	171464	OJAS THAREJA	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
189	171465	RISHABH GUPTA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Mrityunjay Singh & Dr. Yugal	Satisfactory

190	171466	KRITIKA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Mrityunjay Singh & Dr. Rakesh Kanji	Satisfactory
191	171467	JAGRIT ARORA	CSE/IT	Yes	Yes	Yes	06-08-2020	Dr.Mrityunjay Singh & Dr. Rakesh Kanji	Satisfactory
192	171468	PRANJAL SRIVASTAVA	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amol Vasudev & Dr.Vivek Sehgal	Satisfactory
193	171469	HARSHITA SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
194	171470	NAYAN AGGARWAL	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
195	171471	RACHIN JARIAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Mr. Arvind Kumar & Dr.Vivek Sehgal	Satisfactory
196	171473	BHAVYE SHARMA	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr. Aman Sharma & Dr.Monika Bharti	Satisfactory
197	171474	NIMESH BANSAL	CSE/IT	Yes	Yes	Yes	04-08-2020	Dr.Rakesh Kanji & Dr. Ravindra Bhatt	Satisfactory
198	171475	PRAKHAR JAIN	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
199	171476	PRANJAL BHATIA	CSE/IT	Yes	Yes	Yes	06-08-2020	Mr.Surjeet Singh & Dr. Moinka Bharti	Satisfactory
200	171477	KUNAL SINGH	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Amit Kumar & Mr. Parveen Modi	Satisfactory
201	171479	ADITYA AGARWAL	CSE/IT	Yes	Yes	Yes	05-08-2020	Dr.Mrityunjay Singh & Dr.Pradeep Kumar Gupta	Satisfactory

Industrial Training Diary & Report

Student Name	SHAURYA MEHTA	**Roll No.**	141505
Company Name			
Training Supervisor Name		Dr. TIRATH RAJ SINGH	
Training Supervisor Signature			
Internship Start Date		23 - JULY - 2020	
Internship End Date		01 SEPTEMBER - 2020	

Week 1

Day 1 | **Date:** 23 - July - 2020

- Learnt about NGS (NEXT GENERATION SEQUENCING)
- Introduction to NGS.

Day 2 | **Date:** 24-07-2020

- 1st Generation Sequencing.
  - Sanger & Coulson
  - Maxam & Gilbert.

Day 3 | **Date:** 25-07-2020

- Second Generation Sequencing.

-(i) ROCHE /454 sequencing (2005)

Day 4 | **Date:** 27-07-2020

- Studied about

(ii) Illumina /Solexa sequencing (2006)

Day 5 | **Date:** 28-07-2020

(iii) ABI / SoLiD sequencing (IInd Generation)

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Day 6	Date: 29-07-2020

- IInd Generation Sequencing.

(iv) Ion Torrent Sequencing (2010)

Week 2

Day 1	Date: 30-07-2020

- IInd Generation Sequencing.

(v) SMRT Sequencing.

Day 2	Date: 31-07-2020

- IIIrd Generation sequencing.

- Introduction.

Day 3	Date: 01-08-2020

(i) Oxford Nano pore Sequencing.
(IIIrd Generation 2014)

Day 4	Date: 03-08-2020

- Comparison of all the 3 generation mentioned above.
- Learnt about the role of Bioinformatics in NGS.

Day 5	Date: 04-08-2020

- Applications of NGS

(i) Medical diagnostics.

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Day 6	Date: 05-08-2020

• Apps of NGS :-

(ii) Pharmacogenomics

(iii) Personalised medicine.

Week 3

Day 1	Date: 06-08-2020

• Applications of NGS :-

(iv) Forensic biology.

(v) Gene therapy.

Day 2	Date: 07-08-2020

• Applications of NGS :-

(vi) RNA sequencing.

(vii) Identifying mutations.

Day 3	Date: 08-08-2020

• Introduction to RNA sequencing :-

(i) Principle of RNA sequencing.

(ii) Steps in RNA sequencing.

Day 4	Date: 10-08-2020

• RNA Sequencing.

- Different types of methods for RNA Sequencing.

(i) Whole transcriptome sequencing.

Day 5	Date: 11-08-2020

(ii) Target RNA sequencing.

(iii) Small RNA sequencing.

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Day 6	Date: 12 - 08 - 2020

(iv) mRNA sequencing.

- Advantages of RNA Sequencing.

Week 4

Day 1	Date: 13 - 08 - 2020

- Studied about Non-Coding RNA.
- & Alternate Splicing.

Day 2	Date: 14 - 08 - 2020

- Introduction to NGS data analysis:
  - Work flow of NGS data analysis

(i) DNA library prepration.

Day 3	Date: 15 - 08 - 2020

Step 2 in NGS data analyses:

(ii) Assessment of quality.

Day 4	Date: 17 - 08 - 2020

Step III in NGS data analysis:

(iii) Aligning of the sequences.

Day 5	Date: 18 - 08 - 2020

Step IV :

(iv) Identifying Variants.

Date: 19 - 08 - 2020

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step 5 in NGS data analysis:

(v) Annotating Variants.

Week 5

Day 1	Date: 20-05-2020

Step 6 in NGS data analysis:

Visualization of NGS data.

Day 2	Date: 21-05-2020

Step 7

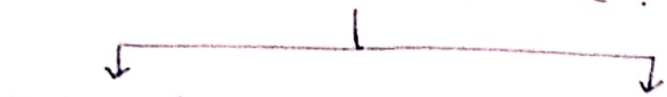
Selection criteria for the Next Generation Sequencing tools.

Day 3	Date: 22-05-2020

- Studied the role of NGS bioinformatics in the identification of the variants.

Day 4	Date: 25-05-2020

- Learnt about structural variance.



Day 5	Date: 25-05-2020

- Handling of Next Generation Sequencing data (NGS)

(i) Analysing and Interpretation of complex NGS data.

Day 6	Date: 26-05-2020

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(•) Learnt about the clinical validation of Variants.
Translation of NGS methods for clinical use.

Week 6

Day 1	Date: 27-08-2020

(•) Studied briefly about
(i) cancer genomics.
(ii) Transcriptomics.

Day 2	Date: 28-08-2020

(•) Studied about:
(iii) Proteomics

Day 3	Date: 29-08-2020

(•) Re-sequencing and its applications.
(•) Learnt about metagenomics.

Day 4	Date: 31-08-2020

(•) Studied about the fragment assembly in Next Generation Sequencing.

Day 5	Date: 01-09-2020

(•) The bad side of Next Generation Sequencing.
(•) Future applications of NGS.

Day 6	Date: 02-09-2020

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(i) Pathways Analysis (ii) Gene Network Analysis.
04-September-2020 | Saumya Mehta
Date | Student Signature

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Industrial Training Diary & Report

Student Name	**Muskan Kapoor**	**Roll No.**	**171501**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr RajKumar**	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020

On the first day of the training, my mentor, I and my colleagues had a discussion on the area of training. We decided it to be Targeting SARS-coV2 main proteases. After this, we were assigned the job to find some relevant literature about COVID-19.

Day 2	**Date:** 19/05/2020

I started reading about the basics of COVID-19 main protease. My main aim was to find answers to what is the main factor causing the disease and how is it useful as a research field in coming time.

Day 3	**Date:** 20/05/2020

Got more literature to read and started reading and marking recent topics of research in this field.

Day 4	**Date:** 21/05/2020

Started reading about different proteases. Asked my mentor to recommend some good literature on proteases especially the main protease

Day 5	**Date:** 22/05/2020

Read about the papers provided by the mentor to find out more about researches in COVID-19. These include drug repurposing, trials on viral infections.

Day 6	**Date:** 23/05/2020

Read more about the topics provided to have a better insight of what drug repurposing can be used for.

Week 2	
Day 1	**Date:** 25/05/2020
Methodology is the main part of this week. Found some existing inhibitors (clinically tested) of Hepatitis C virus (HCV) protease main protease.	
Day 2	**Date:** 26/052020
Read about Hepatitis C virus (HCV) protease main protease as drug target. The focus is kept on Bio-chemistry,structural biology including nomenclature, x-ray co-crystal structure , functions in viral pathogenesis. This was undergone to develop drugs against viral infections	
Day 3	**Date:** 27/05/2020
Read about the Hepatitis C virus (HCV) protease inhibitors from the related literature review.	
Day 4	**Date:** 28/05/2020
Understood the structural and functional activity related to Hepatitis C virus (HCV) protease.	
Day 5	**Date:** 29/05/2020
Explored various databases like Drugbank and Pubchem for each inhibitor of Hepatitis C virus (HCV) protease. Decided to read about one every day and also find out details and uses of each one of them.	

Day 6	**Date:** 30/05/2020
All the information for each inhibitor was compiled into a single tabular table including name, description, structure , clinical trial and citation for the same.	
Week 3	
Day 1	**Date:** 01/06/2020
I stepped to second step of methodology i.e. LIGAND PREPARATION. UCSF CHIMERA explored and studied.	
Day 2	**Date:** 02/06/2020
Explored Pubchem database to get SMILES string for each inhibitors listed in the table created last week.	

Day 3	Date: 03/06/2020
In USCF CHIMERA , structure editing for a ligand was done by using SMILES string we got from Pubchem , followed by minimization of structure	
Day 4	**Date:** 04/06/2020
After minimization of the ligand, gasteiger charges were added to ligand followed by saving a ligand in working directory as .mol2 format.	
Day 5	**Date:** 05/06/2020
Systematically performed all the steps for ligand preparation in UCSF CHIMERA for rest of remaining inhibitors.	

Day 6	Date: 06/06/2020
The same procedure was followed for 2D & 3D structure. By the end of this work ligand preparation was successfully completed.	
Week 4	
Day 1	**Date:** 08/06/2020
This week was for the third step of methodology i.e. protein preparation.	
Day 2	**Date:** 09/06/2020
Explore protein databank to get PDB ID for respective protein and its associated structure was downloaded from RSCB PDB.	
Day 3	**Date:** 10/06/2020
Discovery studio was explored and used to perform steps of protein preparation.	
Day 4	**Date:** 11/06/2020
Open the PDB structure in discovery studio and analyze the structure, amendments were done to the protein to meet requirements of the project.	
Day 5	**Date:** 12/06/2020
This was followed by minimization of protein.	

Day 6	**Date:** 13/06/2020

All the steps for protein preparation were systematically completed using discovery studio followed by saving prepared protein in working directory.

Week 5

Day 1	**Date:** 15/06/2020

This week was for the MOLECULAR DOCKING process.
Autodock software was explored and used to perform this process.

Day 2	**Date:** 16/06/2020

In Autodock, all the steps for docking were performed like adding hydrogens and computing charges.

Day 3	**Date:** 17/06/2020

This was followed by grid generation and ultimately running Autogrid and Autodock to achieve the desired results.

Day 4	**Date:** 18/06/2020

The same procedure was applied to rest of the remaining ligands.

Day 5	**Date:** 19/06/2020

Analyzed 2D & 3D poses through Autodock and discovery studio.

Day 6	**Date:** 20/06/2020

After analyzing the results, one can observe some future aspects which carry potential in research later on.

Week 6

Day 1	**Date:** 22/06/2020

This week was for report preparation, compilation of all the week done till now and started compiling points for the same with approval of training guide.

Day 2	**Date:** 23/06/2020

Started working on the summer industrial training report 2020 which is to be submitted at the end of the training.

Day 3	**Date:** 24/06/2020
Drafted the report by covering each and every parameter, every aspect, all methods done, results and analysis in the report. The content editing completed by end of the day.	
Day 4	**Date:** 25/06/2020
The final report was checked and corrections were made to the report as per mentor's suggestions.	
Day 5	**Date:** 26/06/2020
The report was drafted in the correct format and font. The required references were added to it.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and submitted it to Dr Raj Kumar.	
21/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Aakriti Chauhan	**Roll No.**	171503
Company Name	Jaypee University of Information Technology		
Training Supervisor Name	Prof. Tiratha Raj Singh		
Training Supervisor Signature			
Internship Start Date	15 May 2020		
Internship End Date	30 June 2020		

Week 1

Day 1	**Date:** 15 May 2020

Chose the topic that is “Analysis of various articles on epigenetics of Alzheimers’s disease”. Reviewed the work which was previously done on this topic.

Day 2	**Date:** 16 May 2020

Reviewed literature related to the topic epigentics and extracted some important data from the articles.

Day 3	**Date:** 18 May 2020

Did literature review on the topic Factors that affect Epigenetics (nutrition,age, smoking etc.)

Day 4	**Date:** 19 May 2020

Reviewed literature related to Alzheimers disease.

Day 5	**Date:** 20 May 2020

Did literature review on role of epigenetics (Dna methylation, histone modificarion etc.) in Alzheimers disease.

Day 6	**Date:** 21 May 2020
Did literature review on how DNA methylation causes Alzheimers disease.	

Week 2

Day 1	**Date:** 22 May 2020
Reviewed the litrature on “Alzheimer’s disease epigenetics dna methylation” from PUBMED. Extracted information from 5 articles out of 453. Based on the extracted information a word document was prepared, describing in which of these articles Dna methylation was the major cause of Alzheimer’s disease.	
Day 2	**Date:** 23 May 2020
Extracted information from next 7 articles . Information extracted from next 7 articles was added into the word document.	
Day 3	**Date:** 25 May 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 4	**Date:** 26 May 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 5	**Date:** 27 May 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 6	**Date:** 28 May 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Week 3

Day 1	**Date:** 29 May 2020
Extracted information from next 9 articles . Information extracted from next 9 articles was added into the word document.	
Day 2	**Date:** 30 May 2020
Extracted information from next 9 articles . Information extracted from next 9 articles was added into the word document.	
Day 3	**Date:** 1 June 2020
Extracted information from next 9 articles . Information extracted from next 9 articles was added into the word document.	
Day 4	**Date:** 2 June 2020
Extracted information from next 9 articles . Information extracted from next 9 articles was added into the word document.	
Day 5	**Date:** 3 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 6	**Date:** 4 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Week 4

Day 1	**Date:** 5 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Day 2	**Date:** 6 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Day 3	**Date:** 8 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Day 4	**Date:** 9 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Day 5	**Date:** 10 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	

Day 6	**Date:** 11 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Week 5

Day 1	**Date:** 12 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 2	**Date:** 13 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 3	**Date:** 15 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 4	**Date:** 16 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 5	**Date:** 17 June 2020
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.	
Day 6	**Date:** 18 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Week 6

Day 1	**Date:** 19 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 2	**Date:** 20 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 3	**Date:** 22 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 4	**Date:** 23 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 5	**Date:** 24 June 2020

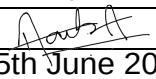
Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document.

Day 6	**Date:** 25 June 2020

Extracted information from next 5 articles . Information extracted from next 5 articles was added into the word document. In total completed 255articles and then compiled the report for the same.

30 June 2020	aakriti
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Garima Sharma	**Roll No.**	171504
Company Name		VERZEO	
Training Supervisor Name		Mr.Aqib Ahmed	
Training Supervisor Signature			
Internship Start Date		5th June 2020	
Internship End Date		10th August 2020	

Week 1

Day 1	**Date:** 5/06/2020
Introduction class	
Day 2	**Date:** 7/06/2020
Introduction to Python: Python fundamentals, Data types, list, dictionary	
Day 3	**Date:** 8/06/2020
Introduction to Python: Array, string operations	
Day 4	**Date:** 10/06/2020
Introduction to pandas and data visualization	
Day 5	**Date:** 12/06/2020
Introduction to pandas and data visualization	

Day 6	**Date:** 14/06/2020
Statistics and probability: Introduction to probability and distribution	

Week 2

Day 1	**Date:**15/06/2020
Statistics and probability: Central limit theorem and hypothesis testing	
Day 2	**Date:**16/06/2020
Exploratory Data Analysis: Exploratory data analysis and feature engineering	
Day 3	**Date:**17/06/2020
Exploratory Data Analysis: Exploratory data analysis and feature engineering	
Day 4	**Date:**18/06/2020
Exploratory Data Analysis: Exploratory data analysis and feature engineering	
Day 5	**Date:** 19/06/2020
Exploratory Data Analysis: Exploratory data analysis and feature engineering	

Day 6	**Date:** 20/06/2020
Exploratory Data Analysis: Exploratory data analysis and feature engineering	

Week 3

Day 1	**Date:**30/06/2020
Introduction to Machine learning and its tools: What is machine learning	
Day 2	**Date:** 2/07/2020
Introduction to machine learning and its tools: Difference between a rule based algorithm and a machine learning algorithm, supervised vs unsupervised algorithm	
Day 3	**Date:**6/07/2020
Introduction to machine learning and its tools: Classification vs Regression	
Day 4	**Date:**7/07/2020
Introduction to machine learning and its tools: training, testing	
Day 5	**Date:**10/07/2020
Introduction to machine learning and its tools: Cross validation data features and its labels	

Day 6	Date: 13/07/2020
Introduction to machine learning and its tools: Pickling and scaling techniques, Error metrics	

Week 4

Day 1	Date:14/07/2020
Machine learning algorithms: Linear regression , forecasting and prediction using regression	
Day 2	**Date:** 16/07/2020
Machine learning algorithms: Linear regression, forecasting and prediction using regression	
Day 3	**Date:**17/07/2020
Machine learning algorithms: Logistic Regression	
Day 4	**Date:** 18/07/2020
Machine learning algorithms: Logistic Regression	
Day 5	**Date:** 19/07/2020
Machine learning algorithms: KNN classification	
Day 6	**Date:**20/07/2020

Support vector machines

Week 5

Day 1	**Date:** 21/07/2020
Support vector machines: K- means, clustering, Random Forest Linear	
Day 2	**Date:** 22/07/2020
Support vector machines: K- means, Clustering, Random Forest Linear	
Day 3	**Date:** 23/07/2020
Minor project on EDA and Data Cleaning	
Day 4	**Date:** 24/07/2020
Minor project on EDA and Dara Cleaning	
Day 5	**Date:** 25/07/2020
Minor project on EDA and Data Cleaning	
Day 6	**Date:** 27/07/2020

Minor project discussion
Week 6
Day 1 **Date:** 28/07/2020
Natural language processing: Introduction to NLTK, Stopwords stemming Lemmetization Named entity recognition, Text classification
Day 2 **Date:** 3/08/2020
Machine learning Implementation: Implementation of all the algorithms using sklearn
Day 3 **Date:** 4/08/2020
Major project: Implementation of machine learning algorithms, finding the best classification algorithm (as per accuracy) and performing EDA and answering questions based on EDA
Day 4 **Date:** 5/08/2020
Major project: Implementation of machine learning algorithms, finding the best classification algorithm(as per accuracy) and performing EDA and answering questions based on EDA
Day 5 **Date:** 6/08/2020
Major project: Implementation of machine learning algorithms, finding the best algorith (as per accuracy) and performing EDA and answering questions based on EDA
Day 6 **Date:** 10/08/2020

Major project: Implementation of machine learning algorithms, finding the best algorithm(as per accuracy) and performing EDA and answering questions based on EDA.	
10/08/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Anjali Sharma	**Roll No.**	171505
Company Name		Jaypee University of Information Technology	
Training Supervisor Name		Dr.Tiratha Raj Singh	
Training Supervisor Signature			
Internship Start Date		15-May-2020	
Internship End Date		30-June-2020	

Week 1

Day 1	**Date:** 15-May-2020

Decided the objective of internship i.e.
"Analysis of various articles on epigenetics of alzheimer's disease".
Reviewed the work which was already done on this topic.

Day 2	**Date:** 16-May-2020

Studied literature about alzheimer's disease.

Day 3	**Date:** 18-May-2020

Studied about the epigenetics of alzheimer's disease. Studied various factors that is biological, genetic factors and other factors which are responsible for alzheimer's disease.

Day 4	**Date:** 19-May-2020

Collected the data on various factors that causes alzheimer's disease.

Day 5	**Date:** 20-May-2020

As their are many processes which led to alzheimer's disease such as histone modifications, DNA methylation etc.But our main aim was to study about how DNA methylation led to alzheimer's disease.
So, studied and reviewed the literature about DNA methylation and how it causes alzheimer's disease.

Day 6	**Date:** 21-May-2020
Studied the literature that "How DNA methylation led to epigenetics of alzheimer's disease". Compiled a short report on the work done.	

Week 2

Day 1	**Date:** 22-May-2020
Searched and studied various articles on pubmed based on "How DNA methylation led to alzheimer's disease".Found 483 articles on pubmed on this topic. So started the next task, that is to study them and collect information related to how DNA methylation led to epigenetics of alzheimer's diseases. (For eg:In some cases it is the genes that causes methylation,in some cases their are certain types of nutrients that are causing methylation. Their are many other causes so our objective is to find them.)	
Day 2	**Date:** 23-May-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 3	**Date:** 25-May-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 4	**Date:** 26-May-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 5	**Date:** 27-May-2020
Studied and collected information from pubmed(Done 5 articles).	

Day 6	**Date:** 28-May-2020
Studied and collected information from pubmed(Done 5 articles).	

Week 3

Day 1	**Date:** 29-May-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 2	**Date:** 30-May-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 3	**Date:** 01-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 4	**Date:** 02-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 5	**Date:** 03-June-2020
Studied and collected information from pubmed(Done 5 articles).	

Day 6	Date: 04-June-2020
Studied and collected information from pubmed(Done 5 articles).	

Week 4

Day 1	Date: 05-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 2	**Date:** 06-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 3	**Date:** 08-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 4	**Date:** 09-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 5	**Date:** 10-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 6	**Date:** 11-June-2020

Studied and collected information from pubmed(Done 5 articles).

Week 5

Day 1	**Date:** 12-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 2	**Date:** 13-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 3	**Date:** 15-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 4	**Date:** 16-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 5	**Date:** 17-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 6	**Date:** 18-June-2020

Studied and collected information from pubmed(Done 5 articles).

Week 6

Day 1	**Date:** 19-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 2	**Date:** 20-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 3	**Date:** 22-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 4	**Date:** 23-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 5	**Date:** 24-June-2020
Studied and collected information from pubmed(Done 5 articles).	
Day 6	**Date:** 25-June-2020
Studied and collected information from pubmed(Done 5 articles).	

26-June-2020 to 30-June-2020 Studied and collected information from rest of the research articles.Completed 255 articles. Compiled the report.	
30-June-2020	Anjali
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Vaibhav Gangta	**Roll No.**	171506
Company Name			
Training Supervisor Name		Dr. Tiratha Raj Singh	
Training Supervisor Signature			
Internship Start Date		16/May/2020	
Internship End Date		30/June/2020	

Week 1

Day 1	**Date:** 16/May/2020

- At the start of the training, I had a meeting with my supervisor and we discussed about the topic in which we would start the training.

Day 2	**Date:** 18/May/2020

- Researched about the project title and the various projects we could implement on the topic and took some ideas about the same.

Day 3	**Date:** 19/May/2020

- Introduction about data mining and including its applications, Healthcare Knowledge Discovery in Database process (KDD).

Day 4	**Date:** 20/May/2020

- Background of Data mining and early methods.
- Data Mining techniques- Classification, Clustering.

Day 5	**Date:** 21/May/2020

- Data Mining Techniques- ARM(Association rule Minng). Basics, Definition.

Day 6	**Date:** 22/May/2020

- I did literature study on the ARM and its application in the world of mrdern science and Bioinformatics field.

Week 2

Day 1	**Date:** 23/May/2020

- ARM method to predict approach and utilize data sets to determine promising phenotyping hypotheses.
- This paper showed the importance of data mining in prediction of secondary phenotype and improving the biological coherence of gene cluster.

Day 2	**Date:** 26/May/2020

- Methodoly for multivariate phenotype-based genome-wide association studies to mine pleiotropic genes.
- The techniques used for predicting some of the disease like diabetes and cancer with the help of data mining techniques.

Day 3	**Date:** 27/May/2020

- Learnt about Privacy Preserving Technique (PPT).
- This is used by major of the companies for privacy of the user data and its application in ARM.

Day 4	**Date:** 28/May/2020

- Growing need of PPT in the current world in Electronic health records which stores huge amount of data of patient's background diagnosis and medical history.
- Read few papers about the same.

Day 5	**Date:** 29/May/2020

APRIORI ALGORITHM-

- Definition
- Algorithm

Day 6	**Date:** 30/May/2020

- Learnt abut few Data mining Tools
- WEKA
- RAPIDMINER

Week 3

Day 1	**Date:** 1/June/2020

DATA MINING TOOLS

- ORANGE
- KNIME

Day 2	**Date:** 3/June/2020

- Learnt to Operate WEKA tool and studied about its functionality in detail.
- Hands on practice in subsequent weeks.

Day 3	**Date:** 4/June/2020

- Data Partition Model and its types-
  - Horizontal Partitioned.
  - Vertical Partitioned.

Day 4	**Date:** 5/June/2020

- Had some basic view about Distributed Association Rule Mining (DARM).
- Aim of DARM, its algorithm, etc

Day 5	**Date:** 8/June/2020

- Frequent Itemset Mining
- Introduction

Day 6	Date: 9/June/2020

- Frequent Itemset Mining example, applications
- Also studied about its applications

Week 4

Day 1	Date: 10/June/2020

- Read Research paper on the topic of Itemset mining and the frequent itemset-based exploration of SNP's

Day 2	Date: 11/June/2020

- Watched Tutorials of using the WEKA tool.
- Continued reading papers

Day 3	Date: 12/June/2020

- Studied about different Bioinformatics applications of Data Mining. This included the following topics which I read the papers about for a couple of days.
- Structural Motif Discovery in Biomolecules.

Day 4	Date: 13/June/2020

- Frequent Annotation mining which is annotation of a molecular entity.
- Itemset mining can also be used to identify relationships between various living entities.

Day 5	Date: 15/June/2020

- Pattern Detection in Quantitative 'omics' Profiles.
- Application called Biclustering was also read about.

Day 6	Date: 16/June/2020

- I studied about the classification accuracy of different Data Mining tools which were discussed above.
- Out of the four, WEKA was the most efficient, computationally cheap and accurate.

Week 5

Day 1	**Date:** 17/June/2020

- Get to know about Primer Binding.
- It's Introduction, application and its rules.

Day 2	**Date:** 18/June/2020

- Algorithm and its implementation were studied in the second day of 5th week of the training.
- Learnt about various softwares as well.

Day 3	**Date:** 19/June/2020

- Understood the pattern mining algorithm with the help of a well illustrated example.
- Did the same for other Bioinformatics applications as well.
- Future perspectives also.

Day 4	**Date:** 20/June/2020

- Got to know about the noise in data, its types and what is it really about.
- Methods to remove noise from dataset.

Day 5	**Date:** 22/June/2020

- Studied market basket analysis in detail as it is the foundation algorithm to the Data Mining work to be done in future.

Day 6	**Date:** 23/June/2020

- Did Research on the various platforms from where we can derive meaningful and reliable data.
- Worked some of the data sets in WEKA tool and analyzed the results.

Week 6

Day 1	**Date:** 24/June/2020

- Started with report writing to be submitted and simultaneously continued with the work.

Day 2	**Date:** 25/June/2020

- Last week was all about gathering information from all the Research Papers.

Day 3	**Date:** 26/June/2020

- Continued with the Report writing and to summarize it in few pages as possible,

Day 4	**Date:** 27/June/2020

- All the points were briefly described so that it can be easily understood.

Day 5	**Date:** 29/June/2020

- Made the necessary changes including grammatical errors, alignment of all the pages and in proper format.

Day 6	**Date:** 30/June/2020

- Compiled the work in the form of short summarized report. Submitted the final report.0

28/July/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	PURVANSHI SHARMA	Roll No.	171507
Company Name		INTERNSHALA	
Training Supervisor Name			
Training Supervisor Signature			
Internship Start Date		22/05/2020	
Internship End Date		03/07/2020	

Week 1

Day 1	Date: 22/05/2020

INTRODUCTION TO PYTHON

Introduction to Python (Developing IDLE)

Day 2	Date: 23/05/2020

Using Python Interpretor (IDLE)

(Executed a few commands)

Day 3	Date: 25/05/2020

Salient features of python

Day 4	Date: 26/05/2020

Basic Python Syntax.

Day 5	Date: 27/05/2020

Basic Python Syntax.

Day 6	Date: 28/05/2020
Getting aquainted to numeric datatypes	

Week 2

Day 1	Date: 29/05/2020
USING VARIABLES IN PYTHON String Datatypes	

Day 2	Date: 30/05/2020
Sequence Datatypes	

Day 3	Date: 1/06/2020
Sequence Datatypes	

Day 4	Date: 2/06/2020
Dictionary Datatypes	

Day 5	Date: 3/06/2020
Dictionary Datatypes	

Day 6	Date: 28/05/2020

Getting aquainted to numeric datatypes

Week 2

Day 1	Date: 29/05/2020

USING VARIABLES IN PYTHON

String Datatypes

Day 2	Date: 30/05/2020

Sequence Datatypes

Day 3	Date: 1/06/2020

Sequence Datatypes

Day 4	Date: 2/06/2020

Dictionary Datatypes

Day 5	Date: 3/06/2020

Dictionary Datatypes

Day 6	Date: 4/06/2020

Datatypes and Variables

Week 3

Day 1	Date: 5/06/2020

BASICS OF PROGRAMMING IN PYTHON

Using functions

Day 2	Date: 06/06/2020

Using functions from built in modules.

Day 3	Date: 08/06/2020

Constructing modules and Packages

Day 4	Date: 09/06/2020

Using Loops

Day 5	Date: 10/06/2020

Understanding Programs and Programming

Day 6	Date: 11/06/2020

Using Conditionals

Week 4

Day 1	Date: 12/06/2020

CONNECTING TO SQL LITE

Using Magic Methods

Day 2	Date: 13/06/2020

Using Magic Methods

Day 3	Date: 15/06/2020

Operator Overloading Using magic methods

Day 4	Date: 16/06/2020

Operator Overloading Using magic methods

Day 5	Date: 17/06/2020

Usage of Various Magic Methods

Day 6	Date: 18/06/2020

Usage of various magic methods

Week 5

Day 1	Date: 19/06/2020

CONNECTING TO SQLLITE.

Connecting to SQL lite database through Python

Day 2	Date: 20/06/2020

Creating records through python

Day 3	Date: 22/06/2020

Insertion of a record through python

Day 4	Date: 23/06/2020

Error handling through python

Day 5	Date: 24/06/2020

Retrieval of records in Python

Day 6	Date: 25/06/2020

Updating records

Week 6

Day 1	Date: 26/06/2020

DEVELOPING A GUI WITH PYQT.

Developing a GUI with PYQT(Using common widgets)

Day 2	Date: 27/06/2020

Designing a menu system

Day 3	Date: 28/06/2020

Layout Managers

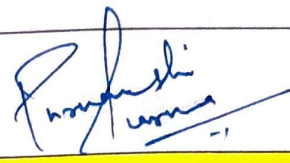
Day 4	Date: 30/06/2020

GUI and event driven programming

Day 5	Date: 1/07/2020

QT Designer

Day 6	Date: 2/07/2020

Final Test preparation and giving it.	
	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Maharishi Kalla	**Roll No.**	171508
Company Name	Center of Excellence in Healthcare and Technology JUIT		
Training Supervisor Name	Dr Narendra Kumar		
Training Supervisor Signature	 Narendra Kumar, 30/07/20		
Internship Start Date	15th May 2020		
Internship End Date	30th June 2020		

Week 1

Day 1	**Date: 15th may 2020**
As the internship starts I have been asked to look for topic to work to work under on the day one.	

Day 2	**Date: 16th may 2020**
I have selected Covid-19 as my topic for Structural Biology research purpose.	

Day 3	**Date: 18th may 2020**
Search for all the available data related to it is asked to be done.	

Day 4	**Date: 19th may 2020**
The data search is in progress.	

Day 5	**Date: 20th may 2020**
Research paper search is in progress related to Covid-19.	

Day 6	**Date: 21st may 2020**

Some research paper found on nature.com, had been asked to study it.

Week 2

Day 1	Date: 22nd may 2020

Study of the structure begins of SARS-CoV-2 its receptors in Humans.

Day 2	Date: 23rd may 2020

The need of study is written and understood, as the emergence and spread of SARS-CoV-2 is endangering Global Health and Economics.

Day 3	Date: 25th may 2020

The study of the structure of the structure through paper is reviewed.

Day 4	Date: 26th may 2020

The structure is download and studied from RCB 2ajf.pdb and 6vw.pdb.

Day 5	Date: 27th may 2020

The downloaded structure are studied under PYMOL.

Day 6	**Date: 28th may 2020**
It is found that SARS-CoV recognizes the same receptor-angiotensin-converting enzyme 2 in Human (ACE2).	

Week 3

Day 1	**Date: 29th may 2020**
I am asked to study about the crystal structure of he RBD receptor while the pymol review is ongoing.	
Day 2	**Date: 30th may 2020**
RBD study is ongoing and it is found that it is complex and several residue change in the SARS-CoV-2 RBD stabilize two virus binding hotspots.	
Day 3	**Date: 1st June 2020**
The structure are further studied from Rcb itself for the purpose of study of Binding Affinity.	
Day 4	**Date: 2nd June**
Study of receptor recognition is started side by side	
Day 5	**Date: 3rd June 2020**
Study of mutation is done and it is found that there are several natural occurring mutation in the SARS-CoV RBM.	

Day 6	Date: 4th June 2020
The Study of mutation is done concluding many points.	

Week 4

Day 1	Date: 5th June 2020
There are recent predictions made on the sequence similarity between SARS-CoV and SARS-CoV-2.	

Day 2	Date: 6th June 2020
The further Study about the prediction are validate by other studies that SARS-Cov-2 also uses ACE-2 as its receptor.	

Day 3	Date: 8th June 2020
Further I am asked about to research and find about the ACE 2 binding Affinity through research paper and studies.	

Day 4	Date: 9th June 2020
Study of Chimeric RBD is done and its is found that it has higher Binding Affinity.	

Day 5	Date: 10th June 2020
Further study of Binding Affinity was done.	

Day 6	Date: 11th June 2020

I was asked to study about the difference between the RBM of SRAS-CoV-2 and SARS-CoV

Week 5

Day 1	Date: 12th June 2020

The further study required the conformation of loops in the ACE-2 binding ridge.

Day 2	Date: 13th June 2020

The study of structure of SARS-Cov 2 and SARS-CoV RBM was done.

Day 3	Date: 16th June 2020

Interface is studied between both RBM ans ACE-2

Day 4	Date: 17th June 2020

Structure of SARS-Cov-2 Chimeric receptor binding domain complex with its receptors human ACE 2 was studied.

Day 5	Date: 18th June 2020

In the research parer important epilopes in the SARS-CoV-2 RBM were identified was reviewed.

Day 6	Date: 19th June 2020

I was asked to study about the methods and processes used for the study.

Week 6

Day 1	Date: 22nd June 2020
Study about the protein expression ans purification method is done.	

Day 2	Date: 23rd June 2020
Study Aboit the protein – protein assay is done.	

Day 3	Date: 24th June 2020
Study about crystallization and structure determination method.	

Day 4	Date: 25th June 2020
Analysis of protein contact residues and protein buried surface area using LIGPLOT+	

Day 5	Date: 29th June 2020
Report preparation was started.	

Day 6	Date: 30th June 2020

Final Summer Internship Report is compiled.

29th July 2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	ANGAM MISHRA	Roll No.	171509
Company Name			
Training Supervisor Name		DR. TIRATHA RAJ SINGH	
Training Supervisor Signature			
Internship Start Date		16 May, 2020	
Internship End Date		30 JUNE, 2020	

Week 1

Day 1	Date: 16 May 2020

→ Introduction to Knowledge Discovery from Mining Association Rules for Heart disease Prediction
→ Overall statistics of people who die as a result of cardiovascular diseases.

Day 2	Date: 17 May 2020

→ Description of Association Rule Mining and its major strength in form of support and confidence.
→ Continuous attribute (Quantitative association Rules) revealing useful insights about data.

Day 3	Date: 18 May 2020

→ Description of Transactional Database and Boolean Matrix.
→ Conversion of Transactional Database into Boolean Matrix
→ Pruning the Boolean Matrix.

Day 4	Date: 19 May 2020

→ Risk factors associated with coronary Heart Disease. (four Major Categories)

Day 5	Date: 20 May 2020

→ I studied about the proposed Method that is about Heart Attack Prediction using Matrix Algorithm.

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→ Discretization of Medical Data and converting it into Boolean Matrix with the generation of frequent item sets

Day 6	Date: 21 May 2020

→ C programs associated with proposed Method.

→ Checking for rows and columns which do not satisfy minimum support.

Week 2

Day 1	Date: 22 May 2020

→ Studying Correlation between different factors such as gender, age, rural population and heart disease.

→ Studying Bar charts for support vs execution time.

Day 2	Date: 23 May 2020

→ Introduction to Association Rule Mining as a Data Mining Technique.

→ Data Mining process

→ Description about Apriori Algorithm.

Day 3	Date: 24 May 2020

→ Application of Association Rule Mining in Market Basket Analysis, Website Navigation Analysis, business domain, Medical diagnosis/ Research

Day 4	Date: 25 May 2020

→ Introduction of Heart and Types of Cardiovascular Diseases with its symptoms.

Day 5	Date: 26 May 2020

→ Prevalence of Cardiovascular Disease

→ Overall statistics of open heart surgies performed in India.

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Day 6	Date: 27 May 2020
→ Various Data mining algorithms for creating some models or to draw vital conclusions and inferences from that Dataset. → These include decision tree, K-means algorithm, ID3 algorithm, support Vector Machine, Naive Bayes	

Week 3

Day 1	Date: 28 May 2020
→ Studying about various Data mining tools such as WEKA, Rapid Miner, TANAGRA, Apache Mahout, MATLAB which provide ready to use implementation of the mining algorithms	
Day 2	**Date: 29 May 2020**
→ Introduction to Literature survey. → Summaries of few research paper that explore computational methods to predict heart diseases	
Day 3	**Date: 30 May 2020**
→ Major drawbacks about classification techniques → Advantages of data cleaning and pruning techniques.	
Day 4	**Date: 31 May 2020**
→ studied about hybrid models and its idea to incorporate several known classification and selection techniques in a single model to give better results.	
Day 5	**Date: 1 June 2020**
→ analysis of heart disease database and how different data mining techniques can be applied on this database.	

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Day 6	Date: 2 June 2020

→ analysis of frequent patterns and calculation of significance weightages of the frequent data.

Week 4

Day 1	Date: 3 June 2020

→ Introduction of knowledge discovery in databases and how problems of association mining can be decomposed into two sub problems.

Day 2	Date: 4 June 2020

→ Problems while dealing with apriori algorithm.

→ Various techniques to improve the efficiency of apriori algorithm such as hash based technique, transaction reduction, partitioning, sampling

Day 3	Date: 5 June 2020

→ Frequent pattern mining through FP-Tree algorithm

Day 4	Date: 6 June 2020

→ analysis of medical data especially in 14 attributes such as age, sex, cp, Blood pressure, cholesterol, Fasting blood sugar, Induced angina, Old peak, slope with its descriptions

Day 5	Date: 7 June 2020

→ Discussing about the problems with professor

Day 6	Date: 8 June 2020

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→ Introduction to another algorithmic approach :- CBARBSN (Cluster Based Association Rule Mining Based on Sequence Number)

Week 5

Day 1	Date: 9 June 2020

→ Studied how to scan the database and partition the transaction Table into equal no. of clusters using skipping fragments.

Day 2	Date: 10 June 2020

→ Calculating sequence no. of each item.
→ Finding out SID of each item
→ Again discovering frequent item sets.

Day 3	Date: 11 June 2020

→ Implementation of algorithm in C language on Pentium 4 processor to assess the efficiency of the proposed method.

Day 4	Date: 12 June 2020

→ Introduction to ANFIS (Adaptive Neuro Fuzzy Inference System)
→ Studied various parameters required for accuracy.

Day 5	Date: 13 June 2020

→ Sensitivity of various classifiers
→ Various classification process such as CRISP-DM (Cross Industry standard process for data mining).

Day 6	Date: 14 June 2020

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→ Studied Neural Network weight optimization by Genetic Algorithm.

Week 6

Day 1	Date: 15 June 2020

→ Introduction to Rule extraction algorithm for diagnosing the CVD.

→ Studied how to arrange linguistic features in descending order with their weights.

Day 2	Date: 16 June 2020

→ ANFIS Architecture
Layer 1: Fuzzification layer Layer 2: Antecedent layer Layer 3: Strengthen normalization layer Layer 4: Consequent layer Layer 5: Inference layer

Day 3	Date: 17 June 2020

→ Analysis and Evaluation of Cleveland dataset for heart disease.

→ Parameters considered in training ANFIS

Day 4	Date: 18 June 2020

→ Studied case-based module to test the status of the patient. Whether heart disease is present or absent from that particular patient.

Day 5	Date: 19 June 2020

→ Number of epochs and hidden layer obtained from results.

→ Studied Reciever Operating Characteristic curve.

Day 6	Date: 20 June 2020

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→ Discussion with Professor on queries related with ANFIS	
29-07-2020	Aagam.
Date	Student Signature

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Industrial Training Diary & Report

Student Name	Garima Singh	**Roll No.**	171510
Company Name			
Training Supervisor Name		Dr. Tirotha Raj Singh	
Training Supervisor Signature			
Internship Start Date		16 | May | 2020	
Internship End Date		30 | Jun | 2020	

Week 1

Day 1 — **Date:** 16 \| May \| 2020

- Introduction to HTML.
- Anatomy of HTML tags, boilerplate code.

Day 2 — **Date:** 18 \| 05 \| 2020

- Intermediate HTML.
- Lists, Tables, Forms,
- Created an HTML used website for CV i.e My personal site.

Day 3 — **Date:** 19 \| 05 \| 2020

- Introduction to CSS.
- Inline CSS, Internal CSS, External CSS.
- CSS selectors and Classes vs IDs.

Day 4 — **Date:** 20 \| 05 \| 2020

- Intermediate CSS.
- Learned and used favicons, used HTML Divs,
- CSS positioning (Static, Relative, Absolute).

Day 5 — **Date:** 21 \| 05 \| 2020

- Font styling in "My personal site".
- CSS property, sizing.

Day 6	Date: 22/05/2020

- Centering element with CSS.
- Learnt about Typography.

Week 2

Day 1	Date: 28/05/2020.

- Introduction to Bootstrap.
- Used Bootstrap Navigation bar.

Day 2	Date: 29/05/2020

- Created a website using HTML, CSS & Bootstrap
- website name: paw-planet (for dog's well being & care)

Day 3	Date: 30/05/2020

- Bootstrap Grid layout system.
- Using Google fonts and other font weights

Day 4	Date: 31/05/2020

- Used Bootstrap containers.
- I got acquainted with Bootstrap Buttons & Font Awesome.

Day 5	Date: 01/06/2020

- Intermediate Bootstrap.
- Bootstrap carousel and implementation

Day 6	Date: 5/06/2020

- Bootstrap cards
- CSS "z-index & stacking order.

Week 3

Day 1	Date: 8/06/2020

→ Learnt about Media Query Breakpoints.
- Code Refactoring.
- Selector priority in CSS.

Day 2	Date: 9/06/2020

- Managing attention with effective User Interface (UI) Design.
→ UX (User Experience Design).

Day 3	Date: 10/06/2020

→ Multiple selectors and implications
- Toggles in Bootstrap).

Day 4	Date: 11/06/2020

→ Wireframing
- Balsamiq → for wireframing.

Day 5	Date: 12/06/2020

- Lorem Ipsum generator
- Flaticon.com.

Day 6	Date: 13/06/2020

- CSS Font stack.
- Boxplot and its usage

Week 4

Day 1	Date: 14/06/2020

- Introduction to Javascript.
- Writing a diry code.
- To add Behaviour to the website.

Day 2	Date: 15/06/2020

- Data types & Javascript variables.
- String Concatenation

Day 3	Date: 16/06/2020

- String length; retuning the number of characters.
- Slicing & Extracting parts of the string.

Day 4	Date: 17/06/2020

- Basic Aisthmetic & the Modulo operator in Javascript.
- Increment and Decrement Expression.

Day 5	Date: 18/06/2020

- Creating and calling functions.
- Parameters and Arguments passed in the functions

Day 6	Date:

Day 6 | 19/06/2020.

- created a BMI calculator and returned values.

Week 5

Day 1	Date: 20/06/2020

- Random Number Generation in Javascript.
- Built an energy calculation giving random values.

Day 2	Date: 21/06/2020

- Control statements: using If-Else. conditionals and Logic.

Day 3	Date: 22/06/2020

- Comparators and Equality.
- Combining Comparators.
- Used conditionals in BMI calculator.

Day 4	Date: 23/06/2020.

- Learnt & implemented Arrays in Javascript.
- While & for loops

Day 5	Date: 24/06/2020

- Did a Fibonacci code challenge with JS

Day 6	Date: 25/06/2020

Day 6

- Implementation of JS and the conditionals used in a website (random) online.

Week 6

Day 1	Date: 26/06/2020

- Adding Event listners to a Button
- a part of DOM manipulation used.

Day 2	Date: 27/06/2020

- Higher order functions.
- passing functions as Arguments.

Day 3	Date: 28/06/2020

- Usage of switch statements in Javascript
- To play sounds on a website.

Day 4	Date: 29/06/2020

- Selecting and manipulating HTML elements, attributes.

Day 5	Date: 30/06/2020

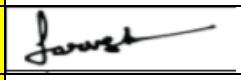
- Structure vs Style vs. Behaviours using DOM & JS.

Day 6	Date: 30/06/2020.

- Text manipulation & Text content property. and manipulation of other elements.

Date	Student Signature

Industrial Training Diary & Report

Student Name	Prerna tiwari	**Roll No.**	171511
Company Name	Internsahala		
Training Supervisor Name	Sarvesh agrawal		
Training Supervisor Signature			
Internship Start Date	15 may 2020		
Internship End Date	26 june 2020		

Week 1

Day 1	**Date:15 may 2020**

First module(topic)-Introduction to python programming started today.
Overview: A complete overview given about industrial training which included important aspects like the need of python programming in todays world ,methods and techniques used ,topics to be covered in the training etc.

Day 2	**Date:16 may 2020**

Important tips: Important tips were given related to the training and the doubts were cleared out by the training supervisor.

Module test: A small module test was conducted after the completion of the very first module of the training

Day 3	**Date:17 may 2020**

Using variables in python- In this module lectures were delivered explaining the various types of variables in python in detail the module had sub- topics of each type of variables used in python such as numeric data types, string data types ,sequence and dictionary data types .
A short assignment task was given to the students at the end of the module to identify the data type and categorize it accordingly.

Day 4	**Date:18 may 2020**

Quiz: A small quiz of approx 7 min. was conducted to test and check the learning so far.

A brief introduction was given about the next module i.e. basic programming with python and introduction was also given about the topics that will be covered in this coming module

Day 5	**Date:19 may 2020**

Basic programming with python-in this module topics like using conditionals, loops and functions to create python program and how to create a basic program using these were taught .
A small quiz section comprising of 5 mcq type question was conducted to test the knowledge of the students

Day 6	**Date:20 may 2020**

Using functions from built in modules and construction of modules and packages were covered in detail.
Method to create packages were taught and explained in detailed .doubts were cleared before the module test

A module test was conducted to test the knowledge gained so far.

Week 2

Day 1	**Date:21 may 2020**

Principles of object-oriented programming –an overview about oops was covered in the very beginning of this module essential features of oops were also taught .
Along with the origin of oops and its usage was covered in this topic.

Day 2	**Date:22 may 2020**

Lectures on declaring a class and creating objects were taught a detailed video lecture on how to use getter and setter methods was also delivered in this video lecture.

A small quiz section was conducted by the end of this topic.
The next topic included inheritance and overriding their importance were explained and how to write a program using these were taught issues were resolved and a small assignment task was given at the end of the topic

Day 3	**Date:23 may 2020**

The next topic included inheritance and overriding their importance were explained and how to write a program using these were taught.

Issues were resolved and a small assignment task was given at the end of the topic

Day 4	**Date:24 may 2020**

Magic methods and its usage was covered in this topic and how can we enable magic methods was explained in this particular topic the importance and use of _init_ method was covered along with operator overloading .
A summary was given after the end of the module comprising of all the important points we have gone through during the module.
A small quiz was conducted at the end to test the learning and marking was done acc. to the no. of correct answers given .

Day 5	Date:25 may 2020
An assignment task was conducted and in which 3 programming question were asked to be performed based on the knowledge gained from the previous modules. Doubts and issues that occurred while writing the program were resolved .	

Day 6	**Date:26 may 2020**
A pdf was provided which comprised of a list of operators ,variables and frequently used magic methods etc. which cleared the concepts learned earlier and the compilation of important data at one place made it very easy to access and understand .	

Week 3

Day 1	**Date:27 may 2020**
Connecting to sqlite databases –started with the module sqlite databases today introduction to sql datbases was given in which statement types in sql were explained A pdf was also provided in the end asking related questions from the topic.	
Day 2	**Date:28 may 2020**
In this topic an overview about RDBMS was given also important points such as how rdbms helps to create,read ,update and delete data in a database was explained also got to know about some popular client server modules such as oracle ,sqlserver,mysql and many more . A brief explaination about ddl was also given. A small quiz was conducted to test the knowledge gained so far.	
Day 3	**Date:29 may 2020**
Creating a sqlite database-In this topic the video lectures delieverd taught how to create a sql databse and also explained about the sql queries in detail for better understanding of the topic. A small assignment task on how to execute sql command was given for better understaning of the topic.	
Day 4	**Date:30 may 2020**
Doubts were cleared if any of the given assignment. A quiz was conducted at the end of the topic to test the learning so far. An overview about the upcoming topic i.e. SQLite studio was given .	
Day 5	**Date:31 may 2020**

Sqlite studio – A video lecture comprising of sqlite studio its uses and how to download sqlite studion\ was given. Moreover how to open a database created previously in command line studio was taught in this topic.

Doubts and issues were cleared if any .
A small quiz session was conducted

Day 6	Date: 1 june 2020
In this topic lectures were delievered on how to update a database in Sqlite and how to create ,delete,read and update a database . A small quiz was conducted at the end of the module.	

Week 4

Day 1	Date:2 june 2020
SQLite databse types- In this topic lectures were delieverd about the sql data types used and its importance. Null ,integer text and blob was also discussed in this topic. A small test was conducted at the end of the topic.	

Day 2	Date:3 june 2020
A pdf file was provided explaining all the important points of SQLite datatypes in detail . A brief introduction about the storage classes was also given in this topic which is considered an important topic in SQLite databases.	

Day 3	Date:4 june 2020
Sql statements- The lectures delieverd taught how to create and write sql statements in SQLite database and how to connect the tables in SQLite data Doubts were cleared and resolved.	

Day 4	Date:5 june 2020
To summarize the module and clear the topics in depth a pdf file was shared which explained the execution of sql queries and creating a SQLite database using SQLite studio . Doubts and issues were cleared if any A module test was organized at the end to test the knowledge	

Day 5	Date:6 june 2020
Accesing SQLite database through python-In this topic teaching was conducted about the relavent features of DB-API And execution of sql queries through python. A small quiz section was conducted at the end of the topic.	

Day 6	**Date:7 june 2020**

Connection method and creating a databse – In this topic the methods defined in connection class were explained in detail .

A short program on creating database uing python was given as practice assignment.

Week 5

Day 1	Date:8 june 2020

This particular topic taught how to insert a new record in a database and how to add new record in the table and add it to SQLite database.
A small quiz was conducted at the end of the topic.

Day 2	Date:9 june 2020

Inserting a new record in the table –leaent aprogram to accept user input for given values in the table
Error handling – the video lectures taught how to handle syntax errors and exception in python in detail with the help of examples.
A quiz was conducted to test the knowledge gained so far.

Day 3	Date:10 june 2020

Lectures taught how to retrieve new records in python using certain commands such as fetchone,select etc.
A small assignment task was given to retrieve new records .
Doubts were cleared if any.

Day 4	Date:11 june 2020

Updating a record –the video lecture taught hoe to update a record in python using update query and also how to link it it to sql database record .

A quiz was given at the end to check the learning so far.

Day 5	Date:12 june 2020

An assignment task was given on to write a program on how to update a record using update query .

Doubts were cleared if any faced during completion of the assignment.

Day 6	Date:13 june 2020

The particular module was summarized mentioning and revising all the important points discussed in the module.
A module test was conducted at the end to check the knowledge of the students.

Week 6

Day 1	Date:14 june-15june 2020

Developing a gui with pyqt-in this overview was given about the development of gui using pyqt toolkit also
A detailed introduction was given about the pyqt toolkit discussing classes in gui and pyqt toolkit
A quiz was conducted to check the knowledge gained so far

Day 2	Date:16 june -17 june 2020

Qt designer - detailed introduction on qt designer was given mentioning all the designer tools for pyqt along with The event handlers used in qt designer .
Doubts were cleared and a small quiz was conducted at the end of the module .

Day 3	Date:18 june-19 june 2020

Layout managers – video consisting of aan overview of layout managers explaining every little information in detail along with procdure to create q form and q grid layout .
A summary was given explaining every important detail in brief .
A quiz was conducted at the end to test the learning so far.

Day 4	Date:20 june -21 june2020

Using common widgets-an overview and the components within this were coverd in th topic.

Topics like qlabel,qpushbutton,qcombopack etc were discussed in detail for better understanding of the topic .

Doubts wer cleared at the end of the module comprising of a 5 min. quiz.

Day 5	Date:22june -23 june 2020

Designing a menu system- finally a database was asked to be designed compiling and using all the knowledge gained so far and also it was made sure that the database worked on the command line prompt.

Doubts were cleared if any.

Day 6	Date:24june2020-26 june 2020

Applications of python in various discip,ines was taught at the end of the training comprising all important aspects such as machine learning and artificial intelligence. Doubts were cleared and issues were resolved . A final test was conducted and certification was provided at the end of the training	
26 june 2020	*Prerna tiwari*
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Riya Dhiman	**Roll No.**	171512
Company Name	Jaypee University of Information Technology		
Training Supervisor Name	Dr. Narendra Kumar		
Training Supervisor Signature	 Narendra Kumar, 30/07/20		
Internship Start Date	16 May 2020		
Internship End Date	30 June 2020		

Week 1

Day 1	**Date: 16/05/2020**

Took systems biology as a field to do my training on.

Day 2	**Date:17/05/2020**

The second day I also decided on what topic I had to work so I took HMDB(human metabolome database) with reference to DrugBank as the topic and started with it.

Day 3	**Date:18/05/2020**

Started Exploring more about HMDB and read more about it on NCBI and some research papers.

Day 4	**Date:19/05/2020**

In HMDB looked for the different metabolites and how HMDB is intended to be used for applications in metabolomics, clinical chemistry, biomarker discovery and so on.

Day 5	**Date:20/05/2020**

Read thoroughly about the different applications of metabolomics in science and how it is working as an emerging technology.

Day 6	**Date:21/05/20**
Coming to an end of the week revised the topics covered and was confident about what's to be done next in the coming weeks.	

Week 2

Day 1	**Date:22/05/2020**
Now moving forward different metabolomics were browsed based on age,gender,BMI,geno,pharmaco and how they are arranged following some pattern like p-value,biospecimen etc.	
Day 2	**Date:23/05/2020**
Looked for the browse section in the database,where protein tab was explored and how the dataset is arranged with the gene name and biospecimen.	
Day 3	**Date:25/05/2020**
How the HMDB contains 3 kinds of data and which formats the HMDB supports for downloading a datset.	
Day 4	**Date:26/05/2020**
Explored the HMDB Metabolite library.	
Day 5	**Date:27/05/2020**

Identification of the diseases related metabolites using HMDB source.

Day 6	**Date:28/05/2020**
Learnt more about the advancements it has brought in this field and is continuing to do so.	

Week 3

Day 1	**Date:29/05/2020**
Also started exploring the KEGG database as it contains high-level functions and utilities of the biological system, such as the cell, from genomic and molecular-level information.	
Day 2	**Date:30/05/2020**
Continued with same today and explored more options on this database.	
Day 3	**Date:01/06/2020**
Studied and understood about different human pathways,diseases related to it.	
Day 4	**Date:02/06/2020**
Learnt more about it and how a dataset file of genes can be extracted from KEGG as csv file and how it can be used further in various analysis.	
Day 5	**Date:03/06/2020**

Simultaneously also read some review articles and research papers on systems biology,HMDB,drugbank.

Day 6	Date:04/06/2020
Gained knowledge more about how systems biology readily lend to their use in several applications in biotechnology and drug discovery.	

Week 4

Day 1	Date:05/06/2020
Moving forward started working with DrugBank.	

Day 2	Date:06/06/2020
How drugbank works as a unique bioinformatics database,contains detailed drug information and drug target information and how is a great help in the pharmaceutical field.	

Day 3	Date:08/06/2020
Explored from different research articles how drugBank contains the exogenous human metabolome.	

Day 4	Date:09/06/2020
Read,Learnt,explored from different resources how since drugbank's discovery this database is used to facilitate in silico drug target discovery,drug design,drug docking or screening.	

Day 5	Date:10/06/2020
Further learnt about how drugBank is leading to the new advancements in the clinical chemistry,drug discovery.	

Day 6	Date:11/06/2020

Also studied how HMDB and DrugBank and related and how one outstands the other.And how both the databases work in the chemogenomic area.

Week 5

Day 1	Date:12/06/2020

This week explored more in depth about the human serum metabolome database.

Day 2	Date:13/06/2020

Started with the basic introduction,gathered some for information from the HMDB database.

Day 3	Date:15/06/2020

Explored how this is serum metabolome is the biggest human metabolome.

Day 4	Date:16/06/2020

Read,looked for many research articles from different sources and read about serum metabolome.

Day 5	Date:17/06/2020

Continued reading the papers.

Day 6	Date:18/06/2020

How serum metabolome database provides a list of the metabolite names, level of verification (confirmed or probable), normal and disease-associated concentration ranges, diseases and references for all (to the best of our knowledge) human serum metabolites that have ever been detected and quantified in the literature.

Week 6

Day 1	Date:19/06/2020

Started with report writing to be submitted and simultaneously continued with the work on metabolites.

Day 2	Date:20/06/2020

Last week was all about gathering information on the databases understood so far and the research papers read.

Day 3	Date:24/06/2020

Continued with the report writing and how to summarize it in a 8-10 page report with proper abstract,introduction,working,figures and conclusion

Day 4	Date:27/06/2020

In the report included all the important points briefly described so that can be understood easily.

Day 5	Date:28/06/2020

Made the necessary changes and any sort of grammatical error,aligned the report in proper format and read it thoroughly before sending it to the supervisor

Day 6	Date:30/06/2020

Compiled the final work done in the form of short summarized report.Submitted the finl report.

29/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Kritika Sharma**	**Roll No.**	**171513**
Company Name		**Jaypee University of Information Technology, Solan**	
Training Supervisor Name		**Dr. Narendra Kumar**	
Training Supervisor Signature		 Narendra Kumar, 28/07/20	
Internship Start Date		15/05/2020	
Internship End Date		30/06/2020	

Week 1

Day 1	**Date:** 18/05/2020
On the first day , me and my guide had a conversation on the area of training. We concluded it to be Protein Interaction Network Analysis in cytoscape software . After this, I was assigned to get information about the software.	
Day 2	**Date:** 19/05/2020
I downloaded the cytoscape software and started getting information about the cytoscape software. .	
Day 3	**Date:** 20/05/2020
I started exploring the software . Also read the command line arguments and their functions in cytoscape.	
Day 4	**Date:** 21/05/2020
Started reading about the basic layout and mechanics of using Cytoscape.	
Day 5	**Date:** 22/05/2020
For getting more knowledge about it , I watched the Basic Expression Analysis Tutorial.	
Day 6	**Date**:23/05/2020
Read about the Network Managements and the Network View Tools.	

Week 2	
Day 1	**Date:** 25/05/2020
I took a small example to understand it better for creating networks.	
Day 2	**Date:** 26/052020
I imported the data and started creating the nested networks.	
Day 3	**Date:** 27/05/2020
Read about the Supported Network File Formats .	
Day 4	**Date:** 28/05/2020
Rea about Node and Edge Column Data and explored by importing the Data table files .	
Day 5	**Date:** 29/05/2020
Gathered the information about the Mapping Identifiers in cytoscape .	
Day 6	**Date**: 30/05/2020
Read about the Column Data Functions and Equations. Also applied the Cytoscape-specific functions and some numeric functions.	

Week 3	
Day 1	**Date:** 01/06/2020
Read about the Finding & Filtering Nodes and Edges , plotted the histogram and scatter charts.	
Day 2	**Date:** 02/06/2020
Applied the Narrowing filters to all the nodes and edges in the network.	
Day 3	**Date:** 03/06/2020
Then I filter out the nodes/edges by Chainable transformers .	
Day 4	**Date:** 04/06/2020
Read about the Edge Interaction Transformer , which was used for adding nodes that are connected to edges that match a particular filter.	
Day 5	**Date:** 05/06/2020
Read about the Navigation & Layout and understood about it .	
Day 6	**Date:** 06/06/2020
Learned about the Styles in cytoscape which gave me ability to encode the table as a property (such as color, size of node, transparency, or font type) of the network.	

Week 4	
Day 1	**Date:** 08/06/2020
For Protein Interaction Network Analysis , I decided to get the Biomarker Panel Data which is Related to Human Esophageal adenocarcinoma .	
Day 2	**Date:** 09/06/2020
Read about the Esophageal adenocarcinoma and the further information's related to it .	
Day 3	**Date:** 10/06/2020
I read about the Biomarker Panel Related to Human Esophageal adenocarcinoma .	
Day 4	**Date:** 11/06/2020
I took possible proteins correlated to esophageal adenocarcinoma which were retrieved from disease query of STRING DataBase.	
Day 5	**Date:** 12/06/2020
Imported the dataset in cytoscape for creating networks.	
Day 6	**Date:** 13/06/2020
The proteins were analyzed via the undirected edges methods by Cytoscape software.	

Week 5	
Day 1	**Date:** 15/06/2020
The main connected component of PPI network was layout by degree values.	
Day 2	**Date:** 16/06/2020
After Analyzing the network , I found one significant cluster .	
Day 3	**Date:** 17/06/2020
The obtained cluster as a sub-network was analyzed and the contributing nodes were classified regarding degree values.	
Day 4	**Date:** 18/06/2020
Then I compared the top hub proteins of cluster and the main connected component .The major candidated biomarker panel was introduced.	
Day 5	**Date:** 19/06/2020
The protein-protein interaction network of disease was constructed with 182 proteins.	
Day 6	**Date:** 20/06/2020
I found the Final Candidate Biomarker Panel Related to Esophageal Adenocarcinoma Including Proteins and their Interactions. The size and color of the nodes were layout by degree value. All of the nodes were connected to each other.	

Week 6	
Day 1	**Date:** 22/06/2020
This week was for the compilation of all the work done till now and started compiling points .	
Day 2	**Date:** 23/06/2020
Started working on the report to be submitted at the end of the training.	
Day 3	**Date:** 24/06/2020
Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:** 25/06/2020
Did all the corrections suggested in the report.	
Day 5	**Date:** 26/06/2020
Put the report in the correct format and added the required references in it.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and submitted it to Dr Narendra Kumar.	
28/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Apurva Garg
Roll No.	171514
Company Name	
Training Supervisor Name	Dr. TIRATHA RAJ SINGH
Training Supervisor Signature	
Internship Start Date	16/May/2020
Internship End Date	30/June/2020

Week 1

Day 1 | Date: 16/May/2020

- Introduction to Biomedical literature.
- Definition of Biomedical.
- Aspects of Biomedical literature in the field of Bioinformation

Day 2 | Date: 17/May/2020.

Different Text Mining Approaches to designed claims.
Introduction to BioNLP.
Biomedical Natural Language Processing.

Day 3 | Date: 18/May/2020.

Biomedical literature in molecular Biology & their different application in the field of Bioinformatics.

Day 4 | Date: 19/May/2020

Introduction to biomedical Documents, Knowledge about unstructural data & pre-defined data.

Day 5 | Date: 20/May/2020

Applications of Text Mining.

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Day 6 | Date: 21/May/2020

Introduction to MEDLINE database, a largest source of biomedical literature, created in 1965.

Week 2

Day 1 | Date: 22/May/2020

Literature Review:

Text Mining In Bioinformatics using Biomedical literature.

Day 2 | Date: 23/May/2020

We studied about different Automation methods for the Information Extraction from large datasets.

Day 3 | Date: 24/May/2020

Introduction to MirTarBase, that is a Bioinformatics database that adopted the text mining tools.

Day 4 | Date: 25/May/2020

Literature Review of another paper, that is Data Mining tools for Biomedical Literature.

Day 5 | Date: 26/May/2020

Connection of Data Mining & Text Mining with data Integration.

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Day 6	Date: 26/May/2020

Gene cluster Identification, that is obtained from Micro Array, is the major Application of Text Mining.

Week 3

Day 1	Date: 28/May/2020.

Studied about diffuent Protein Interaction, that is applied to Biomedical literature for the text.

Day 2	Date: 29/May/2020

Specific Aims of Data Mining which integrate existing text mining tools.

Day 3	Date: 30/May/2020.

Natural Language Processing concepts relevant to Text Mining.

Day 4	Date: 1/June/2020

Different Text Mining Tasks that is used for Biomedical literature.

Day 5	Date: 2/June/2020

Normalization Process used in Text Mining.

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Day 6 | Date: 3| June| 2020

Relationships Extraction Process that identifies the entities that participate in the text.

Week 4

Day 1 | Date: 4| June| 2020

We studied about different Text Mining Toolkits.
- NLTK
- ClearTK & GATE.

Day 2 | Date: 5| June| 2020

Literature Review of Relationship & Event Extraction

Day 3 | Date: 6| June| 2020

Brief Description of Text Mining Process.

Day 4 | Date: 8| June| 2020

After the literature Review, we studied different Algorithms that is used in Text Mining

Day 5 | Date: 9| June| 2020.

Introduction to Naive Bayesian classifier.
- classification.

Day 6 | Date: 10| June| 2020

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Introduction to Neural Networks & their functions.

Week 5

Day 1 | Date: 11/ June/ 2020

After this Algorithm part, we started to learn about Decision Trees Algorithm & their various implementation in Text mining

Day 2 | Date: 12/ June/ 2020

Discussion about Support Vector Machines & different types of margins.

Day 3 | Date: 13/ June/ 2020

Clustering Algorithms
Different Types of Clustering & their Applications

Day 4 | Date: 15/ June/ 2020

Hierarchical clustering & Partitional clustering Algorithms.

Day 5 | Date: 17/ June/ 2020

We completed all the Algorithms parts that are used in Text mining & their various applications

Day 6 | Date: 19/ June/ 2020

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we studied the various process of data mining & their various differences b/w statistics & data mining.

Week 6

Day 1 | Date: 22/ June/ 2020.

Application of Data Mining Technologies

Day 2 | Date: 23/ June 2020

As, we mostly completed the whole knowledge about data mining techniques & their application

Day 3 | Date: 24/ June/ 20 20

We conclude our topic & start preparing report.

Day 4 | Date: 25/ June/ 2020.

Report work.

Day 5 | Date: 26/ June/ 2020

Further discussion with the supervisor for the completion of report.

Day 6 | Date: 29/ June/ 2020

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completion of Report

Date 30/ June/ 2020

Student Signature

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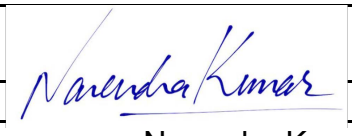
Industrial Training Diary & Report

Student Name	Sarvjeet kaur	**Roll No.**	171515
Company Name			
Training Supervisor Name	Dr Narendra kumar		
Training Supervisor Signature			
Internship Start Date	16/May/2020		
Internship End Date	30/June/2020		

Narendra Kumar,
07/07/20

Week 1

Day 1	**Date:16/May/2020**

I had a talk with my guide where I decided the topic for my Industrial training.

Day 2	**Date:17/May/2020**

- I had a brief introduction about y topic that is IMGT databases

Day 3	**Date:18/May/2020**

- I started with IMGT/LIGM-DB I came to know various ways by which we can perform query searches in it.
- Run the query search and obtained the results.

Day 4	**Date:19/MAY/2020**

- Repeated the same steps for IMGT-DM databases
- Got the results for the same

Day 5	**Date:20/May/2020**

- Had a basic introduction about IMGT PRIMER DM.

- Various methods of performing Query searches in IMGT Primer DB

Day 6	Date:22MAY/2020

- Performed the searches using two methods such as IMGT/PRIMER-DB Accession no,IMGT/PRIMER-DB SET Accession no.
- Obtained the results using these two
- Took screenshots of the results

Week 2

Day 1	Date:23/MAY/2020

- Further explored IMGT/primer-DB and various query search options present it
- Obtained the results for the same.
- Took screenshots of the results

Day 2	Date:24/MAY/2020

- Next I started learning about the IMGT/CLL DATABASE.
- Performed the query search
- Got the results.
- Took the screenshot of the observation.

Day 3	Date:25/MAY/2020

- I started w learning about IMGT /GENE-DB
- Gone through various search criterias such as classification.
- It further included species,gene type functionality,clone name etc.
- Performed same steps as before

Day 4	Date:26/MAY/2020

- Continued exploring IMGT/GENE –DB.
- Been thrugh option localization which contains options like locus name etc
- Performed the query search.
- Got the results
- Took screen shots

Day 5	Date:26MAY/2020

Continued exploring the same database as it contains various query search options

Day 6	Date:30/MAY/2020

- Now I started with IMGT 3D STRUCTUE DATABASE had an introduction about what it is all about.

Week 3

Day 1	Date:1/JUNE/2020

- Continued with IMGT 3D STRUCTURE database
- Performed query search and got the results.
- Took screenshots of the observations

Day 2	Date:4/JUNE/2020

- After that I started with IMGT 2D STRUCTURE DATABASE.
- Repeated the previous steps.

Day 3	Date:5/JUNE/2020

- Continued with IMGT 2D STRUCTURE DATABASE.
- Explored more query search options the query search explored various options.
- Obtained the results for the same.

Day 4	Date:6/JUNE/2020

- Repeated the same steps next day also for the same database only

DAY 5	Date:7/JUNE/2020

- Continued with the same run query search exploring different options and got the results.

Day 6	Date:8/JUNE/2020

- DID query search using allignment

Week 4

Day 1	Date:10/JUNE/2020

- Starting exploring IMGT /MAB -DB
- Repeated same steps

Day 2	Date: 11/JUNE/2020

- Explored other search options in IMGT/MAB-DB
- Obtained the results for the same.
- Took screenshots.

Day 3	Date:12/JUNE/2020

- Explored other search options in IMGT/MAB-DB
- Obtained the results for the same.
- Took screenshots.

Day 4	Date:13/JUNE/2020

- Explored a new option that is IMGT Other Accesses
- Which includes comparing sequence against BLAST, FASTA

Day 5	Date:15/JUNE/2020

- Gone through IMGT LATEST NEWS AND UPDATES

Day 6	Date: 16/JUNE/2020

- Finished with all the latest updates and news

Week 5

Day 1	Date:17/JUNE/2020

- Started with web resources
- Explored four or 5 some of them are IMGT block notes, IMGT POSITIONS etc

Day 2	Date:18/JUNE/2020

- Explored new IMGT webresources
- Repeated the steps as above

Day 3	Date:19/JUNE/2020

- Continued it in the next day also.

Day 4	Date:20/JUNE/2020

- Started exploring IMGT tools
- Explored few of them
- Collected information from the same

Day 5	Date:21/JUNE/2020

Explored more IMGTweb tools.

Day 6	Date:22/JUNE/2020

- Read all the latest news and updates regarding IMGT.

Week 6

Day 1	Date:24/JUNE/2020

- Now I started the work of report writing

Day 2	Date:25/JUNE/2020

- summarize the report into few pages.

Day 3	Date:26/JUNE/2020

- still continued with the procee of report writing

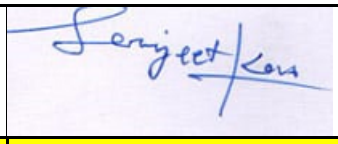
Day 4	Date:27/JUNE/2020

- All the points were briefly described screenshots of the outputs wee pasted so that it can be easily understood.

Day 5	Date:29/JUNE/2020

- Did the spell check and finally submitted corrected the grammatical errors.

Day 6	Date:30/JUNE/2020

• Finally submitted the report	
31/JUNE/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Srishti Thakur	**Roll No.**	171516
Company Name			
Training Supervisor Name	Dr Narendra kumar		
Training Supervisor Signature	 Narendra Kumar, 07/07/20		
Internship Start Date	16/May/2020		
Internship End Date	30/June/2020		

Week 1

Day 1	**Date:16/May/2020**

With my supervisior I decided that I will further continue my minor project as a part of my industrial training which was based on the concept of mhc and how to use it for the purpose of personalized vaccination.

Day 2	**Date:17/May/2020**

- Now I started going through an introduction on IMGT Databases and various types of Imgt databases how to perform searches in them

Day 3	**Date:18/May/2020**

- I explored IMGT/LIGM-DB I came to know various ways by which we can perform searches in it
- Which are search using Accession no search using IMGT-ONTOLOGY concepts and search using bibliographic references.
- Obtained the results for the same

Day 4	**Date:19/MAY/2020**

- Next I explored IMGT/MH- DATABASE.
- Performed searches using it.
- Obtained the results for the same

Day 5	**Date:20/May/2020**

- Had a basic introduction about IMGT PRIMER DM.
- Learnt about it advantages in data standardization
- Various methods of performing Query searches in IMGT Primer DB

Day 6	Date:22MAY/2020

- Performed the searches using two methods such as IMGT/PRIMER-DB Accession no,IMGT/PRIMER-DB SET Accession no.
- Obtained the results using these two

Week 2

Day 1	Date:23/MAY/2020

- Perfomed the searches using IMGT/PRIMER-DB COUPLE Accession no.
- Obtained the results for the same.

Day 2	Date:24/MAY/2020

- Gone through an introduction on IMGT/CLL DATABASE.

Day 3	Date:25/MAY/2020

- I started w learning about IMGT /GENE-DB
- Gone through various search criterias such as classification.
- It further included species,gene type functionality,clone name etc.

Day 4	Date:26/MAY/2020

- Continued exploring IMGT/GENE –DB.
- Been thrugh option localization which contains options like locus name etc
- Performed the query search.
- Got the results

Day 5	Date:26MAY/2020
Repeated the same steps	

Day 6	Date:30/MAY/2020

- Started going through IMGT 3D STRUCTUE DATABASE

Week 3

Day 1	Date:1/JUNE/2020

- Continued with IMGT 3D STRUCTURE database
- Performed query search and got the results.

Day 2	Date:4/JUNE/2020

- Started going through an introduction on IMGT 2D STRUCTURE DATABASE

Day 3	Date:5/JUNE/2020

- Started with IMGT 2D STRUCTURE DATABASE.
- Perfored the query search explored various options.
- Obtained the results for the same.

Day 4	Date:6/JUNE/2020

- Performed search methods in IMGT 2D STRUCTURE DATABASE SUCH as search by entry code
- Search by @ position
- Search by IMGT ONTOLOGY CONCEPTS.

DAY 5	Date:7/JUNE/2020

- Continued with the same run query search exploring different options and got the results.

Day 6	Date:8/JUNE/2020

- DID query search using allignment

Week 4

Day 1	Date:10/JUNE/2020

- Starting exploring IMGT Web tools.
- Explored few of them such as
- IMGT /V-QUEST,IMGT/HighV-QUEST,IMGT/Allele-ALIGN

Day 2	Date: 11/JUNE/2020

- Explored few more IMGT WEB TOOLS.

Day 3	Date:12/JUNE/2020

- Gone through few more web tools.

Day 4	Date:13/JUNE/2020

- Explored a new option that is IMGT Other Accesses
- Which includes comparing sequence against BLAST, FASTA

Day 5	Date:15/JUNE/2020

- Gone through IMGT LATEST NEWS AND UPDATES

Day 6	Date: 16/JUNE/2020

- Finished with all the latest updates and news

Week 5

Day 1	Date:17/JUNE/2020

- Started with IMGT/MAB-DB
- Performed query searching using various crieterias and obtained the results

Day 2	Date:18/JUNE/2020

- Explored other search options in IMGT/MAB-DB
- Obtained the results for the same.

Day 3	Date:19/JUNE/2020

- Continued again with IMGT/MAB-DB
- Explored options like search by proprietary name

Day 4	Date:20/JUNE/2020

- Started exploring IMGT web resources
- Explored few of them
- Collected information from the same
- Name of the few web resources are IMGT REPETOIRE,

Day 5	Date:21/JUNE/2020

Explored more web resources such as IMGT
medical page.
IMGT veterinary page.

Day 6	Date:22/JUNE/2020

Finished exploring all the web resources.

Week 6

Day 1	Date:24/JUNE/2020

- Started with report writing.
- Continued with the work side by side

Day 2	Date:25/JUNE/2020

- Compiled the work done so and summarize the report into few pages.

Day 3	Date:26/JUNE/2020

- Continued with the report writing process

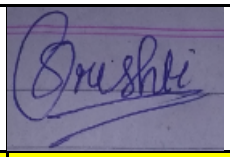
Day 4	Date:27/JUNE/2020

- All the points were briefly described screenshots of the outputs wee pasted so that it can be easily understood.

Day 5	Date:29/JUNE/2020

- Made the necessary changes including the grammatical errors and alignment of the pages in proper format

Day 6	Date:30/JUNE/2020

• Finally submitted the report	
31/JUNE/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	AAKANKSHA GAUTAM	Roll No.	171517
Company Name			
Training Supervisor Name		Dr. Tirathraj Singh	
Training Supervisor Signature			
Internship Start Date		16 May, 2020	
Internship End Date		30 June, 2020	

Week 1

Day 1	Date: 16 May 2020

→ Introduction to Knowledge Discovery from Data Mining Techniques associated with the Personality Traits.

Day 2	Date: 17 May 2020

→ Analyzing all the Personality Traits and their features.

Day 3	Date: 18 May 2020

→ I studied how to predict the personality by analyzing the behaviour of the person is an old technique with the help of researches resources.

Day 4	Date: 19 May 2020

→ Studied the overview of Data Mining Algorithms.

Day 5	Date: 20 May 2020

→ Studied how to train the model accordingly to predict the personality

Day 6	Date: 21 May 2020

→ By knowing about the Personality traits a person can strengthen/develop the other traits accordingly

Week 2

Day 1	Date: 22 May 2020

→ Studied about the online test which would be given by the applicant and helps in predicting the personality.

Day 2	Date: 23 May 2020

→ Studied about how these online tests help an applicant get a job.

Day 3	Date: 25 May 2020

→ I went through some research papers.

Day 4	Date: 26 May 2020

→ Worked on the ideas and their potentials to find different approaches to automated personality classification.

Day 5	Date: 27 May 2020

→ Studied how the problems of Automated Personality Classification can be improved.

Day 6	Date: 28 May 2020

→ Studied more about the problems such as the Dynamic APC.

→ Using Twitter Content to predict the Psychopathy of the users.

Week 3

Day 1	Date: 29 May 2020

→ Using Twitter Content tried predicting significant information.

→ It is often not considered good.

Day 2	Date: 30 May 2020

→ Predicting Personality by considering Educational Game.

→ called as Education Data Mining method for modeling student behaviours.

Day 3	Date: 1 June 2020

→ I studied Eysenck's theory of human personality.

→ basically considers the happiness detection.

Day 4	Date: 2 June 2020

→ I studied about how to predict personality with Social Media.

Day 5	Date: 3 June 2020

→ Studied about an examination of online learning effectiveness using data mining.

Day 6	Date: 4 June 2020

→ Learnt how to apply data mining technique wherein the student data can be assessed.

Week 4

Day 1	Date: 5 June 2020

→ Proposed an Automated Personality Classification system which uses Data Mining techniques to classify the personality of the applicants.

Day 2	Date: 6 June 2020

→ Introduction to an inductive learning algorithm, Naive Bayes Algorithm

→ considered one of the most efficient and effective algorithm that is widely used.

Day 3	Date: 8 June 2020

→ The data obtained by it is considered accurate.

→ Results combines both efficiencies
i.e. optimal time performances with reasonable accuracy.

Day 4	Date: 9 June 2020

→ The data set having the information is converted into frequency table.

Day 5	Date: 10 June 2020

→ Likelihood table is created by finding the probabilities of each and every question.

→ Naive Bayesian equations are then used to calculate the posterior probability of each class.

Day 6	Date: 11 June 2020

→ Another algorithm we use is Support Vector Machine.

→ A type of supervised learning algorithm analyses the data and recognizes pattern for classification purposes.

Week 5

Day 1	Date: 12 June 2020

→ The data set is in the form of point in space divided by either a line or hyperplane.

Day 2	Date: 13 June 2020

→ The data set is now in the form of vectors.

→ The weight of the vectors are calculated.

Day 3	Date: 15 June 2020

→ The vector with highest values are considered

→ The value of the personality related to it is carried out.

→ Finally the prediction of personality type is done.

Day 4	Date: 16 June 2020

→ These two algorithms groups the qualities of the applicants of different streams and a graph is formed to depict which set of candidates would be suitable for a particular post in an organization.

Day 5	Date: 17 June 2020

→ This graph is helpful in screening the candidates and would save the resources of organization.

Day 6	Date: 18 June 2020

Further did some → Discussion with Professor.	
29 June, 2020	Akanksha.
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	CHHAVI THAKUR	**Roll No.**	171518
Company Name		JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY	
Training Supervisor Name		DR. RAJ KUMAR	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020

" SCIENCE HAS EMERGED TODAY AS THE MOST REVOLUTIONARY CO-OPERATIVE ACTIVITY OF MANKIND"

On the first day of my training, my mentor Dr. Raj Kumar briefed me about the AIM and the Main OUTLINE of our project i.e. TARGETING SARS-COV-2 MAIN PROTEASE FOR COVID-19 which is a "Computer Aided Drug Designing" based project.

Day 2	**Date:** 19/05/2020

The formal discussion focusing mainly on the area of the training was made. After that, I was assigned with Research papers related to COVID-19 for the LITERATURE REVIEW.

Day 3	**Date:** 20/05/2020

Literature review about the Covid-19 was read and important information was extracted from it.

Day 4	**Date:** 21/05/2020

Literature review about the Zika virus protease was read and important desired information was extracted from it.

Day 5	**Date:** 22/05/2020

From the literature Review, Analysed the binding properties of existing inhibitors of zika virus protease against SARS-COV-2 main protease.
Day 6 **Date:** 23/05/2020
After reviewing the literature, outline methodology of the project was anticipated.
Week 2
Day 1 **Date:** 25/05/2020
This week was for performing the METHO DOLGY of the project. Started this week by finding the existing inhibitors (clinically tested) each of: zika virus protease as step 1.
Day 2 **Date:** 26/05/2020
Studied about the Zika virus protease as drug target, about its Bio-chemistry and structural biology including its Nomenclature, x-ray co-crystal structure, its crucial function in viral pathogenesis which is studied to develop drugs against chronical viral infectious diseases.
Day 3 **Date:** 27/05/2020
Started finding zika virus inhibitors from the related literature review.
Day 4 **Date:** 28/05/2020
After finding the inhibitors, The structural and functional activity related to it was studied.
Day 5 **Date:** 29/05/2020

The clinical trial phases and structure for each inhibitor was noted by exploring various databases like Drug bank and PubChem.
Day 6 | **Date:** 30/05/2020
All of the information for each inhibitor was compiled into a single tabular table including its name, Description, Structure, Clinical trial phase and at the end, its citation was also added to the table.

Week 3

Day 1 | **Date:** 1/06/2020
This week was for the SECOND STEP of our METHODOLOGY i.e LIGAND PREPARATION. For the ligand preparation, UCSF CHIME RA tool was explored and studied for performing this step.
Day 2 | **Date:** 2/06/2020
Explored PubChem database to get the SMILES string for each inhibitor listed in the table created last week.
Day 3 | **Date:** 3/06/2020
In UCSF Chimera, structured editing for the ligand was done by using the SMILES string we got from the PubChem followed by Minimization of the structure.
Day 4 | **Date:** 4/06/2020
After Minimization of the ligand, Gasteiger charges were added to the ligand Followed by saving the ligand in the working directory a s .mol2 format.
Day 5 | **Date:** 5/06/2020

Systematically performed all the steps for ligand preparation in UCSF Chimera for rest of the remaining inhibitors.

Day 6	**Date:** 6/06/2020

The same procedure was followed for both 2D AND 3D structures.

By the end of this work, ligand preparation for each inhibitor was successfully completed.

Week 4

Day 1	**Date:** 8/06/2020

This week was for the Third step in the methodology i.e PROTEIN PREPARATION.

Day 2	**Date:** 9/06/2020

Explored Protein data bank to get the PDB ID for the respective protein and its associated structure was downloaded from the protein data ban k.

Day 3	**Date:** 10/06/2020

DISCOVERY STUDIO was explored and used to perform the steps of protein preparation.

Day 4	**Date:** 11/06/2020

Opened the PDB structure in discovery studio and analysed the structure, amendments were done to the protein to meet the requirements of the project.

Day 5	**Date:** 12/06/2020

This was followed by minimization of the protein.

Day 6	Date: 13/06/2020

All the steps for protein preparation were systematically completed using Discovery studio followed by saving the prepared protein in the working directory.

Week 5

Day 1	Date: 15/06/2020

This week was for the MOLECULAR DOC KING process.

Autodock software was explored and used to perform this process.

Day 2	Date: 16/06/2020

In Autodock , all the steps for docking were performed like adding hydrogens and computing charges.

Day 3	Date: 17/06/2020

This was followed by grid generation and ultimately running autogrid and autodock to achieve the desired results.

Day 4	Date: 18/06/2020

The same procedure was applied to rest of the remaining ligands.

Day 5	**Date:** 19/06/2020
Analyzed 2D and 3D poses through Autodock and Discovery studio.	
Day 6	**Date:** 20/06/2020
After analysing the results , one can observe some future aspects which carry potential in research later on .	

Week 6

Day 1	**Date:** 22 / 6/2020
This week was for the REPORT PREPARATION, compilation of all the work done till now and started compiling points for the same with the approval of my training mentor.	
Day 2	**Date:** 23 /6/2020
Started working on the Summer Industrial t raining report 2020, which is to be submitted by the end of the training.	
Day 3	**Date:** 24/06/2020
Drafted the report by covering each and every parameter, every aspect, all the methods done, results and analysis in the report. The content editing was being successfully completed by the end of the day.	
Day 4	**Date:** 25 / 6/2020

After the completion of the content editing. All of the required fonts were adjusted, pictures were added to the report to make it more understandable. At last, the cover page of the report was designed.	
Day 5	**Date:** 26 / 6/2020
The first draft was submitted to my mentor .All the corrections were made to the report according to the suggestions of my mentor. The report was finally drafted in the correct format and the required references were added to it.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and the report was submitted to the industrial training mentor, Dr. Rajkumar.	
4/08/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Mehak Kapoor**	**Roll No.**	**171519**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr RajKumar**	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020
On the first day of the training, my mentor, I and my colleagues had a discussion on the area of training. We decided it to be Targeting SARS-coV2 main proteases. After this, we were assigned the job to find some relevant literature about COVID-19.	
Day 2	**Date:** 19/05/2020
I started reading about the basics of COVID-19 main protease. My main aim was to find answers to what is the main factor causing the disease and how is it useful as a research field in coming time.	
Day 3	**Date:** 20/05/2020
Got more literature to read and started reading and marking recent topics of research in this field.	
Day 4	**Date:** 21/05/2020
Started reading about different proteases. Asked my mentor to recommend some good literature on proteases especially the main protease	
Day 5	**Date:** 22/05/2020
Read about the papers provided by the mentor to find out more about researches in COVID-19. These include drug repurposing, trials on viral infections.	

Day 6	**Date:** 23/05/2020

Read more about the topics provided to have a better insight of what drug repurposing can be used for.

Week 2	
Day 1	**Date:** 25/05/2020
Methodology is the main part of this week. Found some existing inhibitors (clinically tested) of HIV-1 main protease.	
Day 2	**Date:** 26/052020
Read about HIV-1 main protease as drug target. The focus is kept on Bio-chemistry,structural biology including nomenclature, x-ray co-crystal structure , functions in viral pathogenesis. This was undergone to develop drugs against viral infections	
Day 3	**Date:** 27/05/2020
Read about the HIV-1 inhibitors from the related literature review.	
Day 4	**Date:** 28/05/2020
Understood the structural and functional activity related to HIV-1.	
Day 5	**Date:** 29/05/2020
Explored various databases like Drugbank and Pubchem for each inhibitor of HIV-1. Decided to read about one every day and also find out details and uses of each one of them.	

Day 6	**Date:** 30/05/2020
All the information for each inhibitor was compiled into a single tabular table including name, description, structure, clinical trial and citation for the same.	

Week 3	
Day 1	**Date:** 01/06/2020
I stepped to second step of methodology i.e. LIGAND PREPARATION. UCSF CHIMERA explored and studied.	
Day 2	**Date:** 02/06/2020
Explored Pubchem database to get SMILES string for each inhibitors listed in the table created last week.	

Day 3	**Date:** 03/06/2020
In USCF CHIMERA , structure editing for a ligand was done by using SMILES string we got from Pubchem , followed by minimization of structure	
Day 4	**Date:** 04/06/2020
After minimization of the ligand, gasteiger charges were added to ligand followed by saving a ligand in working directory as .mol2 format.	
Day 5	**Date:** 05/06/2020
Systematically performed all the steps for ligand preparation in UCSF CHIMERA for rest of remaining inhibitors.	

Day 6	**Date:** 06/06/2020
The same procedure was followed for 2D & 3D structure. By the end of this work ligand preparation was successfully completed.	
Week 4	
Day 1	**Date:** 08/06/2020
This week was for the third step of methodology i.e. protein preparation.	
Day 2	**Date:** 09/06/2020
Explore protein databank to get PDB ID for respective protein and its associated structure was downloaded from RSCB PDB.	
Day 3	**Date:** 10/06/2020
Discovery studio was explored and used to perform steps of protein preparation.	
Day 4	**Date:** 11/06/2020
Open the PDB structure in discovery studio and analyze the structure, amendments were done to the protein to meet requirements of the project.	
Day 5	**Date:** 12/06/2020
This was followed by minimization of protein.	

Day 6	**Date:** 13/06/2020

All the steps for protein preparation were systematically completed using discovery studio followed by saving prepared protein in working directory.

Week 5

Day 1	**Date:** 15/06/2020

This week was for the MOLECULAR DOCKING process.
Autodock software was explored and used to perform this process.

Day 2	**Date:** 16/06/2020

In Autodock, all the steps for docking were performed like adding hydrogens and computing charges.

Day 3	**Date:** 17/06/2020

This was followed by grid generation and ultimately running Autogrid and Autodock to achieve the desired results.

Day 4	**Date:** 18/06/2020

The same procedure was applied to rest of the remaining ligands.

Day 5	**Date:** 19/06/2020

Analyzed 2D & 3D poses through Autodock and discovery studio.

Day 6	**Date:** 20/06/2020

After analyzing the results, one can observe some future aspects which carry potential in research later on.

Week 6

Day 1	**Date:** 22/06/2020

This week was for report preparation, compilation of all the week done till now and started compiling points for the same with approval of training guide.

Day 2	**Date:** 23/06/2020

Started working on the summer industrial training report 2020 which is to be submitted at the end of the training.

Day 3	**Date:** 24/06/2020
Drafted the report by covering each and every parameter, every aspect, all methods done, results and analysis in the report. The content editing completed by end of the day.	
Day 4	**Date:** 25/06/2020
The final report was checked and corrections were made to the report as per mentor's suggestions.	
Day 5	**Date:** 26/06/2020
The report was drafted in the correct format and required references were added to it.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and submitted it to Dr Raj Kumar.	
21/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**AnanyaaKaul**	**Roll No.**	**171801**
Company Name		Jaypee University of Information Technology	
Training Supervisor Name		Dr. Poonam Sharma	
Training Supervisor Signature			
Internship Start Date		15/5/20	
Internship End Date		30/6/20	

Week 1

Day 1	**Date:** 15/5/20
Studied about surfactants and their properties.	
Day 2	**Date:** 16/5/20
Studied about applications of biosurfactants in Day to day life.	
Day 3	**Date:** 17/5/20
Discussed the collected literature with colleagues and supervisor**.**	
Day 4	**Date:** 18/5/20
Studied the different processes of biosurfactant production	

Day 5	**Date:** 19/5/20
Studied phisicochemical properties and characterization of biosurfactants.	

Day 6	**Date:** 20/5/20
Read research papers starting with 'biosurfactants, natural alternatives to synthetic surfactant: physico chemical properties and applications. '	
Week 2	
Day 1	**Date:** 22/5/20
Studied 'production and investigation of the phisicochemical properties of Mel A from glycerol and coconut water.'	
Day 2	**Date: 23**/5/20
Studied 'design and physicochemical characterization Of lysozyme loaded neosomal formulations as a new drug delivery system.'	
Day 3	**Date:** 24/5/20
Studied 'evaluation of physicochemical properties hey and antimicrobial efficacyof monoclinic sulphur nano colloid.'	
Day 4	**Date:** 25/5/20
Studied ' physicochemical characterization of biosurfactants and its potential to remove oil from soil and cotton cloth.'	

Day 5	**Date:** 26/5/20
	studied ‘effects of Silicon surfactant on the properties of open cell flexible polyurethane forms.’

Day 6	**Date:** 27/5/20
	Studied ‘foam properties and detergent abilities of the saponins from Camellia olefera.’
Week 3	
Day 1	**Date:** 29/5/20
	Studied‘potential use of microbial surfactant in microemulsion drug delivery system: a systematic review .’
Day 2	**Date: 30**/5/20
	Studied ‘chemical structure hey, surface properties hey and biological activities of the biosurfactant reduced hey produced by Pseudomonasare aeruginosa LBI from soap stock.’
Day 3	**Date: 31**/5/20
	Studied‘biosurfactants: potential applications in medicine. ‘
Day 4	**Date: 1**/6/20

	Compiled a report on the first paper studied and discussed with the colleagues and supervisor.
Day 5	**Date: 2**/6/20
	Compiled a report on the second paper read.

Day 6	**Date: 3**/6/20
	Discussed the literature with colleagues for better understanding .
Week 4	
Day 1	**Date: 5**/6/20
	Prepared a report on the 3rd paper.
Day 2	**Date: 6**/6/20
	Discuss the report with colleagues and supervisor .
Day 3	**Date: 7**/6/20
	Made a report of the 4th paper.
Day 4	**Date: 8**/6/20

	Discuss the report with colleagues and supervisor .
Day 5	**Date: 9**/6/20
	Prepared a report of the 5th paper studied.
Day 6	**Date: 10**/6/20

	Discuss the report with colleagues and supervisor .
Week 5	
Day 1	**Date: 12**/6/20
	Prepared a report of the 6th paper.
Day 2	**Date: 13**/6/20
	Discuss the report with colleagues and supervisor .
Day 3	**Date:** 14/6/20
	Compiled a report of the 7th paper read.
Day 4	**Date:** 15/6/20

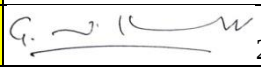
	Discuss the report with colleagues and supervisor .
Day 5	**Date:** 16/6/20
	made a report on the 8th research paper.
Day 6	**Date:** 17/6/20

Discuss the report with colleagues and supervisor .

Week 6	
Day 1	**Date:** 19/6/20
	Compiled a report of the 9th paper.
Day 2	**Date: 20**/6/20
	Discuss the report with colleagues and supervisor .
Day 3	**Date: 21**/6/20
	Compiled a report of the 10th paper.
Day 4	**Date: 22**/6/20

	Had a discussion with the colleague's and supervisor about all the paper studied and shared the information Gained.
Day 5	**Date:** 23/6/20
	Started compiling hey a final report with all the research paper studied, acknowledgements and references.
Day 6	**Date:** 24/6/20
Compiled a final report of the entire work done during the internship and got it approved by the supervisor.	
24/7/20	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Vasudev Singh	**Roll No.**	171802
Company Name	Jaypee University of Information Technology		
Training Supervisor Name	Dr. Garlapati Vijay Kumar		
Training Supervisor Signature	 29/07/2020		
Internship Start Date	15/05/2020		
Internship End Date	30/06/2020		

Week 1

Day 1	**Date:15/05/2020**
Our guide informed me about the topics that we are going to cover during the internship program and provided me some literature study.	
Day 2	**Date:16/05/2020**
I started reading about the basic topics of fermentation technology to get a clear idea about the topic.	
Day 3	**Date:18/05/2020**
Got more literature sources about the same.	
Day 4	**Date:19/05/2020**
Study material was provided via google drive	
Day 5	**Date:20/05/2020**
Thoroughly read the study material which was provided.	
Day 6	**Date:21/05/2020**
Had a discussion over virtual labs.	

Week 2

Day 1	**Date:22/05/2020**
Virtual lab links were provided.	
Day 2	**Date:23/05/2020**
Basics of bioreactor and its theory were thoroughly explained by the virtual lab.	
Day 3	**Date:25/05/2020**
Got familiar with theory and procedure of the lab	
Day 4	**Date:26/05/2020**
Self evaluation was carried out.	
Day 5	**Date:27/05/2020**
Second virtual lab over control characteristics was provided.	
Day 6	**Date:28/05/2020**
Theory and procedure were explained and self evaluation was carried out.	

Week 3

Day 1	**Date:29/05/2020**
Third virtual lab over operation of 15 L bio reactor was provided.	
Day 2	**Date:30/05/2020**

Scale up processes and criteria were studied from bench top to pilot scale.	
Day 3	**Date:01/06/2020**
Theory and procedure both were understood and self evaluation was carried out.	
Day 4	**Date:02/06/2020**
Applications related to fermentation technology were studied.	
Day 5	**Date:03/06/2020**
Fourth virtual lab over Biopolymer production was provided.	
Day 6	**Date:04/06/2020**
The importance of bio polymers and applications were studied.	
Week 4	
Day 1	**Date:05/06/2020**
Biopolymer production by microbes were explained.	
Day 2	**Date:06/06/2020**
Theory and procedure about biopolymer production were studied.	
Day 3	**Date:08/06/2020**
Self evaluation was done.	
Day 4	**Date:09/06/2020**
Other sources of bio polymer were studied.	
Day 5	**Date:10/06/2020**
Had a discussion over biopolymer production techniques.	
Day 6	**Date:11/06/2020**
Alcohol production through fermentation was studied.	
Week 5	
Day 1	**Date:12/06/2020**
Fifth virtual lab over Acetone-butanol-ethanol production was provided.	
Day 2	**Date:13/06/2020**
Theory and procedure were studied.	
Day 3	**Date:15/06/2020**
Self evaluation was done.	
Day 4	**Date:16/06/2020**
Application of acetone-butanol-ethanol were studied.	
Day 5	**Date:17/06/2020**
Sixth virtual lab over propanoic acid fermentation was provided.	
Day 6	**Date:18/06/2020**
Procedure and theory of sixth virtual lab was studied.	

Week 6	
Day 1	**Date:19/06/2020**
Application of propanoic acid was studied.	
Day 2	**Date:20/06/2020**
Seventh virtual lab over 1,3 propanediol fermentation was provided.	
Day 3	**Date:22/06/2020**
Theory and Procedure of 1,3 propanediol fermentation were studied.	
Day 4	**Date:23/06/2020**
Applications of seventh virtual lab were studied.	
Day 5	**Date:24/06/2020**
Future aspects of fermentation technology were explored.	
Day 6	**Date:25/06/2020**
Guide suggested the guidelines for preparing the Industrial training dairy report.	
Date:26/06/2020	
Written the Industrial Training report	
Date:27/06/2020	
Finished the leftover training report and send to guide for corrections	
Date:29/06/2020	
Guide suggested the corrections and done those corrections and sent back to guide for final approval	
Date:30/06/2020	
The final internship report was approved by guide	
28/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Harmeet singh**	**Roll No.**	**171804**
Company Name		**Jaypee university of Information Technology**	
Training Supervisor Name		**Dr. jata Shankar**	
Training Supervisor Signature			
Internship Start Date		**18/05/2020**	
Internship End Date		**27/06/2020**	

Week 1

Day 1	**Date: 18/05/2020**
On the first day of the training my mentor and I had a discussion on the area of training (PCR TECHNIQUES) After this I was assigned for the job to find some relevant literature and history about the PCR Techniques and read about it.	
Day 2	**Date: 19/05/2020**
I started reading about the introductions to PCR. My main aim was to find the answers to what is PCR , how it works and how is it useful as a research field in coming times.	
Day 3	**Date: 20/05/2020**
Got history about pcr to read and how the pcr works in late 90s I also read about water bath pcr and how this pcr is different from modern pcr.	
Day 4	**Date: 21/05/2020**
Started reading about different techniques of pcr and its applications in different fields of research and asked my mentor to recommend some good literature on different topics related to pcr.	

Day 5	Date: 22/05/2020
On this day I read about the discovery of pcr and the exact year of discovery and in detail about the setup of water bath pcr , diagram of water bath pcr and functions of dntps	

Day 6	**Date- 23/05/2020**
Read about the benefits of using pcr in details and also the disadvantages of pcr .	

Week 2

Day 1	date – 25/05/2020
Read about the three key steps to pcr each at different temperature which is denaturation extension and annealing and about the process of heating and cooling	
Day 2	**Date -26/05/2020**
Informed about my mentor about the same and got more topics to read about the pcr such as different techniques of pcr	
Day 3	date – 27/05/2020
I read about the different techniques of pcr such as nested pcr , multiplex pcr ,touchdown pcr and hot start pcr.	
Day 4	**date – 28/05/2020**
Read in detail about the nested pcr and how it is used to increase the specificity of dna amplification reducing unspecific products	

Day 5	date – 29/05/2020	
Read in detail about the multiplex pcr and how it allows amplifications of many target sequences concurrently in the same reaction mixture		

Day -6	date- 30/05/2020	:
Read in detail about the rt pcr known as real time pcr which is the modification of standard pcr and how this technique is used in covid 19 labs		
Week 3		
Day 1	**DATE-1/06/2020**	
On this day I leraned about the different enzymes like phenol and guanidine isothiocynate , rna polymerase which is used in the process of detecting the corona virus with the help of rt pcr		
Day 2	**Date- 2/06/2020**	
On this day I learned about the full process from taking the sample to detection of virus in the rt pcr .		
Day 3	**Date- 3/06/2020**	
Read in detail about the precautions taken while collecting the sample and performing the process on rt pcr		
Day 4	**Date -4/06/2020**	

As told by the mentor i read about different applications in detail like genotyping , cloning ,mutation ,detetction etc	
Day 5	**Date – 5/06/2020**
Gathered information about literature of different applications of pcr and how they are used in different fields.	

Day 6	**Date-6/06/2020**
Read about the research papers available related to the topic	
Week 4	
Day 1	**DATE-8 /06/2020**
My mentor told me to read about different types of pcr and its uses	
Day 2	**Date- 9/06/2020**
As told by the mentor the first type of pcr is Amplified fragment length polymorphism (AFLP) PCR	
Day 3	**Date- 10/06/2020**
On this day I read about second type of pcr which is allele specific pcr and can be used to analyze single nucleotide polymorphism	
Day 4	**Date-11/06/2020**

I read about another type of pcr which is assembly pcr which assemble large DNA oligonucleotides from multiple shorter fragments.

Day 5	**Date-12/06/2020**	
The another type of pcr is Asymmetric PCR which is a variation of PCR used to preferentially amplify one strand of the original DNA more than the other		
Day 6	**Date-13/06/2020**	

I read about another type of pcr which is Colony PCR and it is a method in which, where identification of DNA of interest inserted into the plasmid is obtained by designing the inserted DNA specific primers.
Week 5

Day 1	**Date: 15/06/2020**
I discussed all types of pcr with the mentor and started to prepare the raw report on the types of pcr	
Day 2	**Date: 16/06/2020**
Read about why using only rt pcr technique in the detection of covid 19 in the labs	
Day 3	**Date: 17/06/2020**
Read about how conventional pcr is different from rt pcr	

Day 4	Date: 18/06/2020
Started preparing raw report on the difference between pcr and rt pcr	
Day 5	**Date: 19/06/2020**
Discussed in detail about the mechanisms of different types of pcr and their principles	
Day 6	**Date: 20/06/2020**

Read about how covid 19 virus is detected from rt pcr and its advantages as well as disadvantages	
Week 6	
Day 1	**Date: 22/06/2020**
Starts to prepare a final report on different types of pcr	
Day 2	**Date: 23/06/2020**
Preparing final report on the mechanisms and different types of pcr	
Day 3	**Date: 24/06/2020**

Preparing final report on differences between pcr and rt pcr	
Day 4	**Date: 25/06/2020**
Prepared final report on why only rt pcr used in the covid 19 labs	
Day 5	**Date: 26/06/2020**
Completed first draft of report and sent it for the first review and did all the corrections suggested in the report	
Day 6	**Date: 27/06/2020**
Completed the final draft of the report and submitted to dr jata Shankar	
28/07/2020	**Harmeet**
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Vinay kumar korram**	**Roll No.**	**171805**
Company Name		**Jaypee university of information technology**	
Training Supervisor Name		**Dr. jata Shankar**	
Training Supervisor Signature		*jata shnakar*	
Internship Start Date		**18/05/2020**	
Internship End Date		**27/06/2020**	

Week 1

Day 1	**Date: 18/05/2020**
On the first day of the training my mentor and I had a discussion on the area of training (PCR TECHNIQUES) After this I was assigned for the job to find some relevant literature and history about the PCR Techniques and read about it.	
Day 2	**Date: 19/05/2020**
I started reading about the introductions to PCR. My main aim was to find the answers to what is PCR , how it works and how is it useful as a research field in coming times.	
Day 3	**Date: 20/05/2020**
Got history about pcr to read and how the pcr works in late 90s I also read about water bath pcr and how this pcr is different from modern pcr.	
Day 4	**Date: 21/05/2020**
Started reading about different techniques of pcr and its applications in different fields of research and asked my mentor to recommend some good literature on different topics related to pcr.	
Day 5	**Date: 22/05/2020**

On this day I read about the discovery of pcr and the exact year of discovery and in detail about the setup of water bath pcr , diagram of water bath pcr and functions of dntps

Day 6 **Date- 23/05/2020**

Read about the benefits of using pcr in details and also the disadvantages of pcr .

Week 2

Day 1 date – 25/05/2020

Read about the three key steps to pcr each at different temperature which is denaturation extension and annealing and about the process of heating and cooling

Day 2 **Date -26/05/2020**

Informed about my mentor about the same and got more topics to read about the pcr such as different techniques of pcr

Day 3 date – 27/05/2020

I read about the different techniques of pcr such as nested pcr , multiplex pcr ,touchdown pcr and hot start pcr.

Day 4 **date – 28/05/2020**

Read in detail about the nested pcr and how it is used to increase the specificity of dna amplification reducing unspecific products

Day 5 **date – 29/05/2020**

Read in detail about the multiplex pcr and how it allows amplifications of many target sequences concurrently in the same reaction mixture

Day -6	date- 30/05/2020	**:**
Read in detail about the rt pcr known as real time pcr which is the modification of standard pcr and how this technique is used in covid 19 labs		
Week 3		
Day 1	**DATE-1/06/2020**	
On this day I leraned about the different enzymes like phenol and guanidine isothiocynate , rna polymerase which is used in the process of detecting the corona virus with the help of rt pcr		
Day 2	**Date- 2/06/2020**	
On this day I learned about the full process from taking the sample to detection of virus in the rt pcr .		
Day 3	**Date- 3/06/2020**	
Read in detail about the precautions taken while collecting the sample and performing the process on rt pcr		
Day 4	**Date -4/06/2020**	

As told by the mentor i read about different applications in detail like genotyping , cloning ,mutation ,detetction etc	
Day 5	**Date – 5/06/2020**
Gathered information about literature of different applications of pcr and how they are used in different fields.	

Day 6	**Date-6/06/2020**
Read about the research papers available related to the topic	
Week 4	
Day 1	**DATE-8 /06/2020**
My mentor told me to read about different types of pcr and its uses	
Day 2	**Date- 9/06/2020**
As told by the mentor the first type of pcr is Amplified fragment length polymorphism (AFLP) PCR	
Day 3	**Date- 10/06/2020**
On this day I read about second type of pcr which is allele specific pcr and can be used to analyze single nucleotide polymorphism	
Day 4	**Date-11/06/2020**

I read about another type of pcr which is assembly pcr which assemble large DNA oligonucleotides from multiple shorter fragments.

Day 5	**Date-12/06/2020**	
The another type of pcr is Asymmetric PCR which is a variation of PCR used to preferentially amplify one strand of the original DNA more than the other		
Day 6	**Date-13/06/2020**	

I read about another type of pcr which is Colony PCR and it is a method in which, where identification of DNA of interest inserted into the plasmid is obtained by designing the inserted DNA specific primers.
Week 5

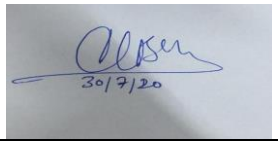
Day 1	**Date: 15/06/2020**
I discussed all types of pcr with the mentor and started to prepare the raw report on the types of pcr	
Day 2	**Date: 16/06/2020**
Read about why using only rt pcr technique in the detection of covid 19 in the labs	
Day 3	**Date: 17/06/2020**
Read about how conventional pcr is different from rt pcr	

Day 4	Date: 18/06/2020
Started preparing raw report on the difference between pcr and rt pcr	
Day 5	**Date: 19/06/2020**
Discussed in detail about the mechanisms of different types of pcr and their principles	
Day 6	**Date: 20/06/2020**

Read about how covid 19 virus is detected from rt pcr and its advantages as well as disadvantages	
Week 6	
Day 1	**Date: 22/06/2020**
Starts to prepare a final report on different types of pcr	
Day 2	**Date: 23/06/2020**
Preparing final report on the mechanisms and different types of pcr	
Day 3	**Date: 24/06/2020**

Preparing final report on differences between pcr and rt pcr	
Day 4	**Date: 25/06/2020**
Prepared final report on why only rt pcr used in the covid 19 labs	
Day 5	**Date: 26/06/2020**
Completed first draft of report and sent it for the first review and did all the corrections suggested in the report	
Day 6	**Date: 27/06/2020**
Completed the final draft of the report and submitted to dr jata Shankar	
28/07/2020	**Vinay**
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Devashish Verma**	**Roll No.**	**171806**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr. Hemant Sood**	
Training Supervisor Signature			
Internship Start Date		**18/05/2020**	
Internship End Date		**27/06/2020**	

Week 1

Day 1	**Date: 18/05/2020**
On the first day of training, I and my mentor had discussion on the area of training. We decided it to be Embryo culture for In micropropagation of new Cicer arietinum (Chickpea) varities.	
Day 2	**Date: 19/05/2020**
I started reading about basics of Inmicropropagation. Main aim of my reading was what are the types of inmicropropagation and what are their importance in the field of biotechnology.	
Day 3	**Date: 20/05/2020**
Weekly discussion with mentor.	
Day 4	**Date: 21/05/2020**
I started reading about Embryo culture in specific and what are the recent advances that are being done related to it.	
Day 5	**Date: 22/05/2020**
Got more literature to read and started reading and marking recent topics of research in this field.	

Day 6	**Date: 23/05/2020**
Weekly discussion with mentor.	

Week 2

Day 1	Date: 25/05/2020
Read more about the topics provided to have a better insight	
Day 2	**Date: 26/05/2020**
Found out about zygotic embryos. Started reading about it.	
Day 3	**Date: 27/05/2020**
Weekly discussion with mentor.	
Day 4	**Date: 28/05/2020**
Found out about somatic embryos which are the most interesting topic out of all. Started reading about it.	
Day 5	**Date: 29/05/2020**
Understood the difference between zygotic and somatic embryos and how they being used to grow a complete plant.	

Day 6	**Date: 30/05/2020**
Discussion with mentor.	
Week 3	
Day 1	**Date: 01/06/2020**
Read about plant hormones and how they can be used in embryo culture technique.	
Day 2	**Date: 02/06/2020**
Found out about certain chemical compositions which can be used as a plant hormone.	
Day 3	**Date: 03/06/2020**
Weekly discussion with mentor.	
Day 4	**Date: 04/06/2020**
Read about Cicer arietinum in detail and their varities.	
Day 5	**Date: 05/06/2020**
Read research papers onAgro bacterium mediated gene transfer.	

Day 6	Date: 06/05/2020
Weekly discussion with mentor.	
Week 4	
Day 1	**Date: 08/06/2020**

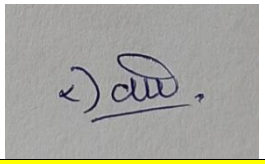
Found out some new varities of Cicer arietinum which are more resistant to diseases which are produced using Agro bacterium mediated gene transfer.	
Day 2	**Date: 09/06/2020**
Read about how Cicer arietinum can be grown using Embryo culture technique.	
Day 3	**Date: 10/06/2020**
Weekly discussion with mentor.	
Day 4	**Date: 11/06/2020**
Read about Embryo rescue technique.	
Day 5	**Date: 12/06/2020**
Read about embryogenesis and embryonic relationship of Cicer arietinum plant.	
Day 6	**Date: 13/06/2020**

Weekly discussion with mentor.

Week 5	
Day 1	**Date: 15/06/2020**
Read about Direct and Indirect somatic embryogenesis.	
Day 2	**Date: 16/06/2020**
Read research papers on different embryo stages of Cicer arietinum.	
Day 3	**Date: 17/06/2020**
Weekly discussion with mentor.	
Day 4	**Date: 18/06/2020**
Found out the best stage for embryo culture of Cicer arietinum.	
Day 5	**Date: 19/06/2020**
Read research papers on Plant growth Regulators.	
Day 6	**Date: 20/06/2020**
Weekly discussion with mentor.	

Week 6

Day 1	**Date: 22/06/2020**
Read about effects of plant growth regulators on induction of somatic embryogenesis.	
Day 2	**Date: 23/06/2020**
Read and found out the different stages of direct and indirect somatic embryogenesis.	
Day 3	**Date: 24/06/2020**
Weekly discussion with mentor.	

Day 4	Date: 25/06/2020
Read more literatures on how Cicer arietinum responses to different plant hormones and embryo culture technique	
Day 5	**Date: 26/06/2020**
Review the literature on Embryo culture of Cicer arietinum.	
Day 6	**Date: 27/06/2020**
Made complete report on be Embryo culture for In micropropagation of new Cicer arietinum (Chickpea) varities.	
30/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Aakanksha Pandey	**Roll No.**	171807
Company Name		JaypeeUniversity of information technology	
Training Supervisor Name		Dr. Poonam Sharma	
Training Supervisor Signature			
Internship Start Date		15/5/20	
Internship End Date		30/6/20	

Week 1

Day 1	**Date:** 18/5/20
Collected data about biosurfactant , gathered literature related to it.	
Day 2	**Date:** 19/05/20
Collected literature related to different types of biosurfactants and and its diverse classes	
Day 3	**Date:** 20/05/20
Discussed the collected literature with the colleagues and supervisor	
Day 4	**Date:** 21/05/20
Gained insights of about production and manufacturing of biosurfactants	

Day 5	**Date:** 22/05/20
Chemical characterization and physicochemical behaviour of biosurfactant was studied	

Day 6	**Date:** 23/05/20
Studied about physicochemical characterization and physicochemical evaluation of microemulsion system for antimicrobial activity of Glycerol monolaurate.	
Week 2	
Day 1	**Date:** 25/05/20
Gained knowledge about evaluation of physicochemical properties and microbial attributes of cooked sausages stuffed in casing modified by surfacrant and lactic acid after immersion vacuum cooling and long term storage	
Day 2	**Date:** 26/05/20
Physicochemical and antimicrobial properties of new rhamnolipids produced by Pseudomonas aeruginosa AT-10 from soybeanOil refinery wastes was studied	
Day 3	**Date:** 27/05/20
Read and gained information about structural and physicochemical characterization of crude biosurfactant produced by Pseudomonas aeruginosa SP-4 Isolated from petroleum contaminated soil	
Day 4	**Date:** 28/05/20
Read about physicochemical and biological effects on detachment and activity recovery of aging biofilm by enzyme and surfactant treatment	

Day 5	**Date:** 29/05/20
Physicochemical and surface-active properties of biosurfactant produced using molassesby a Pseudomonas aeruginosa mutant was studied	

Day 6	**Date:** 30/0520
Studied about physicochemical and functional characterization of biosurfactant produced by Lactococcus lactis 53	
Week 3	
Day 1	**Date:** 1/06/20
Efficient purification of biosurfactant Viscosin from Pseudomonas libanensis strain M9-3 and its physicochemical and biological properties were studied	
Day 2	**Date:** 2/06/20
Studied about Evaluation of tea derived biosurfactant on removing heavy metal ions from dilute waste water by ion flotation	
Day 3	**Date:** 3/06/20
Compiled a report and discussed it with my supervisor and colleagues	
Day 4	**Date:** 4/06/20

Day 5	**Date:** 5/06/20
Compiled 2nd report and discussed it with my supervisor and colleagues	

Day 6	**Date:** 6/06/20
Compiled a report and discussed it with my supervisor and colleagues	

Week 4

Day 1	**Date:** 8/06/20
Compiled another report and discussed it with my supervisor and colleagues	
Day 2	**Date:** 9/06/20
Compiled a report and discussed it with my supervisor and colleagues.	
Day 3	**Date:** 10/06/20
Worked on the mistakes in the report and corrected them	
Day 4	**Date:** 11/06/20

Day 5	**Date:** 12/06/20
Discussed the literature with colleagues to get a better idea about it.	
Day 6	**Date:** 13/06/20

Learned and various insights of biosurfactants.
Week 5
Day 1 **Date:** 15/06/20
Prepared another report about boo properties
Day 2 **Date:** 16/06/20
Discussed the report with supervisor and colleagues.
Day 3 **Date:** 17/06/20
Prepared a report about biosurfactant produced from Lactococcus lactis 53
Day 4 **Date:** 18/06/20

Discussed the report with supervisor and colleagues.	
Day 5	**Date:** 19/06/20
Another report was prepared on biosurfactant fron Pseudomonas aeruginosa SP-4 .	
Day 6	**Date:** 20/06/20

Discuss the report with supervisor and colleagues.

Week 6

Day 1	**Date:** 22/06/20
Prepared 10th report on biosurfactants using the literature related to it.	

Day 2	**Date:** 23/06/20
Discussed the report with supervisor and colleagues.	

Day 3	**Date:** 24/06/20
Had a brief discussion with the colleagues about our respective reports and content Studied	

Day 4	**Date:** 25/06/20
Had a discussion with the supervisor about all the work done until then and gave a summary about it.	

Day 5	**Date:** 26/06/20
Started compiling the entire work along with the references and acknowledgements.	

Day 6	**Date:** 27/06/20

Compiled a final report of all the work done during the internship course and got it approved by the supervisor.	
24-07-20	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Reva Bhardwaj**	**Roll No.**	**171809**
Company Name		**Jaypee University of information technology**	
Training Supervisor Name		**Dr. Ashok Nadda**	
Training Supervisor Signature			
Internship Start Date		15/5/20	
Internship End Date		30/6/20	

Week 1

Day 1	**Date:15/5/20**
Studied about the introduction of immobilization Of enzymes onto nanoparticles.	
Day 2	**Date: 16/5/20**
Studied about various types of immobilization Of enzymes	
Day 3	**Date: 17/5/20**
Studied about heterogeneous biocatalysts and Their parameters	
Day 4	**Date: 18/5/20**
Studied about applications of immobilization	
Day 5	**Date: 19/5/20**

Discussed about applications of immobilization With our mentor

Day 6	**Date: 20/5/20**
Discussed all the things we studied with our mentor	
Week 2	
Day 1	**Date: 22/5/20**
Studied about immobilization efficiency and Its importance	
Day 2	**Date: 23/5/20**
Studied about immobilization yield and how It is different from immobilization efficiency	
Day 3	**Date: 24/5/20**
Discussed immobilization yield and efficiency with our mentor	
Day 4	**Date: 25/5/20**
Studied about immobilization at nanoscale	
Day 5	**Date: 26/5/20**

Studied about various parameters to be Considered when immobilization

Day 6	**Date: 27/5/20**
Discussed all the parameters, rights and wrongs When immobilizing with our mentor	
Week 3	
Day 1	**Date: 29/5/20**
Studied about introduction to BET analysis	
Day 2	**Date: 30/5/20**
Studied about the working of BET and its importance	
Day 3	**Date: 31/5/20**
Discussed the BET analysis with our mentor	
Day 4	**Date: 1/6/20**

Studies about multipoint Bet analysis and how It is different from the standard bet

Day 5	Date: 2/6/20
Studied about protein loading and its role In immobilization	

Day 6	Date: 3/6/20
Discussed the protein loading and multi point Bet with our mentor	

Week 4

Day 1	Date: 5/6/20
Studied about various sources from which Nanoparticle can be derived	

Day 2	Date: 6/6/20
Studied about prepration of nanoparticles	

Day 3	Date: 7/6/20
Discussed about nanoparticles preparation And different sources with our mentor	

Day 4	Date: 8/6/20

Studied about the role of nanoparticles In drug delivery mechanisms	
Day 5	**Date: 9/6/20**
Studied about how drug delivery mechanisms Can boost diagnostic procedures	
Day 6	**Date: 10/6/20**

Discussed the nanoparticles role in drug delivery With our mentor	
Week 5	
Day 1	**Date: 12/6/20**
Studied about electrochemical immobilization Of enzymes	
Day 2	**Date: 13/6/20**
Studied about importance of electrochemical Immobilization of enzymes	
Day 3	**Date: 14/6/20**
Discussed the electrochemical immobilization of enzymes with our mentor	
Day 4	**Date: 15/6/20**

Studied about immobilization types from Research paper
Day 5 | **Date: 16/6/20**
Prepared a raw report on our topic
Day 6 | **Date: 17/6/20**

Discussed about the report on the topic With our mentor
Week 6
Day 1 | **Date: 19/6/20**
Studied about protein inorganic nanohybrids From the reasearch paper
Day 2 | **Date: 20/6/20**
Studied about cross linked enzyme aggregates
Day 3 | **Date: 21/6/20**
Discussed about protein inorganic nanohybrids And cross linked enzyme aggregates with Our mentor
Day 4 | **Date: 22/6/20**

Studied about immobilization of enzymes or Nanoparticles via biometric coating	
Day 5	**Date: 23/6/20**
Discussed about all the things required in a report , all the do's and don'ts to make a final report.	
Day 6	**Date: 24/6/20**
Started making the final report on our Summer internship topic	
24/6/2 0	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Divyansh Rana**	**Roll No.**	**171810**
Company Name		**Jaypee University of information technology**	
Training Supervisor Name		**Dr. Ashok Nadda**	
Training Supervisor Signature			
Internship Start Date		15/5/20	
Internship End Date		30/6/20	

Week 1

Day 1	**Date:15/5/20**
Studied about the introduction of immobilization Of enzymes onto nanoparticles.	
Day 2	**Date: 16/5/20**
Studied about various types of immobilization Of enzymes	
Day 3	**Date: 17/5/20**
Studied about heterogeneous biocatalysts and Their parameters	
Day 4	**Date: 18/5/20**
Studied about applications of immobilization	
Day 5	**Date: 19/5/20**

Discussed about applications of immobilization With our mentor

Day 6	**Date: 20/5/20**
Discussed all the things we studied with our mentor	
Week 2	
Day 1	**Date: 22/5/20**
Studied about immobilization efficiency and Its importance	
Day 2	**Date: 23/5/20**
Studied about immobilization yield and how It is different from immobilization efficiency	
Day 3	**Date: 24/5/20**
Discussed immobilization yield and efficiency with our mentor	
Day 4	**Date: 25/5/20**
Studied about immobilization at nanoscale	
Day 5	**Date: 26/5/20**

Studied about various parameters to be Considered when immobilization

Day 6	**Date: 27/5/20**
Discussed all the parameters, rights and wrongs When immobilizing with our mentor	
Week 3	
Day 1	**Date: 29/5/20**
Studied about introduction to BET analysis	
Day 2	**Date: 30/5/20**
Studied about the working of BET and its importance	
Day 3	**Date: 31/5/20**
Discussed the BET analysis with our mentor	
Day 4	**Date: 1/6/20**

Studies about multipoint Bet analysis and how It is different from the standard bet
Day 5 | **Date: 2/6/20**
Studied about protein loading and its role In immobilization

Day 6	**Date: 3/6/20**
Discussed the protein loading and multi point Bet with our mentor	
Week 4	
Day 1	**Date: 5/6/20**
Studied about various sources from which Nanoparticle can be derived	
Day 2	**Date: 6/6/20**
Studied about prepration of nanoparticles	
Day 3	**Date: 7/6/20**
Discussed about nanoparticles preparation And different sources with our mentor	
Day 4	**Date: 8/6/20**

Studied about the role of nanoparticles In drug delivery mechanisms	
Day 5	**Date: 9/6/20**
Studied about how drug delivery mechanisms Can boost diagnostic procedures	
Day 6	**Date: 10/6/20**

Discussed the nanoparticles role in drug delivery With our mentor	
Week 5	
Day 1	**Date: 12/6/20**
Studied about electrochemical immobilization Of enzymes	
Day 2	**Date: 13/6/20**
Studied about importance of electrochemical Immobilization of enzymes	
Day 3	**Date: 14/6/20**
Discussed the electrochemical immobilization of enzymes with our mentor	
Day 4	**Date: 15/6/20**

Studied about immobilization types from Research paper
Day 5 | **Date: 16/6/20**
Prepared a raw report on our topic
Day 6 | **Date: 17/6/20**

Discussed about the report on the topic With our mentor
Week 6
Day 1 | **Date: 19/6/20**
Studied about protein inorganic nanohybrids From the reasearch paper
Day 2 | **Date: 20/6/20**
Studied about cross linked enzyme aggregates
Day 3 | **Date: 21/6/20**
Discussed about protein inorganic nanohybrids And cross linked enzyme aggregates with Our mentor
Day 4 | **Date: 22/6/20**

Studied about immobilization of enzymes or Nanoparticles via biometric coating	
Day 5	**Date: 23/6/20**
Discussed about all the things required in a report , all the do's and don'ts to make a final report.	
Day 6	**Date: 24/6/20**
Started making the final report on our Summer internship topic	
 **24/6/20**	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Soumi Biswas	**Roll No.**	171811
Company Name		Jaypee University of Information Technology	
Training Supervisor Name		Dr. Jitendraa Vashistt	
Training Supervisor Signature			
Internship Start Date		May 15, 2020	
Internship End Date		June 30, 2020	

Week 1

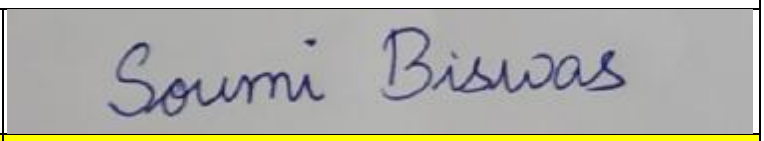
Day 1	**Date: 15/05/2020**
On the first day of training, my mentor provided me with a brief insight on the topic "Proteomics: Technologies and Applications".	
Day 2	**Date: 18/05/2020**
After the first interaction, he guided me to undergo some research on the topic and understand the fundamentals of proteomics.	
Day 3	**Date: 19/05/2020**
On that account, I grasped knowledge from an exceptional internet sites to fulfil the purpose. Later on, I gained knowledge on: what is proteomics, the in-depths of the field and where was its origin.	
Day 4	**Date: 20/05/2020**
Worked on exploring the subject and astonishingly came to know about the objectives of proteomics. Simultaneously, I also worked on clearing the basics.	
Day 5	**Date: 21/05/2020**
From the first interaction, today my mentor had a conversation with me over the things I learnt so far, by myself. Honestly, I'd a few queries which he cleared effectively and later on this day, he told me about the various workflows in proteomics and the sub-divisions of proteomics.	
Day 6	**Date: 22/05/2020**
Read about the types of proteomics study and the proteomics workflows thoroughly.	

Week 2

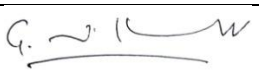
Day 1	**Date: 25/05/2020**
Fairly, I wasn't confident with the understandings of the proteomics workflows. Therefore, I decided to take a transition to watch videos for this purpose. Later on this day, with constant efforts, I finally understood the mechanisms.	
Day 2	**Date: 26/05/2020**
Today, my mentor enquired me about the teachings I learnt so far, followed by a set of questions. Honestly, I answered most of them; followed by he got me introduced to the modern technologies in proteomics. He told me about the different techniques this technology works with, in addition to how these techniques are interpreted by bioinformatics analysis. He further advised me to get myself registered in the NPTEL courses: Introduction to Proteomics course, which will help me in getting command with the techniques.	

Day 3	Date: 27/05/2020
Today, I learnt the conventional techniques, which had three subdivisions: Chromatography-based techniques, ELISA and Western Blotting. The chromatography-based techniques were further sub-divided into: Ion-exchange, Size exclusion and Affinity chromatography. But, as I've studied them earlier so, I revised the principles afresh.	
Day 4	**Date: 28/05/2020**
Yesterday, I distinctly learned the conventional techniques, followed by advanced techniques for today's lesson. The advanced techniques were divided into: Protein microarray, Gel-based approaches, Mass spectrometry and Edman sequencing. Learnt the protein microarray ones.	
Day 5	**Date: 29/05/2020**
Read and learnt gel-based approaches but, didn't understand the 2D-DIGE.	
Day 6	**Date: 30/05/2020**
Got literature on 2D-DIGE and learnt about it.	
Week 3	
Day 1	**Date: 01/06/2020**
Talked to my mentor about the 2D-DIGE. Lately, around the eve he explained me about its principles and I understood completely.	
Day 2	**Date: 02/06/2020**
Learnt the principle of mass spectrometry.	
Day 3	**Date: 03/06/2020**
Read and learnt about edman sequencing but, wasn't confident hence, gathered more information.	
Day 4	**Date: 04/06/2020**
Got literature on edman sequencing and hence, understood the concepts.	
Day 5	**Date: 05/06/2020**
After completion with the advanced techniques, my mentor gave me a brief about the quantitative techniques which were: ICAT, SILAC and iTRAQ.	
Day 6	**Date: 06/06/2020**
Got literature on ICAT, SILAC and iTRAQ and learnt about quantitative proteomics.	
Week 4	
Day 1	**Date: 08/06/2020**
Learnt ICAT labeling: its principle and use.	
Day 2	**Date: 09/06/2020**
Read and learnt about the Stable Isotopic Labeling with Amino Acids in Cell Culture (SILAC): principle and development processes.	

Day 3	Date: 10/06/2020
Got literature about Isobaric tag for relative and absolute quantification (iTRAQ).	
Day 4	**Date: 11/06/2020**
Yesterday after completion of the quantitative techniques, today I started with high-throughput techniques which were further sub-divided into: X-ray crystallography, Mass spectrometry and NMR spectrometry. Learnt the principle of X-ray crystallography.	
Day 5	**Date: 12/06/2020**
Read and learnt about mass spectrometry: principle, m/z values and application.	
Day 6	**Date: 13/06/2020**
Read and understood the significance of m/z values.	
Week 5	
Day 1	**Date: 15/06/2020**
Got literature on NMR spectroscopy and learnt about it.	
Day 2	**Date: 16/06/2020**
Yesterday on completion with high-throughput techniques, today I started learning the bioinformatics analysis; firstly, learnt about the interdisciplinary field bioinformatics.	
Day 3	**Date: 17/06/2020**
Explored software tools used for proteome data exploration available via the Internet. Learnt their descriptions and its use.	
Day 4	**Date: 18/06/2020**
Further learnt about the use of bioinformatics analysis in proteomics.	
Day 5	**Date: 19/06/2020**
Tried using some of the software tools for own curiosity and better understanding of the subject. Gained confidence in the field.	
Day 6	**Date: 20/06/2020**
Explored various sites to get accustomed to bioinformatics analysis.	
Week 6	
Day 1	**Date: 22/06/2020**
After completion with the modern technologies in proteomics, my mentor introduced me to the various applications of proteomics in: Biomarker discovery, Drug discovery and in Food industry.	

Day 2	Date: 23/06/2020
Got literature on applications of proteomics technology in biomarker discovery, learnt about it.	
Day 3	**Date: 24/06/2020**
Got literature on applications of proteomics technology in drug discovery, learnt about it.	
Day 4	**Date: 25/06/2020**
Got literature on applications of proteomics technology in food industry, learnt about it.	
Day 5	**Date: 26/06/2020**
Completed my learning on “Proteomics: Technologies and Applications”, my mentor gave me a summary of the course, also stating the future of proteomics. He instructed me to start preparing the report. Later on this day, I started compiling all the teachings I learnt throughout.	
Day 6	**Date: 29/06/2020**
Made the report, got it checked by my mentor, did the corrections and finally, submitted my completed work to Dr. Jitendraa Vashishtt.	
30/06/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Sugam Singh	**Roll No.**	171812
Company Name		Jaypee University of Information Technology	
Training Supervisor Name		Dr Garlapati Vijay Kumar	
Training Supervisor Signature		 29/07/2020	
Internship Start Date		15/05/2020	
Internship End Date		30/06/2020	

Week 1

Day 1	**Date:** 15/05/2020
I had a discussion with my guide over topic relevant for my training and he suggested some literature study about fermentation technology	
Day 2	**Date:** 16/05/2020
I started studying different topics related to fermentation technology.	
Day 3	**Date:** 18/05/2020
I referred various literature sources to study and build my data bank	
Day 4	**Date:** 19/05/2020
various study material was provided via google drive for reference	
Day 5	**Date:** 20/05/2020
Referred to the study material from google drive	
Day 6	**Date:** 21/05/2020
Had a discussion of performing virtual labs for further training.	

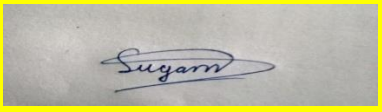
Week 2

Day 1	**Date:** 22/05/2020
Virtual Lab links were provided for the training part.	
Day 2	**Date:** 23/05/2020
Virtual lab about bioractor basics were given and theory involved was explained.	
Day 3	**Date:** 25/05/2020
I familiarized myself with the procedure and theory of the virtual lab.	
Day 4	**Date:** 26/05/2020
Studied the simulation and a self evaluation was carried out.	
Day 5	**Date:** 27/05/2020
Another virtual lab about the control characteristics was Provided.	
Day 6	**Date:** 28/05/2020
Theory was explained and procedure was studied and a self evaluation was done.	

Week 3	
Day 1	**Date:** 29/05/2020
A virtual lab about the operation of a 15 litre bioreactor was provided	
Day 2	**Date:** 30/05/2020
Scale up processes and criteria were studied from bench top to pilot scale.	
Day 3	**Date:** 01/06/2020
Theory involved in scaling up was explained and studied, procedure was understood and self evaluation was done.	
Day 4	**Date:** 02/06/2020
Different applications of fermentation technology were introduced and studied about them.	
Day 5	**Date:** 03/06/2020
A virtual lab about Biopolymer production was provided	
Day 6	**Date:** 04/06/2020
The importance of bio polymers and applications were studied.	
Week 4	
Day 1	**Date:** 05/06/2020
Biopolymer production by microbes was explained.	
Day 2	**Date:** 06/06/2020
Theory and procedure about biopolymer production by microbes was studied.	
Day 3	**Date:** 08/06/2020
A simulation was studied and self evaluation was done.	
Day 4	**Date:** 09/06/2020
Various other sources of biopolymer were studied.	
Day 5	**Date:** 10/06/2020
Different techniques for biopolymer production were studied.	
Day 6	**Date:** 11/06/2020
Various alcohol production through fermentation was studied.	
Week 5	
Day 1	**Date:** 12/06/2020
Virtual lab about Acetone-butanol-ethanol production was provided.	
Day 2	**Date:** 13/06/2020
Theory and procedure were studied.	
Day 3	**Date:** 15/06/2020
Simulations for Acetone-Butanol-Ethanol production were run and self evaluation were done.	

Day 4	**Date:** 16/06/2020
Application and requirements for acetone-butanol-ethanol were studied.	
Day 5	**Date:** 17/06/2020
Another Virtual lab about propanoic acid fermentation was provided	
Day 6	**Date:** 18/06/2020
Procedure and theory of propanoic acid fermentation was studied.	

Week 6

Day 1	**Date:** 19/06/2020
Application of propanoic acid was studied	
Day 2	**Date:** 20/06/2020
A virtual lab about 1,3 propanediol fermentation was given.	
Day 3	**Date:** 22/06/2020
Theory and procedure were studied and simulation were studied.	
Day 4	**Date:** 23/06/2020
Application of 1,3 propanediol were studied	
Day 5	**Date:** 24/06/2020
Future aspects of fermentation were explored and studied.	
Day 6	**Date:** 25/06/2020
Guide given suggestions for preparing the project report	
Date: 26/06/2020	
Worked on the project report	
Date: 27/06/2020	
A report was prepared and submitted with the guide for evaluation.	
Date: 29/06/2020	
Guide suggested the corrections and corrected and send to guide for final approval	
Date: 30/06/2020	
Guide approved the final project report	
Date **28/07/2020**	**Student Signature** 

Industrial Training Diary & Report

Student Name	**Umang Maheshwari**	**Roll No.**	**171813**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr Narendra Kumar**	
Training Supervisor Signature		 Narendra Kumar, 27/07/20	
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020

On the first day of the training, my mentor and I had a discussion on the area of training. We decided it to be synthetic biology. After this, I was assigned the job to find some relevant literature and read about it.

Day 2	**Date:** 19/05/2020

I started reading about the basics of synthetic biology. My main aim was to find answers to what is synthetic biology and how is it useful as a research field in coming time.

Day 3	**Date:** 20/05/2020

Got more literature to read and started reading and marking recent topics of research in this field. I also started actively looking out for the area of research.

Day 4	**Date:** 21/05/2020

Started reading about different areas in synthetic biology. Asked my mentor to recommend some good literature on different topics.

Day 5	**Date:** 22/05/2020

Read about the papers provided by the mentor to find out more about the new and upcoming topics in synthetic biology. These include P4 medicine, genome synthesis and biological circuits.

Day 6	**Date:** 23/05/2020

Read more about the topics provided to have a better insight of what synthetic biology can be used for.

Week 2	
Day 1	**Date:** 25/05/2020
Found out the topic of molecular circuits using synthetic biology most interesting out of all the topics. Started reading more about it.	
Day 2	**Date:** 26/052020
Informed my mentor about the same. Got more literature to read on the topic of biological circuits using synthetic biology.	
Day 3	**Date:** 27/05/2020
Read about the introduction of genetic switches and its uses in the real world.	
Day 4	**Date:** 28/05/2020
Understood what comprises of genetic switches and how are they used and regulated in living systems.	
Day 5	**Date:** 29/05/2020
Got literature about different types of genetic switch elements. Decided to read about one every day and also find out details and uses of each one of them.	

Day 6	**Date:** 30/05/2020
Read the introduction about the first type of genetic switches that are transcriptional regulators. These work by controlling the transcription.	

Week 3	
Day 1	**Date:** 01/06/2020
Read about programmable DNA binding and it's applications in biological systems.	
Day 2	**Date:** 02/06/2020
Got more information and details about Dimerization dependent transcriptional activation.	

Day 3	Date: 03/06/2020
Read about ligand-dependent repressor – another type of genetic control element.	
Day 4	**Date:** 04/06/2020
Gathered information and literature about the rewiring of biological pathways for the use in genetic control switches.	
Day 5	**Date:** 05/06/2020
Read the introduction and uses of post-transcriptional regulators – the second category of genetic control switches.	

Day 6	Date: 06/06/2020
The first category of these is RNA interference. Read about it.	

Week 4

Day 1	Date: 08/06/2020
The second factor for this is mRNA stability. Understood about it.	
Day 2	**Date:** 09/06/2020
Then another one is splicing efficiency. Went through it and got acquainted with it.	
Day 3	**Date:** 10/06/2020
Then studied about protein stability which can also act as a post-transcriptional switch.	
Day 4	**Date:** 11/06/2020
Started reading about what all these elements are capable of doing when they come in a series and form a circuit. These are known as genetic circuits or molecular circuits.	
Day 5	**Date:** 12/06/2020
There are different kinds of arrangements in which these circuits can come and be arranged. Started finding about them.	

Day 6	**Date:** 13/06/2020

Found about some of these arrangements and where are these naturally located in human systems. Started finding about how can these be used synthetically.

Week 5

Day 1	**Date:** 15/06/2020

The first arrangement is gene expression cascades. In this, different genes function in cascades and do complex biological functions.

Day 2	**Date:** 16/06/2020

Next is the Biocomputing that is these circuits can be used as transistors which perform Boolean calculations and decide on that whether there must be a signal of expression or not. These can be further used as computers since they essentially perform the same task.

Day 3	**Date:** 17/06/2020

Then there are Bandpass filters that can be made from these genetic elements. These allow for a specific amount of product to pass and block out the rest. No more or less is allowed.

Day 4	**Date:** 18/06/2020

Another one is a toggle switch. These can change the state between expression to no expression based on the availability of the product.

Day 5	**Date:** 19/06/2020

Another one is an oscillator. It changes the functions based on the periodic movement. Example of this is the circadian rhythm of the human body.

Day 6	**Date:** 20/06/2020

Rewiring of Internal pathway is another type of switch. It is used for changing the default pathway and making something different from it.

Week 6

Day 1	**Date:** 22/06/2020

This week was for the compilation of all the work done till now and started compiling points for the same.

Day 2	**Date:** 23/06/2020

Started working on the report to be submitted at the end of the training.

Day 3	**Date:** 24/06/2020
Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:** 25/06/2020
Did all the corrections suggested in the report.	
Day 5	**Date:** 26/06/2020
Put the report in the correct format and added the required references in it.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and submitted it to Dr Narendra Kumar.	
21/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Diwakar Paliwal	**Roll No.**	171814
Company Name		Jaypee University of Information Technology	
Training Supervisor Name		Dr. Poonam Sharma	
Training Supervisor Signature			
Internship Start Date		18-05-2020	
Internship End Date		30-06-2020	

Week 1

Day 1	**Date:** 18-05-2020

Worked on collecting information about Surfactants, gathering the literature related to it.

Day 2	**Date:** 19-05-2020

Collected literature related to various types of surfactants and focussed on learning the diverse classes of the surfactant molecules.

Day 3	**Date:** 20-05-2020

Discussed about the collected literature with the supervisor and colleagues.

Day 4	**Date:** 21-05-2020

Worked upon the collection of literature and gaining insights about the production and manufacturing techniques related to the synthetic surfactants.

Day 5	**Date:** 22-05-2020

Learned about the use of chemical or synthetic surfactants in various industries and domains.

Day 6	**Date:** 23-05-2020
Focussed on collecting literature articles about Microbial Surfactants. Discussed all the collected information with my supervisor along with submission of a report (1).	

Week 2

Day 1	**Date:** 25-05-2020
Focussed on studying in detail the various properties of the microbial surfactants and had a healthy discussion with my supervisor upon the possible uses of these molecules according to their properties.	
Day 2	**Date:** 26-05-2020
Gathered literature relating to the use of Microbial surfactants as a potent inhibitor of biofilms produced by Pseudomonas aeruginosa, and read it thoroughly.	
Day 3	**Date:** 27-05-2020
Compiled a report (2) about the use of biosurfactant to inhibit the biofilm produced by bacterial species, which tend to spoil food and other items in general.	
Day 4	**Date:** 28-05-2020
Studied some general used biosurfactants in various domains and looked upon the structures of some biosurfactants like Rhamnolipids, caprylic acid etc. Had a good discussion with the supervisor over the structure and the property to inhibit biofilm generation.	
Day 5	**Date:** 29-05-2020
Worked upon collecting information against the production of biosurfactants from various microorganisms and focussed upon learning the sustainable production from low cost waste materials.	

Day 6	**Date:** 30-05-2020

Compiled a report (3) which aimed to establish the sustainable production techniques and use of biosurfactants in food industries as food additives aiming to improve food texture and quality.

Week 3

Day 1	**Date:** 01-06-2020

Discussed with supervisor the work uptil now and further worked upon finding the literature related towards to use of biosurfactants in improving the environmental conditions.

Day 2	**Date:** 02-06-2020

Studied in great detail the potential use of biosurfactants for soil bioremediation thus aiming to decrease the soil pollution and promoting healthy soil characteristics to support plant growth. Compiled a report (4) related to this topic.

Day 3	**Date:** 03-06-2020

Focussed on studying the various parameters for characterisationof biosurfactants which render them fit for use for certain activities. Discussed these parameters in great details with my Supervisor to have a brief idea about the parameters.

Day 4	**Date:** 04-06-2020

Gathered a literature article aiming at degrading the deisel contaminaation present in soil. Studied the article in detail to learn the microorganism capable of degrading deisel which act as contamination in the soil. Compiled a brief report (5) of the related literature.

Day 5	**Date:** 05-06-2020

Compiled a brief report of the above work and familiarized myself with the various available techniques used for the chemical, structural and general characterisation of the biosurfactants.

Day 6	**Date:** 06-06-2020
Having learned about the various techniques used for characterization, discussed about the possible uses of biosurfactants in certain areas owing to their characterization. Also compiled a report (6) for this study.	

Week 4

Day 1	**Date:** 08-06-2020
Briefed my supervisor about the progress made so far and had a discussion about the fields I had explored for the application of biosurfactants.	

Day 2	**Date:** 09-06-2020
Studied about the traditional methods of bisourfactant production and the media components generally used for the production of biosurfactants. Compared it with the production of synthetic surfactants and discussed about the feasibility of using biosurfactants on larger scales.	

Day 3	**Date:** 10-06-2020
Targetted the enhanced production of biosurfactant by Bacillus subtilis by using low cost media supplements and alternatives like Buttermilk and waste generated by poultry farm.	

Day 4	**Date:** 11-06-2020
Compiled a report (7) of the literature collected and discussed up here in this week, having gained significant information about the alternative media that will lead to decreased production costs for biosurfactants.	

Day 5	**Date:** 12-06-2020
Focussed upon gaining insights for isolation of inoculum from various sources and utilizing them for the production of biosurfactants. Studies techniques like Drop collapse test to verify the secretion of biosurfactants by any microorganism.	

Day 6	**Date:** 13-06-2020

Had a discussion with my Supervisor on all the collected information and finding the posiible modifications in various techniques for production and hypothesized the various environmental parameters to be optimized during the microbial fermentation aiming to increase the production of the biosurfactants.

Week 5

Day 1	**Date:** 15-06-2020

Studied about the production of biosurfactants by other living organims like humans, and also found the use of these secreted biosurfactants in pharmaceutical and therapeutics field.

Day 2	**Date:** 16-06-2020

Explored the pharmaceutical domain for the potent uses of biosurfactants and the most commonly used biosurfactants for the production of nanoparticles which are utilized for targeted drug delivery.

Day 3	**Date:** 17-06-2020

Studied the use of biosurfactant as micro-emulsion systems which aided in the production of butter, oil, mayonnaise and other food products like ice cream. Biosurfactants were also utilized for cleaning purposes along with use in cosmetic industries.

Day 4	**Date:** 18-06-2020

Gathered literature related to production of biosurfactant from endophytic fungi found in trees growing in temperate areas.

Day 5	**Date:** 19-06-2020

Compiled a report (8) related to the above literature and explored the property of biosurfactants to act as anti-oxidants thus scavenging the free radical ions. Also studies about the anti-adhesive property of biosurfactants which make them suitable to be used as food additives and aim to protect food spoilage.

Day 6	**Date:** 20-06-2020

Discussed all about the gathered literature with my supervisor and gave a brief summary of what I learned uptil now about microbial surfactants as a whole.

Week 6

Day 1	**Date:** 22-06-2020

Explored the Agriculture field for the probable use of biosurfactants to increase the yield from plant crops. Studies about the microorganisms which secrete metabolites which act as biosurfactants.

Day 2	**Date:** 23-06-2020

Compiled a brief report (9) of the above literature and studies the various plant growth promoters secreted by these microorganisms along with the biosurfactants, also confirmed the plant promoting activities by studying the experimental setups.

Day 3	**Date:** 24-06-2020

Gathered literature showing the use of biosurfactants in food industry serving a potent replacement of egg yolk used in dough formulations for cookie production.

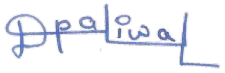
Day 4	**Date:** 25-06-2020

Compiled a report (10) relating the above gathered literature and learned the advantage of using biosurfactant produced by Bacillus species, thus giving high energy yield from cookies as compared to standard formulations having egg yolk.

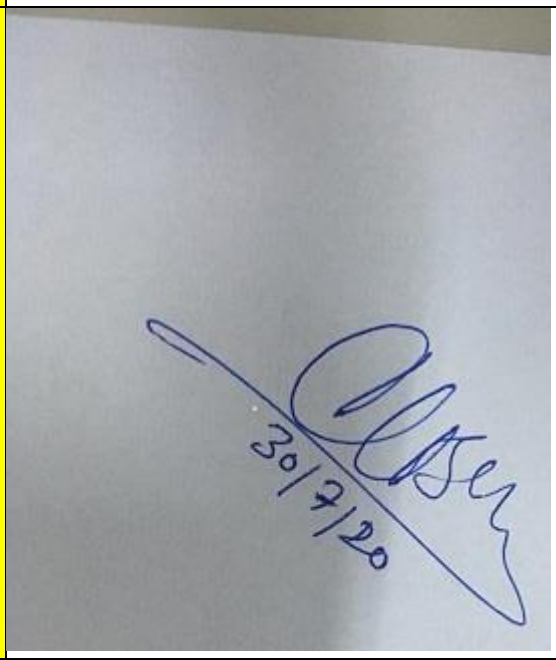
Day 5	**Date:** 26-06-2020

Had a brief discussion with my supervisor about all the work done until now in this internship and gave a brief summary of all my gathered literature and my understanding along with the reports submitted by me. Started putting all my work together along with the references of the literature collected.

Day 6	**Date:** 27-06-2020

Compiled a final report of the overall work done during this Internship program, and got it approved by my Supervisor and finally submitted the report to my Supervisor Dr. Poonam Sharma.	
24-07-2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Ishita kawar	**Roll No.**	171815
Company Name	Through Jaypee University of Information and technology		
Training Supervisor Name	Dr. Hemant Sood		
Training Supervisor Signature			
Internship Start Date	15 May,2020		
Internship End Date	30 june,2020		

Week 1

Day 1	**Date: May 15,2020**
On the first day we did a discussion about the topic of micropropagtion and decided the plant to study about it.	
Day 2	**Date:May16,2020**
Started reading about the plant rhododendron , about it's habitat and it's medicinal properties.	
Day 3	**Date:May17,2020**
Read further about the topic of micropropagation. The research paper studied included the review articles of rhododendron and culturing it under certain specific conditions.	
Day 4	**Date:May18,2020**

Discussion with Dr. Hemant Sood .	
Day 5	**Date:May19,2020**
Read papers regarding the topic more , about micropropagtion and about the plant rhododendron	

Day 6	**Date:May20,2020**
Read more about the topics to have a better insight from sites such as research gate ,Google scholar, scholar library.	

Week 2

Day 1	**Date:May21,2020**
Found out about the medicinal properties of the plant reading review article on Bioactive compounds, health benefits and utilization of Rhododendron: By Vikas Kumar et.al 2018	
Day 2	**Date:May22,2020**
Studied about the uses, and medicinal properties. Studied some review article about the pharmacological effects and uses from research gate .	
Day 3	**Date:May23,2020**
Discussion with Dr. Hemant Sood.	
Day 4	**Date:May24,2020**
Studied more about the uses of the plant and it's healing properties and pharmacological effects and antioxidant properties by reading review articles on Phytochemistry, Traditional uses and Pharmacology of Rhododendron arboreum by authors Som K.et.al 2019	
Day 5	**Date:May25,2020**
Studied about the drawbacks of the plant in medicinal industries and toxicity of the plant rhododendron from a site named springer .com	

Day 6	**Date:May26,2020**
Discussion with my mentor.	

Week 3

Day 1	**Date:June1,2020**
Read about the properties of the plant more and how micropropagtion can help to grow the plant in a sustained environment.	
Day 2	**Date:June2,2020**
Read papers about the micropropagtion of rhododendron and some e-journal from scholar library.	
Day 3	**Date:June3,2020**
Discussion with Dr. Hemant Sood.	
Day 4	**Date:June4,2020**
Got more information about the medicinal properties of plant from sites such as rhodygarden .net and britannica.com.	
Day 5	**Date:June5,2020**
Read more facts and reproduction strategies of the plant from journals at Britannica website.	

Day 6	Date:June6,2020
Discussion with Dr. Hemant Sood	

Week 4

Day 1	Date:June7,2020
Found out more about the topic and various other species of rhododendron and their uses from review article of Som K.et al 2018 on medicinal properties of r.arborendum.	

Day 2	Date:June8,2020
Found out about the mad honey disease and disadvantages of the plant in various sectors .	

Day 3	Date:June9,2020
Discussion with Dr. Hemant Sood regarding the topic.	

Day 4	Date:June10,2020
Analysis of the topic done by reading papers.	

Day 5	Date:June11,2020
Discussion about the papers.	

Day 6	Date:June12,2020

Analysis of the topic done.

Week 5	
Day 1	**Date:june17,2020**
Started to frame a draft of the report.	
Day 2	**Date:june18,2020**
Complied all the information gathered through reading papers .	
Day 3	**Date:june20,2020**
Did a discussion on how to write a report.	
Day 4	**Date:june21,2020**
Prepared of the viva on the given topic and did a little more discussion with my mentor.	
Day 5	**Date:june22,2020**
Started writing the report by gathering more information and compiling it again and again .	
Day 6	**Date:june23,2020**
Report writing	

Week 6

Day 1	Date:june24,2020
Corrected the report with some minor mistakes after discussion with hemant mam.	

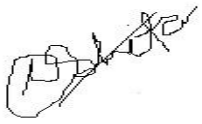
Day 2	Date:june25,2020
Did all the corrections suggested in the report.	

Day 3	Date:june26,2020
Completed the first draft of the report .Sent it for the review.	

Day 4	Date:june27,2020
Did all corrections suggested in the report.	

Day 5	Date:june28,2020
Put the report in correct format and added references to it.	

Day 6	Date:june29,2020
Completed the final draft of the report and submitted to Dr. Hemant Sood	

July30,2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Ekta Choudhary**	**Roll No.**	**171816**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr. Udaybanu**	
Training Supervisor Signature			
Internship Start Date		**16/05/2020**	
Internship End Date		**25/06/2020**	

Week 1

Day 1	**Date: May 16, 2020**

On the first day of training, I had discussion with my guide on the topic of animal cell culture. Then, I started going through the basic introduction related to the animal cell culture and read about it.

Day 2	**Date: May 17, 2020**

I started reading about applications of animal cell culture in various fields such as cell biology & biochemistry, cancer research, virology, genetic engineering etc.

Day 3	**Date: May 18, 2020**

Then, I was assigned to read about instrumentation involved in establishment and maintenance of cell lines.

Day 4	**Date: May 19, 2020**

Started reading about instruments used in cell culture technologies like laminar air flow, centrifuge, haemocytometer, flow cytometry etc.

Day 5	**Date: May 20, 2020**

Read laminar air flow or biosafety cabinet (BSC) in detail which provide protection to the culture from any organism such as fungi, virus, bacteria under aseptic conditions. Then, read about BSC 1, BSC 2 & BSC 3 and efficiency of their HEPA filters.

Day 6	Date: May 21, 2020

Then, read about CO_2 incubator which provide appropriate environment for the growth and development of cells and centrifuge used for the separation of particles from a solution.

Week 2

Day 1	Date: May 23, 2020

Started learning about more instruments such as refrigerator, cryo-storage container, liquid nitrogen container used for storing cell lines.

Day 2	Date: May 24, 2020

Read more about the instruments and made additions to the collected data.

Day 3	Date: May 25, 2020

Revised whatever I have studied so far.

Day 4	Date: May 26, 2020

Started reading about hemocytometer, its principle, usage and applications.

Day 5	Date: May 27, 2020

Studied more about common instruments or equipment used in laboratory such as water bath, microscope, pH meter, aspiration pump etc.

Day 6	Date: May 28, 2020
Got more literature and made additions to the already collected data.	

Week 3

Day 1	Date: May 30, 2020
Read more information about how to use these instruments efficiently.	

Day 2	Date: May 31, 2020
Read precautions related to these instruments and contamination can be prevented.	

Day 3	Date: June 01, 2020
Started studying about flow cytometry which is used to analyze the characteristics of the cells on the basis of laser technique.	

Day 4	Date: June 02, 2020
Then, I was allocated to find literature on any one disorder or disease. I decided to collect data on disorder ‘Dementia’.	

Day 5	Date: June 03, 2020
Started reading about the basic introduction of dementia such as its origin and how it is caused.	

Day 6	Date: June 04, 2020

Started reading about the symptoms of dementia and added it to collected data.

Week 4

Day 1	Date: June 06, 2020
Found more literature and added it to the collected data.	
Day 2	**Date: June 07, 2020**
Revised whatever I have learnt so far.	
Day 3	**Date: June 08, 2020**
Then, started reading different stages of dementia.	
Day 4	**Date: June 09, 2020**
Found more literature on diagnosis of dementia which include different tests used to diagnose dementia.	
Day 5	**Date: June 10, 2020**
Started reading about treatment that can be used to cure the disease.	
Day 6	**Date: June 11, 2020**

Revised the studied data and made more additions.

Week 5

Day 1	Date: June 13, 2020

Then, I was allocated to collect data on basic techniques used in animal cell culture.

Day 2	Date: June 14, 2020

Started with trypsinization of cells including its methodology.

Day 3	Date: June 15, 2020

Then, read about aseptic techniques used in the laboratory to prevent contamination.

Day 4	Date: June 16, 2020

Collected data on passaging of cells. Its procedure was learnt.

Day 5	Date: June 17, 2020

Then, I started reading about how culture is prepared and how plating is done.

Day 6	Date: June 18, 2020

Got acquainted with structure of hemocytometer and found how cells are counted.

Week 6

Day 1	Date: June 20, 2020

Then various prevention measures were understood that should be taken in laboratory in order to avoid contamination.

Day 2	Date: June 21, 2020

Ways of preventing contamination while performing laboratory work were understood.

Day 3	Date: June 22, 2020

Then, collected data on cryopreservation which include its procedure and precaution while cryopreserving the cells.

Day 4	Date: June 23, 2020

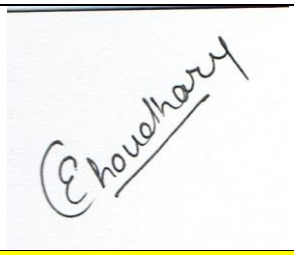
Then, process of thawing of cells was understood.

Day 5	Date: June 24, 2020

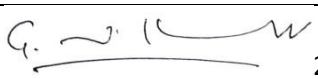
Got information regarding sub-culturing of cells.

Day 6	Date: June 25, 2020

Revised whatever was learnt so far and made additions to the collected data related to animal cell culture techniques. At last, compiled the complete data in final report.

July 29, 2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Charu Thakur	**Roll No.**	**171817**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr. Garlapati Vijay Kumar**	
Training Supervisor Signature		 29/07/2020	
Internship Start Date		15/05/2020	
Internship End Date		30/06/2020	

Week 1

Day 1	**Date:** 15/05/2020
On the first day of the training, my mentor and I had a discussion on the topic of training. We decided it to be Fermentation Technology. After this, I was assigned the job to find some relevant literature and read about it.	
Day 2	**Date:** 16/05/2020
I started reading about bioreactors. My main aim was to understand its working and its various components.	
Day 3	**Date:** 18/05/2020
Got more literature to read and started reading and marking recent topics of research in this field. I also started actively looking out for the area of research.	
Day 4	**Date:** 19/05/2020
Started reading about the AG fermenter. Also, read about the pH control method which is dependent on various parameters.	
Day 5	**Date:** 20/05/2020
Read about the papers provided by the mentor to find out more about bioreactors. Learned about the basics of operating a bioreactor: login control, priming tubes, setting parameters like ph, temperature, DO etc.	
Day 6	**Date:** 21/05/2020
Got more literature to read on the topic before moving forward.	

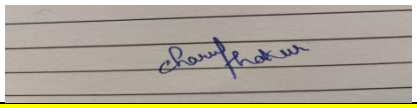
Week 2

Day 1	**Date:** 22/05/2020
Got some literature about the Biopolymer Production by Microbes.	
Day 2	**Date:** 23/052020
Read about the Microbial Biopolymer Production by R. eutropha NRRL B14690.	
Day 3	**Date:** 25/05/2020
Gathered information about the Media Preparation and Bioreactor cultivation.	
Day 4	**Date:** 26/05/2020
Read about the method involved. Understood the protocol.	
Day 5	**Date:** 27/05/2020
Understood about the kinetic profile of different fermentations by studying the graph.	
Day 6	**Date:** 28/05/2020
Researched more about the Microbial Biopolymer Production.	

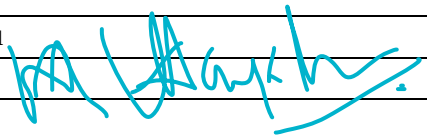
Week 3	
Day 1	**Date:** 29/05/2020
Read about another type of production: Acetone-Butanol-Ethanol Production.	
Day 2	**Date:** 30/05/2020
Got more information about the Clostridium acetobutylicurn strain ATCC 824 which was used for production of Acetone-Butanol-Ethanol. Read more about the media preparation for the same.	
Day 3	**Date:** 01/06/2020
Read about the Flask and Bioreactor development.	
Day 4	**Date:** 02/06/2020
Gathered information about the Analytical protocols like dry weight, glucose (DNS method) and, solvent and acid concentration (Gas Liquid Chromatography).	
Day 5	**Date:** 03/06/2020
Read and understood the protocol.	
Day 6	**Date:** 04/06/2020
Read some more research paper on the topic to understand the basic working and result formation.	
Week 4	
Day 1	**Date:** 05/06/2020
Read about another type of production: Propanoic Acid Production.	
Day 2	**Date:** 06/06/2020
Gathered information about the organism involved: Propionibacterium acidipropionici ATCC 4875. Studied about the inoculum preparation.	
Day 3	**Date:** 08/06/2020
Read about the bioreactor cultivation.	
Day 4	**Date:** 09/06/2020
Started reading about what this method is capable of doing, and how it's done.	
Day 5	**Date:** 10/06/2020
Read about the Analytical Protocol: Biomass Estimation and Substrate/Product Estimation.	
Day 6	**Date:** 11/06/2020
Understood about the basic working and result formation.	
Week 5	
Day 1	**Date:** 12/06/2020
Read about “1, 3 Propanediol Fermentation”.	
Day 2	**Date:** 13/06/2020
Understood about the fermentation process involved and did some more research on the topic.	
Day 3	**Date:** 15/06/2020
Gathered information about medium requirement, culture used ,mechanism etc.	
Day 4	**Date:** 16/06/2020
Gathered information about the setup for fermentation bioreactor and how its done.	
Day 5	**Date:** 17/06/2020
Read about 1,3-PD MODEL EQUATIONS and how these equations describe batch dynamics of growth & 1,3-PD production.	

Day 6	**Date:** 18/06/2020
Read more research papers to understand the process better.	

Week 6

Day 1	**Date:** 19/06/2020
This week was for the compilation of all the work done till now and started compiling points for the same.	
Day 2	**Date:** 20/06/2020
Started working on the report to be submitted at the end of the training.	
Day 3	**Date:** 22/06/2020
Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:** 23/06/2020
Did all the corrections suggested in the report.	
Day 5	**Date:** 24/06/2020
Put the report in the correct format.	
Day 6	**Date:** 25/06/2020
Guide given suggestions to make the project report	
Date: 26/06/2020	
Worked on the project report	
Date: 27/06/2020	
Completed the final draft of the report and submitted to guide for correction	
Date: 29/06/2020	
Guide suggested the modifications and corrected those and send back to guide for final approval.	
Date: 30/06/2020	
Guide approved the project report.	
27/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Rachita Gupta	**Roll No.**	171818
Company Name		Jaypee University of Information Technology, Waknaghat	
Training Supervisor Name		Dr. Udayabanu	
Training Supervisor Signature			
Internship Start Date		May 16, 2020	
Internship End Date		June 25, 2020	

Week 1

Day 1	**Date: May 16, 2020**
After a discussion with my guide on the topic of animal cell culture, I started with the basics such as how cell lines are established and their potential applications in various fields.	

Day 2	**Date: May 17, 2020**
After this, I was allocated the activity to locate some applicable writing and read about instrumentation involved in establishment and maintenance of cell lines.	

Day 3	**Date: May 18, 2020**
In order to learn about the current methodologies involved, I studied about the history of cell lines as to how they came into existence along with different categories of tissue culture.	

Day 4	**Date: May 19, 2020**
Started reading about instrumentation involved in cell culture technologies, like equipment, reagents, etc.	

Day 5	**Date: May 20, 2020**
Read detailed description about laminar flow hoods which provide aseptic work area during laboratory experiments and incubator for growth of cell lines.	

Day 6	**Date: May 21, 2020**
Learnt about water purification and media filtration devices, including their types and market producers.	

Week 2

Day 1	**Date: May 23, 2020**
Started learning more about different media filtration devices provides by LifeAssure.	
Day 2	**Date: May 24, 2020**
Revised what I have learnt so far.	
Day 3	**Date: May 25, 2020**
Made additions to the already collected data.	
Day 4	**Date: May 26, 2020**
Got more literature to read and started reading and marking recent instruments involved. I also started actively looking out for the area of research.	
Day 5	**Date: May 27, 2020**
Found information related to the most common and important instruments involved in laboratory: automated cell counters and storage tanks- refrigerators, freezer and cryogenic storage.	

Day 6	**Date: May 28, 2020**
Collected data regarding water baths, their types, etc. and imaging systems involved in visualizing cell lines.	

Week 3

Day 1	**Date: May 30, 2020**
Studied advantages and applications of imaging systems in cell lines.	
Day 2	**Date: May 31, 2020**
Collected more information regarding how to use these instruments efficiently and carefully. Read precautions related to these instruments and how to prevent contamination at all costs.	
Day 3	**Date: June 01, 2020**
Started studying about electroporation instruments used in cell culture laboratories to study the basics of transgenics.	
Day 4	**Date: June 02, 2020**
Recent advances in electroporation devices such as Neon Transfection system for cell suitability was studied.	
Day 5	**Date: June 03, 2020**
Types of aspiration pump including peristaltic and vacuum were studied.	

Day 6	Date: June 04, 2020
Glassware and plasticware as utilized in culture laboratory, such as flasks, pipettes, etc. were studied. Holding capacity of different volumes of flasks was learnt.	

Week 4

Day 1	Date: June 06, 2020
The technique of flow cytometry was studied to monitor hybridoma cell cultures, changes in DNA, RNA, etc. during the growth cell culture.	
Day 2	**Date: June 07, 2020**
Revised what I have learnt so far and made additions to the already collected data.	
Day 3	**Date: June 08, 2020**
Started collecting information on Alzheimer's Disease.	
Day 4	**Date: June 09, 2020**
Learnt about the origin and associated symptoms of Alzheimer's disease.	
Day 5	**Date: June 10, 2020**
Got acquainted with diagnostic techniques of AD including testing equalization, CT Scan, and identifying affected genes.	
Day 6	**Date: June 11, 2020**

Causes and factors that increase the risk of acquiring AD were studied and understood.
Week 5
Day 1 | **Date: June 13, 2020**
Neuroimaging and genetic biomarkers involved in diagnosis of AD were studied.
Day 2 | **Date: June 14, 2020**
Got acquainted with cerebrospinal fluid, peripheral fluid-based and cell-based biomarkers for AD diagnosis.
Day 3 | **Date: June 15, 2020**
Acclimated with the technique of trypsinization. Its methodology was learnt.
Day 4 | **Date: June 16, 2020**
Learnt aseptic techniques used in laboratory for a carrying out the experiment without any contamination.
Day 5 | **Date: June 17, 2020**
Collected information on successful passaging of cells. Learnt about live cell density, etc. required for sub-culturing.
Day 6 | **Date: June 18, 2020**
Got acquainted with culture plating and preparation techniques.

Week 6

Day 1	Date: June 20, 2020
Structure of hemocytometer was acclimated and procedure of counting cells was learnt.	

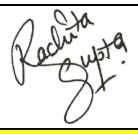
Day 2	Date: June 21, 2020
Ways of preventing contamination while performing laboratory work were understood.	

Day 3	Date: June 22, 2020
Working of FBS, DMSO and isopropanol were learnt in order to understand cryopreservation. Procedure and precaution while cryopreserving the cells were acclimated.	

Day 4	Date: June 23, 2020
Procedure of thawing of cells was learnt.	

Day 5	Date: June 24, 2020
Got acquainted with sub-culturing of cells.	

Day 6	Date: June 25, 2020
Revised what was done so far and gathered additional data related to animal cell culture techniques.	

July 27, 2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Vitasta Jalali	**Roll No.**	171819
Company Name		Jaypee university of information and technology	
Training Supervisor Name		Dr. Sudhir Kumar	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:18/05/2020**

On the first day of the training, my mentor and I had a discussion on the topic of training. First sir told to revise long preservation techniques of fungus.

Day 2	**Date:19/05/2020**

Then we decided our topic that was ATCC. I was asked to gather basic information about it that what is ATCC and its work on basic level.

Day 3	**Date:20/05/2020**

I read more about ATCC i.e. kind of preservation done in that and how it is done.

Day 4	**Date:21/05/2020**

Then we read about some qualifications which are required in ATCC.

Day 5	**Date:22/05/2020**

Then categories of qualification in which qualifications are categorized.

Day 6	***Date:23/05/2020***
Exploring of ATCC website a little more.	

Week 2

Day 1	***Date:25/05/2020***
Then I read about the ordering steps by which a culture is ordered from the ATCC website.	
Day 2	***Date:26/05/2020***
There focusing area that on what that website focuses while preserving the cultures.	
Day 3	***Date:27/05/2020***
Then I got know about the collection of cultures there which were very large in number.	
Day 4	***Date:28/05/2020***
Different type of cultures preserved in it and their number.	
Day 5	***Date:29/05/2020***
Requirements of people for handling a particular type of culture in ATCC.	

Day 6	***Date:30/05/2020***
Then discussed with my mentor after reading literature , then got more literature more topics to study.	

Week 3

Day 1	***Date:1/06/2020***
About working of ATCC read little information.	
Day 2	***Date:2/06/2020***
Begin with an ATCC bacterial strain.	
Day 3	***Date:3/06/2020***
Read about item sheet in which information about strain is written and sent.	
Day 4	***Date:4/06/2020***
About classification changes.	
Day 5	***Date:5/06/2020***
Then got to know the planning and preparation of medium for the strain.	

Day 6	***Date:6/06/2020***
How to open a glass ampoule.	

Week 4

Day 1	***Date:8/06/2020***
Then read about opening double-vial preparations and opening single-vial preparations.	

Day 2	***Date:9/06/2020***
Then read about preserving bacterial cultures in frozen state.	

Day 3	***Date:10/06/2020***
Then we read about the fungal long-term preservation techniques.	

Day 4	***Date:11/06/2020***
Continued it as many techniques were there to learn. I read cryopreservation technique in which 2 strategies were there that are slant culture and slide cut culture.	

Day 5	***Date:12/06/2020***
Read about lyophilization.	

Day 6	***Date:13/06/2020***

Lyophilization have few stages in which it occurs read about that.
Week 5
Day 1 ***Date:15/06/2020***
About next technique paraffin strategy and safeguarding in distilled water.
Day 2 ***Date:16/06/2020***
More techniques i.e. protection on paper and agar incline societies.
Day 3 ***Date:17/06/2020***
Learned about how naming of fungi is done.
Day 4 ***Date:18/06/2020***
I also learned about bacterial preservation techniques.
Day 5 ***Date:19/06/2020***
Compared fungal preservation techniques and bacterial preservation techniques learned some difference between them.
Day 6 ***Date:20/06/2020***

Read more about them discussed with my mentor got to know about them that what is difference and much more.

Week 6

Day 1	***Date:22/06/2020***
Looked over all the topics being studied, revised them.	

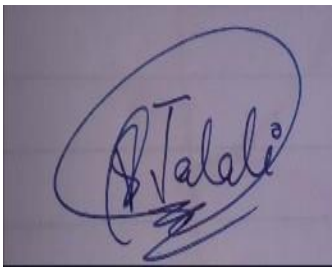
Day 2	***Date:23/06/2020***
The notes which were made in whole 5 weeks I started compiling it in a proper manner.	

Day 3	***Date:24/06/2020***
Completed the first draft of the report and sent it for the first review.	

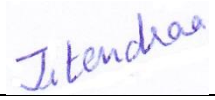
Day 4	***Date:25/06/2020***
Did the corrections suggested and questions which were supposed to answer and mention in my report.	

Day 5	***Date:26/06/2020***
Summarized the report in correct format.	

Day 6	***Date:27/06/2020***
Completed the final draft of the report and submitted it to my mentor Dr. Sudhir Syal	

21/07/2020	
Date	***Student Signature***

Industrial Training Diary & Report

Student Name	**Naveeta Karar**	**Roll No.**	**171820**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr Jitendraa Vashistt**	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		30/06/2020	

Week 1

Day 1	**Date:** 18/05/2020
On the first day of the training, my mentor and I had a discussion about Proteomics technology and Benefits of proteomics. started reading about the Introduction of proteomic technology.	
Day 2	**Date:** 19/05/2020
Started reading about what is proteomic, various applications of proteomics and what is the use of proteomics.	
Day 3	**Date:** 20/05/2020
Started reading about structural levels of proteins	
Day 4	**Date:** 21/05/2020
Read about understanding the proteomics allows for characterization of proteins, and understanding of protein interactions.	
Day 5	**Date:** 22/05/2020
Read more about the branches of proteomics.	

Day 6	**Date:** 23/05/2020
Read more about the techniques used in proteomics and various applications of proteomics	

Week 2	
Day 1	**Date:** 25/05/2020
Started reading about the factors that affect the proteome of a cell	
Day 2	**Date:** 26/05/2020
Read about why proteomic is important, and used in large scale study of proteins with many functions	
Day 3	**Date:** 27/05/2020
Why proteomic is dynamic and much more complex than genome	
Day 4	**Date:** 28/05/2020
Read more about the identifications and functions of a protein	
Day 5	**Date:** 29/05/2020
Then read about methods utilise in proteomics	

Day 6	**Date:** 30/05/2020
Got more information of proteins and various applications.	
Week 3	
Day 1	**Date:** 01/06/2020
Read about advantages of study of proteomics and why proteomics	
Day 2	**Date:** 02/06/2020
Read about what is the purpose of doing gel electrophoresis	

Day 3	**Date:** 03/06/2020
Read about protein separation by SDS-PAGE	
Day 4	**Date:** 04/06/2020
Read importance of proteins and various applications	
Day 5	**Date:** 05/06/2020
Read about functionality of proteomics	

Day 6	**Date:** 06/06/2020
Read about gel electrophoresis, mass spectrometry of proteins and peptides	

Week 4

Day 1	**Date:** 08/06/2020
Read about describes the operating principles as well as the applications of these instruments.	
Day 2	**Date:** 09/06/2020
Then proteomics research, basic research and applied research	
Day 3	**Date:** 10/06/2020
Read applications and most common used stains.	
Day 4	**Date:** 11/06/2020
Read more about Identify all the genes that are turned on in that particular cell.	
Day 5	**Date:** 12/06/2020
Sample preparation and labelling read about it.	
Day 6	**Date:** 13/06/2020

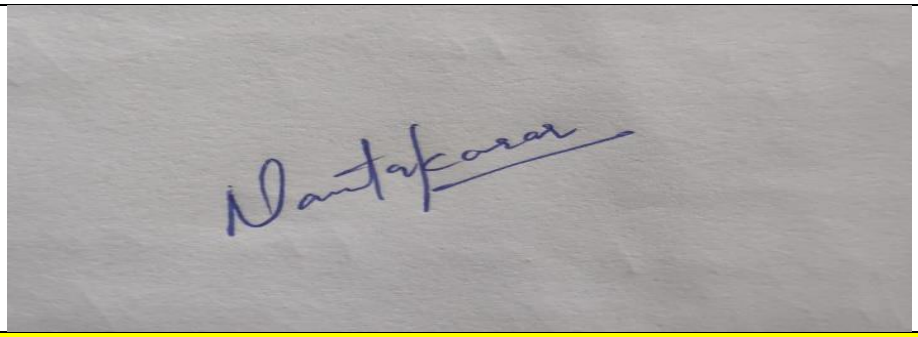
Then again read applications of proteomic technology.

Week 5

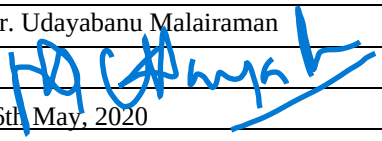
Day 1	Date: 15/06/2020
Read about what are the goals of proteomic technology.	
Day 2	**Date:** 16/06/2020
Then more read about why is the study of proteomics important.	
Day 3	**Date:** 17/06/2020
Read about the functionality of the proteomics	
Day 4	**Date:** 18/06/2020
Read the protein identification techniques and usage of these techniques	
Day 5	**Date:** 19/06/2020
Read about physical properties.	
Day 6	**Date:** 20/06/2020
Then flow chart for designing a proteomic Experiment	

Week 6

Day 1	Date: 22/06/2020
This week was for the compilation of all Done the work	

Day 2	**Date:** 23/06/2020
Started working on the report to be submitted at the end of the training.	
Day 3	**Date:** 24/06/2020
Completed the first draft of the report.	
Day 4	**Date:** 25/06/2020
Did all the corrections suggested in the report.	
Day 5	**Date:** 26/06/2020
Put the report in the correct format and other added required references in it.	
Day 6	**Date:** 27/06/2020
Then completed the final draft of the report and submitted it to Dr Jitendraa Vashistt.	
27/06/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Jigyasa	**Roll No.**	171821
Company Name	Jaypee University Of Information Technology		
Training Supervisor Name	Dr. Udayabanu Malairaman		
Training Supervisor Signature			
Internship Start Date	16th May, 2020		
Internship End Date	26th June, 2020		

Week 1

Day 1	**Date:** 16th May, 2020

On the first day of training, my mentor and I had a discussion on the area of training. We decided it to Animal Cell Culture.

Day 2	**Date:** 18th May, 2020

I was assigned to find some relevant literature and read about it. I started reading about the basics of Animal Cell Culture.

Day 3	**Date:** 19th May 2020

Got more literature to read and started noting down the laboratory designs and layouts, and various technologies.

Day 4	**Date:** 20th May 2020

Got more topics of research in this field. I also started actively looking out for more literature,

Day 5	**Date:** 21st May 2020

I found out more about the new and upcoming topics in Animal Cell culture. These include in-vitro propagation and cultivation techniques.

Day 6	**Date:** 22nd May 2020
Read more about the topics provided to have a better insight of what Animal Tissue culture can be used for.	

Week 2

Day 1	**Date:** 23rd May 2020
I have started searching about different types of tissue culture and started reading about them.	
Day 2	**Date:** 25th May 2020
Read about the instrumentation needed for Animal Tissue Culture.	
Day 3	**Date:** 26th May 2020
Understood different instruments and how are they used.	
Day 4	**Date:** 27th May 2020
Got more literature. Decided to read about them every day and also find out details and uses of each of them.	
Day 5	**Date:** 28th May 2020
I have made a list of different equipments and characterized them.	

Day 6	**Date:** 29th May 2020
I have gained insights about different areas- preparation, washing and cleaning, and sterilization and characterized instruments on the basis of areas they are used in.	

Week 3

Day 1	**Date:** 30th May 2020
Read about Laminar Flow Hood and Inverted Microscope and also explored different literatures for their uses.	
Day 2	**Date:** 1st June 2020
Read about various other instruments- Hemocytometer slide, Cell counter, refrigerator, periplasmic pump, centrifuge and incubator.	
Day 3	**Date:** 2nd June 2020
Read about the various instruments and other specific things needed in preparation area like water purifier, weighing balance, pH meter, conductivity meter and osmometer.	
Day 4	**Date:** 3rd June 2020
Got Literature to read about hot room which is used for incubation of large number of stirrer cultures. Shelves and trolleys should also be there for sharing and transporting glassware.	
Day 5	**Date:** 4th June 2020
Read about walk-in-cold room or large refrigerator which is needed for bulk long term storage of media and nutrients.	

Day 6	**Date:** 5th June 2020
Read about different types of sterilization and the equipments used for them.	

Week 4

Day 1	**Date:** 6th June 2020
I have read about different cell culture media and uses.	
Day 2	**Date:** 8th June 2020
Got more literature on cell culture media and understood about the different components used in these media.	
Day 3	**Date:** 9th June 2020
I have started reading about how we can use cell culture techniques in detecting diseases.	
Day 4	**Date:** 10th June 2020
Got more literature on various diseases but as my discussion with the guide finally decided to read and understand Type 2 Diabetes Mellitus.	
Day 5	**Date:** 11th June 2020
Started reading about various factors determining Type Diabetes Mellitus.	
Day 6	**Date:** 12th June 2020

I have read about various metabolites that found to be positively related to Type 2 Diabetes Mellitus and also read about various biomarkers for the disease.

Week 5

Day 1	**Date:** 13th June 2020

I have started exploring about Animal Cell Culture procedure.

Day 2	**Date:** 15th June 2020

Got literature from the guide regarding various techniques of Animal Cell culture and their procedures.

Day 3	**Date:** 16th June 2020

I have started reading about the functioning and uses of Hemocytometer (Cell counting slide).

Day 4	**Date:** 17th June 2020

I have started studying about various aseptic techniques used while cell culture experiments as this is very essential.

Day 5	**Date:** 18th June 2020

I have started studying about primary culturing and trypsinization.

Day 6	**Date:** 19th June 2020

I have started reading about maintaining cell lines and sub-culturing and have also gained insights on cryopreservation.

Week 6

Day 1	**Date:** 20th June 2020

This week was for compilation of all the work done till now and started compiling points for the same.

Day 2	**Date:** 22nd June 2020

Started working on the report to be submitted at the end of the training.

Day 3	**Date:** 23rd June 2020

Completed the first draft of the report. Sent it for first review.

Day 4	**Date:** 24th June 2020

Did all the corrections suggested in the report.

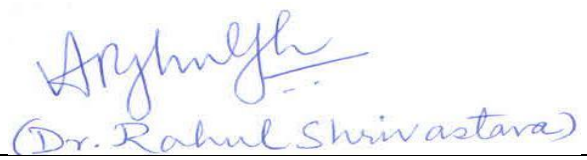
Day 5	**Date:** 25th June 2020

Put the report in the correct format added the required references in it.

Day 6	**Date:** 26th June 2020

Completed the final draft of the report and submitted to Dr. Udayabanu Malairaman.	
29th July, 2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Kirti Arora**	**Roll No.**	**171823**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name & Signature		 (Dr. Rahul Shrivastava)	
Internship Start Date		15/05/2020	
Internship End Date		30/06/2020	

Week 1

Day 1	**Date:** 15/05/2020
On the very first day of the training, my mentor and I had a discussion on the area of training. We decided it to be innovation so far made in COVID-19. After this, I was assigned the job to find some relevant literature and read about it.	
Day 2	**Date:** 16/05/2020
I started reading about its origin and evolution of Pathogenic coronavirus. My main aim was to find answers to what Coronavirus is and how it originates as a research field in coming time.	
Day 3	**Date:** 18/05/2020
Got more literature to read and started reading and Find out its keys to Diagnosis, treatment and Prevention of SARS. I also started actively looking out for my area of interest.	
Day 4	**Date:** 19/05/2020
Started reading about different areas in Covid-19. Asked my mentor to recommend some good literature on different topics.	
Day 5	**Date:** 20/05/2020
Read about the papers provided by the mentor to find out more about the innovations and research in COVID-19. These include Different Modalities to fight the virus which includes 6 feet social distancing or more to reduce aerosols based spread from infected person, clean surface agents with antiviral activity, PPE, Drug development for specific target of virus, vaccine development, enhancing immunity with nutraceuticals and food, exploring alternative Medicine.	

Day 6	**Date:** 21/05/2020
Read more about the topics provided to have a better insight of what is my area of interest.	

Week 2

Day 1	**Date:** 22/05/2020
Found out the topic of Innovations made so far in COVID-19 Vaccine most interesting out of all the topics. Started reading more about it.	
Day 2	**Date:** 23/052020
Informed my mentor about the same. Got more literature to read on the topic of What is the process of vaccine development.	
Day 3	**Date:** 25/05/2020
Read about the General Process of vaccine development and read literature about the same in Clinical Vaccine development by Seunghoon Han.	
Day 4	**Date:** 26/05/2020
Got an overview of different stages of Vaccine Development, Vaccine testing and Approval Process in another Review Literature by Centres for disease Control and Prevention.	
Day 5	**Date:** 27/05/2020
Got to know about the Anatomy of COVID-19 virus which is important to break it down and stop its entering into the cells of Host.	

Day 6	**Date:** 28/05/2020
Till the second week I came to know about its mode of transmission, General process of Vaccine development.	

Week 3

Day 1	**Date:** 29/05/2020

Got to know about the Candidate Vaccine in clinical evaluation, First vaccine that reached was University of Oxford (WHO) it started its trial in the month of May.

Day 2	**Date:** 30/05/2020
Got more information and details about the different Candidate Vaccine such as Cansino Biological Inc. , Moderna and many more.	
Day 3	**Date:** 01/06/2020
Read about the platform used in Oxford Vaccine, Moderna & Wuhan Institute of Biological Products.	
Day 4	**Date:** 02/06/2020
Gathered information and literature about the different types of Vaccine using in COVID-19 case which includes inactivated, live-attenuated subunit, conjugate with Adjuvant.	
Day 5	**Date:** 03/06/2020
Read about the Novavax in research article stated that it used an adjuvanted with matrix M to enhance the immune response.	

Day 6	**Date:** 04/06/2020
BioTech/Fosun/Pharma/Pfizer uses an innovative gene-based technology known as mRNA. Read about it in more detail.	

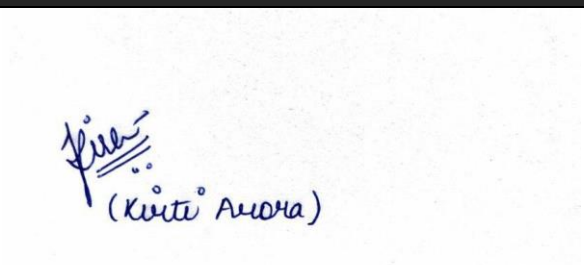
Week 4

Day 1	**Date:** 05/06/2020
Read about Monoclonal Antibodies used as a vaccine by Utrecht University. Understood about it.	
Day 2	**Date:** 06/06/2020
Then another one vaccine candidate used as Blood Plasma transfers (Convalescent Plasma). Went through it and got acquainted with the process in detail.	
Day 3	**Date:** 08/06/2020

Thoroughly study the Platform used for treatment of every vaccine candidates.
Day 4 | **Date:** 09/06/2020
Started reading about the vaccine candidate in Newspaper to get an overview of the vaccine candidate.
Day 5 | **Date:** 10/06/2020
Read about the new technology Stem cells by Abu Dhabi Stem Cell Centre used as a vaccine.
Day 6 | **Date:** 11/06/2020

Read about the candidate and type of candidate vaccine draft by World Health Organization.
Week 5
Day 1 | **Date:** 12/06/2020
Sinovac entered the phase ½ trial, platform used inactivated.
Day 2 | **Date:** 13/06/2020
Platform 1. Non-Replicating Viral Vector used by University of Oxford, Cansino Biological Inc., Gamaleya Research Institute 2. Inactivated- Wuhan Institute of Biological Products, Beijing Institute of Biological Products, Sinovac, and Institute of Medical Biology.
Day 3 | **Date:** 15/06/2020
Read about the apps helping social distancing and avoid close contact with infected persons by different countries such as Aarogya Setu App, Crowdless, Sodar and many more.
Day 4 | **Date:** 16/06/2020
Another Candidate vaccine reached the human trial phase- Inovio.
Day 5 | **Date:** 17/06/2020
On the regular basis checked the draft by the WHO. 18 candidate vaccines in clinical evaluation as on 17th June by World Health Organization.
Day 6 | **Date:** 18/06/2020

Another Candidate Vaccine by ICMR & Bharat Biotech Limited Covaxin had reached the human trial phase 1 and used inactivated strain of COVID-19.

Week 6	
Day 1	**Date:** 19/06/2020
This week was for the compilation of all the work done till now and started compiling points for the same.	
Day 2	**Date:** 24/06/2020
Started working on the report to be submitted at the end of the training.	
Day 3	**Date:** 25/06/2020
Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:** 27/06/2020
Attended Webinar by Dr. B.R. Ambedkar National Institute of Technology, Jalandhar on Innovations against COVID-19; start-up opportunities for medical informatics, biopharma and biomedical products and some content of Webinar in Report also. Did all the corrections suggested in the report.	
Day 5	**Date:** 28/06/2020
Put the report in the correct format as per the mentor guidelines and added the required references in it.	
Day 6	**Date:** 02/06/2020
Completed the final draft of the report and submitted it to Dr Rahul Shrivastava.	
25/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Ayush Tyagi	**Roll No.**	**171824**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr. Harish Changotra**	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020
On the first day of the training, my mentor and I had a discussion on the topic of training. We decided it to be Cancer and SNPs relation. After this, I was assigned the job to find some relevant literature and read about it.	
Day 2	**Date:** 19/05/2020
I started reading about Cancer and its various factors and mechanisms. My main aim was to find exact relation between Cancer and single nucleotide polymorphism.	
Day 3	**Date:** 20/05/2020
Got more literature to read and started reading and marking recent topics of research in this field. I also started actively looking out for the area of research.	
Day 4	**Date:** 21/05/2020
Started reading about different areas in Cancer and snps. Also, read about the different methods of DNA isolation.	
Day 5	**Date:** 22/05/2020
Read about the papers provided by the mentor to find out more about snps, cancer and DNA isolation. In these DNA isolation Incyte's two different methods, stated as organic and inorganic.	

Day 6	**Date:** 23/05/2020

Read about the inorganic method of DNA isolation, and their relation with cancer cells and snps.

	Week 2
Day 1	**Date:** 25/05/2020
Found some relation between snps and genotyping involving the diagnosis of the most prominent disease of all time, Cancer.	
Day 2	**Date:** 26/052020
Informed my mentor about the same. Got more literature to read on the topic of genotyping of snps.	
Day 3	**Date:** 27/05/2020
Read about pcr (polymerase chain reaction) and its importance in various biological field.	
Day 4	**Date:** 28/05/2020
Understood what comprises of PCR and how are they used to diagnose other diseases or genetic changes.	
Day 5	**Date:** 29/05/2020
Got literature about different types of pcr. Decided to read about one every day and also find out details and uses of each one of them.	

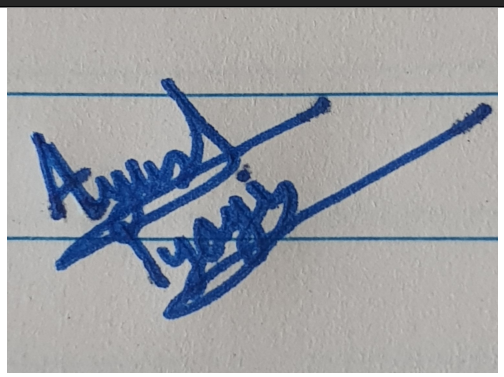
Day 6	**Date:** 30/05/2020
Read the introduction about the 3rd type of pcr which was, artificial restriction fragment length polymorphism (T-ARMS) PCR.	
	Week 3
Day 1	**Date:** 01/06/2020
Read about the details and chemicals related with the stated pcr method.	
Day 2	**Date:** 02/06/2020

Got more information about the applications and the drawbacks related with T-ARMS PCR.	
Day 3	**Date:** 03/06/2020
Read about the comparisons related with the different types of pcr and their mechanism.	
Day 4	**Date:** 04/06/2020
Gathered information and literature about the genotyping of single nucleotide polymorphism by T-ARMS pcr method.	
Day 5	**Date:** 05/06/2020
Read the introduction and its mechanism.	

Day 6	**Date:** 06/06/2020
. Read some more research paper regarding genotyping through T-ARMS pcr method.	
	Week 4
Day 1	**Date:** 08/06/2020
Studied about this method in detail, took help of my PhD scholar as this method was giving me a hard time.	
Day 2	**Date:** 09/06/2020
Studied whatever paper she has listed for the respected topic.	
Day 3	**Date:** 10/06/2020
Done comparison of the papers with T-ARMS pcr method.	
Day 4	**Date:** 11/06/2020

Started reading about what this method is capable of doing, and how it's done.
Day 5 | **Date:** 12/06/2020
There are different kinds of arrangements done for the genotyping of snps for diagnosis of various diseases.
Day 6 | **Date:** 13/06/2020

Found about site-directed mutagenesis or, what we can also say as mutagenic primers which are used to create a restriction enzyme site and amplify the desired DNA fragment in this particular method.
Week 5
Day 1 | **Date:** 15/06/2020
The first arrangement which was site directed mutagenesis helps to create an artificial restriction fragment length polymorphism for almost all naturally occurring DNA polymorphism.
Day 2 | **Date:** 16/06/2020
Next is its mechanism, chemicals used, drawbacks, etc. has been studied for gathering further information about it.
Day 3 | **Date:** 17/06/2020
Then how the process of amplification, and genotyping is done through T-ARMS PCR method has been studied.
Day 4 | **Date:** 18/06/2020
Its importance has been kept in mind... One of which include how this method can digest the sequence containing snap if it is recognized by the created restriction enzyme/site with the help of mutagenic primers.
Day 5- Another one is how it optimizes pcr reaction.
Day 6 | **Date:** 20/06/2020
PCR amplification followed by agarose gel electrophoresis to check whether the desired region is amplified or not. Followed by restriction digestion and then gel electrophoresis of digested products to check the genotypes.

	Week 6
Day 1	**Date:** 22/06/2020
This week was for the compilation of all the work done till now and started compiling points for the same.	
Day 2	**Date:** 23/06/2020
Started working on the report to be submitted at the end of the training.	
Day 3	**Date:** 24/06/2020
Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:** 25/06/2020
Did all the corrections suggested in the report.	
Day 5	**Date:** 26/06/2020
Put the report in the correct format.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and submitted it to Dr Harish Changotra.	
21/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Neha Verma	**Roll No.**	171825
Company Name		Jaypee University of Information Technology	
Training Supervisor Name & Signature			
Internship Start Date		15/5/2020	
Internship End Date		30/6/2020	

Week 1

Day 1	**Date: 15/5/20**

On the first day of training my mentor and I had a discussion on the area of training. We decided it to be "How to write a review article."
After this, I was assigned the job to find some relevant literature and read about it.

Day 2	**Date: 16/5/20**

My main aim was review article compilation, summarization, and synthesize information available on it. Six steps to write a review article are-
1) Choose a topic
If you are trying to select a topic to write about be sure you select a topic which matches your assignment.

Day 3	**Date: 18/5/20**

The topic you choose should allow you to fulfill all the required elements of an assignment and the topic chosen should be something in which you are interested in learning.It does not need to be a topic of which you are already well informed.

Day 4	**Date: 19/5/20**

The topic selected should be something for which yo can find credible source of information which shape and support your theories, arguments or conclusion. And narrow the topic down to a specific focus of an investigation.

Day 5	**Date: 20/5/20**

Day 6	**Date: 21/5/20**

Refer to various resources for gathering information such as newspaper articles, journals, publications, books and online websites.

Week 2

Day 1	**Date: 22/5/20**

2) Create your thesis and organize your notes A thesis statement clearly identifies the topic being discussed, includes the point discussed in the paper. Thesis statement is used to generate interest in your topic and encourage your audience to continue reading.
Personal opinion should be supported with facts and statistics otherwise you wold just be an opinionated person rather than a good writer.

Day 2	**Date: 25/5/20**
In order to make your writing interesting, you should develop a thesis statement that is arguable, not factual. Thesis should always be stated in your introduction usually at the end of the first paragraph.	
Day 3	**Date: 26/5/20**
Now you need to organize the information that you have collected from different sources. Divide your notes into three sections, notes on the right, keywords and questions on the left and conclusion at the bottom.	
Day 4	**Date: 27/5/20**
Create charts and tables which provides visual review for memorization of facts.Note anything that you do not understand by underlining and highlighting to remind you to ask the instructor later on.	
Day 5	**Date: 28/5/20**
Day 6	**Date: 29/5/20**
Make short notes and flashcards, organize important points and ideas.	
Review your article again after 24 hours to help fix new information to it and this will also help you to memorize the information.	

Week 3

Day 1	**Date: 1/6/20**
3) Make an outline and find more information An outline is a tool used to organize written ideas about a topic or thesis into a logical order. Writers uses outline in order to know which topic to cover in what order.	
Day 2	**Date: 2/6/20**
Creating an outline is really about structuring a paper. As you create an outline, think about what you are trying to explain in your paper and what format or structure allows you to do that in a clear and organized way.Be sure that whatever format you choose make sense for your paper.	
Day 3	**Date: 3/6/20**
Find information or content that support your points and ideas.You can refer to various resources, books, journals, newspaper articles, reports and websites too.	
Day 4	**Date: 4/6/20**
Some databases are topic specific , so look through various websites to get full knowledge for your topic.	
Day 5	**Date: 5/6/20**
Day 6	**Date: 8/6/20**
Finally, don't ignore information. You can find different articles that have different views on same topic but when you dig deeper into them it is clear that they are not. Just because you find one article stating that it is true does not necessarily mean that it is proven fact.	

Be sure to evaluate the website you use. Consider limiting your search to web page addresses or urls that include .gov or .edu . Search using Google, Binge or similar search engine.

Week 4

Day 1	Date: 9/6/20
4) Writing introduction and body of the paper. Depending on the style of the paper the introduction will need to reflect the proper tone or define the purpose of the topic that is your paper narrative, expository, persuasive, descriptive and creative?	
Day 2	**Date: 10/6/20**
Introduce what the topic of paper will be and why is it important. The development of your paper can make or break your paper. However, you can make the process easier by choosing a topic that you are already familiar with or excites you to learn more about.	
Day 3	**Date: 11/6/20**
Introduction should not start with a definition and it should not provide a lot of background information. It should not be more than one paragraph longer and should be simple not confusing.	
Day 4	**Date: 12/6/20**
Now since you have collected a lot of information and already read a lot about them, so instead of writing from them you should now write in your own language and try to define your ideas in your ways instead of copying sentences and facts from others. Working from your own ideas will help you to avoid plagiarism.	
Day 5	**Date: 13/6/20**
If you quot something from word to word, you need to cite your source . use quotation marks and site the source of the quote. You'll also need to give more information about it in your reference section.	
Day 6	**Date: 15/6/20**

If something is a common fact than you don't need to mention where the idea comes from eg "Bill Gates is a billionaire."This is a common fact and you can find it in various trustworthy sources.

Week 5

Day 1	Date: 16/6/20
5) Write conclusion and set your rough draft aside for a while. Conclusion is the final paragraph of your paper. A conclusion rounds out a paper and signals that the discussion has been completed.	
Day 2	**Date: 17/6/20**
A conclusion should not contain any new idea, it should not offer nay new example and also it should not reach any new conclusion.	
Day 3	**Date: 18/6/20**
A conclusion wrap up all the points that you have made in the research paper.A good conclusion shows that you have done what you have set out to do- and prove your thesis.It also reveals the implication and significance of the information in the paper.	
Day 4	**Date: 19/6/20**

Setting your rough draft aside for a while means that keeping your paper that is completed but not polished. That is the paper you have written has grammatical errors and other mistakes that need to be checked so far.

Day 5	Date: 20/6/20

Submit your paper to the Grammarly , an automated proofreading service. This will remove all your typing errors or the grammatical orders.

Day 6	Date: 22/6/20

Week 6

Day 1	Date:23/6/20

6) Edit or revise your paper and submit it

When you revise or edit your paper focus on the ideas and the organization as well as grammar, spelling and punctuation.

Day 2	Date:25/6/20

Check all the necessary details of the research paper and ensure that all sources are cited properly to avoid any plagiarism. Include all of the items cited into reference page.

Day 3	Date:26/6/20

Ensure that your intentions and all the points are clear in the essay. All the arguments should be well supported and well reasoned.

Day 4	Date:27/6/20

Ask your instructor or teacher for any help in the concepts which you have still not understood and do not feel any hesitation.

Day 5	Date:28/6/20

Submit your assignment before date and do corrections if any suggested by your instructor or mentor.

Day 6	Date:30/6/20

Completed the report and submitted to Dr Rahul Shrivastava.

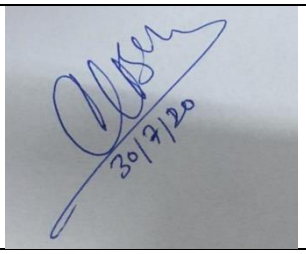
Submitted assignment on 29/6/2020



Neha Verma(171825)

Submit your paper to the writing lab an online tutoring centre that provides you with the feedback of your writing skills which further allows you to create a better paper and become a stronger writer.

Industrial Training Diary & Report

Student Name	**YUKTI**	**Roll No.**	**171826**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr. Hemant Sood**	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date: 18/05/2020**

On the very first day of training, I and my supervisor had a discussion on the area and topic of our interest for training. We decided it to be related to virus elimination and Micropropagation of some commercial plant. So, I was assigned the job to find the plant of my interest and do research on it.

Day 2	**Date: 19/05/2020**

I started with basics by learning about different techniques of Micropropagation and how can this be used for virus elimination. But I was still confused regarding the plant for research.

Day 3	**Date: 20/05/2020**

Discussed about my topic and plants on which I could continue my research with my supervisor. We decided the plant to be potato. My topic for training was " Production of Disease-free potatoes through Mericloning".

Day 4	**Date: 21/05/2020**

Started searching for relevant literature and online platforms to learn the techniques required for my research.

Day 5	**Date: 22/05/2020**

First of all, I searched and read the research papers which taught me about different disease-causing organisms in potato and how to detect and identify them using various techniques.

Day 6	**Date: 23/05/2020**
Had a talk with my supervisor regarding my progress and research for the training. She guided me so that I could do better and helped me understand the topics that I was not able to understand.	
Week 2	
Day 1	**Date: 25/05/2020**
Read more literature and continued to learn about the in vitro techniques to grow disease-free potato tubers.	
Day 2	**Date: 26/05/2020**
Meristem culture/ Mericloning is the technique which could give best results for disease-free potato tubers.	
Day 3	**Date: 27/05/2020**
Discussed with my supervisor and continued my research.	
Day 4	**Date: 28/05/2020**
Understood the technique of Mericloning.	
Day 5	**Date: 29/05/2020**

Took practical knowledge about Mericloning using virtual labs.

Day 6	**Date: 30/05/2020**
Informed my mentor about what I had learned and she corrected my mistakes.	
Week 3	
Day 1	**Date: 01/06/2020**
Researched more techniques which could enhance the productivity of disease-free potatoes.	
Day 2	**Date: 02/06/2020**
Found out that cryotherapy and chemotherapy can also be used along with meristem culturing for high yield.	
Day 3	**Date: 03/06/2020**
Discussion with the mentor.	
Day 4	**Date: 04/06/2020**
Read about cryotherapy and its pros and cons while using it with meristem culture.	
Day 5	**Date: 05/06/2020**

Read about chemotherapy and chemicals that can be used with meristem culture.

Day 6	Date: 06/06/2020
My knowledge and learning was corrected by my mentor and helped me in better understanding of my topic.	

Week 4

Day 1	Date: 08/06/2020
More literature was read and found out more ways to increase yield and production.	
Day 2	**Date: 09/06/2020**
Research helped me find more ways such as thermotherapy and electrotherapy for virus elimination.	
Day 3	**Date: 10/06/2020**
My mentor guided me to work in the right direction.	
Day 4	**Date: 11/06/2020**
Read about thermotherapy and learnt the technique in association with meristem culture.	
Day 5	**Date: 12/06/2020**

Read about electrotherapy and ways to use this technique in my training.	
Day 6	**Date: 13/06/2020**

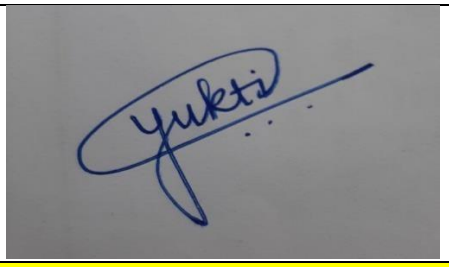
Discussed about these techniques with my mentor.
Week 5

Day 1	**Date: 15/06/2020**
Found about post-eradication techniques for production of disease-free of potato tubers.	
Day 2	**Date: 16/06/2020**
Learnt about Real-Time PCR as a post-eradication method.	
Day 3	**Date: 17/06/2020**
Discussed Real- Time PCR with my supervisor.	
Day 4	**Date: 18/06/2020**
Learnt about DAS-Elisa.	
Day 5	**Date: 19/06/2020**
Read about the technique of DAS-ELISA and how to use it in production of disease-free potatoes through Mericloning.	

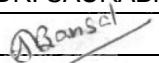
Day 6	Date: 20/06/2020
Discussion with mentor regarding the training and she asked to make report for Summer training.	

Week 6	
Day 1	**Date: 22/06/2020**
This week was for compilation of all the work done till now. Started compiling points for the same.	
Day 2	**Date: 23/06/2020**
Started to work for the report to be submitted.	
Day 3	**Date: 24/06/2020**
Completed first draft of report and sent it for review to my supervisor.	
Day 4	**Date: 25/06/2020**
Did corrections in the report that were suggested.	
Day 5	**Date: 26/06/2020**
Compiled the report and added required references.	
Day 6	**Date:27/06/2020**

Completed final draft of report and submitted it to my supervisor Dr. Hemant Sood.

25/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	YASHKIRTI GARG	**Roll No.**	171827
Company Name	JAYPEE UNIVERSITY OF INFORMATION AND TECHNOLOGY		
Training Supervisor Name	DR. SAURABH BANSAL		
Training Supervisor Signature			
Internship Start Date	15 May 2020		
Internship End Date	30 June, 2020		

Week 1

Day 1	**Date: 15 may, 2020**
On the first day of training, my mentor and I had a discussion over the area of training. The topic of my preference was "protein purification techniques". After this I was assinged the enzyme named Arginase and all the further report was to made under this topic. I was asked to find all relevant literature on this enzyme.	

Day 2	**Date:16 may, 2020**
I started reading about the Arginase enzyme, its working in the living system and applications in the biological world. I read about its extraction from the microbes using conventional and recombinant technology.	

Day 3	**Date:17 May, 2020**
I read about its various uses in the biological systems and about various diseases related to its deficiency and over production in the human body.	

Day 4	Date:18 May, 2020
I got more literature related to the various methods that were employed in the extraction of Arginase from various sources like bacteria and yeasts along with the various assays that were used for the identification and checking the activity of arginase.	
Day 5	**Date:19 May, 2020**
I was asked to make a flow chart for better understanding of the purification techniques used in the extraction.	
Day 6	**Date:20 May, 2020**
I drew various flow charts explaining the process of Arginase purification from the very initial steps of bacteria culturing to cell homoginization taking it further to using various purification techniques like Gel Filtration Chromatography, Ion Exchnage Chromatography, Affinity Chromatography.	
Week 2	
Day 1	**Date:22May, 2020**
I was asked to write about the characteristics of the organisms that produced the Arginase enzyme. I collected the literarture and all relevant information about the bacteria and fungi that produce the Arginase enzyme the information consisted of the type of cell, its mophology, type of respiration associated with it, source of its extraction of the organism and its pathogenic nature etc.	
Day 2	**Date:23 May, 2020**

All the collected information was written down in the from of a table for easy access. The selected organisms were *Bacillus subtilis* and *Saccharomyces cerevisiae*	
Day 3	**Date:24 May, 2020**
Collected the data about the culture conditions of the above organisms. The conditions involved about the medium composition, temperature, pH, aeration, agitation speed, volume and about the harvest.	
Day 4	**Date:25 May, 2020**
Found the information about Gel Chromatography which is one of the most used technique in the extraction of proteins.	
Day 5	**Date:26 May, 2020**
Read about its working and principle, also studied about its procedure.	
Day 6	**Date:27 May, 2020**
Read about the applications and advantages of Gel Filtetration Chromatography.	

Week 3

Day 1	Date:29 May, 2020
I collected the litrature about Ion Exchange Chromatography.	

Day 2	Date:30 May, 2020
I read about its working and principle.	

Day 3	Date:31 May, 2020
I read about its procedure of working	

Day 4	Date:1 June, 2020
I read about the applications and advantages of the Ion Exchnage Chromatography technique.	

Day 5	Date:2 June, 2020
I collected the literature about Affinity Chromatography.	
Day 6	**Date:3 June, 2020**
I read about the working and the principle of Affinity Chromatography.	

Week 4

Day 1	Date:5 June, 2020
I read about the procedure used in the purification of Arginase from various sources.	
Day 2	**Date:6 June, 2020**
I read about the application and advantages of this Chromatographic method.	
Day 3	**Date:7 June, 2020**

I was told to collect the information about the Arginase enzyme activity, so I collected all the relevant information on the methods used for the assay of Arginase enzyme activity.

Day 4	Date:8 June, 2020

I got to know about the measurment of Ornithin values in the samples which were checked by using the qulitative and quantitaive techniques like the TLC and HPLC methods.

Day 5	Date:9 June, 2020

I read about the Radioisotopic Assay for the Arginase activity where an isotope of carbon was used for its radioactivity detection later after the reaction was completed using a liquid scintillating counter.

Day 6	Date:10 June, 2020

I read about the determination of Arginase activity by Ornithin-Ninhidrin reaction and its absorbance was later checked using a spectrophotometer.

Week 5

Day 1	Date:12 June, 2020

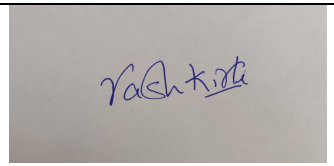
All the above information was compiled as a a flow chart to make it easy for understanding and data access.

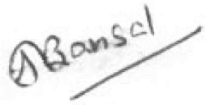
Day 2	**Date:13 June, 2020**
I was told to collect the information about various resins used in the column of various techniques.	
Day 3	**Date:14 June, 2020**
I studied about the application and advantages of Sephadex resin.	
Day 4	**Date:15 June, 2020**
I studied and collected information about the application and advantage of Sepharose resin	
Day 5	**Date:16 June, 2020**
I collected and studied the information about the application and advantage of Sephacryle resin.	

Day 6	Date:17 June, 2020
As the final stage of the training I was told to find about the trouble shooting processes used while using various purification techniques of Arginase enzymes.	

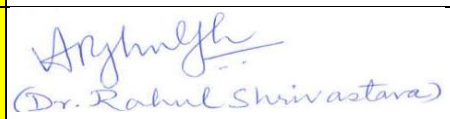
Week 6

Day 1	Date:19 June, 2020
I studied about the various trouble shooting methods used in the Gel Filtration, Ion xchange and Affinity Chromatography.	
Day 2	**Date:20 June, 2020**
A final report was asked to be prepared summarising all the work done during the training period	
Day 3	**Date:21 June, 2020**
I prepared an intial draft of the report.	
Day 4	**Date:22 June, 2020**

The initial draft was edited.	
Day 5	**Date:23 June, 2020**
A final draft with proper references was prepared and shown to my mentor. He suggested further addition of information and asked me to make certain changes.	
Day 6	**Date:24 June, 2020**
All the suggested changes were done and a final report was submitted to the mentor on the given date.	
27 June, 2020.	
Date	**Student Signature**



Industrial Training Diary & Report

Student Name	ISHITA	**Roll No.**	171828
Company Name	Jaypee University of Information Technology		
Training Supervisor Name and Signature	 (Dr. Rahul Shrivastava)		
Internship Start Date	15/5/2020		
Internship End Date	30/6/2020		

Week 1

Day 1	**Date:15/5/20**

At first day of training my mentor and I had discussion on the purpose of training. He apprised me about the steps to review article and told me to first what is important for our paper.

Day 2	**Date:16/5/20**

Summary of the steps they outline as well as a step-by-step method for writing a literature review.
1) decide area of research: Exploring topic that we are willing to work with for considerable amount of time.
To study the concept clearly I was starting reading about basic knowledge of literature and follow the steps what my mentor taught me.

Day 3	**Date:18/5/20**

Then my mentor told me to choose your interest topic and give me a rough and short write up about what is your interest regarding the training and chosen topic antibody engineering.

Day 4	**Date:19/5/20**

I started searching collective some knowledge and to develop the research topic, broaden my thinking and creativity. Considering an area which interests me and has high importance to profession. tart writing about the topic i.e antibody engineering which I have known of.

Day 5	**Date:20/5/20**

Purpose of the research has to be very clear. Fine tuning the topic by experimenting with key word; Search until satisfied with the retrieval results.

Day 6	**Date:21/5/20**

Checking if we have adequate resources and material to help writing the review. Exploring variety of resources: Journals, books, online information.

Week 2	
Day 1	Date:22/5/20
Step Two: Search for the literature: Learning about how keywords are so important in case of library databases. Brainstorming keywords related to our research questions.	
Day 2	Date:23/5/20
Conducting a comprehensive bibliographic search of books and articles in my area. Read the abstracts online and download and/or print those articles that pertain to your area of research.	
Day 3	Date:25/5/20
To find specify information, all narrower terms are collected. Having range of keywords is significant. Study about how antibodies formed in invitro or invivo conditions.	
Day 4	Date:26/5/20
Read about the introduction of antibodies and its uses and need in human body.	
Day 5	Date:27/5/20
Got literature about different types of techniques to produce antibodies. Decided to read about one every day and also find out details and uses of each one of them.	
Day 6	Date:28/5/20
Read the introduction about the first technique that are hybridoma technology that providing a reliable source of monoclonal antibodies (mAbs) of known specificity.	
Week 3	
Day 1	Date:29/5/20
Step 3 evaluation time Making sure that resources and information is authoritative, reliable, relevant and most useful in supporting the research.	
Day 2	Date:30/5/20
Start reading about how monoclonal antibodies made/synthesise and bind with the antigen. Study about antigen antibodies interaction	
Day 3	Date:1/6/20
After studying lots of information and paper I found the first human monoclonal antibody was engineered using phage display and choosing antigen-specific binders from blood lymphocyte libraries.	

Day 4	Date:2/6/20
Studying lot about monoclonal antibodies I was on the situation that engineered monoclonal antibodies needs specific binding affinity.	
Day 5	**Date:3/6/20**
Then I talked to my mentor for some doubts regarding why engineered monoclonal antibodies are capable of binding with high affinity and high specificity to molecular targets that are classically seen in diseased conditions, but this is absent in normal cells.	

Day 6	Date:4/6/20
Then studied engineered antibodies work using several known activities.	

Week 4

Day 1	Date:5/6/20
Step 4 analysis: Analyse the evaluated data and After evaluation of retrieved sources, exploring of what has been found and what is missing. Content collected needs to be analyzed. Breaking study into parts, understand each part, assessing strength of evidence, drawing conclusions.	
Day 2	**Date:6/6/20**
Critically reviewing each sources' methods, procedure, data validity. Considering each source approach towards the topic.	
Day 3	**Date:8/6/20**
Starts studying about different methods of antibody engineering one by one.	
Day 4	**Date:9/6/20**
Studied about recombinant monoclonal antibodies which involves repertoire cloning, CRISPR/Cas9, or phage display/yeast display technologies.	
Day 5	**Date:10/6/20**
1. Studied some other methods i.e. Chimeric antibodies/humanized antibodies where I studied about generations of antibodies.	

Day 6	Date:11/6/20

Exploring recombinant DNA, "chimeric" or "humanized" DNA through cell culture yielded part-mouse, part-human antibodies.

Week 5

Day 1	Date:12/6/20

Step 5 Synthesis:
Literature review should synthesize ideas with observations to create map of scholarly conversation about the topic. Also, mentioning gaps or areas of further research.

Day 2	Date:13/6/20

Start learning and finding application of antibodies engineering for the treatment of several diseases

Day 3	Date:15/6/20

Finding and researching more and more diagnostic tests which can detect diseases.
There were many different applications I found.

Day 4	Date:16/6/20

I started compiling all the various application and diagnostic method.

Day 5	Date:17/6/20

Studying about cancer treatment in which there are many monoclonal antibodies. The use of monoclonal antibodies for cancer treatment is very encouraging.

Day 6	Date:18/6/20

All applications including treatment of cancer, monoclonal antibodies were all compiled.

Week 6

Day 1	Date:19/6/20

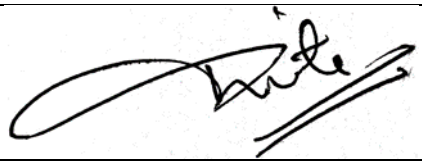
This week was for the compilation of all the work done till now and started compiling points for the same.

Step 6 Writing and Presenting:
Including thesis statement in the literature and writing the perceptions clearly. Demonstrating through investigation in relation to topic.

Day 2	Date:20/6/20

Started working on the report to be submitted at the end of the training.
Writing critical discussions, comparing opinions; relating our study to previous ones, showing gaps in research.
Compiling primary questions and subject areas involved.

Day 3	Date:22/6/20
Writing an introduction which gives quick idea of review article, such as central theme or organizational pattern. Scope, method, problem statement, thesis etc. to be written. Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:23/6/20**
Writing the final draft and making further corrections.	
Day 5	**Date:24/6/20**
Concluded the report. Wrote reference management and Endnote.	
Day 6	**Date:25/6/20**
Submitted the final draft after giving it a through reading.	

24/7/20	

Industrial Training Diary & Report

Student Name	KHUSHI MAHESHWARI	Roll No.	171829
Company Name		SANWARIA SWEETS PVT. LTD.	
Training Supervisor Name		MR. NAVDEEP SORYAN	
Training Supervisor Signature			
Internship Start Date		1st JUNE 2020	
Internship End Date		15th JULY 2020	

Week 1

Day 1	Date: 1st JUNE 2020

On the first day of training, after reaching to the factory I was introduced to my training mentor and the quality department team under whom I was about to complete my training for 6 weeks.
(personal introduction along with the team members)

Day 2	Date: 2nd JUNE 2020

After introduction, my supervisor explained me about the topic on which we'll be carrying forward our training.
TOPIC: "QUALITATIVE ANALYSIS OF TRADITIONAL INDIAN SWEETS AND NAMKEEN PRODUCTS"

Day 3	Date: 3rd JUNE 2020

The day was well focused towards the basic introduction about quality analysis and quality control . Explaining about how the protocols are applied in food industries to bring best out of the product.

Day 4	Date: 4th JUNE 2020

Started reading about the how quality analysis is done in different products apart from what are manufactured in the company.

Day 5	Date: 5th JUNE 2020

Read about what new techniques are coming up to easily analyze the quality of raw material and finished good accurately in less time and cost.

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Day 6	Date: 6th JUNE 2020
Last day of every week is kept for getting the information checked with the supervisor and reporting what I have learned. (continued studying over internet about the analysis protocols)	
Week 2	
Day 1	**Date: 8th JUNE 2020**
Week 2 was fully focused upon listing of products and their ingredients with detailed information and categorizing them under different headings. (from where what ingredients come that is of best quality)	
Day 2	**Date: 9th JUNE 2020**
Learned about what are the basic ingredients used each and everywhere and how they are sorted and cleaned accordingly. Starting with coming from the supplier to weighing them and to separate them according to the quality, size, color.	
Day 3	**Date: 10th JUNE 2020**
The day was dedicated towards learning hoe the machines works with less labor involvement in producing large amount of finished goods in less duration of time starting from mixing the raw material, adding spices and flavoring agents proceeding towards mixing, baking, heating, packaging and so on.	
Day 4	**Date: 11th JUNE 2020**
Raw material processing machines, intermediate machines for cooking and baking and finally the packaging machines used for packing products that are easily transported to the various delivery stations with less damage and that are good for the consumption.	
Day 5	**Date: 12th JUNE 2020**
Differentiating export quality products in different categories , labelling all the products and doing the paper work that was done by the team members.	



Day 6	Date: 13th JUNE 2020
Reporting to supervisor about what I learned in week 2 and getting things corrected	
Week 3	
Day 1	**Date: 15th JUNE 2020**
The week was focused towards plant and lab visit to know about various sections of complete plant including the laboratory and on the first day learned about which section is involved in doing which work.	
Day 2	**Date: 16th JUNE 2020**
Company produces ample number of products which are produced in different sections divided accordingly. Supervisor told me about the plant's division in 4 directions (EAST, WEST, NORTH, SOUTH) Each section is dedicated to produce specific product.	
Day 3	**Date: 17th JUNE 2020**
Each block is engaged in prescribed work with complete machinery and labor in clean and hygienic environment. Making list of each of products that are manufactured in each block and accordingly proceeding for tests.	
Day 4	**Date: 18th JUNE 2020**
Introduction about all the laboratory equipment used to analyze the products from raw material to the finished good. Learning on how the instrument works and their standard operating procedures.	
Day 5	**Date: 19th JUNE 2020**
Analysis of the results with the standard table issued by FSSAI to all the food industries engaged in producing specific product.	

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Day 6	Date: 20th JUNE 2020
Reporting to the supervisor what I learned in the last 5 days with detailed information and done corrections whatever was told.	
Week 4	
Day 1	**Date: 22nd JUNE 2020**
The first day started with the introduction to all the tests that will be performed in the next 2 weeks for the qualitative analysis of the raw material and finished good.	
Day 2	**Date:23rd JUNE 2020**
For every test to be performed, each time the raw material, dough and finished good is taken for analysis from every batch. For raw material, to be more specific tests are performed in triplets. Supervisor taught me about the first 3 tests that will be performed in the week	
Day 3	**Date:24th JUNE 2020**
TEST 1- Moisture analysis (moisture content in raw material, dough, finished products) Detailed SOP was learned and performed experiment [redacted]	
Day 4	**Date:25th JUNE 2020**
TEST 2- Acidity % The test was performed for the namkeen products which involve addition of various eatable acidic materials for taste and texture.	
Day 5	**Date:26th JUNE 2020**
TEST 3- Salt% The test was performed again for the namkeen products using titration technique with various reagents.	
Day 6	**Date:27th JUNE 2020**

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On the last day, revision of all the test was done along with matching the result with the standard table and checking whether the products is having everything in correct amount. Reporting the results to the supervisor.
Week 5
Day 1 **Date:29th JUNE 2020**
The day focused to repeat the test of last week if the result came up to be wrong. If not, then the next 3 tests were performed. Supervisor explained about the protocols how to perform them.
Day 2 **Date:30th JUNE 2020**
TEST 4- Peroxide Value estimation in the sample Test performed with the fresh and old sample using solvent and KI solution.
Day 3 **Date:1st JULY 2020**
TEST 5- Free Fatty Acid% The test was performed using indicator ,NaOH and ethyl alcohol
Day 4 **Date:2nd JULY 2020**
TEST 6- Water Chloride % The test was performed using potassium chromate and silver nitrate
Day 5 **Date:3rd JULY 2020**
The test performed in the week were compared with the standard and corrections were done if the results came out to be wrong.
Day 6 **Date:4th JULY 2020**



On the last day of the week, reported to the supervisor regarding the tests performed and what I learned from them.
Week 6
Day 1 **Date:5th JULY 2020**
In the last week of training, last 3 tests were performed. Also, if some test were not done properly in the last week were performed again with complete procedure. In the last week, I also learned about some other products that company produces like bakery products including biscuits and different type of breads.
Day 2 **Date: 6th JULY 2020**
TEST 7- Water Hardness Test The test was performed using various reagents along and results was compared with the standard table that are mentioned in the final report.
Day 3 **Date: 7th JULY 2020**
TEST 8- Volatile Oil% The test was performed using 2 machines which gives results in different time duration and checking which one is more appropriate in giving results accurately. Also learned about the working of Soxhlet apparatus.
Day 4 **Date: 8th JULY 2020**
TEST 9- Moisture % in sample using Dean and Stark Method The test is completely dedicated towards calculating the moisture content in all the spices used for preparing namkeen products.
Day 5 **Date:9th JULY 2020**
Compiling all the test over a single sheet and revising all of them from starting. Studied about the ingredients that are produced in-house by the company for preparing dishes. Also studied about how the quality of milk is checked that is solely used for preparing Sweets.
Day 6 **Date: 10th JULY 2020**
Last day of the week is dedicated towards getting more information about the tests and related aspects. 3-4 days were kept for compiling the work in a report that will be used for future assistance.

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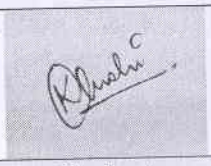
From 11th JULY 2020 onwards till 15th JULY 2020, after completing all the work related to lab, I started preparing my report under the guidance of my supervisor with searching more about how qualitative analysis is done over internet.
All the corrections were done and after getting final report checked and signed by supervisor, it was submitted to the parent organization and the company.

28 JULY 2020	
Date	**Student Signature**

For SANWARIA SWEETS PVT. LTD.

A.G.M. H.R./ADMIN

SANWARIA SWEETS PRIVATE LIMITED JAIPUR

Industrial Training Diary & Report

Student Name	MEGHA	**Roll No.**	171830
Company Name	Jaypee University Of Information Technology		
Training Supervisor Name	Dr. Saurabh bansal		
Training Supervisor Signature			
Internship Start Date	15/5/2020		
Internship End Date	30/6/2020		

Week 1

Day 1	**Date:15/5/20**

On the first day of training, my mentor and I had a discussion over the area of training. The topic of my preference was "protein purification techniques". After that I was assigned the enzyme named phytase and all the further report was to made under this topic. I was asked to find relevant literature in this enzyme.

Day 2	**Date:16/5/20**

Started reading about the phytase enzyme, it's applications and uses.

Day 3	**Date:18/5/20**

Read about various sources of phytase enzyme and the chemical reaction of phytase.

Day 4	**Date:19/5/20**

I got more literature related to the various methods that were employed in the extraction of phytase from various sources like bacteria and yeast along with the various assay that were used for the identification and checking the activity of phytase.

Day 5	**Date:20/5/20**

I was asked to make a flow chart for better understanding of the purification techniques used in the extraction.

Day 6	**Date:21/5/20**
I drew various flow charts explaining the process of phytase purification from the very initial steps of bacteria culturing and studied about gel filtration chromatography, ion exchange chromatography and affinity chromatography.	
Week 2	
Day 1	**Date:22/5/20**
I was asked to write about the characteristics of the organisms that produces the phytase enzyme. I collected the literature and all the relevant information about the bacteria and fungi that produces phytase enzyme. (Type of cell, it's morphology, sources of its extraction and pathogenic nature etc.)	
Day 2	**Date:23/5/20**
All the collected information was written down in the form of a table for easy assay. The selected organisms were lactobacillus caryniformis, Bacillus subtilis and Candida melibiosica.	
Day 3	**Date:25/5/20**
Collected the data about the culture conditions of the above organism. The conditions involved about the medium composition, temperature, agitation speed and volume etc.	
Day 4	**Date:26/5/20**
Found the information about gel filtration chromatography which is one of the most used technique in the extraction of proteins.	
Day 5	**Date:27/5/20**
Read about it's working and principles, and also studied about it's procedure.	

Day 6	**Date:28/5/20**
Read about the application and advantages of gel filtration chromatography.	
Week 3	
Day 1	**Date:29/5/20**
I collected the literature about ion exchange chromatography.	
Day 2	**Date:30/5/20**
Read about it's working and principle.	
Day 3	**Date:1/6/20**
Read about it's procedure of working.	
Day 4	**Date:2/6/20**
Read about the applications and advantages of the ion exchange chromatography.	
Day 5	**Date:3/6/20**
I collected the literature about the affinity chromatography.	

Day 6	Date:4/6/20
Read about the working and principle of affinity chromatography.	
Week 4	
Day 1	**Date:5/6/20**
Read about the procedure used in the purification of phytase from various sources.	
Day 2	**Date:6/6/20**
Studied about the application and advantages of this chromatographic methods.	
Day 3	**Date:8/6/20**
I was then told to collect the information about the phytase enzyme activity, so I collected relevant information on methods used for the assay of phytase enzyme activity.	
Day 4	**Date:9/6/20**
I got to know about the determination of protein concentration by the coomassive blue G-250 dye binding assay for phytase from Aspergillus Niger.	
Day 5	**Date:10/6/20**
I read about the Bradford protein assay which is a quantitative assay.	
Day 6	**Date:11/6/20**

I was asked to write the reaction and procedure of Bradford protein assay.

Week 5	
Day 1	**Date:12/6/20**
All the above information was copied as a flow chart to make it easy to understand.	
Day 2	**Date:13/6/20**
Then, was asked to collect the information about the various resins used in the column of various techniques.	
Day 3	**Date:15/6/20**
Studies about the Sephadrx resin, and about it's application and advantages.	
Day 4	**Date:16/6/20**
Collected information about the application and advantages of Sepharose resin.	
Day 5	**Date:17/6/20**
Then studied and collected all the information about the Sephacryl resin.	
Day 6	**Date:18/6/20**
Collected information about the application and advantages of Sepharose resin.	

Then studied and collected all the information about the Sephacryl resin.After that I was asked to find about the troubleshoots used while doing various purification techniques of phytase enzyme.

Day 1
Studied about the various trouble shooting me on, ion exchange and affinity chromatography
Date / ***Student Signature***

where my mentor asked me my purpose of choosing this topic and asked some basic questions regarding this training

Day 2	**Date:23/6/20**
A final report was asked to be prepared, summarising all the work done during the training period.	
Day 3	**Date:22/6/20**
I prepared a initial draft of the report.	
Day 4	**Date:23/6/20**
The initial draft was edited.	
Day 5	**Date:24/6/20**
A final draft with proper references, was prepared and shown to my mentor. He suggested further addition of information and asked me to make further changes.	
Day 6	**Date:25/6/20**
All the suggested changes were done and a final report was submitted to the mentor on the given date.	

Industrial Training Diary & Report

Student Name	Amanjot Singh Malhotra	**Roll No.**	171831
Company Name		Jaypee University of Information Technology	
Training Supervisor Name		Dr. Harish Changotra	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020

"SCIENCE HAS EMERGED TODAY AS THE MOST REVOLUTIONARY CO-OPERATIVE ACTIVITY OF MANKIND"
On the first day of my training, my mentor Dr. Harish Changotra briefed me about the AIM and the OUTLINE of our project i.e. GENOTYPING OF SINGLE NUCLEOTIDE POLYMORPHISM By applying PCR RFLP method.

Day 2	**Date:** 19/05/2020

The formal discussion focusing on the main area of training was made. After that I was assigned with Research papers related to our topic for the LITERATURE REVIEW.

Day 3	**Date:** 20/05/2020

Literature review was done on Single Nucleotide Polymorphism and important information was extracted from it.

Day 4	**Date:** 21/05/2020

Literature review was done on SNP GENOTYPING and the desired points were noted accurately.

Day 5	**Date:** 22/05/2020

Literature review was done on Genotyping single nucleotide polymorphism applying pcr-rflp method and the main concept was studied properly.

Day 6	**Date:** 23/05/2020

After reviewing the literature, outline methodology of the project was created.

Week 2

Day 1	**Date:** 25/05/2020

Read and studied about PCR (polymerase chain reaction) and its importance in various biological fields.

Day 2	**Date:** 26/05/2020

Each and every component and parameter which comprises PCR was understood in order to study its use of diagnosing various diseases and genetic changes.

Day 3	**Date:** 27/05/2020

Read about various PCR methods , their pros and cons were noted.

Day 4	**Date:** 28/05/2020

The most convenient , simple , inexpensive and accurate method was selected for the project i.e PCR- RFLP method.

Day 5	**Date:** 29/05/2020

The whole protocol for the PCR- Restriction fragment length polymorphism was studied properly .

Day 6	**Date:** 30/5/2020
Applications associated with PCR-RFLP method was studied.	

Week 3

Day 1	**Date:** 1/6/2020
This week was for the experimental design of the project.	
Day 2	**Date:** 2/06/2020
Explored REBASE database and restriction enzymes were selected to meet the requirement of the project.	
Day 3	**Date:** 3/06/2020
This was followed by PRIMER designing , Explored primer3 software and snp_cutter to find the appropriate Restriction sites and for designing amplification primers for producing PCR products.	
Day 4	**Date:** 4/06/2020
Procedure for DNA isolation was studied.	
Day 5	**Date:** 5/06/2020
Template preparation for PCR-RFLP method was studied.	

Day 6	Date: 6/06/2020
All the controls were noted and made for the project.	

Week 4

Day 1	Date: 8/06/2020
This week was for analyzing the materials , reagents and equipment required for the pcr- rflp method.	
Day 2	**Date:** 9/06/2020
All of the material reagents with their required amount were noted.	
Day 3	**Date:** 10/06/2020
The function of each material reagent required were studied.	
Day 4	**Date:** 11/06/2020
Precaution related to each reagent is noted cautiously .	
Day 5	**Date:** 12/06/2020
All required equipments were noted . Function and use of each equipment was studied.	
Day 6	**Date:** 13/06/2020

Precautions related to the usage of each equipment were studied.

Week 5

Day 1	Date: 15/06/2020

This week was for the understanding of the procedure to be carried out for PCR-RFLP method.

Day 2	Date: 16/06/2020

PCR amplification of DNA samples with their timing of occurrence was studied.

Day 3	Date: 17/06/2020

PCR set up to amplify a single DNA sample and more than one DNA sample for digestion of single and multiple restriction enzymes respectively was studied.

Day 4	Date: 18/06/2020

The concept of "GEL ELECTROPHORESIS" was studied.

Day 5	Date: 19/06/2020

Applied the concept of gel electrophoresis for the analysis of PCR products.

Day 6	Date: 20/06/2020

ALL of the troubleshooting problems and precaution associated with each step of the procedure was noted and highlighted. Followed by the anticipation of results.

Week 6

Day 1	Date: 22/06/2020

This week was for the REPORT PREPARATION, compilation of all the work done till now by compiling all the necessary points with the approval of my training guide.

Day 2	Date: 23/06/2020

Drafted the report by covering each and every parameter , every aspect, all of the methods done results and analysis in the report. The content editing was successfully done by the end of the day.

Day 3	Date: 24/06/2020

This was followed by adjusting the fonts and addition of images to make the concept more understandable.

Day 4	Date: 25/06/2020

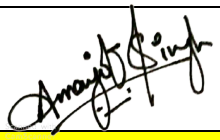
Completed the first draft of the report and sent to the respective guide.

Day 5	Date: 26/06/2020

The report was corrected and related references were added to it.

Day 6	Date: 27/06/2020

Completed the final draft of the report and submitted to the training guide, Dr. Harish Changotra.

4/08/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Rishab Roy	**Roll No.**	171832
Company Name		Jaypee university of information and technology	
Training Supervisor Name		Dr. Sudhir Kumar	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:18/05/2020**

On the first day of the training, my mentor and I had a discussion on the topic of training. First sir told to revise long preservation techniques of fungus.

Day 2	**Date:19/05/2020**

Then we decided our topic that was ATCC. I was asked to gather basic information about it that what is ATCC and its work on basic level.

Day 3	**Date:20/05/2020**

I read more about ATCC i.e. kind of preservation done in that and how it is done.

Day 4	**Date:21/05/2020**

Then we read about some qualifications which are required in ATCC.

Day 5	**Date:22/05/2020**

Then categories of qualification in which qualifications are categorized.

Day 6	**Date:23/05/2020**
Exploring of ATCC website a little more.	

Week 2

Day 1	**Date:25/05/2020**
Then I read about the ordering steps by which a culture is ordered from the ATCC website.	
Day 2	**Date:26/05/2020**
There focusing area that on what that website focuses while preserving the cultures.	
Day 3	**Date:27/05/2020**
Then I got know about the collection of cultures there which were very large in number.	
Day 4	**Date:28/05/2020**
Different type of cultures preserved in it and their number.	
Day 5	**Date:29/05/2020**
Requirements of people for handling a particular type of culture in ATCC.	

Day 6	**Date:30/05/2020**
Then discussed with my mentor after reading literature , then got more literature more topics to study.	

Week 3

Day 1	**Date:1/06/2020**
About working of ATCC read little information.	
Day 2	**Date:2/06/2020**
Begin with an ATCC bacterial strain.	
Day 3	**Date:3/06/2020**
Read about item sheet in which information about strain is written and sent.	
Day 4	**Date:4/06/2020**
About classification changes.	
Day 5	**Date:5/06/2020**
Then got to know the planning and preparation of medium for the strain.	

Day 6	Date:6/06/2020
How to open a glass ampoule.	

Week 4

Day 1	Date:8/06/2020
Then read about opening double-vial preparations and opening single-vial preparations.	
Day 2	**Date:9/06/2020**
Then read about preserving bacterial cultures in frozen state.	
Day 3	**Date:10/06/2020**
Then we read about the fungal long-term preservation techniques.	
Day 4	**Date:11/06/2020**
Continued it as many techniques were there to learn. I read cryopreservation technique in which 2 strategies were there that are slant culture and slide cut culture.	
Day 5	**Date:12/06/2020**
Read about lyophilization.	
Day 6	**Date:13/06/2020**

Lyophilization have few stages in which it occurs read about that.
Week 5
Day 1 **Date:15/06/2020**
About next technique paraffin strategy and safeguarding in distilled water.
Day 2 **Date:16/06/2020**
More techniques i.e. protection on paper and agar incline societies.
Day 3 **Date:17/06/2020**
Learned about how naming of fungi is done.
Day 4 **Date:18/06/2020**
I also learned about bacterial preservation techniques.
Day 5 **Date:19/06/2020**
Compared fungal preservation techniques and bacterial preservation techniques learned some difference between them.
Day 6 **Date:20/06/2020**

Read more about them discussed with my mentor got to know about them that what is difference and much more.

Week 6

Day 1	Date:22/06/2020
Looked over all the topics being studied, revised them.	

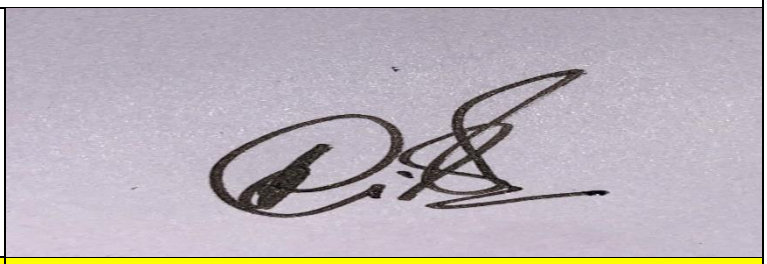
Day 2	Date:23/06/2020
The notes which were made in whole 5 weeks I started compiling it in a proper manner.	

Day 3	Date:24/06/2020
Completed the first draft of the report and sent it for the first review.	

Day 4	Date:25/06/2020
Did the corrections suggested and questions which were supposed to answer and mention in my report.	

Day 5	Date:26/06/2020
Put the report in correct format .	

Day 6	Date:27/06/2020
Completed the final draft of the report and submitted it to my mentor Dr. Sudhir Syal	

16-08-2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Manvhi Rastogi	**Roll No.**	171834
Company Name		Jaypee University of Information Technology	
Training Supervisor Name & Signature			
Internship Start Date		15/5/2020	
Internship End Date		30/6/2020	

Week 1

Day 1	**Date: 15/5/20**

Review Articles compile, summarize, critique and synthesize available information on a topic. 6 steps of writing it-

1) Selecting a research topic. Exploring topic that we are willing to work with for considerable amount of time.

Day 2	**Date: 16/5/20**

The topic to be chosen should interest the person. To develop the research topic, broaden your thinking and creativity. Considering an area which interests us and has high importance to profession.

Day 3	**Date: 18/5/20**

Choosing relevant topic and taking care. Subject should meet the assignment/ research requirements. Reviewing guidelines and seeking clarifications from professor.

Day 4	**Date: 19/5/20**

Making notes on the scope of the topic. Sometimes the chosen topic may be too broad. Focusing on few concepts and limiting the scope.

Day 5	**Date: 20/5/20**

Purpose of the research has to be very clear. Fine tuning the topic by experimenting with key word; Search until satisfied with the retrieval results.

Day 6	**Date: 21/5/20**

Checking if we have adequate resources and material to help writing the review. Exploring variety of resources: journals, books, online information.

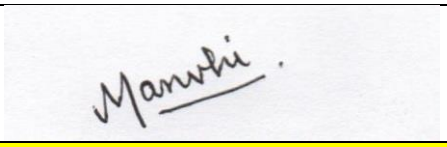
Week 2

Day 1	Date: 22/5/20
2) Search Learning about how keywords are so important in case of library databases. Brainstorming keywords related to our research question.	
Day 2	**Date: 25/5/20**
Identifying key concepts in research and brainstorming related terms of our concepts. Keywords are main idea and concepts of topic and they should be put together for information.	
Day 3	**Date: 26/5/20**
To find specify information, all narrower terms are collected. Having range of keywords is significant.	
Day 4	**Date: 27/5/20**
Broader terms are also used and collected to find general information. We should have alternate search options also, for finding resources.	
Day 5	**Date: 28/5/20**
Also, taking care of similar terms and thinking of all synonyms as well. To find information about related topics, related terms are also searched.	
Day 6	**Date: 29/5/20**
Learning to identify appropriate terms to describe topic and find best results. Making list of narrow terms, broader terms, similar terms and related terms.	

Week 3	
Day 1	**Date: 1/6/20**
3) Evaluate Making sure that resources and information is authoritative, reliable, relevant and most useful in supporting the research.	
Day 2	**Date: 2/6/20**
Criteria like author's aim, to what extent it has been achieved, what knowledge does it add, missing key points etc are to be checked.	
Day 3	**Date: 3/6/20**
Methodology or approach used for research is considered. Approach should be objective, results valid.	
Day 4	**Date: 4/6/20**
Methods used like qualitative/ quantitative analysis/ review of theory, comparative, case study etc is evaluated. Analytical framework used to discuss the results.	
Day 5	**Date: 5/6/20**
What problems, hypothesis we mention and the evidence that text relay on are seen. The evidences are to be effective, conclusions are to be drawn and justified.	
Day 6	**Date: 8/6/20**
Evaluation of writing style is also very important. It should suit the intended audience. Organizing text in suitable way.	

Week 4	
Day 1	**Date: 9/6/20**
4) Analyze After evaluation of retrieved sources, exploring of what has been found and what is missing.	
Day 2	**Date: 10/6/20**
Content collected needs to be analyzed. Breaking study into parts, understand each part, assessing strength of evidence, drawing conclusions.	
Day 3	**Date: 11/6/20**
Critically reviewing each sources' methods, procedure, data validity. Considering each source approach towards the topic.	
Day 4	**Date: 12/6/20**
Identifying the gaps in research. Defining the key terms and nothing key statistics. Determining emphasis, strengths and weaknesses.	
Day 5	**Date: 13/6/20**
Critique research methods used in studies. Identifying major patterns, categories, relationships and inconsistencies.	
Day 6	**Date: 15/6/20**
Recognizing specific aspects of the topic, analyzing any gaps in the literature. Using only current and up-to date sources. The whole content needs to be analyzed.	

Week 5	
Day 1	**Date: 16/6/20**
5) Synthesis Literature review should synthesize ideas with observations to create map of scholarly conversation about the topic. Also, mentioning gaps or areas of further research.	
Day 2	**Date: 17/6/20**
Studying many ideas from books, articles etc. and highlighting important points as well as observations of related texts.	
Day 3	**Date: 18/6/20**
Thesis is properly defined and to check it should neither support nor refute an argument. It should be well defined and supported by various sources.	
Day 4	**Date: 19/6/20**
Comparing and contrasting information from multiple sources and citing them.	
Day 5	**Date: 20/6/20**
Critical analysis of source material is essential. Making connections between different sources (supporting and refuting arguments, different concepts, methodologies etc.)	
Day 6	**Date: 22/6/20**
Bringing together review results and making creative connections between unrelated research and identifying any gaps.	

Week 6	
Day 1	**Date: 23/6/20**
6) Writing and Presenting Including thesis statement in the literature and writing the perceptions clearly. Demonstrating through investigation in relation to topic.	
Day 2	**Date: 24/6/20**
Writing critical discussions, comparing opinions; relating our study to previous ones, showing gaps in research. Compiling primary questions and subject areas involved.	
Day 3	**Date: 25/6/20**
Organizing the literature review into proper structure- an introduction, body and the conclusion. Learning and using only specialized vocabulary in discipline.	
Day 4	**Date: 26/6/20**
Writing an introduction which gives quick idea of review article, such as central theme or organizational pattern. Scope, method, problem statement, thesis etc. to be written.	
Day 5	**Date: 29/6/20**
Then writing the body of the article. It contains the discussion of sources. Structuring the discussion chronologically (discussing all the themes present within research).	
Day 6	**Date: 30/6/20**
Writing conclusion in which we need to mention concise summary of our review and providing suggestions for future research.	
24/7/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Nayanika Sharma	**Roll No.**	171835
Company Name	Jaypee University of Information Technology, Waknaghat		
Training Supervisor Name	Dr. Udayabanu		
Training Supervisor Signature			
Internship Start Date	May 16, 2020		
Internship End Date	June 25, 2020		

Week 1

Day 1	**Date: May 16, 2020**

After a discussion with my guide on the topic of animal cell culture, I started with the basics such as how cell lines are established and their potential applications in various fields.

Day 2	**Date: May 17, 2020**

After this, I was allocated the activity to locate some applicable writing and read about instrumentation involved in establishment and maintenance of cell lines.

Day 3	**Date: May 18, 2020**

In order to learn about the current methodologies involved, I studied about the history of cell lines as to how they came into existence along with different categories of tissue culture.

Day 4	**Date: May 19, 2020**

Started reading about instrumentation involved in cell culture technologies, like equipment, reagents, etc.

Day 5	**Date: May 20, 2020**

Read detailed description about laminar flow hoods which provide aseptic work area during laboratory experiments and incubator for growth of cell lines.

Day 6	**Date: May 21, 2020**
Learnt about water purification and media filtration devices, including their types and market producers.	

Week 2

Day 1	**Date: May 23, 2020**
Started learning more about different media filtration devices provides by LifeAssure.	
Day 2	**Date: May 24, 2020**
Revised what I have learnt so far.	
Day 3	**Date: May 25, 2020**
Made additions to the already collected data.	
Day 4	**Date: May 26, 2020**
Got more literature to read and started reading and marking recent instruments involved. I also started actively looking out for the area of research.	
Day 5	**Date: May 27, 2020**
Found information related to the most common and important instruments involved in laboratory: automated cell counters and storage tanks- refrigerators, freezer and cryogenic storage.	

Day 6	**Date: May 28, 2020**
Collected data regarding water baths, their types, etc. and imaging systems involved in visualizing cell lines.	

Week 3

Day 1	**Date: May 30, 2020**
Studied advantages and applications of imaging systems in cell lines.	
Day 2	**Date: May 31, 2020**
Collected more information regarding how to use these instruments efficiently and carefully. Read precautions related to these instruments and how to prevent contamination at all costs.	
Day 3	**Date: June 01, 2020**
Started studying about electroporation instruments used in cell culture laboratories to study the basics of transgenics.	
Day 4	**Date: June 02, 2020**
Recent advances in electroporation devices such as Neon Transfection system for cell suitability was studied.	
Day 5	**Date: June 03, 2020**
Types of aspiration pump including peristaltic and vacuum were studied.	

Day 6	Date: June 04, 2020
Glassware and plasticware as utilized in culture laboratory, such as flasks, pipettes, etc. were studied. Holding capacity of different volumes of flasks was learnt.	

Week 4

Day 1	Date: June 06, 2020
The technique of flow cytometry was studied to monitor hybridoma cell cultures, changes in DNA, RNA, etc. during the growth cell culture.	
Day 2	**Date: June 07, 2020**
Revised what I have learnt so far and made additions to the already collected data.	
Day 3	**Date: June 08, 2020**
Started collecting information on uses of animal cell cultures in disease identification.	
Day 4	**Date: June 09, 2020**
Learnt about the origin and associated symptoms of different diseases like Cancer, Alzheimer Disease etc	
Day 5	**Date: June 10, 2020**
Got acquainted with diagnostic techniques of Animal Cell Culture including testing equalization, CT Scan, and identifying affected genes.	
Day 6	**Date: June 11, 2020**

Causes and factors that increase the risk of acquiring AD were studied and understood.

Week 5

Day 1	Date: June 13, 2020
Neuroimaging and genetic biomarkers involved in diagnosis of AD were studied.	
Day 2	**Date: June 14, 2020**
Got acquainted with cerebrospinal fluid, peripheral fluid-based and cell-based biomarkers for AD diagnosis.	
Day 3	**Date: June 15, 2020**
Acclimated with the technique of trypsinization. Its methodology was learnt.	
Day 4	**Date: June 16, 2020**
Learnt aseptic techniques used in laboratory for a carrying out the experiment without any contamination.	
Day 5	**Date: June 17, 2020**
Collected information on successful passaging of cells. Learnt about live cell density, etc. required for sub-culturing.	
Day 6	**Date: June 18, 2020**
Got acquainted with culture plating and preparation techniques.	

Week 6

Day 1	Date: June 20, 2020
Structure of hemocytometer was acclimated and procedure of counting cells was learnt.	

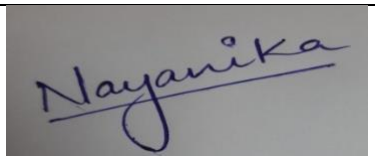
Day 2	Date: June 21, 2020
Ways of preventing contamination while performing laboratory work were understood.	

Day 3	Date: June 22, 2020
Working of FBS, DMSO and isopropanol were learnt in order to understand cryopreservation. Procedure and precaution while cryopreserving the cells were acclimated.	

Day 4	Date: June 23, 2020
Procedure of thawing of cells was learnt.	

Day 5	Date: June 24, 2020
Got acquainted with sub-culturing of cells.	

Day 6	Date: June 25, 2020
Revised what was done so far and gathered additional data related to animal cell culture techniques.	

July 27, 2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	Shivani Chaturvedi	**Roll No.**	**171837**
Company Name		**Jaypee University of Information Technology**	
Training Supervisor Name		**Dr. Harish Changotra**	
Training Supervisor Signature			
Internship Start Date		18/05/2020	
Internship End Date		27/06/2020	

Week 1

Day 1	**Date:** 18/05/2020
On the first day of the training, my mentor and I had a discussion on the topic of training. We decided it to be Cancer and SNPs relation. After this, I was assigned the job to find some relevant literature and read about it.	
Day 2	**Date:** 19/05/2020
I started reading about Cancer and its various factors and mechanisms. My main aim was to find exact relation between Cancer and single nucleotide polymorphism.	
Day 3	**Date:** 20/05/2020
Got more literature to read and started reading and marking recent topics of research in this field. I also started actively looking out for the area of research.	
Day 4	**Date:** 21/05/2020
Started reading about different areas in Cancer and snps. Also, read about the different methods of dna isolation.	
Day 5	**Date:** 22/05/2020

Read about the papers provided by the mentor to find out more about snps, cancer and dna isolation. In these Dna isolation inckydes twi different methods, stated as organic and inorganic.

Day 6	**Date:** 23/05/2020
Read about the inorganic method of dna isolation, and their relation with cancer cells and snps.	
	Week 2
Day 1	**Date:** 25/05/2020
Found some relation between snps and genotyping involving the diagnosis of the most prominent disease of all time, Cancer.	
Day 2	**Date:** 26/052020
Informed my mentor about the same. Got more literature to read on the topic of genotyping of snps.	
Day 3	**Date:** 27/05/2020
Read about pcr(polymerase chain reaction) and it's importance in various biological field.	
Day 4	**Date:** 28/05/2020
Understood what comprises of PCR and how are they used to diagnose other diseases or genetic changes.	
Day 5	**Date:** 29/05/2020
Got literature about different types of pcr. Decided to read about one every day and also find out details and uses of each one of them.	

Day 6	**Date:** 30/05/2020

Read the introduction about the 3rd type of pcr which was, artificial restriction fragment length polymorphism (A-RFLP) PCR.

Week 3	
Day 1	**Date:** 01/06/2020
Read about the details and chemicals related with the stated pcr method.	
Day 2	**Date:** 02/06/2020
Got more information about the applications and the drawbacks related with A-RFLP PCR.	
Day 3	**Date:** 03/06/2020
Read about the comparisons related with the different types of pcr and their mechanism.	
Day 4	**Date:** 04/06/2020
Gathered information and literature about the genotyping of single nucleotide polymorphism by A-RFLP pcr method.	
Day 5	**Date:** 05/06/2020
Read the introduction and its mechanism.	

Day 6	**Date:** 06/06/2020
. Read some more research paper regarding genotyping through a-rflp pcr method.	

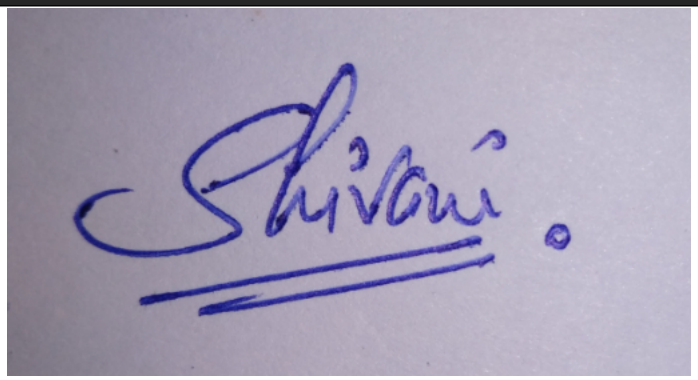
Week 4	
Day 1	**Date:** 08/06/2020
Studied about this method in detail, took help of my phd scholar as this method was giving me a hard time.	
Day 2	**Date:** 09/06/2020
Studied whatever paper she has listed for the respected topic.	
Day 3	**Date:** 10/06/2020
Done comparison of the papers with a-rflp pcr method.	
Day 4	**Date:** 11/06/2020
Started reading about what this method is capable of doing, and how it's done.	
Day 5	**Date:** 12/06/2020
There are different kinds of arrangements done for the genotyping of snps for diagnosis of various diseases.	
Day 6	**Date:** 13/06/2020

Found about site-directed mutagenesis or, what we can also say as mutagenic primers which are used to create a restriction enzyme site and amplify the desired dna fragment in this particular method.

Week 5	
Day 1	**Date:** 15/06/2020
The first arrangement which was site directed mutagenesis helps to create an artificial restriction fragment length polymorphism for almost all naturally occurring DNA polymorphism.	
Day 2	**Date:** 16/06/2020

Next is its mechanism, chemicals used, drawbacks, etc has been studied for gathering further information about it.	
Day 3	**Date:** 17/06/2020
Then how the process of amplification, and genotyping is done through A-RFLP PCR method has been studied.	
Day 4	**Date:** 18/06/2020
It's importance has been kept in mind... One of which include how this method can digest the sequence containing snp if it is recognized by the created restriction enzyme/site with the help of mutagenic primers.	
Day 5- Another one is how it optimizes pcr reaction.	
Day 6	**Date:** 20/06/2020
PCR amplification followed by agarose gel electrophoresis to check whether the desired region is amplified or not. Followed by restriction digestion and then gel electrophoresis of digested products to check the genotypes.	

# Week 6	
Day 1	**Date:** 22/06/2020
This week was for the compilation of all the work done till now and started compiling points for the same.	
Day 2	**Date:** 23/06/2020

Started working on the report to be submitted at the end of the training.	
Day 3	**Date:** 24/06/2020
Completed the first draft of the report. Sent it for the first review.	
Day 4	**Date:** 25/06/2020
Did all the corrections suggested in the report.	
Day 5	**Date:** 26/06/2020
Put the report in the correct format.	
Day 6	**Date:** 27/06/2020
Completed the final draft of the report and submitted it to Dr Harish Changotra.	
21/07/2020	
Date	**Student Signature**

Industrial Training Diary & Report

Student Name	**Divyanshu Bhuraita**	**Roll No.**	**171840**
Company Name		**Jaypee University of information technology**	
Training Supervisor Name		**Dr. Ashok Nadda**	
Training Supervisor Signature			
Internship Start Date		15/5/20	
Internship End Date		30/6/20	

Week 1

Day 1	**Date:15/5/20**
On the first day I studied about the introduction of immobilization of enzymes onto nanoparticles.	
Day 2	**Date: 16/5/20**
Studied about random and site-directed immobilization.	
Day 3	**Date: 17/5/20**
Studied about various types of immobilization	
Day 4	**Date: 18/5/20**
Studied about heterogenous biocatalysts and their parameters	
Day 5	**Date: 19/5/20**
On the 5th day we discussed about applications of immobilization with our mentor	
Day 6	**Date: 20/5/20**
Discussed all the things we studied with our mentor	

Week 2

Day 1	**Date: 22/5/20**
Studied about various immobilization techniques and studied the affinity-tag binding.	
Day 2	**Date: 23/5/20**

Studied about adsoption on glass	
Day 3	**Date: 24/5/20**
Studied about entrapment and cross linkage	
Day 4	**Date: 25/5/20**
Studied about immobilization by covalent bond	
Day 5	**Date: 26/5/20**
Studied about various parameters to be Considered when immobilization	

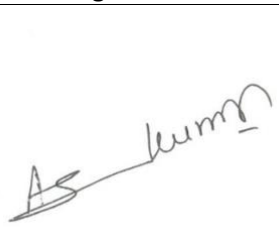
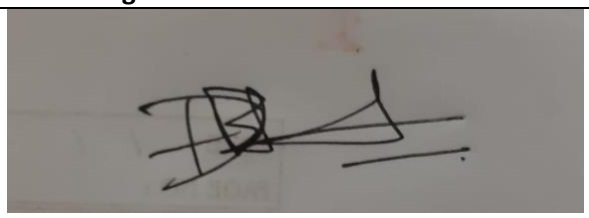
Day 6	**Date: 27/5/20**
Discussed all the parameters, rights and wrongs When immobilizing with our mentor	
	Week 3
Day 1	**Date: 29/5/20**
Studied about commerial use of immobilization	
Day 2	**Date: 30/5/20**

Studied about the convenience and economical use	
Day 3	**Date: 31/5/20**
Discussed the commerical uses with our mentor	
Day 4	**Date: 1/6/20**
Studies about immobilization of a Substrate for Enzymatic Reactions	
Day 5	**Date: 2/6/20**
Studied about advantages and applications of immobilization	

Day 6	**Date: 3/6/20**
Studied the disadvantages and more applications of immobilization	
	Week 4
Day 1	**Date: 5/6/20**
Studied about various sources from which Nanoparticle can be derived	
Day 2	**Date: 6/6/20**
Studied about prepration of nanoparticles	
Day 3	**Date: 7/6/20**
Discussed about nanoparticles preparation	

And different sources with our mentor	
Day 4	**Date: 8/6/20**
Studied about the role of nanoparticles In drug delivery mechanisms	
Day 5	**Date: 9/6/20**
Studied about how drug delivery mechanisms Can boost diagnostic procedures	
Day 6	**Date: 10/6/20**

Discussed the nanoparticles role in drug delivery With our mentor	
	Week 5
Day 1	**Date: 12/6/20**
Studied about immobilization efficiency and it's importance	
Day 2	**Date: 13/6/20**
Studied about immobilization yield and how it is different from immobilization efficiency	
Day 3	**Date: 14/6/20**
Discussed immobilization yield and efficiency with our mentor	
Day 4	**Date: 15/6/20**
Studied about immobilization at nanoscale	
Day 5	**Date: 16/6/20**
Prepared a raw report on our topic	
Day 6	**Date: 17/6/20**

Discussed about the report on the topic With our mentor	
	Week 6
Day 1	**Date: 19/6/20**
Studied about supports or Matrix used in immobilization	
Day 2	**Date: 20/6/20**
Studied more in detail about different types of supports	
Day 3	**Date: 21/6/20**
Studied about natural and synthetic matrixes	
Day 4	**Date: 22/6/20**
Studied about inorganic supports and the advantages and disadvantages of different types of supports and what is best for immobilisation	
Day 5	**Date: 23/6/20**
Day 6	**Date: 24/6/20**
Started making the final report on our Summer internship topic	
Teacher's sign	**Student's sign-**
 24/6/20	
Date	**Student Signature**

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JUIT/WKG/BT-BI/20-21/059

Date: 07/09/2020

CERTIFICATE

This is to certify that **Mr. SHAURYA MEHTA** (Enrollment No. 141505) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Next Generation Sequencing** from **July 23' 2020 to September 4 ' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/010

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MUSKAN KAPOOR** (Enrollment No. 171501) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Targeting Sars-Cov-2 Main Protease for Covid-19** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Raj Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/011

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAKRITI CHAUHAN** (Enrollment No. 171503) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Analysis of various articles on Epigenetic of Alzheimer's Disease** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/012

Date: 26/08/2020

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This is to certify that **Ms. ANJALI SHARMA** (Enrollment No. 171505) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Analysis of Various Articles on Epigenetics of Alzheimer's Disease** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

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(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VAIBHAV GANGTA** (Enrollment No. 171506) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Data Mining in Biomedical Literature** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
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Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. MAHARISHI KALLA** (Enrollment No. 171508) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Structural Analysis of SARS-CoV-2** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAGAM MISHRA** (Enrollment No. 171509) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Summer Training on HealthCare Monitoring System Based Upon Features for CVD** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. GARIMA SINGH** (Enrollment No. 171510) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Website Development** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/016

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. RIYA DHIMAN** (Enrollment No. 171512) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Exploring Human Metabolome Database(HMDB) and DrugBank with reference to Metabolomics** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
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Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
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Prof. Sudhir Kumar
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. KRITIKA** (Enrollment No. 171513) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Protein Interaction Network Analysis** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. APURVA GARG** (Enrollment No. 171514) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Text Mining in Biomedical Literature** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/020

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SARVJEET KAUR** (Enrollment No. 171515) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **IMGT Database** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY JUIT WAKNAGHAT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/021

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SRISHTI THAKUR** (Enrollment No. 171516) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **IMGT Database** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY JUIT WAKNAGHAT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/022

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAKANKSHA GAUTAM** (Enrollment No. 171517) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Automated Personality Classification using Data Mining Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY JUIT WAKNAGHAT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/023

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. CHHAVI THAKUR** (Enrollment No. 171518) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **TARGETING SARS-CoV-2 MAIN PROTEASE FOR COVID-19** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Raj Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Fax : +91-01792-245362

JUIT/WKG/BT-BI/20-21/024

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MEHAK KAPOOR** (Enrollment No. 171519) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **TARGETING SARS-COV-2 MAIN PROTEASE FOR COVID-19** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Raj Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/010

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MUSKAN KAPOOR** (Enrollment No. 171501) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Targeting Sars-Cov-2 Main Protease for Covid-19** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Raj Kumar

(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/011

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAKRITI CHAUHAN** (Enrollment No. 171503) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Analysis of various articles on Epigenetic of Alzheimer's Disease** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/012

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ANJALI SHARMA** (Enrollment No. 171505) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Analysis of Various Articles on Epigenetics of Alzheimer's Disease** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/013

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VAIBHAV GANGTA** (Enrollment No. 171506) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Data Mining in Biomedical Literature** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/014

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. MAHARISHI KALLA** (Enrollment No. 171508) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Structural Analysis of SARS-CoV-2** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/015 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAGAM MISHRA** (Enrollment No. 171509) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Summer Training on HealthCare Monitoring System Based Upon Features for CVD** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. GARIMA SINGH** (Enrollment No. 171510) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Website Development** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/016 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. RIYA DHIMAN** (Enrollment No. 171512) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Exploring Human Metabolome Database(HMDB) and DrugBank with reference to Metabolomics** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/018 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. KRITIKA** (Enrollment No. 171513) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Protein Interaction Network Analysis** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/019

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. APURVA GARG** (Enrollment No. 171514) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Text Mining in Biomedical Literature** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/020 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SARVJEET KAUR** (Enrollment No. 171515) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **IMGT Database** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/021 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SRISHTI THAKUR** (Enrollment No. 171516) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **IMGT Database** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/022 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAKANKSHA GAUTAM** (Enrollment No. 171517) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Automated Personality Classification using Data Mining Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Tiratha Raj Singh
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/023 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. CHHAVI THAKUR** (Enrollment No. 171518) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **TARGETING SARS-CoV-2 MAIN PROTEASE FOR COVID-19** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Raj Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/024 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MEHAK KAPOOR** (Enrollment No. 171519) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **TARGETING SARS-COV-2 MAIN PROTEASE FOR COVID-19** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Raj Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

INTERNSHALA TRAININGS

Certificate of Training

Purvanshi Sharma

from **Jaypee University Of Infornation Technology** has successfully completed a six weeks online training on **Programming with Python** from 22nd May, 2020 to 3rd July, 2020. The training consisted of Introduction to Python, Using Variables in Python, Basics of Programming in Python, Principles of Object-oriented Programming (OOP), Connecting to SQLite Database, Developing a GUI with PyQT and Application of Python in Various Disciplines modules. Purvanshi scored 95% marks in the final assessment and is a top performer in the training. We wish Purvanshi all the best for the future.

Sarvesh Agrawal
Founder & CEO, Internshala

Date of certification: 2020-06-22 Certificate no. : 4E597DD9-CD05-7D95-488A-8591FE8006D8

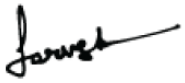
For certificate authentication, please visit https://trainings.internshala.com/verify_certificate

INTERNSHALA TRAININGS

Certificate of Training

Prerna Tiwari

from **JAYPEE UNIVERSITY OF INFORMATION AND TECHNOLOGY** has successfully completed a six weeks online training on **Programming with Python** from 15th May, 2020 to 26th June, 2020. The training consisted of Introduction to Python, Using Variables in Python, Basics of Programming in Python, Principles of Object-oriented Programming (OOP), Connecting to SQLite Database, Developing a GUI with PyQT and Application of Python in Various Disciplines modules. We wish Prerna all the best for the future.



Sarvesh Agrawal
Founder & CEO, Internshala

Date of certification: 2020-07-02 Certificate no. : 7F0161D4-0BA3-1848-4A9F-A65D26FE1B49

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JUIT/WKG/BT-BI/20-21/025

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ANANYAA KAUL** (Enrollment No. 171801) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physico-Chemical Evaluation of Biosurfactants for their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY * WAKNAGHAT * JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/026

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VASUDEV SINGH** (Enrollment No. 171802) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/027

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. HARMEET SINGH** (Enrollment No. 171804) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **PCR Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jata Shankar
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY * WAKNAGHAT * JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/028

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VINAYKORRAM** (Enrollment No. 171805) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **PCR TECHNIQUES** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jata Shankar
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/029

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DEVASHISH VERMA** (Enrollment No. 171806) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Embryo Culture For In-vitro Micropropagation of New Cicer arietinum (Chickpea) Varities** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Hemant Sood
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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CERTIFICATE

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Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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CERTIFICATE

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Dr. Ashok Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
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(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SOUMI BISWAS** (Enrollment No. 171811) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Proteomics: Technologies and Application** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Jitendraa

Dr. Jitendraa Vashistt
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/034

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. SUGAM SINGH** (Enrollment No. 171812) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/035

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. UMANG MAHESHWARI** (Enrollment No. 171813) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Molecular Circuits Using Synthetic Biology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/036

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DIWAKAR PALIWAL** (Enrollment No. 171814) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physico-Chemical Evaluation of Biosurfactants for their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/025

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ANANYAA KAUL** (Enrollment No. 171801) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physico-Chemical Evaluation of Biosurfactants for their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/026

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VASUDEV SINGH** (Enrollment No. 171802) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/027

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. HARMEET SINGH** (Enrollment No. 171804) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **PCR Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jata Shankar
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/028

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VINAYKORRAM** (Enrollment No. 171805) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **PCR TECHNIQUES** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Jata Shankar
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

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JUIT/WKG/BT-BI/20-21/029

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DEVASHISH VERMA** (Enrollment No. 171806) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Embryo Culture For In-vitro Micropropagation of New Cicer arietinum (Chickpea) Varities** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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CERTIFICATE

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(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
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CERTIFICATE

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Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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CERTIFICATE

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Jitendraa

Dr. Jitendraa Vashistt
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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CERTIFICATE

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Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
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(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Date: 26/08/2020

CERTIFICATE

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(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY * WAKNAGHAT * JUIT

Prof. Sudhir Kumar
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Fax : +91-01792-245362

JUIT/WKG/BT-BI/20-21/037

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ISHITA KAWAR** (Enrollment No. 171815) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Micropropagation of Rhododendron** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Hemant Sood
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/038

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. EKTA CHOUDHARY** (Enrollment No. 171816) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/039

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. CHARU THAKUR** (Enrollment No. 171817) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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JUIT/WKG/BT-BI/20-21/040

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. RACHITA GUPTA** (Enrollment No. 171818) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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JUIT/WKG/BT-BI/20-21/041

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. VITASTA JALALI** (Enrollment No. 171819) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Study on ATCC** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Prof. Sudhir Kumar
(Training Supervisor)
(Head, Department of Biotechnology and Bioinformatics)

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/042

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NAVEETA KARAR** (Enrollment No. 171820) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Proteomic Technology, Techniques and Usage** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jitendraa Vashistt
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/025

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ANANYAA KAUL** (Enrollment No. 171801) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physico-Chemical Evaluation of Biosurfactants for their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/026

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VASUDEV SINGH** (Enrollment No. 171802) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
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Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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JUIT/WKG/BT-BI/20-21/027

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. HARMEET SINGH** (Enrollment No. 171804) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **PCR Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jata Shankar
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/028

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. VINAYKORRAM** (Enrollment No. 171805) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **PCR TECHNIQUES** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jata Shankar
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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JUIT/WKG/BT-BI/20-21/029

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DEVASHISH VERMA** (Enrollment No. 171806) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Embryo Culture For In-vitro Micropropagation of New Cicer arietinum (Chickpea) Varities** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Hemant Sood
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/030

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. AAKANKSHA PANDEY** (Enrollment No. 171807) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physicochemical Evaluation of Biosurfactants For Their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/031

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. REVA BHARDWAJ** (Enrollment No. 171809) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Immobilization of Enzymes onto the Nanoparticles and their Characterization Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Ashok Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/032

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DIVYANSH RANA** (Enrollment No. 171810) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Immobilization of Enzymes onto the Nanoparticles and their Characterization Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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JUIT/WKG/BT-BI/20-21/033

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SOUMI BISWAS** (Enrollment No. 171811) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Proteomics: Technologies and Application** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Jitendraa Vashistt
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/034

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. SUGAM SINGH** (Enrollment No. 171812) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/035

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. UMANG MAHESHWARI** (Enrollment No. 171813) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Molecular Circuits Using Synthetic Biology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Narendra Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/036

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DIWAKAR PALIWAL** (Enrollment No. 171814) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physico-Chemical Evaluation of Biosurfactants for their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
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Prof. Sudhir Kumar
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Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
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Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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CERTIFICATE

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Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. RACHITA GUPTA** (Enrollment No. 171818) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/041

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. VITASTA JALALI** (Enrollment No. 171819) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Study on ATCC** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Prof. Sudhir Kumar
(Training Supervisor)
(Head, Department of Biotechnology and Bioinformatics)

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/042

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NAVEETA KARAR** (Enrollment No. 171820) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Proteomic Technology, Techniques and Usage** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jitendraa Vashistt
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/036

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DIWAKAR PALIWAL** (Enrollment No. 171814) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Physico-Chemical Evaluation of Biosurfactants for their Potential Applications in Biotechnology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Poonam Sharma
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/037

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ISHITA KAWAR** (Enrollment No. 171815) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Micropropagation of Rhododendron** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Hemant Sood
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/038

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. EKTA CHOUDHARY** (Enrollment No. 171816) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/039

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. CHARU THAKUR** (Enrollment No. 171817) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Fermentation Technology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Garlapati Vijay Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/040

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. RACHITA GUPTA** (Enrollment No. 171818) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/041

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. VITASTA JALALI** (Enrollment No. 171819) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Study on ATCC** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Prof. Sudhir Kumar
(Training Supervisor)
(Head, Department of Biotechnology and Bioinformatics)

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NAVEETA KARAR** (Enrollment No. 171820) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Proteomic Technology, Techniques and Usage** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Jitendraa Vashistt
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/043

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. JIGYASA** (Enrollment No. 171821) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Technologies** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/044

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. KIRTI ARORA** (Enrollment No. 171823) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Innovations Made so far in Covid-19 Vaccines** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Supervisor &Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/045

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. AYUSH TYAGI** (Enrollment No. 171824) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Genotyping of Single Nucleotide Polymorphisms by Applying TARMS-PCR Method** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Harish Changotra
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/046

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NEHA VERMA** (Enrollment No. 171825) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Introduction to Chemical Pharmacology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Coordinator & Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/047

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. YUKTI** (Enrollment No. 171826) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Production of Disease-free Potatoes via Mericloning** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Hemant Sood
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY JUIT WAKNAGHAT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/048

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. YASHKIRTI GARG** (Enrollment No. 171827) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Chromatographic Techniques used for Arginase Purification** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Saurabh Bansal
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY * WAKNAGHAT * JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/049

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ISHITA** (Enrollment No. 171828) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Antibody Engineering** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Supervisor & Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY * WAKNAGHAT * JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/050

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MEGHA SHARMA** (Enrollment No. 171830) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Phytase and Different Chromatography Techniques used for it's Purification** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Saurabh Bansal
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY JUIT WAKNAGHAT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/057

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. AMANJOT SINGH MALHOTRA** (Enrollment No. 171831) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Genotyping of Single Nucleotide Polymorphismby Applying Pcr-Rflp Method** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Harish Changotra
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY * WAKNAGHAT * JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/058

Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. RISHAB ROY** (Enrollment No. 171832) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Study on ATCC(American Type Culture Collection)** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Prof. Sudhir Kumar
(Training Supervisor)
(Head, Department of Biotechnology and Bioinformatics)

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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JUIT/WKG/BT-BI/20-21/051

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MANVHI RASTOGI** (Enrollment No. 171834) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **VACCINATION** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Supervisor & Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/052

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NAYANIKA SHARMA** (Enrollment No. 171835) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Udayabanu, M
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

JUIT

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/053

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. SHIVANI CHATURVEDI** (Enrollment No. 171837) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Genotyping Single Nucleotide Polymorphism Applying ARFLP-PCR Method** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Harish Changotra
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. DIVYANSHU BHURAITA** (Enrollment No. 171840) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Immoblisation of Enzymes, Economical and Commercial uses, and their Methods and Characterization Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Ashok Kumar
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. JIGYASA** (Enrollment No. 171821) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Technologies** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

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(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. KIRTI ARORA** (Enrollment No. 171823) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Innovations Made so far in Covid-19 Vaccines** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Supervisor &Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Mr. AYUSH TYAGI** (Enrollment No. 171824) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Genotyping of Single Nucleotide Polymorphisms by Applying TARMS-PCR Method** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Harish Changotra
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/046

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NEHA VERMA** (Enrollment No. 171825) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Introduction to Chemical Pharmacology** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Coordinator & Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/047 Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. YUKTI** (Enrollment No. 171826) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Production of Disease-free Potatoes via Mericloning** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Hemant Sood
(Training Supervisor)
Associate Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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JUIT/WKG/BT-BI/20-21/048

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. YASHKIRTI GARG** (Enrollment No. 171827) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Chromatographic Techniques used for Arginase Purification** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Saurabh Bansal
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. ISHITA** (Enrollment No. 171828) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Antibody Engineering** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
(Training Supervisor & Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MEGHA SHARMA** (Enrollment No. 171830) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Phytase and Different Chromatography Techniques used for it's Purification** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Saurabh Bansal
(Training Supervisor)
Assistant Professor, Department of Biotechnology and Bioinformatics

Dr. Rahul Shrivastava
(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
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JUIT/WKG/BT-BI/20-21/051

Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. MANVHI RASTOGI** (Enrollment No. 171834) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **VACCINATION** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

During this training period the candidate was sincere and hard working. We wish for a bright future and success in his/her studies and career.

Dr. Rahul Shrivastava
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Associate Professor, Department of Biotechnology and Bioinformatics

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Date: 26/08/2020

CERTIFICATE

This is to certify that **Ms. NAYANIKA SHARMA** (Enrollment No. 171835) studying Bachelor of Technology (B.Tech.) Degree in Biotechnology and Bioinformatics of Jaypee University of Information Technology (JUIT), Waknaghat, has successfully completed his/ her SIX WEEKS In-house virtual mode Summer Training in the area of **Animal Cell Culture Techniques** from **May 15' 2020 to June 30' 2020** at the Department of Biotechnology and Bioinformatics, JUIT Waknaghat.

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Dr. Udayabanu, M
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(Training Coordinator)
Associate Professor, Department of Biotechnology and Bioinformatics

Prof. Sudhir Kumar
(Head, Department of Biotechnology and Bioinformatics)

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Tel.: 0141-2700648, E-mail : officekanha@gmail.com

15.07.2020

TO WHOM SO EVER IT MAY CONCERN

This is to certify that Miss Khushi Maheshwari student of Jaypee University of Information Technology (JUIT), Solan, HP has successfully completed Training for 1 Month and 15 Days W.e.f. 01.06.2020 to 15.07.2020 with the Quality Assurance and Control Department at M/s Sanwaria Sweets Pvt. Ltd. (Kanha), Jaipur.

During her training she has undergone 1 project and has successfully submitted the respective report of that project. She has submitted project on:

1. **Qualitative Analysis of Traditional Indian Sweets and Namkeen Products**

The Project submitted by her was excellent and added value to the organization.

She has shown a great amount of reliability, sincerity and willingness to learn and is capable of working in a multi-sectoral team. We wish her success in all future endeavors.

For Sanwaria Sweets Pvt. Ltd.,

For SANWARIA SWEETS PVT. LTD.

Lokpal Singh
(Assistant General Manager-HR & Admin.)

Regd. Office :

J-6, Himmat Nagar, Near Gopalpura Fly Over, Tonk Road, Jaipur-302018, Rajasthan

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Next Generation Sequencing (NGS) Data Analysis

Industrial Training

.



Supervisor: Dr Tiratha Raj Singh

Shaurya Mehta

141505

Btech Bioinformatics

Training Period: 6 weeks

CONTENTS:

- **Acknowledgment.**
- **Abstract.**
- **Introduction to NGS.**
- **Role of Bioinformatics in NGS.**
- **Applications of NGS.**
- **Introduction to RNA sequencing.**
- **Types of methods for RNA sequencing.**
- **Non Coding RNA.**
- **Alternate Splicing.**
- **NGS data analysis.**
- **Structural Variome.**
- **Handling of NGS data.**
- **Metagenomics,**
- **Future Applications of NGS.**

Acknowledgment

At the very beginning, I would like to express my deepest to almighty GOD for giving me the strength and the composure to finish the report.

Words actually will never be enough to express how grateful I am, but never the less I will try my level best to express my gratefulness toward some people.

At first, I would like to express my indebtedness to Jaypee University of Information and Technology. I want to remember my department, teachers, and family especially my internship supervisor, my mentor, **Dr Tiratha Raj Singh** for backing me up in my downs, without your support it was nearly impossible for me to complete my Industrial Training. I would like to

convey my sincere gratitude to my honorable teacher **Dr Rahul Shrivastava, Dr Sudhir Syal (H.O.D**). Without their guidance and support, this report would not have seen the light of day.

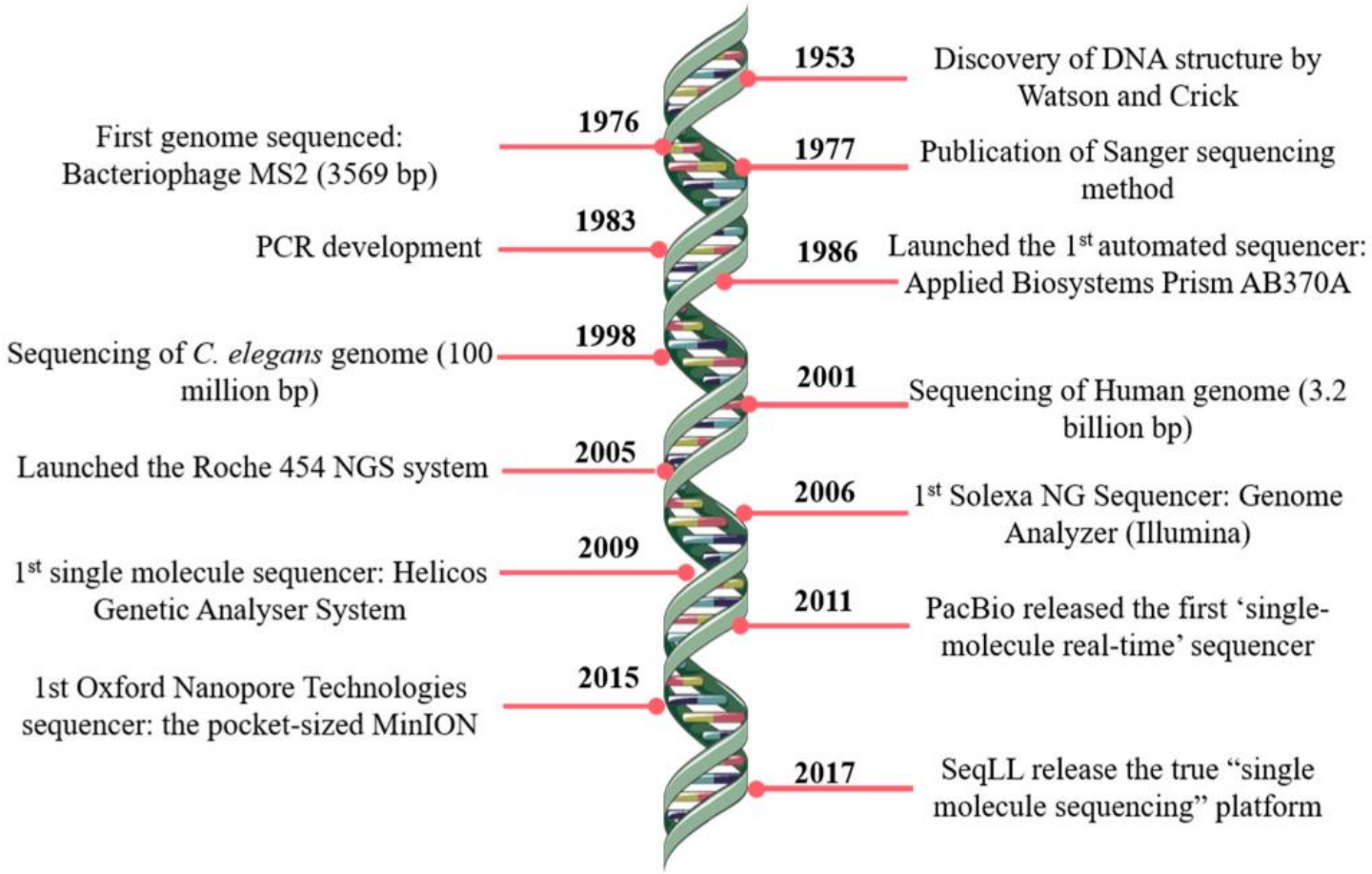
Abstract:

Next-generation sequencing (NGS) technologies using DNA, RNA, or methylation sequencing have impacted enormously on the life sciences. NGS is the choice for large-scale genomic and transcriptomic sequencing because of the high-throughput production and outputs of sequencing data and the lower cost compared to the traditional Sanger first-generation sequencing method. The vast amounts of data generated by NGS have broadened our understanding of structural and functional genomics through the concepts of "omics" ranging from basic genomics to integrated systeomics, providing new insight into the workings and meaning of genetic conservation and diversity of living things. NGS today is more than ever about how different organisms use genetic information and molecular biology to survive and reproduce with and without mutations, disease, and diversity within their population networks and changing environments. Next generation sequencing (NGS), massively parallel or deep sequencing are related terms that describe a DNA sequencing technology which has revolutionized genomic research. Using NGS an entire human genome can be sequenced within a single day

Introduction:

Deoxyribonucleic acid, commonly known as DNA, contains the blueprints of life. Within its structures are the codes required for the assembly of proteins and non-coding RNA – these molecular machineries affect all the biological systems that create and maintain life. By understanding the sequence of DNA, researchers have been able to elucidate the structure and function of proteins as well as RNA and have gained an understanding of the underlying causes of disease. Next Generation Sequencing (NGS) is a powerful platform that has enabled the sequencing of thousands to millions of DNA molecules simultaneously. This powerful tool is

revolutionizing fields such as personalized medicine, genetic diseases, and clinical diagnostics by offering a high throughput option with the capability to sequence multiple individuals at the same time.



First-generation DNA sequencing:

The first generation of sequencing technology is based on the chain termination method developed by Sanger and Coulson in 1975 or the chemical method (chain degradation) invented by Maxam and Gulbert during 1976 and 1977. And Sanger in 1977 judged the first genome sequence belonging to Phage X174 with the whole length of 5375 bases. Since then, human beings have acquired the ability to snoop the nature of the genetic difference of life, and also it is a beginning of the genomic era. Researchers continue to improve the Sanger method during performance. In 2001, it was based on the improved Sanger method that the first human genome map was completed. The core principle of Sanger method is that ddNTP cannot form phosphodiester bond during the synthesis of DNA, due to the lack of hydroxyl in its 2 'and 3'. So it can be used to interrupt the DNA synthesis reaction. Add a certain proportion of ddNTP with radioactive isotope label, including ddATP, ddCTP, ddGTP and ddTTP, into four DNA

synthesis reaction systems respectively. After gel electrophoresis and autoradiography, the DNA sequences of the samples can be determined according to the position of the electrophoretic band.

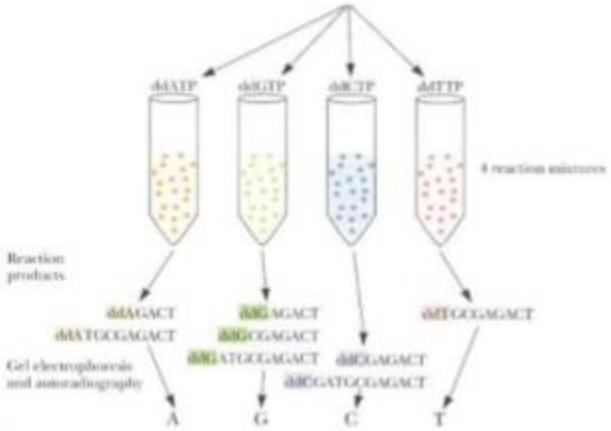
In addition to Sanger method, it is worth noting that during the period of sequencing technology development, there are many other sequencing technologies emerging, such as pyrophosphate sequencing method, ligation enzyme method and so on. Among these, pyrophosphate sequencing method was later used by Roche company for 454 technique, while the ligation enzyme method was used for SOLID technique by ABI company. The common core method shared by both of them was to use dNTP which can interrupt DNA synthesis, similar to ddNTP in Sanger method.

All in all, the first generation of sequencing technology has the read-length ability of 1000bp with the 99.999% accuracy, which are the main feature. However, its high cost, low throughput and other disadvantages result in a serious impact on its real large-scale application. Therefore, the first generation of sequencing technology is not the most ideal sequencing method. Undergoing development and improvement, the second generation of sequencing technology was born symbolized by Roche's 454 technology, Illumina's Solexa, Hiseq technology, and ABI's Solid technology. The second generation of sequencing technology cannot only greatly reduce sequencing cost, but also dramatically increase the speed of sequencing, maintaining high accuracy. The turn-around time of the second generation sequencing technology to complete a human genome project can just be one week, while that using the first generation sequencing technology to achieve the same goal is three years. However, the read length of the second generation of sequencing technology is much shorter than that of the first generation.

SANGER SEQEUNCING

- Chain termination method of DNA sequencing.
- It involves following components:

a) 1. Primer
b) 2. DNA template
c) 3. DNA polymerase
d) 4. dNTPs(A,T,G,C)
e) 5. ddNTPs



- 4 Steps:
  1. Denaturation
  2. Primer attachment and extension of bases
  3. Termination
  4. Poly acrylamide gel electrophoresis

Second-generation DNA sequencing:

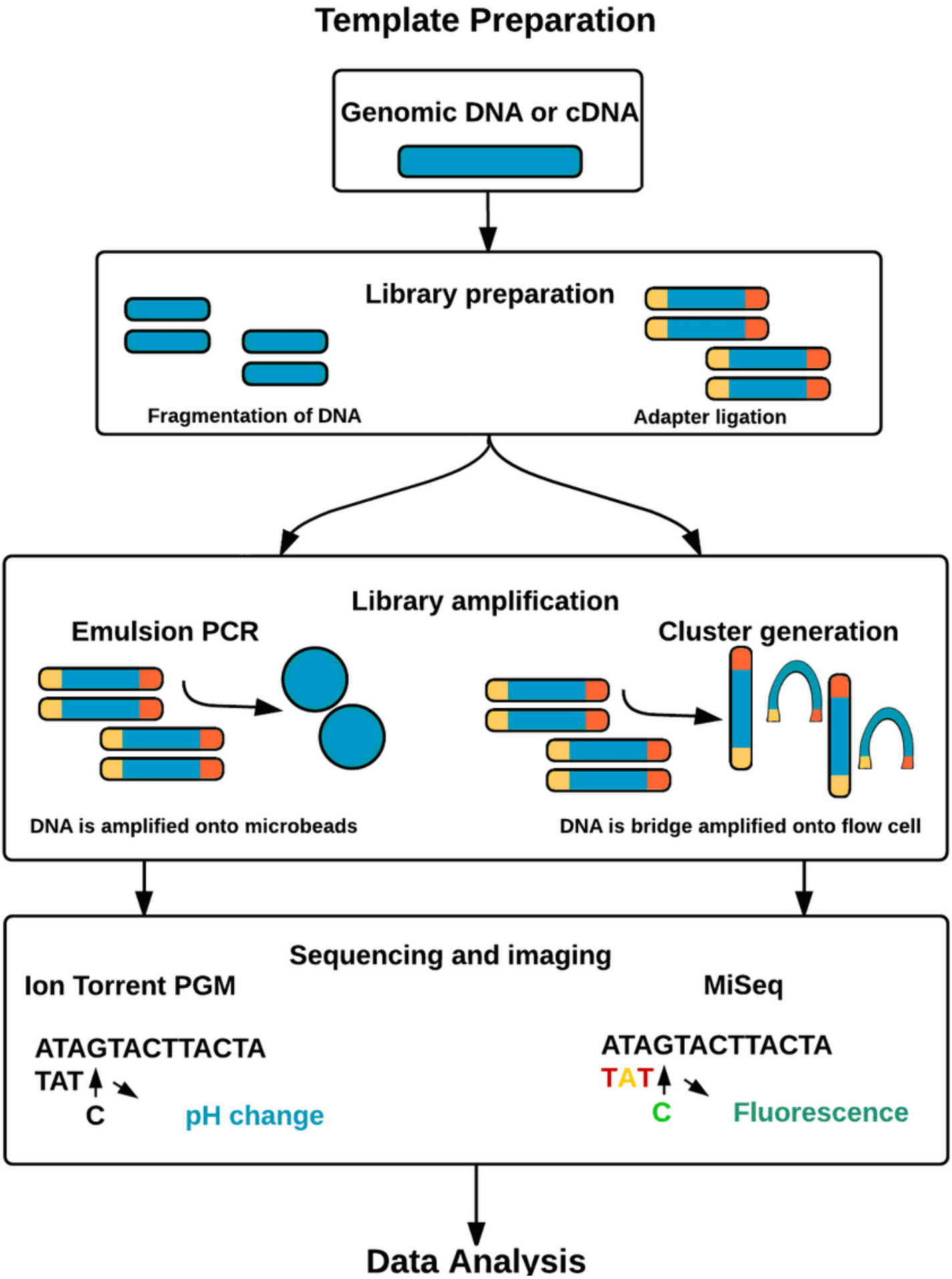
The first generation of sequencing was dominant for three decades especially Sanger sequencing, however, the cost and time was a major stumbling block. In 2005 and in subsequent years, have marked the emergence of a new generation of sequencers to break the limitations of the first generation. The basic characteristics of second generation sequencing technology are: the generation of many millions of short reads in parallel, he speed up of sequencing the process compared to the first generation, the low cost of sequencing and he sequencing output is directly detected without the need for electrophoresis. Short read sequencing approaches divided under two wide approaches: sequencing by ligation (SBL) and sequencing by synthesis (SBS), and are mainly classified into three major sequencing platforms: Roche/454 launched in 2005, Illumina / Solexa in 2006 and in 2007 the ABI/SOLiD. We will briefly describe these commonly utilized sequencing platforms.

Roche/454 sequencing:

Roche/454 sequencing appeared on the market in 2005, using pyrosequencing technique which is based on the detection of pyrophosphate released aier each nucleotide incorporation in the new synthetic DNA strand. The pyrosequencing technique is a sequencing-by-synthesis approach. DNA samples are randomly fragmented and each fragment is attached to a bead whose surface carries primers that have oligonucleotides complementary to the DNA fragments so each bead is associated with a single fragment. Then, each bead is isolated and amplified using PCR emulsion which produces about one million copies of each DNA fragment on the surface of the bead. The beads are then transferred to a plate containing many wells called picotiter plate (PTP) and the pyrosequencing technique is applied which consists in activating of a series of downstream reactions producing light at each incorporation of nucleotide. By detecting the light emission aier each incorporation of nucleotide, the sequence of the DNA fragment is deduced. The use of the picotiter plate allows hundreds of thousands of reactions occur in parallel, considerably increasing sequencing throughput. The latest instrument launched by Roche/454 called GS FLX+ that generates reads with lengths of up to 1000 bp and can produce ~1Million reads per run. The Roche/454 is able to generate relatively long reads which are easier to map to a reference genome. The main errors detected of sequencing are insertions and deletions due to the presence of homopolymer regions. Indeed, the identification of the size of homopolymers should be determined by the intensity of the light emitted by pyrosequencing. Signals with too high or too low intensity lead to under or overestimation of the number of nucleotides which causes errors of nucleotides identification.

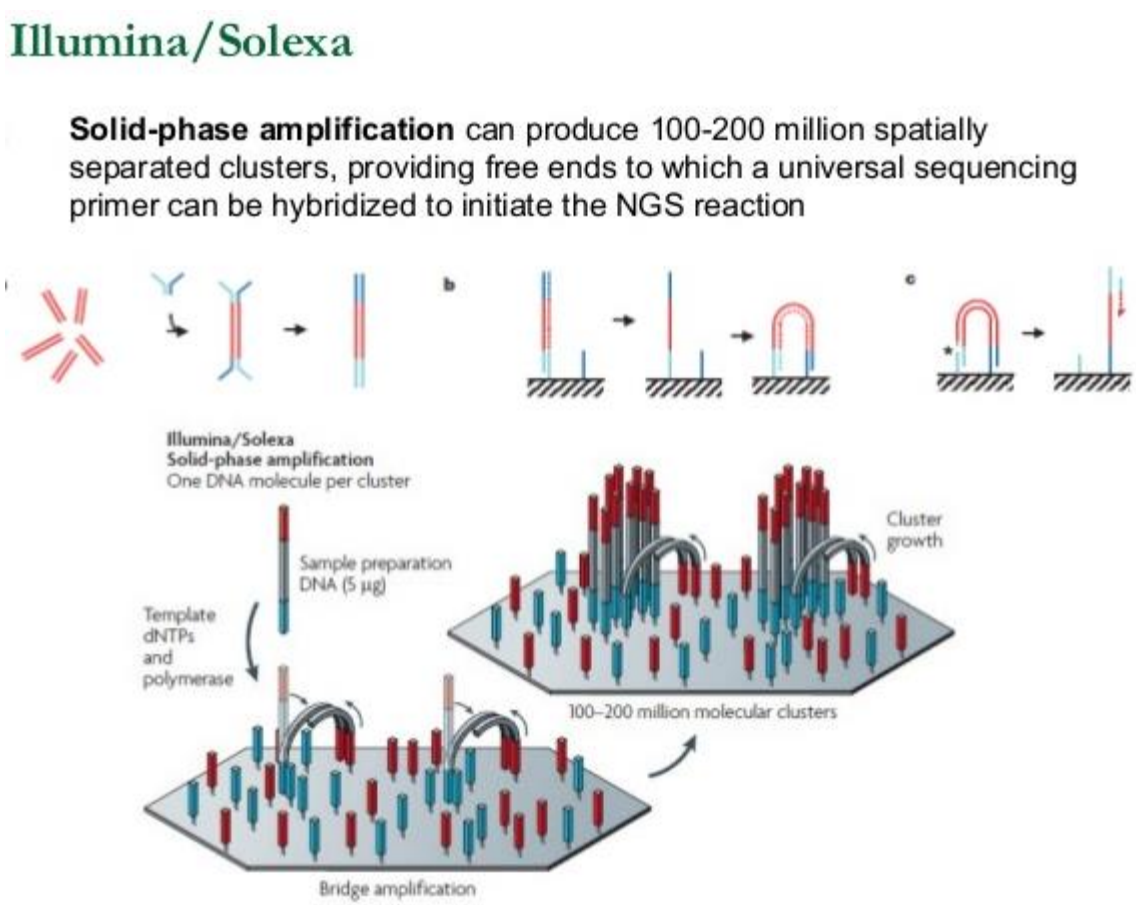
Ion torrent sequencing:

Life Technologies commercialized the Ion Torrent semiconductor sequencing technology in 2010. It is similar to 454 pyrosequencing technology but it does not use fluorescent labeled nucleotides like other second-generation technologies. It is based on the detection of the hydrogen ion released during the sequencing process. Specifically, Ion Torrent uses a chip that contains a set of micro wells and each has a bead with several identical fragments. The incorporation of each nucleotide with a fragment in the pearl, a hydrogen ion is released which change the pH of the solution. This change is detected by a sensor attached to the bottom of the micro well and converted into a voltage signal which is proportional to the number of nucleotides incorporated. The Ion Torrent sequencers are capable of producing reads lengths of 200 bp, 400 bp and 600 bp with throughput that can reach 10 Gb for ion proton sequencer. The major advantages of this sequencing technology are focused on read lengths which are longer to other SGS sequencers and fast sequencing time between 2 and 8 hours. The major disadvantage is the difficulty of interpreting the homopolymer sequences (more than 6 bp) which causes insertion and deletion error with a rate about ~1%


Template Preparation
Genomic DNA or cDNA
Library preparation
Fragmentation of DNA
Adapter ligation
Library amplification
Emulsion PCR
Cluster generation
DNA is amplified onto microbeads
DNA is bridge amplified onto flow cell
Sequencing and imaging
Ion Torrent PGM
MiSeq
ATAGTACTTACTA
TAT
C
pH change
ATAGTACTTACTA
TAT
C
Fluorescence
Data Analysis

Illumina/Solexa sequencing:

The Solexa Company has developed a new method of sequencing. Illumina Company purchased Solexa that started to commercialize the sequencer Ilumina/Solexa Genome Analyzer (GA). Illumina technology is sequencing by synthesis approach and is currently the most used technology in the NGS market. During the first step, the DNA samples are randomly fragmented into sequences and adapters are ligated to both ends of each sequence. Then, these adapters are fixed themselves to the respective complementary adapters, the latter are hooked on a slide with many variants of adapters (complementary) placed on a solid plate. During the second step, each attached sequence to the solid plate is amplified by "PCR bridge amplification that creates several identical copies of each sequence; a set of sequences made from the same original sequence is called a cluster. Each cluster contains approximately one million copies of the same original sequence. The last step is to determine each nucleotide in the sequences, Illumina uses the sequencing by synthesis approach that employs reversible terminators in which the four modified nucleotides, sequencing primers and DNA polymerases are added as a mix, and the primers are hybridized to the sequences. Then, polymerases are used to extend the primers using the modified nucleotides. Each type of nucleotide is labeled with a fluorescent specific in order for each type to be unique. The nucleotides have an inactive 3'-hydroxyl group which ensures that only one nucleotide is incorporated. Clusters are excited by laser for emitting a light signal specific to each nucleotide, which will be detected by a coupled-charge device (CCD) camera and Computer programs will translate these signals into a nucleotide sequence. The process continues with the elimination of the terminator with the fluorescent label and the starting of a new cycle with a new incorporation. The first sequencers Illumina/Solexa GA has been able to produce very short reads ~35 bp and they had an advantage in that they could produce paired-end (PE) short reads, in which the sequence at both ends of each DNA cluster is recorded. The output data of the last Illumina sequencers is currently higher than 600 Gb and lengths of short reads are about 125 bp. Details on Illumina sequencers. One of the main drawbacks of the Illumina/Solexa platform is the high requirement for sample loading control because overloading can result in overlapping clusters and poor sequencing quality. The overall error rate of this sequencing technology is about 1%. Substitutions of nucleotides are the most common type of errors in this technology, the main source of error is due to the bad identification of the incorporated nucleotide.



ABI/SOLiD sequencing:

Supported Oligonucleotide Ligation and Detection (SOLiD) is a NGS sequencer Marketed by Life Technologies. In 2007, Applied Biosystems (ABI) has acquired SOLiD and developed ABI/SOLID sequencing technology that adopts by ligation (SBL) approach. He ABI/SOLiD process consists of multiple sequencing rounds. It starts by attaching adapters to the DNA fragments, fixed on beads and cloned by PCR emulsion. These beads are then placed on a glass slide and the 8-mer with a fluorescent label at the end is sequentially ligated to DNA fragments, and the color emitted by the label is recorded. Then, the output format is color space which is the encoded form of the nucleotide where four fluorescent colors are used to represent 16 possible combinations of two bases. He sequencer repeats this ligation cycle and each cycle the complementary strand is removed and a new sequencing cycle starts at the position n-1 of the template. The cycle is repeated until each base is sequenced twice. He recovered data from the color space can be translated to letters of DNA bases and the sequence of the DNA fragment can be deduced. ABI/SOLiD launched the first sequencer that produce short reads with length 35 bp and output of 3 Gb/run and continued to improve their sequencing which increased the length of reads to 75 bp with an output up to 30 Gb/run. The strength of ABI/SOLiD platform is

high accuracy because each base is read twice while the drawback is the relatively short reads and long run times. The errors of sequencing in this technology is due to noise during the ligation cycle which causes error identification of bases. The main type of error is substitution.

SMRT sequencing:

Pacific Biosciences (http//www.pacificbiosciences.com/) developed the first genomic sequencer using SMRT approach and it's the most widely used third-generation sequencing technology. Pacific Biosciences uses the same fluorescent labeling as the other technologies, but instead of executing cycles of amplification nucleotide, it detects the signals in real time, as they are emitted when the incorporations occur. It uses a structure composed of many SMRT cells; each cell contains microfabricated nanostructures called zeromode waveguides (ZMWs) which are wells of tens of nanometers in diameter microfabricated in a metal film which is in turn deposited onto a glass substrate. These ZMWs exploit the properties of light passing through openings with a diameter less than its wavelength, so light cannot be propagated. Due to their small diameter, the light intensity decreases along the wells and the bottom of the wells illuminated. Each ZMW contains a DNA polymerase attached to their bottom and the target DNA fragment for sequencing. During the sequencing reaction, the DNA fragment is incorporated by the DNA polymerase with fluorescent labeled nucleotides (with different colors). Whenever a nucleotide is incorporated, it releases a luminous signal that is recorded by sensors. The detection of the labeled nucleotides makes it possible to determine the DNA sequence. Compared to SGS, Pacific Bioscience technology has several advantages. The preparation of the sample is very fast, it takes 4 to 6 hours instead of days. In addition, the long-read lengths, currently averaging ~10 kb but individual very long reads can be as long as 60 kb, which is longer than that of any SGS technology. Pacific Biosciences sequencing platforms have a high error rate of about 13% dominated by insertions and deletions errors. These errors are randomly distributed along the long read.

Third Generation of Sequencing:

The second-generation of sequencing technologies previously discussed have revolutionized the analysis of DNA and have been the most widely used compared to the first generation of sequencing technologies. However, the SGS technologies generally require PCR amplification step which is a long procedure in execution time and expansive in sequencing price. Also, it became clear that the genomes are very complex with many repetitive areas that SGS

technologies are incapable to solve them and the relatively short reads made genome assembly more difficult. To remedy the problems caused by SGS technologies, scientists have developed a new generation of sequencing called “third generation sequencing”. These third generations of sequencing have the ability to offer a low sequencing cost and easy sample preparation without the need PCR amplification in an execution time significantly faster than SGS technologies. In addition, TGS are able to produce long reads exceeding several kilobases for the resolution of the assembly problem and repetitive regions of complex genomes. There are two main approaches that characterize TGS: The single molecule real time sequencing approach (SMRT) that was developed by Quake laboratory and the synthetic approach that rely on existing short reads technologies used by Illumina (Moleculo) and 10xGenomics (https://www.10xgenomics.com) to construct long reads. The most widely used TGS technology approach is SMRT and the sequencers that have used this approach are Pacific Biosciences and Oxford Nanopore sequencing (specifically the MinION sequencer).

Oxford Nanopore sequencing:

The Oxford Nanopore sequencing (ONT) was developed as a technique to determine the order of nucleotides in a DNA sequence. In 2014, Oxford Nanopore Technologies released the MinION device that promises to generate longer reads that will ensure a better resolution structural genomic variants and repeat content. It’s a mobile single-molecule Nanopore sequencing measures four inches in length and is connected by a USB 3.0 port of a laptop computer. This device has been released for testing by a community of users as part of the MinION Access Program (MAP) to examine the performance of the MinION sequencer [50]. In this sequencing technology, the first strand of a DNA molecule is linked by a hairpin to its complementary strand. He DNA fragment is passed through a protein nanopore. When the DNA fragment is translated through the pore by the action of a motor protein attached to the pore, it generates a variation of an ionic current caused by differences in the moving nucleotides occupying the pore. This variation of ionic current is recorded progressively on a graphic model and then interpreted to identify the sequence. He sequencing is made on the direct strand generating the “template read” and then the hairpin structure is read followed by the inverse strand generating the “complement read”, these reads is called "1D". If the “temple” and “complement” reads are combined, then we have a resulting consensus sequence called “two direction read” or "2D". Among the advantages offered by this sequencer: first, it’s low cost and small size. Then, the sample is loaded into a port on the device and data is displayed on the screen and generated without having to wait till the run is complete. And, MinION can provide very long reads exceeding 150 kb which can improve the contiguity of the denovo assembly. However, MinION produces a high error rate of ~12% distributed about ~3% mismatches, ~4% insertions and ~5% deletions. The ONT technology has continued to evolve. Recently, a new

instrument has emerged called "PromethION"; it is the bigger brother of the MinION. It is an autonomous worktable sequencer with 48 individual flow cells each with 3000 pores (equivalent to 48 MinIONs) operating at 500 bp per second which is sufficiently powerful to achieve an ultra-high throughput needed for sequencing large genomes such as the human genome. Although the PromethION is not commercially available, the ONT announces that it is capable of producing ~2 to 4 Tb for a duration of 2 days and a length of reads which can attain 200 Kb which puts this sequencer in competition with the PacBioRSII sequencer from pacific biosciences in terms of read length and HiSeq sequencer from Illumina in cost.

	First generation	Second generation	Third generation
Fundamental technology	Size-separation of specifically end-labeled DNA fragments	Wash-and-scan SBS	Single molecule real time sequencing
Resolution	Averaged across many copies of the DNA molecule	Averaged across many copies of the DNA molecule	Single DNA molecule
Current raw read accuracy	High	High	Lower
Current read length	Moderate (800-1000 bp)	Short (generally much shorter than Sanger sequencing)	> 1000 bp
Current throughput	Low	High	High
Current cost	High cost per base, Low cost per run	Low cost per base, High cost per run	Low cost per base, High cost per run
RNA-sequencing method	cDNA sequencing	cDNA sequencing	Direct RNA sequencing
Time to result	Hours	Days	< 1 day
Sample preparation	Moderately complex, PCR amplification is not required	Complex, PCR amplification is required	Various
Data analysis	Routine	Complex (due to large data volumes & short reads)	Complex
Primary results	Base calls with quality values	Base calls with quality values	Base calls with quality values

Adapted from Schadt, et al. Hum Mol Genet 2010[13]

Error Rate:

	illumina	Roche 454 SEQUENCING	ion torrent by life technologies	PACIFIC BIOSCIENCES
Read length, bp	25-250	400-1100	200-400	1000-5000
Error rate	0.01-1%	1%	1-2%	10-13%
Error type	Mismatches	Indels & Mismatches	Indels & Mismatches	Indels & Mismatches
Comments	Error rate grows to the end of the read	Problems with homopolymers	Problems with homopolymers	
Cost per 1 mbp, $	0.05 - 0.5	30	0.5 - 5	2

Bioinformatics: DNA and RNA data analysis:

Bioinformatics is a major rate-limiting step for NGS technology with respect to overcoming the growing challenges of storage, analysis, and interpretation of NGS data. There are at least four tiers of nucleotide sequence analysis to consider when using the NGS platforms. The first is generation of sequence reads using the software integrated within the sequencing instruments that convert the raw signals into base calling with short reads of nucleotide sequences and associated quality scores. The second is the alignment and assembly of contigs and scaffolds and variant detection. The third is annotation, data integration, and visualization of the assembled sequence. The fourth is the amalgamation of all the data from the different NGS platforms into a single, coherent, bioinformatics output with accessible links and tools for general and particular biological or forensic interest.

The raw sequencing signals produced by the manufacturer's sequencing machine or system are converted into nucleotide bases of short read data (base calling) with base quality scoring using the system's FASTQ format or the native raw data file formats (Illumina, SFF, HDF5, CG, or

SOLID). Storage of raw signal (image) and sequencing data as short read archives in the FASTQ format or native raw data file formats is a problem in regard to computing resources for many research sequencing laboratories and commercial service providers. Thus, the conversion of FASTQ files to the more compact Sequence Alignment Map (SAM) format and its compressed Binary Alignment Map (BAM) format is recommended because it is easier to read and process for later bioinformatics analysis. The safe storage of the original raw sequences is important for bioinformatics analysis and corrections because it is the source of the initial sequencing errors that are either filtered out or left within the final assembled sequence. Quality checks are necessary to remove reads with low phred levels, sequence errors, and sequences such as primers, vectors, adapters, tags, and tails that were introduced experimentally during the preparation of the sequencing libraries. Errors or biases associated with raw reads from the Illumina, Roche, and SOLiD platforms are mainly fluorophore-dependent errors, whereas the non-fluorophore platforms such as Ion Torrent produce their own unique errors and biases. Therefore, many different signal and image detection programs and base calling algorithms still need to be developed and tested in an attempt to improve the accuracy of base calling. The raw sequence data (a mixture of raw files and other metadata) from the NGS technologies can be submitted to the NCBI Sequence Read Archive database for DNA studies and to Gene Expression Omnibus and ArrayExpress for mRNA-seq or ChIP-Seq studies in order to receive a database accession number and to reference the raw sequence data in scientific publications. The Sequence Read Archive (SRA) at NCBI also provides a fee-free, downloadable SRA computing toolkit to read the raw graphs and files from the different NGS platforms and to convert between different file formats. Archive files in the SRA format (.sra) are converted into the FASTQ or SAM/BAM formats for input to downstream analysis using software programs to undertake the second tier analysis of sequence alignment (spliced and genomic), assembly, and variant detection.

Applications of NGS

NGS technologies have many applications such as DNA-sequencing and assembly to determine an unknown genome without any preparation or search for variations among genome samples, RNA-sequencing, to analyze gene expression and to predominantly identify DNA regions of DNA binding proteins, for example, transcription factors etc. The most important application of NGS is in identifying mutations. Commonly, short i.e. 50–250 bp NGS reads are initially mapped to a reference genome and after that from the mapped data, variations are detected. While most of the NGS applications concentrate on identification of single nucleotide variations (SNVs) or small insertions/deletions (indels), structural variation including translocations, bigger indels, and copy number variation (CNV) can also be recognized from similar data. Structural variation discovery can be performed from whole genome NGS data or “targeted” data including exomes or gene panels. While targeted sequencing incredibly

increments sequencing coverage or depth of specific genes, it might present predispositions in the data that require particular computational analysis. Since the past few years, there have been extensive advances in methods used to identify structural variations and a full coverage of variations from SNVs; balanced translocations to CNV can now be identified with reasonable sensitivity from either whole genome or targeted NGS data. Such methods are connected to clinical testing where they can supplement fluorescence in situ hybridization or array-based testing. The identification of structural DNA variation has since quite a while ago assumed a part in the diagnosis of cancer and Mendelian disorders, originating before the approach of current DNA sequencing. Structural DNA variation is found in a DNA region larger than 1 kb and incorporates a few classes, for example, translocations, inversions, insertions/deletions (indels) and copy number variations (CNVs).

NGS-based diagnostics implement some portion of the clinical genomic testing in which a limited set of genes are targeted and not the entire genome and exome. Such diagnostics are routinely offered by more than 250 commercial and academic laboratories. One of the key elements of NGS-based diagnostics is its capacity to identify a full coverage of hereditary variation, offering the possibility to significantly streamline testing by utilizing a single analysis platform. For instance, prognostic assessment of acute myeloid leukemia for the most part requires the utilization of various advances including PCR and fragment sizing to detect FLT3 internal tandem duplications and NPM1 insertions, Sanger sequencing to identify CEBPA, IDH1/2, and DNMT3A mutations, and FISH to identify MLL, RARA, CBFB, and RUNX1 rearrangements. Such complicated assessments require very well trained staff with prohibitive cost. Thus, NGS-based testing can identify SNVs, insertions and translocations in a single test, considerably bringing down cost as compared with that of a conventional workup.

Single-cell sequencing is used for characterization of cancer heterogeneity. Cancer heterogeneity is caused due to different factors such as tissue hierarchies, clonal evolution, rare cells and dynamic cell states. With single-cell sequencing, it can be characterized in a large population of cells and molecular properties influencing clinical outcomes like prognosis and treatment, and can be determined in contrast to bulk sequencing, in which significant information is lost as the molecular profile represents an average phenotype over a large number of cells.

Table 1. NGS platforms currently employed.

Sr. No.	Platform	Read length	Sequencing approach
1	Illumina/ Solexa, Illumina, Inc.	30–40 bp	Sequencing by synthesis with reversible terminators
2	ABI/SOLiD, Applied Biosystems	35 bp	Massively parallel sequencing by Ligation
3	454/Roche FLX system, Roche Applied Science	200–300 bp	Pyrosequencing on solid support
4	Ion Torrent	200 bp	Proton detection

NGS technologies are utilized to produce whole genome data, create exome data (all coding sequences in the genome), or target particular genes or loci of interest. While whole genome data is by and large low coverage (8–30 bp coverage) and reasonable for the discovery of constitutional variations, by targeting on sequencing to particular genes or regions of interest, the coverage might be expanded to 1000 or higher, allowing more delicate assessment of gene variations and subclonal populations in cancer.

RNA Sequencing- Principle, Steps, Methods and Applications:

Ribonucleic acid is a type of nucleic acid majorly involved in the gene expression, gene regulation and coding/decoding of information.

mRNA- messenger RNA is a coding sequence of a gene implicated in the synthesis of protein, approximately, 4% of RNA pool consists of mRNA while rest are non-coding RNAs.

Though approximately 90% of RNA are non-coding, those are important for performing various functions**.**

For example,

- tRNA- transfers the amino acid to the ribosomal site, while the translation.
- rRNA- ribosomal RNA helps in translation.
- microRNA- gene expression and regulation of gene expression.
- siRNA- protects a cell from the exogenous RNAs.

An mRNA is a single-stranded nucleic acid transcribed from a gene and from which the protein is translated.

The mRNA or transcript contains only the coding sequences from a gene. Thus it only possesses the sequences which are required in the protein formation.
Henceforth, by analysing an mRNA, the expression pattern of the related gene can be determined.
Also, total RNA examination gives us an idea about which genes are linked to the protein formation and which are not.
Means, the amount of total RNA, mRNA and ncRNA can be determined by studying the total RNA.
Transcriptomics is the study of the entire mRNA- often called as transcriptomes or total RNA present in a cell or cell population.
By analysing the transcriptome of a cell, the entire pool of the gene expression can be examined. One of the important techniques used in transcriptomics studies is RNA sequencing.
The transcriptome of an organism is larger, complex and more uncertain, unlike the genome.
The transcriptome varies in different condition and a different environment. Lifestyle, diet, exercise, environment, conditions and other external factors play a significant role in transcriptome regulation.

Principle of RNA sequencing:

RNA sequencing is a next-generation, high throughput RNA sequencing and quantification method used for studying the transcriptomics and gene expression.
A cDNA is constructed from total mRNA through the process of reverse transcription and fragmented. Simultaneous, adaptor ligation and library preparation are practised before doing sequencing.
The sequencer reads and quantifies the cDNA complementary to the mRNA.

Steps in RNA-seq:

- RNA isolation
- cDNA synthesis
- Adaptor ligation
- Library preparation
- DNA fragmentation
- Sequencing
- Downstream applications

RNA isolation:

- The first step in the RNA sequencing is the isolation of total RNA, mRNA or ncRNA for the experiment.
- Isolating RNA is a tedious process in comparison with DNA isolation. The RNA can be breakdown easily. Also, the chance of contamination is high in RNA isolation.
- Thus extra care must be taken while isolating RNA and expert hand in required to do so. High yield pure RNA is must require for RNA sequencing.
  The purity and quantity of the RNA are measured using the Nanodrop or qubit.

Reverse transcriptase PCR:

Another innovative set up for RNA sequencing is to do reverse transcriptase PCR in which the RNA is reverse transcribed into DNA.
Using a special type of polymerase known as DNA reverse transcriptase, the cDNA is synthesised from the mRNA.
Learn more on RT PCR here: Reverse transcriptase PCR.

Second strand cDNA synthesis:

After the cDNA synthesized from the mRNA, the second strand DNA synthesis is must required. For that, PCR is performed using the normal Taq DNA polymerase in conventional PCR.
The Polymerase adds dNTPs to the growing DNA strand using the primer set.

Library preparation:

The first step in the library preparation or NGS library preparation starts with the fragmentations.
Using the special type of restriction endonucleases whole set of ds cDNA is fragmented for the NGS.

Library purification:
The entire library is purified using the ready to use DNA purification kit.
In the last step, it is very crucial to purify the entire fragment library for that the concentration of the library is assessed using the quantitative PCR or bioanalyzer.

DNA sequencing:
Now the sample is sequenced in the high throughput NGS machine which reads the sequence as well as quantifies the nucleic acid as well.
The chemistry behind sequencing the cDNA is depends on which platforms we are using, although, the widely used method is the use of fluorescence chemistry.
In the sequencer, individual fragments are “read” separately and sequenced. The final data are sent to the bioinformatics lab for post-sequencing analysis.

Different RNA sequencing methods:

Whole Transcriptome sequencing:

The whole transcriptome of a cell or tissue- all RNAs (mRNA, tRNA, rRNA, sncRNA, microRNA and siRNA) are sequenced and quantified. In other words, we can say, Both novel, as well as known transcripts, can be sequenced.

For doing it, the entire set of RNA is extracted from the tissue sample.

Target RNA sequencing:

A gene-specific, cluster of gene-specific, a pathway-specific or disease-related transcriptomes is sequenced in the target-specific RNA sequencing.

Target RNA sequencing is more affordable and accurate than the whole Transcriptome sequencing. Moreover, less amount of RNA sample is required for doing the experiment.

Small RNA sequencing:

One of the most emerging techniques in RNA-sequencing is to study the smaller non-coding RNA of a cell because those are associated with so many functions in a genome.

Smaller RNA molecules such as miRNA, siRNA and piRNA can be quantified and sequenced through the NGS based RNA sequencing method for various applications.

mRNA sequencing:

Sequence the entire mRNA transcript using poly(A) tail selection used for gene expression studies. Using mRNA sequencing known as well as novel transcript alteration can be detected.

Advantages of RNA sequencing:

One of the pivotal advantages of RNA sequencing is the no need for prior sequence information. As the entire process is not based on the probe-based chemistry, prior sequence information for designing the probe is not required here.

More accurate and sensitive gene expression study can be done.

Broader dynamic range.

Capture both known as well as novel alterations of the transcript, even if no sequence information is available.

Even though no reference sequence information is available, RNA sequencing can be applied for any species.

Related: Synthetic Genome- Methods, Applications And Challenges.

Alternate Splicing:

Alternative splicing, or alternative RNA splicing, or differential splicing, is a regulated process during gene expression that results in a single gene coding for multiple proteins. In this process, particular exons of a gene may be included within or excluded from the final, processed messenger RNA (mRNA) produced from that gene. Consequently, the proteins translated from alternatively spliced mRNAs will contain differences in their amino acid sequence and, often, in their biological functions (see Figure). Notably, alternative splicing

allows the human genome to direct the synthesis of many more proteins than would be expected from its 20,000 protein-coding genes.

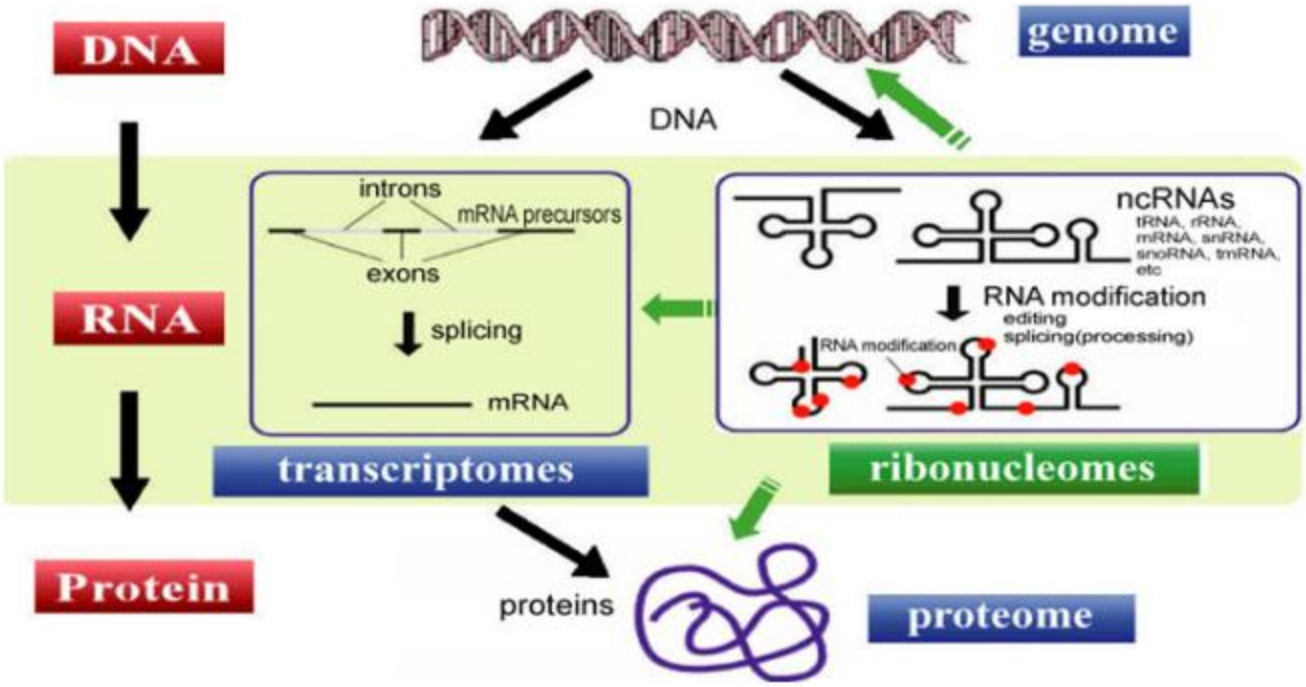
Alternative splicing occurs as a normal phenomenon in eukaryotes, where it greatly increases the biodiversity of proteins that can be encoded by the genome; in humans, ~95% of multi-exonic genes are alternatively spliced. There are numerous modes of alternative splicing observed, of which the most common is exon skipping. In this mode, a particular exon may be included in mRNAs under some conditions or in particular tissues, and omitted from the mRNA in others.

The production of alternatively spliced mRNAs is regulated by a system of trans-acting proteins that bind to cis-acting sites on the primary transcript itself. Such proteins include splicing activators that promote the usage of a particular splice site, and splicing repressors that reduce the usage of a particular site. Mechanisms of alternative splicing are highly variable, and new examples are constantly being found, particularly through the use of high-throughput techniques. Researchers hope to fully elucidate the regulatory systems involved in splicing, so that alternative splicing products from a given gene under particular conditions ("splicing variants") could be predicted by a "splicing code".

Abnormal variations in splicing are also implicated in disease; a large proportion of human genetic disorders result from splicing variants. Abnormal splicing variants are also thought to contribute to the development of cancer, and splicing factor genes are frequently mutated in different types of cancer.

Non Coding RNA:

A non-coding RNA (ncRNA) is a functional RNA molecule that is transcribed from DNA but not translated into proteins. Epigenetic related ncRNAs include miRNA, siRNA, piRNA and lncRNA. In general, ncRNAs function to regulate gene expression at the transcriptional and post-transcriptional level. Those ncRNAs that appear to be involved in epigenetic processes can be divided into two main groups; the short ncRNAs (<30 nts) and the long ncRNAs (>200 nts). The three major classes of short non-coding RNAs are microRNAs (miRNAs), short interfering RNAs (siRNAs), and piwi-interacting RNAs (piRNAs). Both major groups are shown to play a role in heterochromatin formation, histone modification, DNA methylation targeting, and gene silencing.



Metagenomics:

Metagenomics is the study of genetic material recovered directly from environmental samples. The broad field may also be referred to as environmental genomics, ecogenomics or community genomics.

While traditional microbiology and microbial genome sequencing and genomics rely upon cultivated clonal cultures, early environmental gene sequencing cloned specific genes (often the 16S rRNA gene) to produce a profile of diversity in a natural sample. Such work revealed that the vast majority of microbial biodiversity had been missed by cultivation-based methods.

Because of its ability to reveal the previously hidden diversity of microscopic life, metagenomics offers a powerful lens for viewing the microbial world that has the potential to revolutionize understanding of the entire living world. As the price of DNA sequencing continues to fall, metagenomics now allows microbial ecology to be investigated at a much greater scale and detail than before. Recent studies use either "shotgun" or PCR directed sequencing to get largely unbiased samples of all genes from all the members of the sampled communities.

Sequencing and assembly of DNA:

DNA sequencing of whole chromosomes or whole genomes, targeted regions, such as exome, can be carried out. This can be performed via two ways: first, by considering availability of a reference genome and second is through de novo sequencing when no reference sequence is available. The fundamental principle behind the reference genome approach comprises of three general steps; firstly, DNA molecules are separated into smaller fragments at random positions by using restriction enzymes or mechanical forces. After that, a sequencing library comprising of such fragments of known insert size is made, and in the third step, these fragments are sequenced and mapped back to a known reference sequence. The general method is broadly known as shotgun sequencing, this sequencing and assembly process is depicted in Fig. Owing to sequencing again, where there is no previously catalogued reference sequence for the given organism, the small sequenced fragments are assembled into contigs (gatherings of overlapping, continuous fragments) and the consensus sequence is obtained from these contigs.

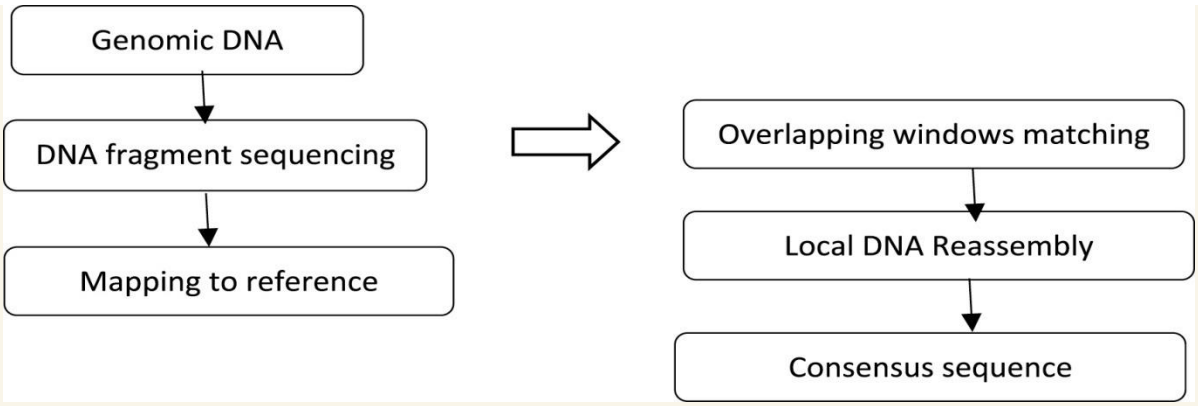


Fig. Sequencing and assembly of DNA.

As stated previously, there are three implementations of NGS. In whole genome sequencing (WGS), sequencing of the entire genome is carried out including regulatory elements responsible for hereditary diseases. It requires more time and cost, and so it is being replaced by whole exome sequencing. In whole exome sequencing (WES), all exons are sequenced; this is advantageous as compared to WGS because the cost of sequencing has been reduced. With WES, genes associated with cancer, diabetes, immunologic disorders, and other disease conditions can be identified. This sequencing is preferably used for identifying mutations such as SNPs, INDELS etc. In genetic disorders and for enhancing the precision of

diagnosis of patients . The measure of both raw and processed data for whole exome sequencing is orders of magnitude smaller than for whole genome sequencing. Transcriptome sequencing includes sequencing of cDNA fragments, created by reverse transcription of RNA with which researchers can study RNA expression and splicing profile.

Introduction to NGS data analysis:

Workflow of NGS data analysis:

First, the DNA library is prepared and samples are sequenced using NGS platform. Then, quality assessment of NGS reads is carried out and reads are aligned with the reference genome. After that, variant identification and annotation is performed followed by visualization. Further prioritization and filtration of identified variations is followed by validation of the generated results in the lab

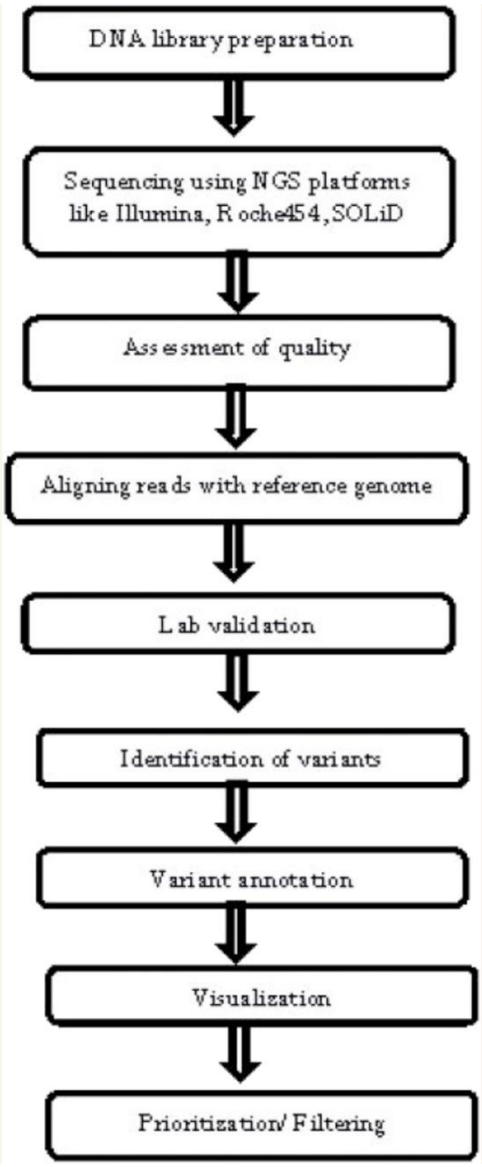


Fig. Workflow depicting computational analysis of NGS data.

NGS instruments give higher throughput data at an immense speed by sequencing a huge number of short DNA fragments in parallel. The three most commonly utilized platforms Roche 454, Illumina and ABI SOLiD sequence DNA by measuring and analyzing signals, which are discharged amid the formation of the second DNA strand, however the contrast in how the second strand is created. Keeping in mind the end goal to create detectable signals, template DNA is divided into small fragments, amplified and immobilized on a glass slide before sequencing.

Subsequent to finishing lab work and the real sequencing, the researcher will have a huge amount of raw data to be further processed. The analysis of the data can be divided into five particular steps (Fig.): (i) quality assessment of the raw data, (ii) read alignment to a reference genome, (iii) variant identification, (iv) annotation of the variants and (v) data visualization.

- ***Assessment of quality:***

In this step, quality of NGS reads is evaluated to remove, correct or trim the reads not meeting the standards. Errors such as base calling errors, poor quality reads etc. are assessed in this step. For this, tools such as FASTQC are used, which assesses the quality by considering the above mentioned errors with calculation of quality scores.

- ***Aligning sequences:***

  After assessing the quality of NGS reads, the reads are aligned to the reference genome. For that UCS(University of Santa Cruz) and GRC (Genome Reference Consortium) are mainly used as sources of human reference genome. There are some issues in selecting alignment software; the first is solving the problem of ambiguity in mapping short reads to the reference genome, which can be solved by considering paired-end reads as a better option. Secondly, mutations generated from reads with many mismatches have to be discarded from further analysis steps.

- ***Identifying variants:***

  Variant identification is a very important part of NGS data analysis. In this, sequence coverage is a main parameter, as identified mutations should be supported by several reads. Tools of variant identification are divided into 4 categories: (i) germline callers, (ii) somatic callers, (iii) Copy Number Variants (CNV) identification and (iv) Structural Variants (SV) identification. In case of rare diseases, germline mutations are focused while in cancer, somatic mutations are targeted for detection. Structural variant identification tools identify SVs such as inversions, translocations or large INDELS as well as CNVs which are the simplest form of SVs only.

- ***Annotating variants****:*

  Annotation of variants provides biological significance by identifying disease causing variants. Annotation of SNPs and INDELs is provided via computational annotation tools by providing links to pertaining databases such as dbSNP etc. Yohe S and co-workers have identified and annotated 1102 variants of inherited disorders across the 568 genes using the ANNOVAR tool combined with SIFT, PolyPhen2 and Provean annotation scores to evaluate the functional significance of novel variants.

- ***Visualizing NGS data***:

  After annotating the variants, they are visualized using visualization tools and genome browsers. By visualizing the variants, we can obtain information about variants, such as mapping quality, aligned reads, annotation information which includes consequence, impact of variants, scores of different annotation tools, etc. Paula Paulo and co-workers have identified and visualized functionally deleterious germline mutations in novel genes in early-onset/familial prostate cancer using Geneticist Assistant tool.

- ***NGS tools selection criteria****:*

For identifying variations, germline and somatic variant callers can be selected if: (i) they use Binary Alignment/Map (BAM) or pileup and Sequence alignment/map (SAM) format as input and (ii) the tools offer output effects in the Variant Call Format (VCF). SVs and CNVs detection tools are used after the acceptance of SAM/BAM as input format. For annotating variations, requirements of annotation packages are: (i) It should accept VCF as input format and (ii) It should integrate results from other software. GUI availability, VCF, SAM and BAM support are required for visualization of results.

Role of NGS informatics in identifying variants:

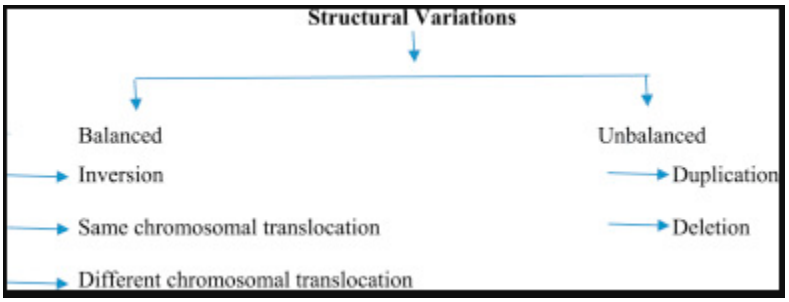
Algorithms for detection of structural variation from NGS data depend on one or more of the criteria: discordant paired-end reads, split reads, or depth of coverage. Discordant paired reads are read pairs that do not map together within the regular manner: the paired ends may additionally map to different chromosomes or to the identical chromosome either inside the incorrect orientation or inside the proper orientation, however, as an instance, too far apart inside the chromosome. Split reads are single reads that map to the genome discontinuously: the primary part of the read maps to one genomic area and the remainder to another. Because of the short read lengths currently available from NGS data, split reads are greatly beneficial and reliable from paired-end data, in which one end maps uniquely to the genome, serving as an "anchor," and the other end is a split read. Finally, the depth of sequencing coverage local to a selected point in the genome provides proof of structural variation. While changes in read depth over large regions often suggest copy number variations, greater diffused variant in sequence coverage is generally seen close to the breakpoints of other types of structural variation.

The overall performance of any approach for detection of structural variation relies on the form of sequencing data. For detection of translocations, split-read methods require sufficient sequence coverage so that the translocation breakpoints are supported by numerous split reads. Similarly, indels can be detected from exome (or targeted-capture) data using paired- or split read methods most effectively if at least one of the breakpoints falls within or near the captured regions.

Epigenetic alterations have been observed in many diseases like cancer, viral infection etc. Due to epigenetic alteration like methylation, gene expression is affected but gene sequence is not. These methylation are stable, inheritable and reversible, thus can serve as attractive targets for therapy. Hypermethylation genes have been detected in different types of cancer like breast cancer, leukemia, prostate cancer etc. Thus, they can be used in prediction of disease outcomes. Using NGS platforms single-molecule sequencing can be performed with the help of methylation-specific probes. Detection of epigenetic alterations is proving to be a promising tool for diagnosis and treatment of cancer patients. Application of MGMT (O6-methylguanine-DNA methyltransferase) hypermethylation in glioma patients is the best example of methylation marker in clinical usage.

Structural variome:

Variation in more than one nucleotide is called the structural variome. There are two major classes of structural variations: balanced and unbalanced variations. Balanced variations do not change content of DNA while unbalanced variations change the content of DNA. Inversion, same chromosomal translocation and different chromosomal translocation are subtypes of balanced structural variations, while duplication and deletion are subtypes of unbalanced structural variations.



Structural variations can be detected by five types of methods. First is the Pair-end mapping (PEM) method. In this type, the two ends of the DNA fragment are sequenced and uniquely mapped to the reference genome. Second is the Single-end method in which single ends of multiple DNA fragments are sequenced and mapped with the reference genome at different positions, which forms overlapping in read mapping. The third type is Translocation and inversion detection. In interchromosomal translocations, one member of the pair maps to one chromosome and its mate to every other. And in inversions or intrachromosomal translocations, the two ends map to the equal chromosome, however in the wrong orientation or the wrong distance apart. Fourthly is Copy number variant detection which can be defined as stretches of DNA, longer than a kilobase, which is present in the genome with an abnormal number of copies that include large deletions and duplications, as well as unbalanced translocations. Large deletions are less difficult to detect than smaller indels using paired-end methods, as they are easily identified from normal variation within the insert size. Large duplications are harder to discover, as there may be no single read or read pair spanning the insertion. And the fifth type is Insertion and deletion detection. Indels are common in human genome and make a contribution to genetic diversity and human diseases. In the clinical molecular oncology laboratory, the detection of small (<10 bp) and medium (>10 but <1 kb) indels is important to many cancers. Of specific clinical importance are the NPM1 insertion, FLT3 internal tandem duplication (FLT3-ITD), KIT exon 8 indels in acute myeloid leukemia

and EGFR exons 19 and 21 insertions and deletions in lung cancers .By Sanger sequencing or gel capillary based sizing methods, small-and medium sized indels are typically simple to detect. Indel detection via NGS methods has been challenging largely because of the short read lengths generated by using NGS methods. In general, small indels can be called with reasonable sensitivity from NGS data, despite the fact that the specificity has a tendency to be low. Further, most indel detection software detect deletions over insertions because of inherited bias in the tool, as inserted sequences are more difficult to align to the reference sequences.

Handling of NGS data

While analyzing NGS data, a number of intermediate analysis files and result files are generated that are collectively very large in size i.e., 100's of GB, TB and even reaching petabytes. Interpretation of these complex NGS data files especially for aggregated large amounts of variations or heterogeneous sequencing data is challenging in terms of translating data to knowledge for clinical applications. Also, processing power, memory (RAM) and data storage are hardware bottlenecks in computational analysis that can be overcome by high performance computational resources, but increase the computational cost. After analyzing the NGS data, the next step is handling of the resultant NGS data, which is carried out by employing machine learning based methods. Machine learning is a descendent of the statistical model fitting method, which extracts the information from data by building probabilistic models. Efficient machine learning methods study huge amounts of generated NGS data comparatively and evolutionarily. Good classification and regression results can be yielded by machine learning methods like Support Vector Machines, Artificial Neural Network. Weizhong Zhao and coworkers have employed machine learning methods for evaluating the performance of the NGS data set for the Salmonella enterica strains. The analysed NGS data can be classified with these methods to obtain clinically significant results.

Clinical validation of variants:

Translation of NGS methods for clinical use is a very important and challenging task that is carried out by validation of different performance characteristics. Clinical validation of NGS data is performed by measuring different parameters like analytical sensitivity that is defined as an ability of the assay to detect true sequence variants i.e. false-negative rate, analytical specificity that is defined as probability of the assay to not detect mutations where none are present i.e. false-positive rate. Accuracy is the measure of sequencing accuracy and error rates and precision are the measure of reproducibility of mutation detection by the assay and inter-user reproducibility. In a related work, researchers have clinically validated 30 known mutations of more than 100 inherited

diseases with 100% analytical sensitivity and 100% analytical specificity for 18 samples of patients in whom pathogenic mutations were previously identified.

Cancer genomics, transcriptomics and proteomics:

Cancer genomics is a branch of genomics which deals with study of cancer-associated genes, and it identifies oncogenes or tumor-suppressor genes for clinical diagnostics. Cancer genome sequencing is also one of the aspects of cancer genomics in which DNA or RNA sequences of cancer cells are identified and characterized, by sequencing of the tumor and normal tissues. The first cancer genome sequencing report was generated in 2006, in which 13,023 genes were sequenced in 11 breast and 11 colorectal tumors. With cancer genomics, many cancer specific genes and mutations have been identified from the nucleotide sequence. It has been observed that a greater number of mutations were found to be located in the exome part and a lesser number of mutations in the intron part of the DNA sequence.

Cancer transcriptomics is a branch of transcriptomics which deals with the study of RNA transcripts associated with cancer. With RNA Transcriptome sequencing, it is possible to identify transcription start sites, promoter region sites and splicing sites that play an important role in human disease. For assembly of RNA sequencing reads, the reference genome is not required, so gene expression of non-model organisms can be studied without the need of any existing genome resource. Transcriptome sequencing is performed for coding and non-coding RNAs; it has been observed that many non-coding RNAs have been implicated in the disease causing state of cancer. With transcriptomics, more accurate and earlier diagnosis of cancer is possible, which proves very beneficial to oncologists and patients.

Proteomics is the next step in the Biosystems studies after genomics and transcriptomics. Cancer proteomics involves study of cancer associated proteins. Proteomics is complicated as compared to genomics and transcriptomics as proteome differs from cell to cell over time while genome and Transcriptome are somewhat constant. The Cancer Proteome Atlas has provided quantitative protein expression data of around 200 proteins from 4000 tumor samples with matched corresponding data from the Cancer Genome Atlas. In cancer proteomics, protein databases are analyzed to evaluate gene expression at the proteome level. The biology of cancer patients can also be understood with proteomics by extracting biological information from serum and tissue. With Onco-proteogenomics, tumor-derived DNA, RNA and protein measurements can be linked, and thus it is possible to identify tumor-specific peptides.

Bad side of NGS:

Due to massive-parallel sequencing – commonly known as next generation sequencing – we can obtain whole exomes (and even genomes!) of multiple samples, in a matter of days. This crazy amount of data poses a challenge for bioinformatics. Therefore, development of a streamlined, highly automated pipeline to facilitate data analysis is a critical step in analyzing NGS data.

There are some concerns prior to the analysis that should be taken into consideration:

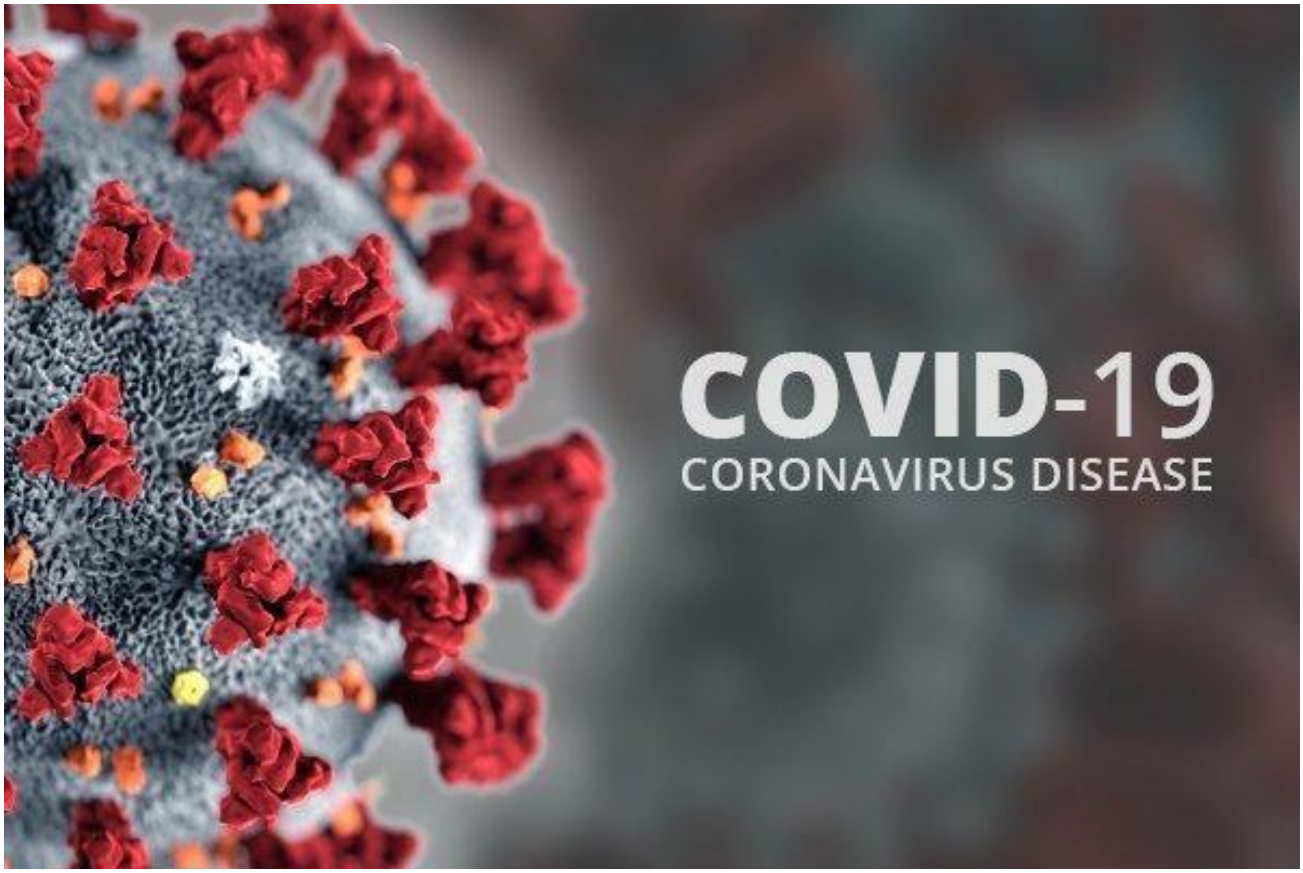
- Run quality metrics – most NGS platforms indicate how the run is going, and if the library is yielding good sequencing results (error rate, sequence alignment); and
- Sequencing coverage metrics – the data that shows whether your target is being sequenced, and how many sequences it has produced (coverage). You should always aim to have good coverage – with higher coverage you can have more confidence in your results, and trust that what you are obtaining in your results is actually there. If you are not obtaining a good coverage it might mean that there is something not working quite right – either in the pool preparation protocol, in the lab bench, in the sequencing protocol, or there might be something wrong with your sample. It means it's time for some good old fashioned troubleshooting

Current scenario of NGS and future prospects:

The current review has highlighted the benefits of NGS vis-à-vis conventional sequencing technologies such as low cost, high throughput for detecting a range of all possible mutations such as SNP, INDELs, CNVs and SVs, and thus proving to be a valuable clinical diagnostic tool for routine mutation profiling of tumors. Tools such as Fast QC, htSeq and platforms such as Galaxy and Persistent system's SanGeniX are employed for detection of the quality of short reads and NGS data analysis, respectively. Now, major clinical implementations of NGS include characterization of Ebola virus infection in West Africa, and identification of trait loci of Type-1 diabetes by resequencing of candidate genes. With NGS to study cancer genome architecture, it is possible to overcome drug resistance by identifying molecular mechanisms. For example, in the field of clinical oncology, markers are needed to identify molecular mechanisms of drug resistance to tamoxifen or aromatase inhibitors among estrogen receptor (ER)-positive patients, to trastuzumab among HER2-positive patients, and new biomarkers and drugs for triple-negative (ER/progesterone receptor/HER2) disease. However, extraction of clinically significant data from the vast amount of generated NGS data and data storage are the challenges that researchers are trying to resolve. But despite these challenges, NGS will likely prove to be a potential molecular diagnostic tool that will eventually replace currently used diagnostic tools. Thus, in the field of clinical oncology, by enabling treatment for dynamic genomic changes in individual tumors, we can emphatically state that NGS will propel personalized medicine.

REFRENCES:

- https://www.sciencedirect.com
- https://geneticeducation.co.in
- https://www.whatisepigenetics.com/
- https://journals.plos.org/
- https://en.wikipedia.org/
- https://www.ncbi.nlm.nih.gov
- https://www.nature.com/
- https://www.longdom.org/open-access/nextgeneration-sequencing-ngsbased-clinical-testing-is-recommended-for-the-detection-of-gene-mutations-associated-with-familial-my-2469-9853-1000153.pdf
- https://www.longdom.org/next-generation-sequencing-applications.html
- Harris SR, Cartwright EJ, Török ME, et al. Whole-genome sequencing for analysis of an outbreak of meticillin-resistant Staphylococcus aureus: a descriptive study. Lancet Infect Dis 2013;13:130–6 [PMC free article] [PubMed] [Google Scholar]



TARGETING SARS-CoV-2 MAIN PROTEASE FOR COVID-19

TARGERTING SARS-CoV-2 MAIN PROTEASE FOR COVID-19

A Report

Submitted in fulfillment of the requirements for the internship in the degree of

BACHELOR OF TECHNOLOGY
IN
BIOINFORMATICS

Under the supervision of

Dr. Raj Kumar
Assistant professor

By

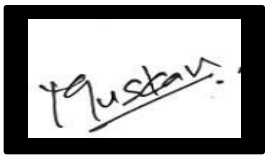
Muskan Kapoor
(171501)

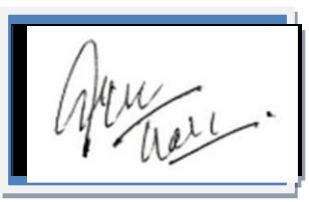
to

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

WAKNAGHAT, SOLAN – 173 234

HIMACHAL PRADESH, INDIA

Student's Signature : 

Supervisor Signature: 

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Muskan Kapoor

(171501)

TABLE OF CONTENT

CONTENT	PAGE NO.
Abstract	**6**
Chapter 1: Introduction	**7-9**
• **1.1 General**	
• **1.2 Drug –Repurposing**	
• **1.3 Protease Inhibitors**	
• **1.4 Why is it called $3CL^{pro}$ or M^{pro}**	
• **1.5 Structure**	
• **1.5.1 Domains of SARS-CoV $3CL^{pro}$ or M^{pro}**	
• **1.5.2 SARS-CoV-2 M^{pro} is a dimer**	
Chapter 2: Methodology	**11-23**
• **2.1 Finding existing inhibitors**	
• **2.1.1 About HCV**	
• **2.1.1.1 Proteases of HCV**	
• **2.2 Table of Protease Inhibitors**	
• **2.3 Ligand Preparation**	
• **2.3.1 For 2D Structures**	
• **2.3.2 For 3D Structures**	
• **2.4 Protein Preparation**	
• **2.5 Grid Generation**	
• **2.6 Docking**	
• **2.6.1 Auto Grid**	
• **2.6.2 Auto Dock**	

- **2.7 Analyzing 2D 3D Poses**
- **2.7.1 Through Auto Dock**
- **2.7.2 Through Discovery Studio**
- **2.7.3 Binding Energy**
- **2.8 Software's used**

Chapter 3: Literature Review **24-28**

- **3.1 Review of Literature**
- **3.2 Summary**

Chapter 4: Conclusions **29**

Chapter 5: Future scope **30**

References **31**

ABSTRACT

A newly come to light severe acute respiratory syndrome corona virus 2 reported 7 months ago in Wuhan, China better known as COVID_19 has become the current health concern to the entire world ,and declared a pandemic by the World Health Organization (WHO). Precautionary measures remain the sole obliging tactic to cease the human to human transmissions till any effective method of treatment or vaccine is developed. Amidst the pandemic, research and development of new molecule is labor-intensive and tedious process. In this report we have used Drug repurposing method, it is a concept of identifying therapeutically potent molecule from the library of pre-existing molecules. The main protease of SARS-CoV-2 (M^{pro}) is a critical target for designing potent antiviral agents against COVID-19. It aims at analyzing binding properties of existing inhibitors using molecular docking of other viral proteases. In this report HCV virus is used against SARS-CoV-2.

INTRODUCTION

1.1 General

The recent outbreak of a novel corona virus disease (COVID-19), occurring from a severe acute respiratory syndrome (SARS), which is now considered as a global pandemic. WHO, on 30 January 2020, declared this outbreak as Public Health Emergency of International Concern and later on 11 February 2020 named it as COVID-19. According to the data of WHO currently (as on July 4, 2020), more than 11,206,722 COVID-19 cases have been confirmed globally, and the number of death toll rose to 5, 29,403 which are increasing exponentially. To date no specific medications have been developed, and therefore considering the risk factors associated with this disease, there is an urgent need for a treatment method to treat this disease in order to limit the transmission.

1.2 Drug-Repurposing

It is also known as drug repositioning, is a drug development strategy predicated on the reuse of existing licensed drugs for new medical indications. Among all the treatment strategies, the uses of already known viral medications have great advantages as the pharmacokinetics, pharmacodynamics, and safety profiles of these drugs have already been established. This drug repurposing strategy has gained significance as they are expected to be faster with less investment.

1.3 Protease Inhibitors

Preliminary studies revealed Lopinavir/ritonavir combined therapy as a potential inhibitor of the virus. Along with these two drugs, many other antiviral drugs have also been screened. Recently, anti-malarial drug chloroquine (and hydroxychloroquine have been reported to have certain curative effect on COVID-19. Numerous reports to identify

the potential inhibitors of novel corona virus (COVID-19) have recently been published using computational methods .The transcription of the genomic RNA inside the cell generates a polypeptide which is proteolytically cleaved by the main protease (MPro which is also known as 3CLPro or chymotrypsin-like protease) at 11 different sites to produce proteins necessary for the replication of the virus. Inhibition of the activity of the main protease is expected to block the viral replication as no human proteases are known having similar cleavage specificity. Therefore MPro is one of the most explored drug targets among the corona viruses that plays a major role in the translation and replication of new generation viruses from the viral genomic.

1.4 Why it is called $3CL^{pro}$ or M^{pro}

The functional polypeptides are released from the polyproteins by extensive proteolytic processing. This is primarily achieved by 33.1-kD HCoV 229E main proteinase (M^{pro}), which is frequently also called 3C-like proteinase ($3CL^{pro}$) to indicate a similarity of its cleavage-site specificity to that observed for picoronavirus 3C proteinases.

1.5 Structure

SARS-CoV-2 was found to be a positive-sense, single-stranded RNA virus belonging to the genus Betacoronavirus. Phylogenetic analysis revealed that SARS-CoV-2 is closely related (88–89% similarity) to two bat-derived SARS-like corona viruses, namely bat-SL-CoVZC45 (GenBank accession no. **MG772933.1**) and bat-SL-CoVZXC21 (GenBank accession no. **MG772934.1**), but it is more distant from SARS-CoV (~79% similarity) and Middle East respiratory syndrome corona virus (MERS-CoV) (~50% similarity). RNA-based metagenomic next-generation sequencing approach was applied to identify a human coronavirus from two pneumonia cases during the Wuhan outbreak in 2019. Its entire genome was 29 881 bp in length. Phylogenetic analysis indicates that SARS-CoV-2 is similar to the corona virus circulating in *Rhinolophus* (horseshoe bats), with 98.7% nucleotide similarity to the partial RNA-dependent RNA polymerase (*RdRp*) gene of the bat corona virus strain BtCoV/4991 (GenBank **KP876546**, 370 bp sequence of *RdRp*) and 87.9% nucleotide similarity to bat corona virus strain bat-SL-CoVZC45 and bat-SL-

CoVZXC21. Evolutionary analysis based on ORF1a/1b, S and N genes suggests that SARS-CoV-2 is more likely a novel corona virus that was independently introduced from animals to humans. Based on the findings of genomic investigations and the presence of some bats and live animals in the seafood market in Wuhan, SARS-CoV-2 may have originated from bats or bat droppings associated with contaminated materials in the market or surrounding region. At this time, there are no specific vaccines or treatments for COVID-19. However, there are many ongoing clinical trials evaluating potential treatments.

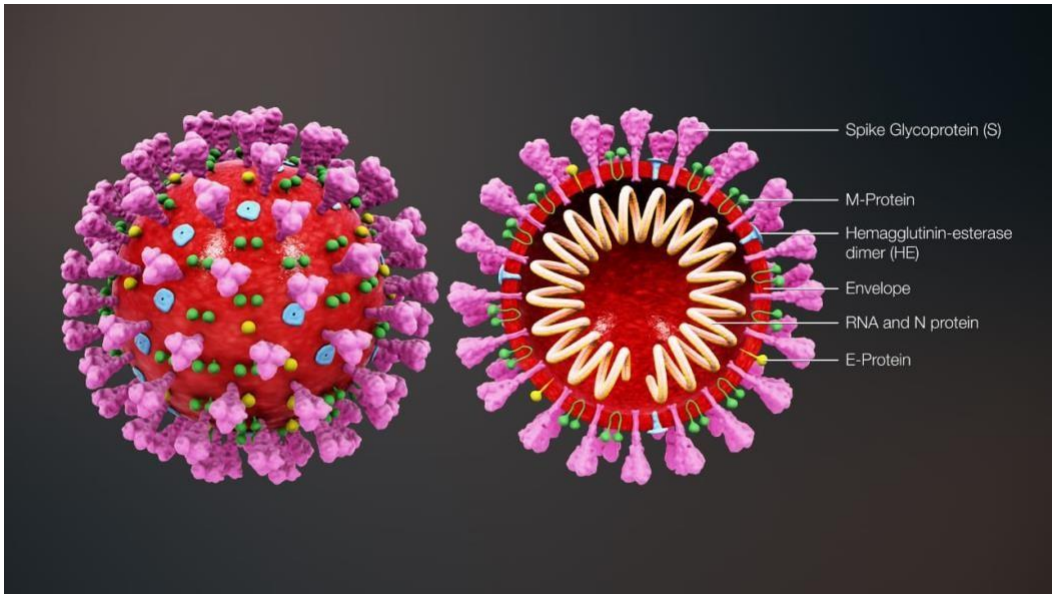


Fig1: Structure of COVID-19

1.5.1 Domains of SARS-CoV 3CL^{pro} or M^{pro}

The 3DstructureofSARS-CoV-2Mpro (PDB ID. 6Y2G), is made up of three domains, where domain I, II and III spans across 8-101, 102-184 and 201-306 amino acid residues, respectively. Domain I and II mainly consists of b-barrels while domain III mainly consists of a-helices. The substrate/active site of binding is located at the cleft of domain I and II, which consists of two catalytic residues, namely, HIS41 and CYS145.

It has following features:

- ✓ SARS-CoV M^{pro} and SARS-CoV-2 M^{pro} share more than 96% similarity

- ✓ Therefore, their 3D structures are highly similar
- ✓ Substrate/inhibitors bind to the same binding site
- ✓ Substrate/inhibitor binding site lies between domain-I and domain-II

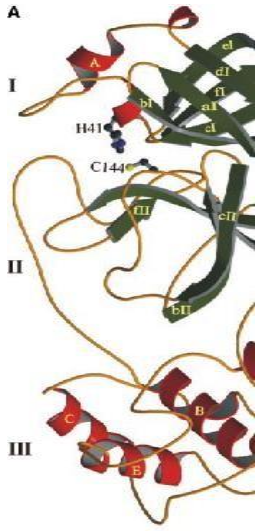


Fig2: Domain

1.5.2 SARS-CoV-2 M^{pro} is a dimer

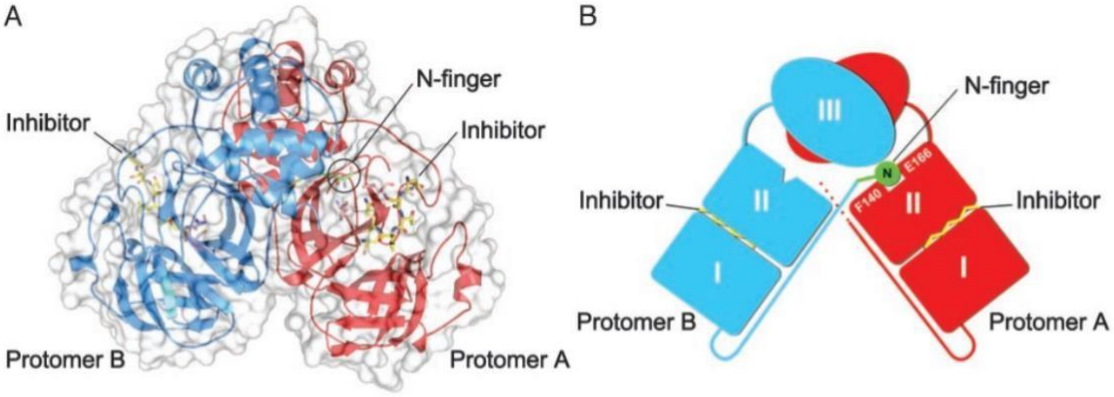


Fig. 1. The SARS-CoV M^{pro} dimer structure complexed with a substrate-analogue hexapeptidyl CMK inhibitor. (*A*) The SARS-CoV M^{pro} dimer structure is presented as ribbons, and inhibitor molecules are shown as ball-and-stick models. Protomer A (the catalytically competent enzyme) is red, protomer B (the inactive enzyme) is blue, and the inhibitor molecules are yellow. The N-finger residues of protomer B are green. The molecular surface of the dimer is superimposed. (*B*) A cartoon diagram illustrating the important role of the N-finger in both dimerization and maintenance of the active form of the enzyme.

Fig3: Dimer

METHODOLGY

2.1 Finding existing inhibitors

Found 13 existing inhibitors for HCV (clinically tested). We will use these inhibitors to check their binding with SARS-CoV-2 M^{pro} using molecular docking.

2.1.1 About HCV (Hepatitis-C)

Hepatitis C is a liver infection caused by the hepatitis C virus (HCV). Hepatitis C is spread through contact with blood from an infected person. Today, most people become infected with the hepatitis C virus by sharing needles or other equipment used to prepare and inject drugs. For some people, hepatitis C is a short-term illness, but for more than half of people who become infected with the hepatitis C virus, it becomes a long-term, chronic infection. Chronic hepatitis C can result in serious, even life-threatening health problems like cirrhosis and liver cancer. People with chronic hepatitis C can often have no symptoms and don't feel sick. When symptoms appear, they often are a sign of advanced liver disease. There is no vaccine for hepatitis C. The best way to prevent hepatitis C is by avoiding behaviors that can spread the disease, especially injecting drugs. Getting tested for hepatitis C is important, because treatments can cure most people with hepatitis C in 8 to 12 weeks.

2.1.1.1 Protease Inhibitors of Hepatitis-C

The hepatitis C virus (HCV) specific protease inhibitors are a class of agents that block the enzymatic activity of the HCV NS3 protease region that is necessary for protein processing required for viral replication. The combination of an HCV protease inhibitor with other antiviral agents with activity against HCV (such as peginterferon, ribavirin, and the direct acting agents that block the NS5A and NS5B regions of the virus) leads to marked decrease in HCV replication and eradication of the infection in a high proportion of patients with chronic hepatitis C. At least four HCV protease inhibitors have been approved for use

in the United States (boceprevir, paritaprevir, simeprevir, telaprevir), and many more are in preclinical or clinical development (asunaprevir, danoprevir, faldaprevir, grazoprevir, sovaprevir, vedroprevir).

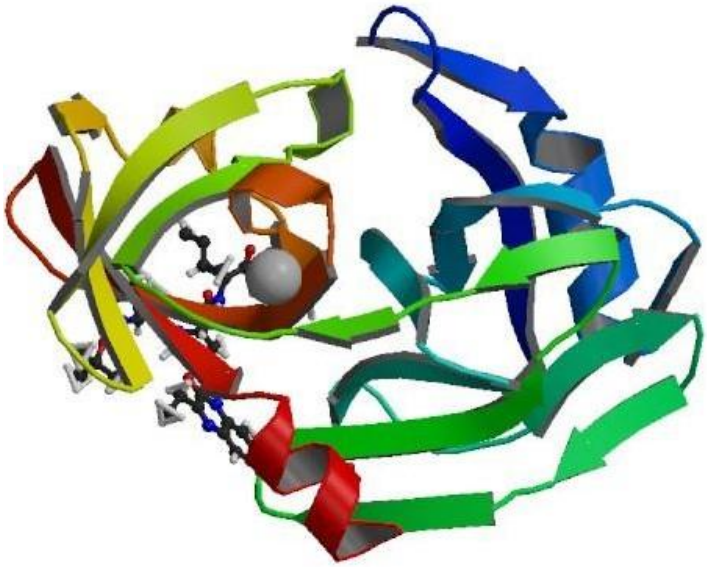
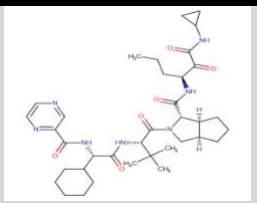
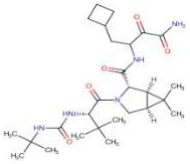
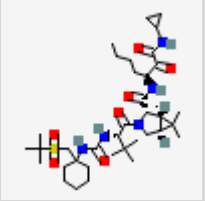
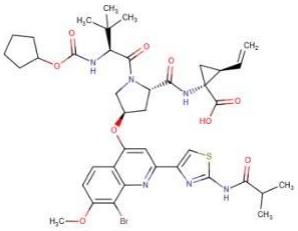
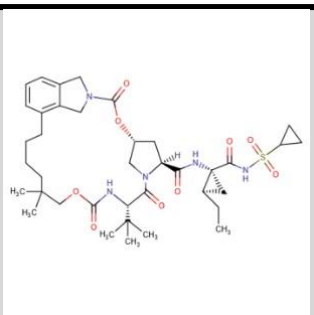
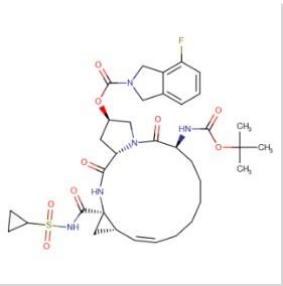
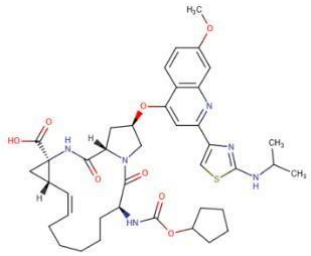
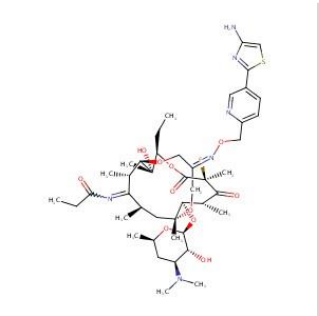


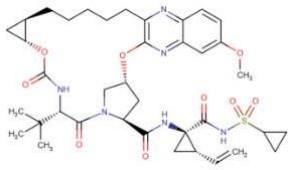
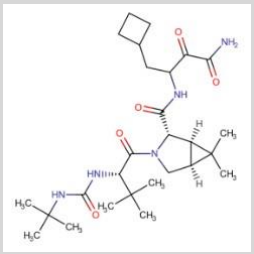
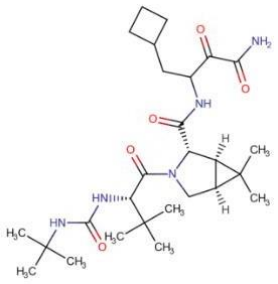
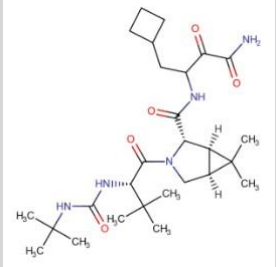
Fig4: HCV inhibitors

2.2 Table of Protease Inhibitors

TABLE

SNO	NAME /AGENT	DETAILS OF CLINICAL TRIALS	CITATION	TYPE	STRUCTURE
1	Telaprevir(Vx-950)	Filed	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Linear	
2	Boceprevir(SCH 503034)	Filed	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Linear	
3	Narlaprevir(SCH 900518)	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Linear	
4	BI 201335/ Faldaprevir	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Linear	

5	Vaniprevir(MK- 7009)	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Macrocyclic	
6	Beclabuvir/BMS-791325	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Macrocyclic	NA
7	Danoprevir(IMN191/RG7227)	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Macrocyclic	
8	Ciluprevir(GS-9256*)	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Macrocyclic	
9	Paritaprevir (ABT-450*)	Phase II	_ 2011 European Association for the Study of the Liver. Published by Elsevier B.V. All rights reserved.[1]	Macrocyclic	

10	Grazoprevir	Phase II/III	https://www.drugbank.ca/categories/DBCAT002768[2]	Macrocyclic	
11	Simeprevir	Phase II ongoing	https://www.drugbank.ca/categories/DBCAT002768[2]	Macrocyclic	
12	Voxilaprevir	Phase III	https://www.drugbank.ca/categories/DBCAT002768[2]	Macrocyclic	
13	Glecaprevir	Phase II/III	https://www.drugbank.ca/categories/DBCAT002768[2]	Macrocyclic	

2.3 Ligand Preparation

2.3.1 For 2D Structures

1. Open UCSF Chimera
2. Open PubChem in the browser and type inhibitor name.
3. Get the SMILES string
4. Go to UCSF Chimera Tools -> Structure Editing -> Build Structure -> SMILES string (Paste the SMILES string that we have copied from pubChem) -> Apply -> Close.
5. Now we have our ligand molecule built.
6. Again Tools -> Structure Editing -> Minimize Structure (here set steepest descent steps: 1000 and Conjugate gradient steps:1000) -> Minimize
7. Now Add hydrogens will pop-up click OK, then Assign Charges to minimize select Gasteiger and enter OK. This will show the net charge of the molecule. Click OK.
8. Save ligand to the working directory: save as .mol2

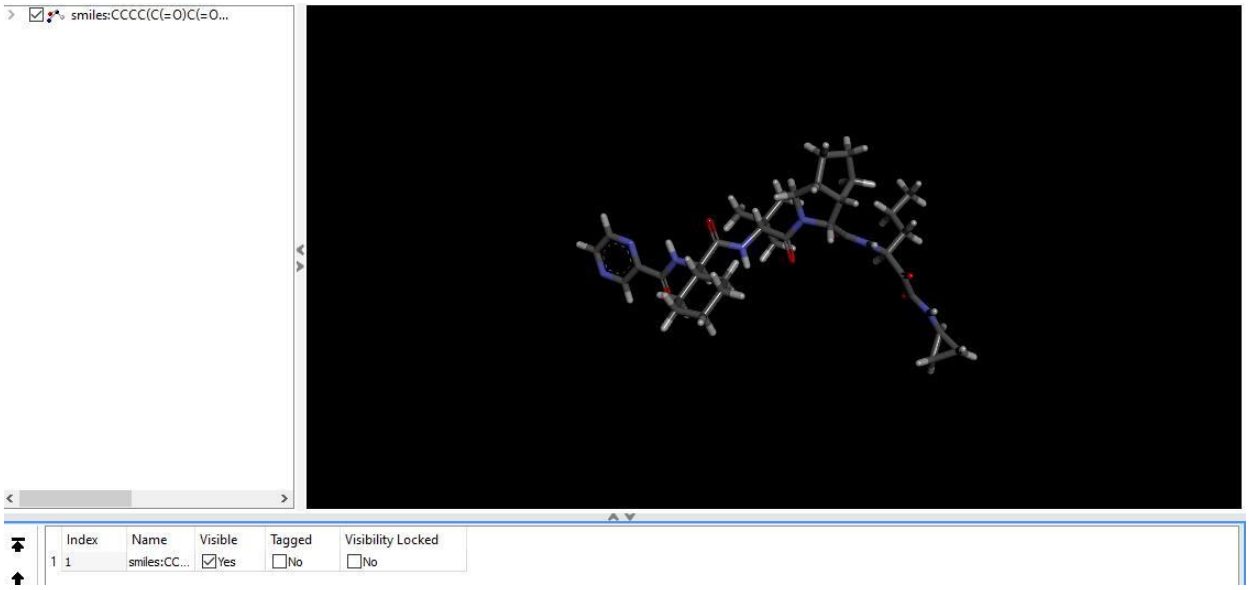


Fig5: Telaprevir

2.3.2 For 3D Structures

1. Open UCSF Chimera

2. Open PubChem in the browser and type inhibitor name.
3. Download the 3D structure as .SDF and open it in UCSF Chimera.
4. Again Tools -> Structure Editing -> Minimize Structure (here set steepest descent steps: 1000 and Conjugate gradient steps:1000) -> Minimize
5. Now Add hydrogens will pop-up click OK, then Assign Charges to minimize select Gasteiger and enter OK. This will show the net charge of the molecule. Click OK.
6. Save ligand to the working directory: save as .mol2

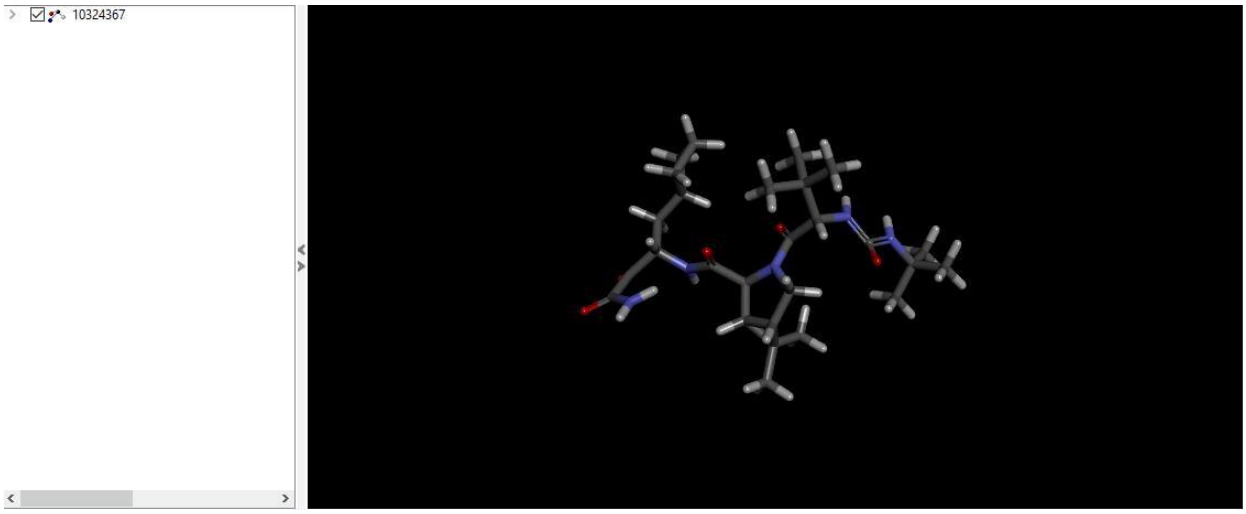


Fig 6: Boceprevir

2.4 Protein Preparation

PDB ID: 6Y2G

1. Open Discovery studio.
2. Open RSCB PDB from web browser and search for PDB ID.
3. Download the structure as PDB.
4. Open the pdb structure in Discovery studio.
5. The pdb structure 6Y2G has 2 chains – A and B.
6. Delete chain B .
7. Only keep Ligand A(O6K402) as reference and delete all other ligands.
8. Go to macromolecule -> prepare protein -> clean protein -> show clean report.

9. Now go to minimize protein -> select protein -> select algorithm -> Yes.

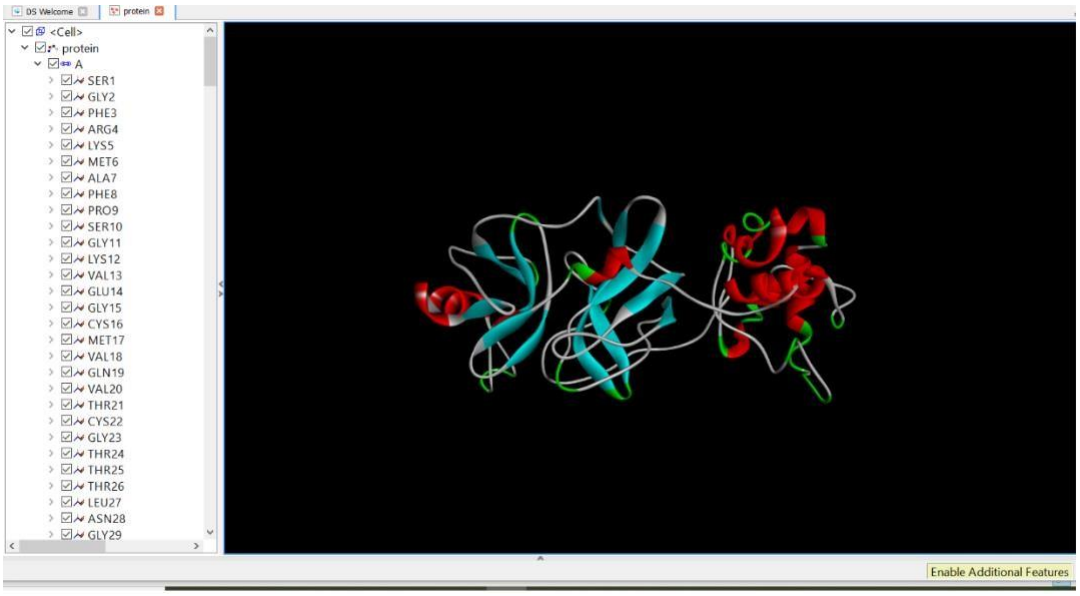


Fig7 Minimized protein

2.5 Grid Generation

1. File -> Read Molecule -> 6Y2G.pdb
2. Edit -> Delete Water
3. Edit -> Hydrogens -> Add H -> All polar -> Ok
4. Edit -> Charges -> Add Kollman charges
5. Edit -> Charges -> Compute Gastegier charges
6. Atoms -> Assign AD4 type
7. File -> Save -> Write PDBQT
8. Select -> Select from string -> Residue sets -> Ligands -> Dismiss
9. Ligand -> Input -> Open -> .mol2 files -> Ok
10. Ligand -> Output -> Write PDBQT
11. Select ->Select from string -> Residue sets -> Ligands -> Add-> Dismiss
12. Grid -> Macromolecule -> Choose -> 6Y2G -> Save as .pdbqt
13. Grid -> Set map types -> Choose ligand
14. Grid -> Grid Box -> Centre -> Centre on ligand

15. File -> Close saving current
16. Grids -> Output -> gpf -> save as grid.gpf

2.6 Docking

2.6.1 Auto Grid

1. Run -> Auto-Grid -> Program Pathname -> Browse -> C Drive -> (XProgram Files) -> The Scripps Research Institute -> Autodock -> 4.2.6 -> autogrid.
2. For parameter filename -> Browse ->grid.gpf.
3. Automatically a log filename file grid.glg will be created -> Launch

2.6.2 Auto Dock

1. Docking -> Macromolecule -> RigidFilename -> 6Y2G.pdb
2. Docking -> Ligand -> Choose -> .mol2 file -> Accept
3. Docking -> Output -> Lamarkian -> Save as dock.dpf
4. Run -> Auto-Dock -> Program Pathname -> Browse -> C Drive -> (XProgram Files) -> The Scripps Research Institute -> Autodock -> 4.2.6 -> autodock.
5. For parameter filename -> Browse ->dock.dpf.
6. Automatically a log filename file dock.dlg will be created -> Launch

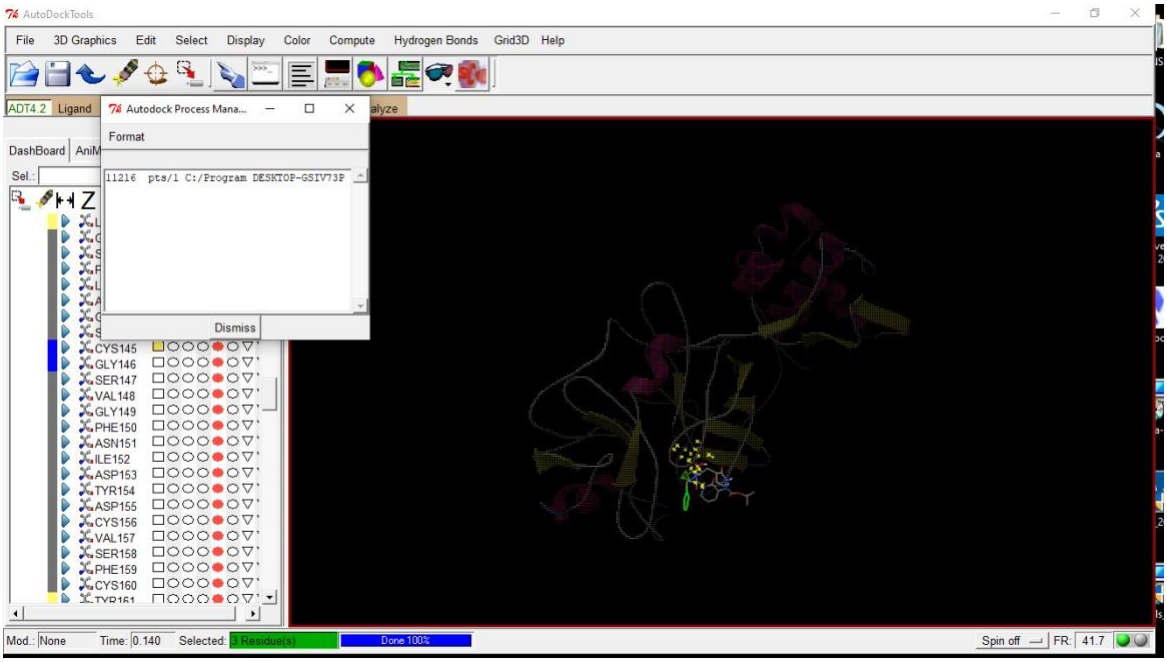


Fig 8 Autodock

2.7 Analyzing 2D and 3D Poses

2.7.1 Through Auto dock

- Analyze -> Docking -> Open -> File Location -> dock.dlg.
- Analyze -> Conformations -> Play Rank by Energy(Best pose appears)

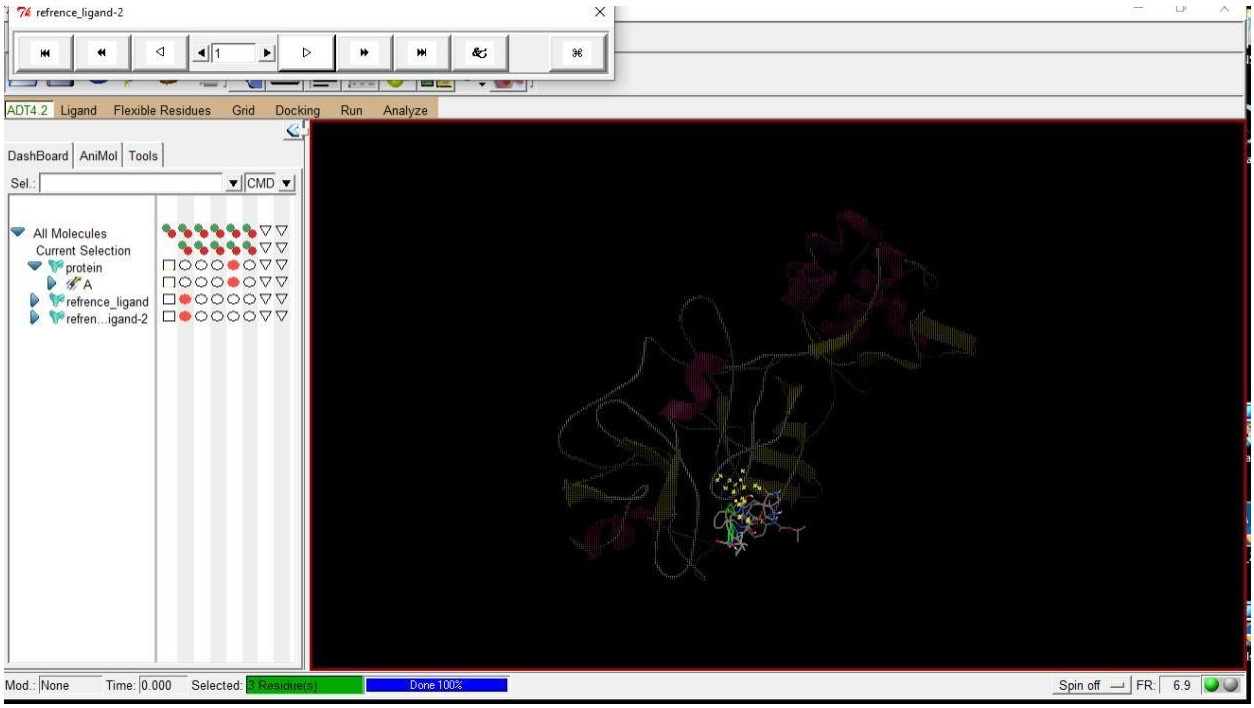


Fig 9 Best Pose from 10 different poses

2.7.2 Through Discovery Studio

- File -> Open -> Protein
- Convert ->dock.dlg to dock.pdb
- Delete everything except coordinates
- Remove lower remaining part
- Drag pdb file from notepad
- Check every dock model and pose

2.7.3 Binding Energy

Minimum binding energy of only on cluster is obtained and a best pose is created.

Cluster Rank	Lowest Binding Energy	Run	Mean Binding Energy	Num in Clus	Histogram 5 10 15 20 25 30 35
1	-5.93	9	-5.84	2	##
2	-5.58	4	-4.82	2	##
3	-5.41	1	-4.76	2	##
4	-5.38	5	-5.38	1	#
5	-4.71	8	-4.71	1	#
6	-4.31	10	-4.31	1	#
7	-3.75	6	-3.75	1	#

Number of multi-member conformational clusters found = 3, out of 10 runs.

RMSD TABLE

Rank	Sub-Rank	Run	Binding Energy	Cluster RMSD	Reference RMSD	Grep Pattern
1	1	9	-5.93	0.00	29.89	RANKING
1	2	3	-5.76	1.27	29.81	RANKING
2	1	4	-5.58	0.00	30.59	RANKING
2	2	7	-4.07	1.96	31.48	RANKING
3	1	1	-5.41	0.00	30.35	RANKING
3	2	2	-4.11	1.92	30.82	RANKING
4	1	5	-5.38	0.00	29.03	RANKING
5	1	8	-4.71	0.00	30.84	RANKING
6	1	10	-4.31	0.00	30.33	RANKING
7	1	6	-3.75	0.00	31.15	RANKING

Fig 10 Binding Energy

2.8 Software's used

We used UCFS Chimera a molecular visualization tool, was used to visualize the results obtained from the server. Discovery Studio Visualizer was further employed in

order to prepare the docked poses and 2 D interaction plots. Autodock 4.2.6 ; a suite of automated docking tools was practiced to predict how small molecules bind to receptor of known 3D structures. While browsing the web we exploited PubChem , Drugbank and NCBI.

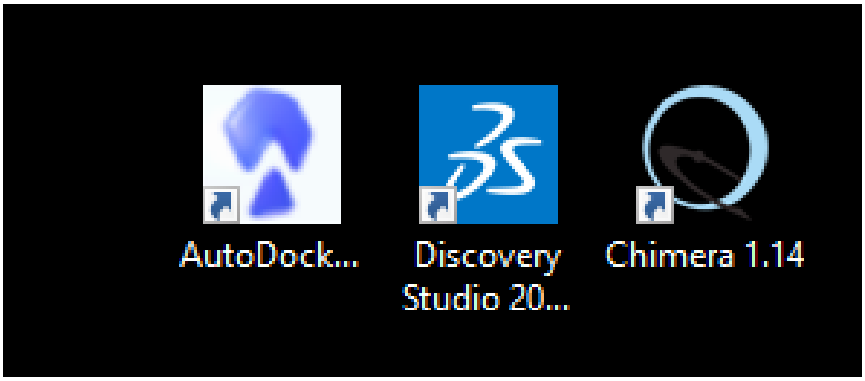


Fig11: Tools used

LITERATURE REVIEW

3.1 Review of Literature

The coronavirus disease 2019 (COVID-19) pandemic caused by severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) is a global health emergency. The virus has been named severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) because the RNA genome is about 82% identical to that of the SARS coronavirus (SARS-CoV), both viruses belong to clade b of the genus Betacoronavirus. The best-characterized drug targets among coronaviruses is the main protease (Mpro, also called 3CLpro). Along

with the papain-like protease(s), this enzyme is essential for processing the polyproteins that are translated from the viral RNA. The Mpro operates at no fewer than 11 cleavage sites on the large polyprotein 1ab (replicase 1ab, ~790 kDa). The recognition sequence at most sites is Leu-Gln↓(Ser, Ala, Gly) (↓ marks the cleavage site). Inhibiting the activity of this enzyme would block viral replication. Because no human proteases with a similar cleavage specificity are known, such inhibitors are unlikely to be toxic. The three-dimensional structure is highly similar to that of the SARSCoV Mpro, as expected from the 96% sequence identity.

The chymotrypsin-like and picornavirus 3C protease–like domains I and II (residues 10 to 99 and 100 to 182, respectively) are six-stranded antiparallel

b barrels that harbor the substrate-binding site between them. Domain III (residues 198 to 303), a globular cluster of five helices, is involved in regulating the dimerization of the Mpro, mainly through a salt-bridge interaction between Glu290 of one protomer and Arg4 of the other.They used this crystal structure to dock the a-ketoamide 13a which suggested that the pyridine ring might have some steric clash with the side chain of Gln189. However, in their previous work, they had found Gln189 to be quite flexible, and therefore we went ahead with 13a as a lead. However, relative to 11r (IC50 = 0.18 ± 0.02 mM), the structural modification led to some loss of inhibitory activity against the main protease of SARS-CoV-2 (IC50 = 2.39 ± 0.63 mM) cyclopropyl in 13b. Through the nucleophilic attack of the catalytic Cys145 onto the a-keto group of the inhibitor, a thiohemiketal is formed in a reversible reaction. The oxyanion (or hydroxyl) group of this thiohemiketal is stabilized by a hydrogen bond from His41, whereas the amide oxygen of 13b accepts a hydrogen bond from the main-chain amides of Gly143, Cys145, and partly Ser144, which form the canonical “oxyanion hole” of the cysteine protease. It is an advantage of the a-ketoamides that their warhead can interact with the catalytic center of the target proteases through two hydrogen-bonding interactions rather than only one, as with other warheads such as aldehydes or Michael acceptors . To assess the absorption-distribution-metabolism-excretion (ADME) properties of the pyridine containing a-ketoamides, they investigated compound 13a and 13b .The ADME parameters of 13b were similar to those of 13a. In

addition, binding to human plasma proteins was found to be 90%. The Cmax of 13b is around 37% of the Cmax detected for 13a, although the 13b dosage was lower by a factor of ~7. In addition, 13b showed a less rapid clearance relative to 13a. During the pharmacokinetic study with 13b, we monitored its lung tissue levels. After 4 hours, 13b was still found at ~13 ng g−1 in lung tissue. This lung tropism of 13a and 13b is beneficial given that COVID-19 affects the lungs. In addition 13b was nebulized using an inhalation device at 3mg kg−1. After 24 hours, 13b was found at 33 ng g−1 in lung tissue. Thus, this study provides a useful framework for development of pyridone-containing inhibitors toward anticoronaviral drugs. To date no specific medications have been developed, and therefore considering the risk factors associated with this disease, there is an urgent need for a treatment method to treat this disease in order to limit the transmission. This study is focused on the repurposing/identification of compounds with a sole aim to expedite the identification of specific drugs for the treatment

of COVID-19. Among all the treatment strategies, the uses of already known

viral medications have great advantages as the pharmacokinetics, pharmacodynamics, and safety profiles of these drugs have already been established. This drug repurposing strategy has gained significance as they are expected to be faster with less investment .

Recently, anti-malarial drug chloroquine and hydroxychloroquine along with some antiviral drugs have been reported to have certain curative effect on COVID-19. Due to diverse bioactivity and less toxicity, naturally occurring bioactive

flavonoid molmolecules have also been screened for their potential therapeutic effects. The MPro is one of the most explored drug target among the corona

viruses that plays a major role in the translation and replication of new generation viruses from the viral genomic RNA The 3D structure of SARS-CoV-2 Mpro (PDB ID. 6Y84), is made up of three domains, where domain I, II and III spans across 8-101, 102-184 and 201-306 amino acid residues, repectively. Domain I

and II mainly consists of b-barrels while domain III mainly consists of a-helices .The substrate/active site of binding is located at the cleft of domain I and II, which

consists of two catalytic residues, namely, HIS41 and CYS145 .Here in this report, a total of 33 compounds belonging to different classes (i) control drugs, (ii) natural products, (iii) anti-virals, (iv) anti-fungals, (v) anti-nematodes and antiprotozoal
were identified to investigate their inhibitory effects towards MPro by molecular docking analysis. Ritonavir, hydroxychloroquine, penciclovir and lopinavir are known drugs that have been screened for the treatment of COVID-19. The reason for them being used as control drugs in the study is that, lopinavir/ritonavir combination,
and anti-malarial drug hydroxychloroquine has recently been found to be a potential inhibitor of the virus, Considering the diverse pharmaceutical
properties of the natural products including anti-viral properties, a total of 17 compounds: curcumin, demethoxycurcumin, (-)-Epigallocatechin gallate (EGCG), (-)-epigallocatechin, (EGC), hesperidin, myricitrin, puerarin, scutellarin, rutin, quercitrin, capsaicin, ursolic acid, glabridin, apiin, rhoifolin, glycyrrhizin,
and vitexin were screened for their inhibitory potential against SARS-CoV-2 Mpro. Azidothymidine, indinavir, tipranavir, and saquinavir are the well-known anti-viral drugs while diethylcarbamazine, primaquine, mepacrine, artemisinin and niclosamide are the anti-nematodes and emetine, an anti-protozoal drug ,
which have also been screened for their inhibitory potentials. Further, two anti-fungals, namely, fluconazole and itraconazole were also docked to
the main protease of COVID-19. The 3 D coordinates of the ligands were
obtained from ChemSpider as a .mol file and further geometry optimization was carried out in ArgusLab using PM3 methods .The drug likeliness of a molecule is indicated by the Lipinski's rule of five parameters (molecular weight <500 Da,
no more than 5 hydrogen bond donors, no. of hydrogen bond acceptors should be less than 10 and logP should not be greater than 5. The Lipinski's rule of five parameters were obtained from the SWISSADME server. The crystal structure of MPro (PDB ID: 6Y84) was obtained from Protein Data Bank (PDB) . The obtained structure was a dimer of two homologous amino acid chains (A and B). The chain A was used for molecular docking. Water molecules were removed from the PBD using PyMOL .

The final PDB file of the protease and geometry optimized ligand structures were selected for molecular docking analyses in the SwissDock server. According to the SwissDock server, the binding modes of the ligands are ranked according
to their fullfitness score, therefore the conformers having the minimum fullfitness score were analyzed for further evaluations. The fullfitness score and the free binding energy associated with each corresponding docked pose were calculated and results were seen. Within the control drugs , the best pose was found to be of penciclovir with a fullfitness score of -1314.77 kcal/mol followed by ritonavir. Looking to naturally occurring compounds curcumin had best fulfitness score(-1236.50 kcal/mol). Coming forward to anti-fungal drugs Flucanazole (-1168.54 kcal/mol). The anti-viral drug with Azidothymidine (-1324.25 kcal/mol) and anti-nematodal and anti-protozoal drugs with Diethylcarbamazine(-1272.14 kcal/mol).
Among all the molecules, the inhibition activity of rutin was found to be the highest as its DG value (_9.55 kcal/mol) is the minimum, followed by ritonavir (_9.52 kcal/mol), emetine (_9.07 kcal/mol), hesperidin (_9.02 kcal/mol), and indinavir(_8.84 kcal/mol).

3.2 Summary of Literature Review

We used a-ketoamide13b inhibitor as our reference compound for our project based on the results of above mentioned article, whereas some reference inhibitors were also used including penciclovir, hydroxychloroquine according to fullfitness score and free energy from the results drawn.

CONCLUSION

Cutting edge chemical science technology and computer-aided drug design (CADD) is bringing together leading minds from across the world to help tackle the COVID-19 crisis. The recent outbreak of novel coronavirus disease-19 (COVID-19) calls for and welcomes possible treatment strategies using drugs on the market. It is very efficient to apply computer-aided drug design techniques to quickly identify promising drug repurposing candidates, especially after the detailed 3D structures of key viral proteins are resolved. The virus causing COVID-19 is SARS-CoV-2. Taking advantage of a recently released crystal structure of SARS-CoV-2 main protease in complex with a covalently bonded

inhibitor, we have successfully proposed a study focused on the repurposing/identification of compounds with a sole aim to expedite the identification of specific drugs for the treatment of COVID-19.A great application of drug repurposing is to identify drugs that were developed for treating other diseases to treat a new disease. Drug repurposing can be achieved by conducting systematic drug–drug target interaction (DTI)

analyses by using various tools like UCSF Chimera(ligand preparation), Discovery studio(protein preparation) and autodock4 (molecular docking) followed by binding free energy calculations.

FUTURE SCOPE

Discovery and development of a new drug is generally known as a very complex process which takes a lot of time and resources. So now a day's computer aided drug design approaches are used very widely to increase the efficiency of the drug discovery and development course. Various approaches of CADD are evaluated as promising techniques according to their need, in between all these structure-based drug design and ligand-based drug design approaches are known as very efficient and powerful techniques in drug discovery and development. These both methods can be applied with molecular docking to virtual screening for lead identification and optimization. In the recent times computational tools are widely used in pharmaceutical industries and research areas to improve effectiveness and efficacy of drug discovery and development Pipeline, through it we can find the most promising drug candidate in a very cost-effective way. It always provides

a hope for betterment in drug discovery area. In the past years through Computer aided drug design many impressive researches are achieved so it will play a very much important role in the near future. With the current achievement's, there is a promising future of computer aided drug design to aid drug discovery of many more curatives in covid-19 for future.

REFERENCES

[1] Halfon, P., & Locarnini, S. (2011). Hepatitis C virus resistance to protease inhibitors. Journal of hepatology, 55(1), 192-206.

[2] https://www.drugbank.ca

[3] https://www.rcsb.org/

[4]https://pubchem.ncbi.nlm.nih.gov/

[5] Aanouz, I., Belhassan, A., El-Khatabi, K., Lakhlifi, T., El-Ldrissi, M., & Bouachrine, M. (2020). Moroccan Medicinal plants as inhibitors against SARS-CoV-2 main protease: Computational investigations. Journal of Biomolecular Structure and Dynamics, 1-9

[6]https://www.who.int/

[7] Cheung, G., & Sundram, F. (2017). Understanding the progression from physical illness to suicidal behavior: A case study based on a newly developed conceptual model. Clinical gerontologist, 40(2), 124-129.

ANALYSIS OF VARIOUS ARTICLES ON EPIGENETICS OF ALZHEIMERS DISEASE

Final Report

(15 May2020 to 30 June 2020)

Submitted by

Aakriti Chauhan 171503

B-TECH in Bioinformatics (6 sem)

Name of Supervisor – Dr. Tiratha Raj Singh



BACHELOR OF TECHNOLOGY IN BIOINFORMATICS

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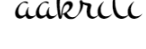
Candidates Declaration

I hereby declare that the work presented in the report entitled **"ANALYSIS OF VARIOUS ARTICLES ON EPIGENETICS OF ALZHEIMERS DISEASE"** in partial fulfillment of the requirements for the award of the degree of Bachelor of Technology in Bioinformatics submitted in the **Department of Biotechnology and Bioinformatics, Jaypee University of Information and Technology, Wakanaghat** is an authentic record of my own work carried out over a period from May 2020 to June 2020 under the supervision of **Prof Tiratha Raj Singh**.

Aakriti Chauhan 171503



This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Prof Tiratha Raj Singh

Associate Professor

Biotechnology and Bioinformatics

Dated:30-06-220

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I give my greatest acknowledgement to my **Parents** for all round support during studies. The endless sacrifices from my parents have made me what I am today.

CONTENTS

Sno.	Title	Page No.
1	Introduction	5-14
2	Materials and Methods	15-16
3	Results and Discussion	17-18
4	Conclusion	19
5	References	20-22

INTRODUCTION

Alzheimer's disease (AD) is a major form of senile dementia, characterized by progressive memory and neuronal loss combined with cognitive impairment. Alzheimer's disease and other dementias are a major and increasing global health challenge, with 40–50 million people currently living with dementia. 701 cases per 100000 population in 1990 and 712 cases per 100000 population in 2016, constituting an increase of 1·7%. However, because of population ageing and growth, the number of people affected by Alzheimer's more than doubled since 1990 and almost 44 million prevalent cases were estimated globally in 2016. Age-standardized prevalence was 1·17 (1·17–1·18) times higher in females than in male[1]. The AD is characterized by linguistic decline, irreversible and progressive cognitive impairment, memory loss and eventually cell death [2].

AD is characterized by the accumulation of extracellular senile plaques containing amyloid –β (Aβ) peptides and intracellular neurofibrillary tangles, which together with cerebral atrophy and neuronal cell death, comprise the hallmark features of the disease. The AD brain is also characterized by the presence of "inflammatory" response, even at prodromal stages. These responses result in activation of astroglia and microglia cells, which can activate several signaling pathways(Wyss-Coray,2006;Avlia-Munoz and Arias,2014) to produce inflammatory signals such as cytokines and reactive oxygen species (ROS), leading to oxidative stress, which further leads to neuronal dysfunction .

Alzheimer's disease is multifactorial disorder that is determined by genetic and environmental factors as well as their interactions. Population-based prospective study is the major epidemiological approach to identifying influential factors for chronic multifactorial diseases. Age is the most powerful determinant of Alzheimer's disease, and gene mutations contribute to a small proportion of all cases. The strong association of Alzheimer's disease with increasing age may partially reflect the cumulative effect of different risk and protective factors over the lifespan, including the effect of complex interactions of genetic susceptibility, psychosocial factors, biological factors, and environmental exposures experienced over the lifespan. Evidence from epidemiological, neuroimaging, and neuropathological research, supports the role of

genetic, vascular, and psychosocial factors in the development of Alzheimer's disease, whereas evidence for the etiologic role of dietary or nutritional factors, occupational exposures, and inflammation is less clear.

GENETIC FACTORS

Mutations in amyloid precursor protein, presenilin-1, and presenilin-2 genes can cause early- onset familial Alzheimer's disease that account for no more than 5% of all cases. The majority of AD cases are sporadic, with considerable heterogeneity in their risk profiles and neuropathological features.

a) Apolipoprotein E ε4 (APOE ε4)

   The APOE ε4 allele is the only established susceptibility gene for both early- and late-onset Alzheimer's disease, and is a susceptibility gene, being neither necessary nor sufficient for the development of Alzheimer's disease

b) Family history

   Individuals who have a parent, brother or sister with Alzheimer's are more likely to develop the disease than those who do not have a first-degree relative with Alzheimer's.

c) Plasma lipid levels

BIOLOGICAL RISK FACTORS

Increasing age is a well-established risk factor for Alzheimer's disease. The incidence of Alzheimer's disease almost doubles with every 5 years of age . Female sex is often associated with an increased risk of AD, especially at the oldest-old age . Men seem to be at greater risk for vascular dementia than women.

VASCULAR DISORDERS AND RISK FACTORS

A number of vascular risk factors and disorders have been linked to Alzheimer's disease, but some factors may have a differential association with the risk of Alzheimer's disease depending on the age when the exposure is assessed.

a) Blood pressure
b) Cardiovascular diseases
c) Cerebrovascular diseases
d) Diabetes mellitus
e) Overweight and obesity
f) Hyperlipidemia
g) The metabolic syndrome
h) Alcohol consumption
i) Cigarette smoking
j) Diet and nutrients

PSYCHOSOCIAL FACTORS

Psychological factors include social economic status, education attainment in early life, and work complexity in adult-life and leisure activities. Evidence from epidemiological research has been accumulating that some psychosocial factors and healthy lifestyle may postpone the onset of dementia, possibly by enhancing cognitive reserve.

a) Social economic status
b) High education
c) Physical activity
d) Mentally stimulating activity
e) Social network and social engagement
f) Depression

OTHER FACTORS

a) Inflammation
b) Hormone replacement therapy
c) Occupational exposures
d) Head trauma and traumatic brain injury

Factors	Systematic review	Results
Overweight and obesity	Meta-analysis of ten studies. Sixteen articles on 15 prospective studies with 3.2-36 years follow-up	Overweight: Dementia RR 1.26 (95% CI 1.10–1.44); Alzheimer's disease 1.35 (95% CI 1·19–1.54) Obesity: Dementia RR 1.64 (95% CI 1.34-2.00); Alzheimer's disease RR 2.04 (95% CI 1.59-2.62)
Smoking	Meta-analysis of four prospective studies with 2–25 years follow-up in over 17 000 people. In the four studies the dementia ORs were 3·17 (95% CI 1.37–7.35), 1.42 (1.07–1.89), 1.60 (1.00–2.57), and 1.63 (1.00–2.67)	Dementia RR 2.2 (95% CI 1.3–3.6)
Physical activity	13 prospective studies focusing on Alzheimer's disease, dementia, or both, with at least 150 000 participants	Dementia RR 0.72 (95% CI 0.60–0.86); Alzheimer's disease 0.55 (95% CI 0.36–0.84)
Cognitive reserve (intelligence, occupation, and education)	22 prospective studies with at least 29 000 participants followed up for a median of 7.1 years	Dementia OR 0.54 (95% CI 0.49–0.59)
Alcohol	15 longitudinal studies with 2–8 years follow-up and at least 14 000 participants	Dementia RR 0.74 (95% CI 0.61–0.91); Alzheimer's disease 0.72 (0.61–0.86)

Medical conditions		
Midlife hypertension	At least 15 years follow-up in most studies, with at least 16 000 participants	Four of five longitudinal studies focusing on midlife hypertension suggested that it is a significant risk factor for incident dementia (RR 1.24–2.8 in different studies) The biggest differences were reported in studies using 160/95 mm Hg as the threshold for hypertension
Stroke	16 studies with at least 25 000 participants, mainly included patients aged 65 years and over	12 of 16 studies showed significant association between stroke and incident dementia, with overall doubling of incidence
Diabetes	15 prospective cohort studies	Dementia RR 1.47 (95% CI 1.25–1.73); Alzheimer's disease RR 1.39 (95% CI 1.16–1.66)

Factors	Systematic review	Results
Midlife hypercholesterolemia	18 studies, but only five assessed high cholesterol specifically in midlife. All five midlife studies had over 15 years follow-up and a total of over 15 000 participants	Four of five longitudinal studies in midlife suggested a significant positive association between high total cholesterol and incident dementia. For overall difference the RR was 1·4–3·1
Intervention studies		
Hypertension	12 091 participants between the three trials (SHEP, SYST-EUR, and SCOPE) with mean follow-up of 3·3 years. Only SYST-EUR reported significant benefit	OR 0.89 (95% CI 0.69–1.16) for incident dementia
Statins for prevention of dementia	26 340 participants between the two trials (PROSPER and HPS), with follow-up of 3·2 and 5 years. Cognition was measured with different instruments at different timepoints	Neither of the two trials reported significant benefit of statin therapy
Vitamins B12 or folate	Four trials in older people without existing cognitive impairment	Three trials showed no benefit. One trial (the only that selected participants based on increased homocysteine) reported benefit with respect to global function

RR=relative risk. OR=odds ratio. SHEP=Systolic Hypertension in the Elderly Program. SYST-EUR=Systolic Hypertension in Europe. SCOPE=Study on Cognition and Prognosis in the Elderly. PROSPER=PROspective Study of Pravastatin in the Elderly at Risk. HPS=Heart Protection Study.

Alzheimer disease is characterized by progressive cognitive decline usually beginning with impairment in the ability to form recent memories, but inevitably affecting all intellectual functions and leading to complete dependence for basic functions of daily life, and premature death. The pathological manifestations of Alzheimer disease include diffuse and neurotic extracellular amyloid plaques and intracellular neurofibrillary tangles accompanied by reactive microgliosis, dystrophic neurites, and loss of neurons and synapses.

National Institute of Neurological and Communicative Disorders and Stroke and the Alzheimer Disease and Related Disorders Association (NINCDSADRDA) developed a uniform set of criteria to enable clinicians and researchers to maintain consistency in the diagnosis. They included aspects of medical history, clinical examination, neuropsychological testing, and laboratory assessments which have been remarkably reliable and valid for the diagnosis of AD over the past three decades. Criteria recently been updated with major advances in

neuropsychological assessment, brain imaging and the neuropathological, biochemical and genetic understanding of this disease, revisions were considered a necessity.

The prevalence rates for AD also rise exponentially with age, increasing markedly after 65 years. There is almost a 15-fold increase in the prevalence of dementia, predominately Alzheimer disease, between the ages of 60 and 85 years . Countries like North America and Western Europe have at age 60 the highest prevalence of dementia (6.4 and 5.4% of the population at age 60), followed by Latin America (4.9%) and China and its developing western-Pacific neighbors (4.0%). The annual incidence rates (per 1000) for these countries were estimated at 10.5 for North America, 8.8 for Western Europe, 9.2 for Latin America and 8.0 for China and its developing western-Pacific neighbors, increasing exponentially with age in all countries, especially through the seventh and eighth decades of life.

ANTECEDENT RISK FACTORS THAT INCREASE THE RISK OF ALZHEIMER DISEASE

Table 1. Factors that modify the risk of Alzheimer disease

Antecedent	Direction	Possible mechanisms
Cardiovascular disease	Increased	Parenchymal destruction Strategic location ↑ Aβ deposition
Smoking	Increased	Cerebrovascular effects Oxidative stress
Hypertension	Increased and decreased	Microvascular disease
Type II diabetes	Increased	Cerebrovascular effect Insulin and Aβ compete for clearance
Obesity	Increased	Increased risk of type II diabetes inflammatory
Traumatic head injury	Increased	↑Aβ and amyloid precursor protein deposition
Education	Decreased	Provides cognitive reserve
Leisure activity	Decreased	Improves lipid metabolism, mental stimulation
Mediterranean diet	Decreased	Antioxidant, anti-inflammatory
Physical activity	Decreased	Activates brain plasticity, promotes brain vascularization

Interventions toward Alzheimer's disease

Current evidence tends to support the notion that dementia onset may be postponed by implementing interventions toward the potential etiologic factors (both risk and protective

factors) (ie, primary prevention) and by early detection (ie, secondary prevention), whereas appropriate care and pharmacotherapy for patients with AD and dementia (ie, tertiary prevention) may help stabilize cognitive functions, reduce agitation, control neuropsychiatric symptoms, and improve the quality of life.

Interventions toward primary prevention

Primary intervention strategies

Theoretically, even if the mechanisms of vascular and psychosocial factors being involved in the pathogenesis and clinical expression of AD are still not fully understood, primary prevention seems possible as most vascular factors and disorders, psychosocial factors, and lifestyle factors are modifiable or amenable to management.38,175 One intervention strategy is to target vascular pathways, including management of midlife high blood pressure and obesity, high blood glucose level, and diabetes. In addition, preventing recurrent cerebrovascular disease and maintaining sufficient cerebral blood perfusion by adequately managing heart failure and avoiding very low blood pressure may help postpone clinical expression of the dementia syndrome, especially among very old people. The second strategy is to maintain the more active and socially integrated lifestyles by establishing extensive social networks and frequently participating in social, physical, and intellectually stimulating activities, which may reduce the risk or delay the onset of AD.38,132Taken together, the most effective strategy may be to encourage people implementing multiple preventive measures throughout the life course, including high educational attainment in childhood and early adulthood, active control of vascular factors and disorders over adulthood, and maintenance of mentally, physically, and socially active lifestyles during middle age and later in life.

Intervention trials toward primary prevention

The main clinical and intervention trials toward primary prevention by targeting the possible risk and protective factors for AD and dementia are summarized in Table II.160,161,176-182 Antihypertensive treatments in reducing the risk of dementia and AD have been tested in a few clinical trials. The pooling analysis of the 2007 Cochrane review, based essentially on three clinical trials (SHEP,183 Syst-Eur,184 and SCOPE185), found no convincing evidence that

blood pressure-lowering therapy among elderly individuals with hypertension could prevent dementia. However, in this review the SCOPE trial, which did not show any effect of blood pressure-lowering treatment by candesartan on the risk of dementia, was actually not a placebo-controlled trial due to ethical considerations. By contrast, the placebo-controlled PROGRESS trial among individuals with cerebrovascular disease (transient ischemic attacks and stroke), which did find a beneficial effect of antihypertensive therapy on cognitive function related to recurrent stroke, was not included.186 The cognition sub study of the double-blind placebo- controlled Hypertension in the Very Elderly Trial (HYVET-COG) among people 80+ years found a nonsignificant reduction in the risk of dementia related to antihypertensive treatment. Encouragingly, when data from this clinical trial were pooled together with those from three other double-blind placebo-controlled trials (SHEP, Syst-Eur, and PROGRESS), antihypertensive treatment could reduce the risk of dementia by 13% (hazard ratio, 0.87; 95% CI, 0.76–1.00; P=0.045).177 It is worthwhile to notice that dementia or AD was the secondary end point in all major clinical trials of antihypertensive therapy, with a relatively short period of follow-up because the trials had to be terminated when benefits of the treatments were clearly shown in terms of primary end points (usually cardiac and cerebrovascular disease). In this context, if the beneficial effect of lowering blood pressure on dementia is not as strong as for cardiovascular disease, a longer period of observation is needed to demonstrate any significant beneficial effect. Estrogen therapy among postmenopausal women has been linked to a considerably lower risk of AD and dementia in numerous observational studies, but the large-scale clinical trial of the Women's Health Initiative Memory Study (WHI-MS) showed that estrogen therapy alone or in combination with progestin did not reduce incidence of probable dementia and mild cognitive impairment (MCI); instead, the active treatments with estrogen and estrogen plus progestin were found to be associated with a twofold increased risk for both dementia and MCI.178,179 It has been argued that in the WHI-MS hormone replacement therapy was given 10 to 15 years after the menopause when the "window of critical time" for putative beneficial effects of estrogen therapy may have been missed.187 Other major clinical trials of primary prevention against dementia, such as those with NSAIDs and vitamin E supplementation, have so far failed to confirm any efficacy against dementia and AD (Table II), while more clinical trials (eg, use of cholesterol-lowering drugs and blood glucose lowering drugs) are ongoing.188,189 The lack of

success in most primary prevention trials underscores the need of new strategies in future intervention studies.

Secondary prevention

Alzheimer's disease is characterized by a preclinical phase, possibly lasting years, during which progressive neurodegeneration in the brain is occurring before typical clinical symptoms (eg, cognitive deficits and subtle cognitive disturbances) become detectable.193 Theoretically, detection of AD at early stage may provide an opportunity for implementing therapeutic intervention to more effectively delay its progression to clinical dementia. However, there remains a challenge as to how to identify individuals during the preclinical phase of the disease, although some clinical markers, neuroimaging biomarkers, and biochemical markers have been investigated.194 First, numerous studies have suggested that deficits in specific cognitive domains such as episodic memory and verbal ability are conceivable up to 10 years before the dementia syndrome can be clinically diagnosed, with a more evident decline occurring over the final few years. The term "mild cognitive impairment" has been used in clinical settings to identify individuals with isolated memory loss (i.e., "amnestic" type MCI), which is more likely to represent the preclinical phase of Alzheimer dementia. However, population-based follow-up studies have frequently shown that individuals with MCI represent a very heterogeneous group in terms of prognosis195,196; although elderly persons with MCI had increased risk of progressing to dementia, a substantial proportion remained stable or even reverted to normal during the next few years. Second, biochemical markers in serum and cerebrospinal fluid such as β-amyloid and τ-protein have been proposed for early detection of AD, but these markers are not sufficiently reliable in making diagnosis of AD in the presymptomatic phase.39,194 Finally, during the last decade neuroimaging has emerged as a useful tool to define AD at both preclinical and early clinical phases of the disease. For example, the amyloid positron emission tomography imaging tracer ligands offer opportunity for measuring β-amyloid in the brain in vivo, which provides the possibility for early diagnosis and for monitoring the course of anti amyloid therapy in AD.197,198 Furthermore, the medial-temporal lobe atrophy seen on volumetric MRI has been used in the identification of MCI and early AD as well as in the assessment of progression of MCI and early AD.199,200 Successful secondary prevention relies on both reliable detection of the disease at an early stage and availability of efficacious

interventions for slowing down progression of the disease. However, while efforts are being made to find ways to effectively counteract the course of AD, some methodological issues facing research on disease-modifying therapies and interventions remain a challenge.

Tertiary prevention

The tertiary prevention aims to avoid functional disability, and if possible, to improve quality of life for patients with AD. Cognitive training may help maintain cognitive function, slow down cognitive decline, and improve wellbeing for people with mild dementia. Current medications widely used for AD and dementia, including cholinesterase inhibitors (donepezil, rivastigmine, and galantamine) and the N-methyl-D-aspartate-receptor antagonist (memantine), are designed to target clinical symptoms of the disease such as cognitive and neuropsychiatric disturbances.201 The efficacy of antioxidant treatments in AD has not been proven. For example, the Cochrane review found no evidence of efficacy of vitamin E in the treatment of AD and in the prevention of progression of MCI to AD,203 although the randomized clinical trials of the Physicians' Health Study II suggested that a long-term β-carotene supplementation might provide cognitive benefits among men.204 Furthermore, high-dose B vitamin supplements did not slow down cognitive decline among individuals with mild to moderate AD.205 Intensive research is ongoing in an attempt to develop disease-modifying drugs by targeting the key neuropathological processes in AD such as β-amyloid protein.206

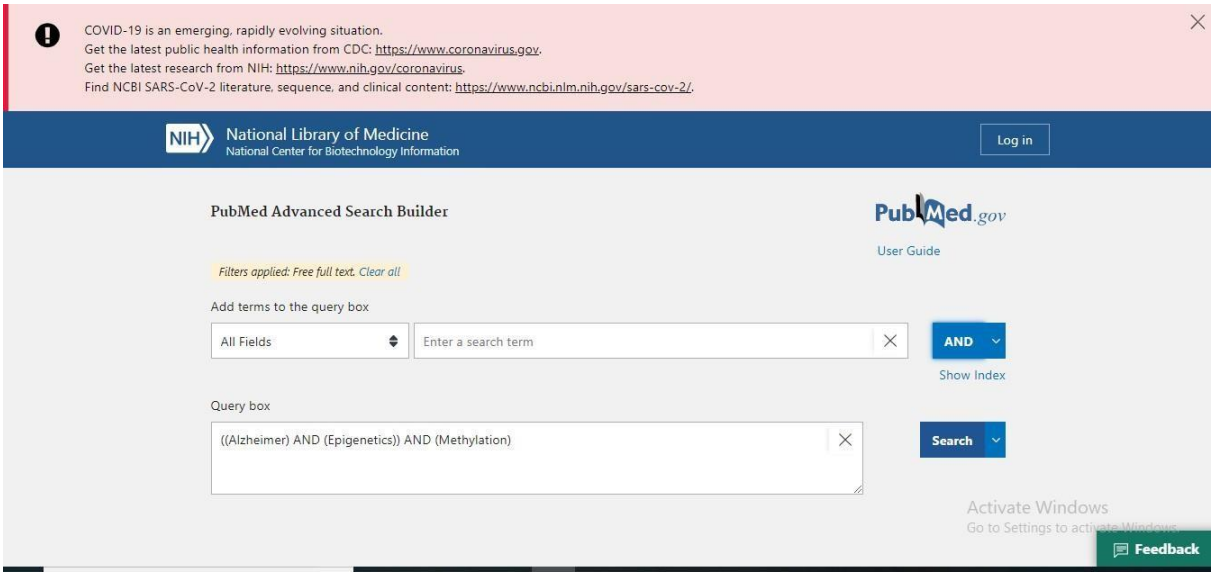
Materials and Methods

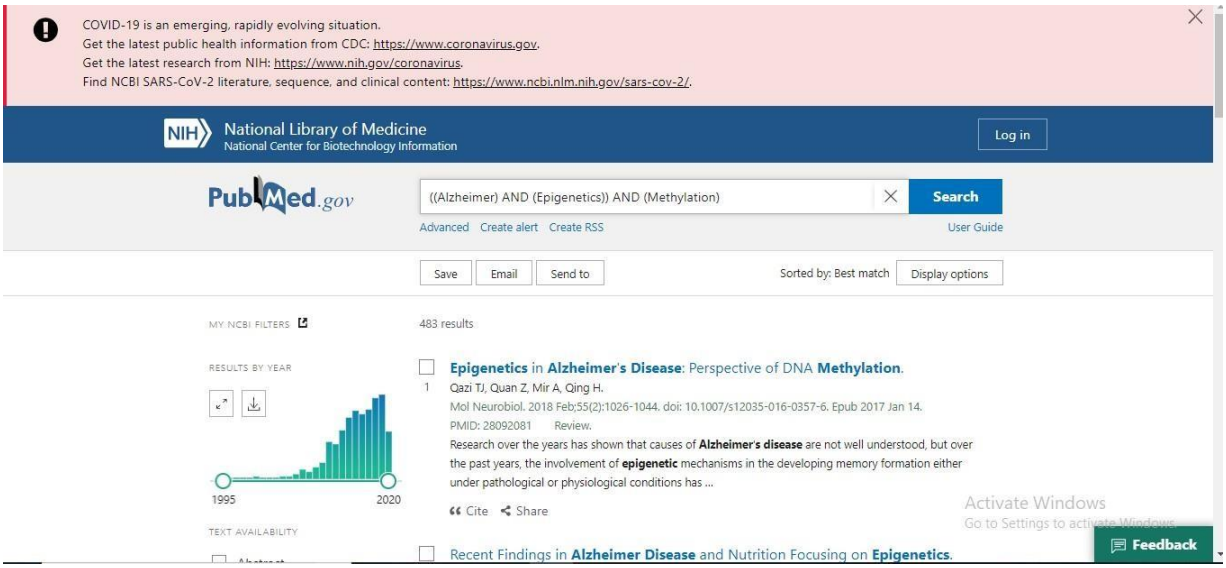
Retrieval of information for the database

A database is an organized collection of data, generally stored and accessed electronically from a computer system. In order to make a database on epigenetics of alzheimer disease, literature review was done. As in epigentics our main focus was on methylation,so the literature in which methylation was the main cause of alzheimer disease were studied. The articles are searched on the pubmed.

PubMed comprises more than 30 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites. **PubMed** is a free search engine accessing primarily the MEDLINE database of references and abstracts on life sciences and biomedical topics. The United States National Library of Medicine (NLM) at the National Institutes of Health maintain the database as part of the Entrez system of information retrieval.

Advance search on PubMed was done for reviewing the literature




COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov.
Get the latest research from NIH: https://www.nih.gov/coronavirus.
Find NCBI SARS-CoV-2 literature, sequence, and clinical content: https://www.ncbi.nlm.nih.gov/sars-cov-2/.
National Library of Medicine
National Center for Biotechnology Information
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((Alzheimer) AND (Epigenetics)) AND (Methylation)
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483 results
RESULTS BY YEAR
1995
2020
TEXT AVAILABILITY
1 Epigenetics in Alzheimer's Disease: Perspective of DNA Methylation.
Qazi TJ, Quan Z, Mir A, Qing H.
Mol Neurobiol. 2018 Feb;55(2):1026-1044. doi: 10.1007/s12035-016-0357-6. Epub 2017 Jan 14.
PMID: 28092081 Review.
Research over the years has shown that causes of Alzheimer's disease are not well understood, but over the past years, the involvement of epigenetic mechanisms in the developing memory formation either under pathological or physiological conditions has ...
Cite Share
Recent Findings in Alzheimer Disease and Nutrition Focusing on Epigenetics.
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Go to Settings to activate Windows.
Feedback

Results and Discussion

By doing advance search in PubMed 483 results were obtained.

So, from those 483 articles we collected information on how methylation is playing a role in epigenetics of Alzheimer disease.

Following are the results obtained (here only 9 articles are mentioned, but this is done for 255 articles):

Sno.	NAME OF THE RESEARCH ARTICLE	Role of methylation	RELATION WITH METHYLATION
1	Recent Findings in Alzheimer Disease and Nutrition Focusing on Epigenetics	YES	The current review focuses on the epigenetic mechanisms of AD and how nutrition can influence the course of this disease through regulation of gene expression, according to the latest scientific findings. Epigenetics is becoming a very attractive subject for researchers because it can shed light on unknown aspects of complex diseases like AD. DNA methylation, histone modifications, and microRNAs are the principal epigenetic mechanisms involved in AD pathophysiology. Nutrition is an environmental factor that is related to AD through epigenetic pathways. Vitamin B-12, for instance, can alter the one-carbonmetabolismand thus interfere in the DNA methylation process.
2	Epigenetics and DNA methylomic profiling in Alzheimer's disease and other neurodegenerative diseases	YES	. This review discuss advances that have been made toward understanding the role of epigenetic processes in neurodegenerative disorders, with a particular focus on Alzheimer's disease. And also a brief overview of DNA modifications, followed by a summarization of studies of DNA modifications in Alzheimer's disease and other neurodegenerative diseases.
3	The epigenetics of aging and neurodegeneration	YES	They review current knowledge about the major epigenetic mechanisms, including DNA methylation and DNA demethylation, chromatin remodeling and noncoding RNAs, as well as the involvement of these mechanisms in normal aging and in the pathophysiology of the most common neurodegenerative diseases.
4	Role of Genetics and Epigenetics in the Pathogenesis of Alzheimer's Disease and Frontotemporal Dementia	YES	In this review, an overview of the current genetic and epigenetic progresses in AD and FTD is provided, with particular focus on 1) causative genes, 2) genetic risk factors and disease modifiers, and 3) epigenetics, including methylation, non-coding RNAs and chromatin remodeling.

5	DNA methylation analysis on purified neurons and glia dissects age and Alzheimer's disease-specific changes in the human cortex	YES	The current review focuses on how cell sorting strongly enhances the robust detection of disease-related DNA methylation changes even in a relatively small cohort. Numerous genes with cell-type-specific methylation signatures and document differential methylation dynamics associated with aging specifically in neurons such as CLU, SYNJ2 and NCOR2 or in glia RAI1,CXXC5 and INPP5A were identified
6	Could Alzheimer's Disease Originate in the Periphery and If So How So?		It is shown that the presence of the APOE ε4 allele, altered miRNA expression and epigenetic dysregulation in the promoter region and exon 1 of TREM2, as well as ANK1 hypermethylation and altered levels of histone post-translational methylation leading to increased transcription of TNFA, could variously explain increased levels of peripheral and central inflammation found in AD. In particular, as a result of increased activity of triggering receptor expressed on myeloid cells 2 (TREM-2), the presence of the apolipoprotein E4 (ApoE4) isoform, and changes in ANK1 expression, with subsequent changes in miR-486 leading to altered levels of protein kinase B (Akt), mechanistic (previously mammalian) target of rapamycin (mTOR) and signal transducer and activator of transcription 3 (STAT3), all of which play major roles in microglial activation, proliferation and survival, there is activation of microglia, leading to the subsequent (further) production of cytokines, chemokines, nitric oxide, prostaglandins, reactive oxygen species, inducible nitric oxide synthase and cyclooxygenase-2, and other mediators of inflammation and neurotoxicity. These changes are associated with the development of amyloid and tau pathology, mitochondrial dysfunction (including impaired activity of the electron transport chain, depleted basal mitochondrial potential and oxidative damage to key tricarboxylic acid enzymes), synaptic dysfunction, altered glycogen synthase kinase-3
			(GSK-3) activity, mTOR activation, impairment of autophagy, compromised ubiquitin-proteasome system, iron dyshomeostasis, changes in APP translation, amyloid plaque formation, tau hyperphosphorylation and neurofibrillary tangle formation.
7	Epigenetic Factors in Late-Onset Alzheimer's Disease: MTHFR and CTH Gene Polymorphisms, Metabolic Transsulfuration and Methylation Pathways, and B Vitamins	YES	DNA methylation and other epigenetic factors are important in the pathogenesis of late-onset Alzheimer's disease (LOAD). Methylenetetrahydrofolate reductase (MTHFR) gene mutations occur in most elderly patients with memory loss. MTHFR is critical for production of S-adenosyl-L-methionine (SAM), the principal methyl donor. A common mutation (1364T/T) of the cystathionine-γ-lyase (CTH) gene affects the enzyme that converts cystathionine to cysteine in the transsulfuration pathway causing plasma elevation of total homocysteine (tHcy) or hyperhomocysteinemia—a strong and independent risk factor for cognitive loss and AD.
8	Epigenetics and Pharmacology	YES	Epigenetic regulation of gene activity has been shown to be important in maintaining normal phenotypic activity of cells, as well as having a role in development and diseases such as cancer and neurodegenerative disorders such as Alzheimer's. Newer classes of drugs regulate epigenetic mechanisms to counteract disease states in humans. The reports in this issue describe some advances in epigenetic understanding that relate to human disease, and our ability to control these mechanisms by pharmacological means. Increasingly the importance of epigenetics is being uncovered - it is pharmacology that will have to keep pace.
9	Alzheimer's disease pathogenesis: Is there a role of folate?	YES	Epigenetic modifications, including changes in DNA methylation, have been implicated in a wide range of diseases including neurologicaldiseases such as Alzheimer's. The role of dietary folate in providing methyl groups required for maintenance and modulation of DNA methylation makes it a

Till now literature review of 255 articles were done out of 483.

Conclusion

In the present study an attempt has been made to analyze the role or effect of epigenetics on Alzheimer's disease. Alzheimer disease is a chronic neurodegenerative disorder, and its complexity makes its cure an unsolved problem for the time being. A novel pathophysiologic aspect, that of epigenetics, promises the explanation of many medical mysteries including etiology and pathophysiology of AD. Epigenetic biomarkers can be a very helpful tool for the researchers to find the exact nutrients needed to create specific remedies, and maybe the same biomarkers can even be used in patient screening in the future. In this way, nutrition might grow to become a useful preventive and even a therapeutic alternative against AD, especially if combined with other antidementia interventions, such as acetylcholinesterase inhibitors, brain exercise, physical training, etc.

References

[1] Nichols, Emma, et al. "Global, regional, and national burden of Alzheimer's disease and other dementias, 1990–2016: a systematic analysis for the Global Burden of Disease Study 2016." The Lancet Neurology 18.1 (2019): 88-106.

[2] Blass, John P. "Alzheimer's disease and Alzheimer's dementia: distinct but overlapping entities." Neurobiology of aging 23.6 (2002): 1077-1084.

[3] Davies, Peter, and A. J. F. Maloney. "Selective loss of central cholinergic neurons in Alzheimer's disease." The Lancet 308.8000 (1976): 1403.

[4] De Jager, P.L.; Srivastava, G.; Lunnon, K.; Burgess, J.; Schalkwyk, L.C.; Yu, L.; Eaton, M.L.; Keenan, B.T.; Ernst, J.; McCabe, C.; et al. Alzheimer's disease: Early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nat. Neurosci. 2014, 17, 1156– 1163. [CrossRef][PubMed]

[5] Lunnon,K.;Smith,R.;Hannon,E.;DeJager,P.L.;Srivastava,G.;Volta,M.;Troakes,C.;Al-Sarraj,S.;Burrage,J.; Macdonald, R.; et al. Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nat. Neurosci. 2014, 17, 1164–1170. [CrossRef]

[6] Shewale SJ, Huebinger RM, Allen MS, Barber RC. The potential role of epigenetics in Alzheimer's disease etiology. Biol Syst 2013;2:114.

[7] Balazs R. Epigenetic mechanisms in Alzheimer's disease. Degener Neurol Neuromuscul Dis 2014;4:85–102.

[8] Landgrave-Gómez J, Mercado-Gómez O, Guevara-Guzmán R. Epigenetic mechanisms in neurological and neurodegenerative diseases. Front Cell Neurosci 2015;9:58.

[9] Pezzi JC, Ens CM, Borba EM, Schumacher-Schuh AF, de Andrade FM, Chaves ML, Fiegenbaum M, Camozzato AL. DNA methyltransferase haplotype is associated with Alzheimer's disease. Neurosci Lett 2014;579:70–4.

[10] Chouliaras L, Mastroeni D, Delvaux E, Grover A, Kenis G, Hof PR, Steinbusch HW, Coleman PD, Rutten BP, van den Hove DL. Consistent decrease in global DNA methylation and hydroxymethylation in the hippocampus of Alzheimer's disease patients. Neurobiol Aging 2013;34:2091–9.

[11] Condliffe D, Wong A, Troakes C, Proitsi P, Patel Y, Chouliaras L, Fernandes C, Cooper J, Lovestone S, Schalkwyk L, et al. Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. Neurobiol Aging 2014;35:1850–4. 12. Wang J, Yu JT, Tan MS, Jiang T, Tan L. Epigenetic mechanisms in Alzheimer's disease: implications for pathogenesis and therapy. Ageing Res Rev 2013;12:1024–41.

[12] Fujiki R, Hashiba W, Sekine H, et al. GlcNAcylation of histone H2B facilitates its monoubiquitination. Nature. 2011; 480:557–60. [PubMed: 22121020]

[13] Xu Q, Yang C, Du Y, et al. AMPK regulates histone H2B O-GlcNAcylation. Nucleic Acids Res. 2014; 42:5594–604. [PubMed: 24692660]

[14] He Y, Roth C, Turkenburg JP, Davies GJ. Three-dimensional structure of a Streptomyces sviceus GNAT acetyltransferase with similarity to the C-terminal domain of the human GH84 OGlcNAcase. Acta Crystallogr D Biol Crystallogr. 2014; 70:186–95. [PubMed: 24419391]

[15] Zhang Q, Liu X, Gao W, et al. Differential regulation of the ten-eleven translocation (TET) family of dioxygenases by O-linked β-N-acetylglucosamine transferase (OGT). J Biol Chem. 2014; 289:5986–96. [PubMed: 24394411]

[16] Harwood KR, Hanover JA. Nutrient-driven O-GlcNAc cycling - think globally but act locally. J Cell Sci. 2014; 127:1857–67. [PubMed: 24762810]

[17] Myers SA, Panning B, Burlingame AL. Polycomb repressive complex 2 is necessary for the normal site-specific O-GlcNAc distribution in mouse embryonic stem cells. Proc Natl Acad Sci US A. 2011; 108:9490–5.

[18] Medford HM, Porter K, Marsh SA. Immediate effects of a single exercise bout on protein OGlcNAcylation and chromatin regulation of cardiac hypertrophy. Am J Physiol Heart Circ Physiol. 2013; 305:H114–23. [PubMed: 23624624]

[19] Cox EJ, Marsh SA. Exercise and diabetes have opposite effects on the assembly and O-GlcNAc modification of the mSin3A/HDAC1/2 complex in the heart. Cardiovasc Diabetol. 2013; 12:101. [PubMed: 23835259]

[20] Ito R, Katsura S, Shimada H, et al. TET3-OGT interaction increases the stability and the presence of OGT in chromatin. Genes Cells. 2014; 19:52–65. This paper demonstrates that the TET3-OGT interactions stabilize OGT on chromatin. [PubMed: 24304661]

MACHINE LEARNING WITH PYTHON

A report submitted in partial fulfilment of the requirements for the degree of

BACHELOR OF TECHNOLOGY

Internship with

VERZEO

(5/06/2020-10/08/2020)

By

Garima Sharma

Batch-BI-61

Roll no. - 171504



DEPT. OF BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, SOLAN, H.P-173234

TABLE OF CONTENT

S.no	Topics	Page No.
1.	Acknowledgement	1
2.	Student Declaration	2
3.	Introduction	3
4.	Description of Industry	4
5.	Description of work	5-6
6.	Detailed description of work	7-13
7.	Conclusion	14-15
8.	Appendices	16

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I, Garima Sharma would like to express my sincerest gratitude to the TnP cell(Jaypee University of Information Technology, Solan, H.P.).I would also like to thank Dr. Sudhir Kumar, HOD Department of Biotechnology and Bioinformatics; who has been a constant support through all my endeavours; for providing me with this wonderful opportunity for the fulfilment of requirements of the Internship (2020) with a report on

MACHINE LEARNING WITH PYTHON

STUDENT DECLARATION

I, Garima Sharma, hereby declare that the presented report of internship titled "**MACHINE LEARNING WITH PYTHON**" is uniquely prepared by me after the completion of 45 days' training at VERZEO (online).

I also confirm that the report is only prepared for my academic requirement, not for any other purpose.

GARIMA SHARMA

Bachelor of Technology

Department of Biotechnology and Bioinformatics

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INTRODUCTION

Basic Introduction to my Internship

The online training, **Machine Learning with Python,** is a 2 months training program covering essential concepts on the building block of Machine Learning. Our advancements of technology have now lead us to a new realm of possibilities, Machine Learning. It has the ability to learn by itself without human interference with the help of data.

I learnt basic python first, that helps in Data analysis, deploy algorithms, etc.

Then, EDA was learnt for cleaning the data, before any analysis could be done.

Using python, Machine learning algorithms were learned and applied in code for Data analysis. Algorithms identify and observe the data, clean it, find patterns, and make/suggest decisions that helps humans ease their workload. It replicates the way humans understand the data.

There are various categories of machine learning algorithms:

- Supervised
- Semi-supervised
- Unsupervised

DESCRIPTION OF INDUSTRY

Verzeo is an upskilling e-learning platform headquartered in Bengaluru, India. It uses machine learning and artificial intelligence to assist students in gaining technological knowledge and skills required for employment.

Verzeo was founded in 2017 by Vungarala V Subhramanyam. The idea behind verzeo is to bridge the gap between the classroom environment and work-space environment by training students in new technological skills. The platform works online and offline, and provides training to UG and PG students. Upskilling happens in the fields of cloud computing, artificial intelligence, machine learning, cyber security, blockchain technology, augmented reality, web development, virtual reality, and other technology-related programs.

Post the learning, students get internship opportunities with multinational companies (This time gold partner **Microsoft**). Their offline centres are in Mumbai, New Delhi, Bengaluru, Chennai, and Hyderabad, and focuses on students from Tier 2 and Tier 3 Institutes.

In April 2018, Verzeo raised undisclosed seed funding and $5 million from high net-worth individuals in September of the same year.

DESCRIPTION OF WORK

In my internship I was required to complete the course on basic Python, basics of Statistics and probability and EDA for data cleaning in the first month.

In the second month I was required to learn the basics of Machine learning, the algorithms of machine learning and apply those algorithms for data analysis, data visualization, make/suggest decisions.

I was given 2 projects in the second month:

- Mini Project
- Major Project

OVERVIEW OF THE PROJECTS

- **MINI PROJECT:** The mini project was an individual project. The mini project was based on EDA and data cleaning. A tmdb-dataset was given, which I was asked to clean and perform EDA on it. After the above step, I was asked to answer four out of 6 given questions based on the dataset, I answered 6 of them. The questions were answered using Python in Anaconda (Spyder).

- **MAJOR PROJECT:** The major project was a group project, which was done in a group of 8 people. An Information.csv file was given, containing a twitter dataset.

  We were required to clean the dataset and perform EDA on the given dataset, after that answering any two questions on the dataset. Thereafter, we were required to find the best suited machine learning algorithm based on accuracy. At the end we were required to write a summarised write-up of the above work.

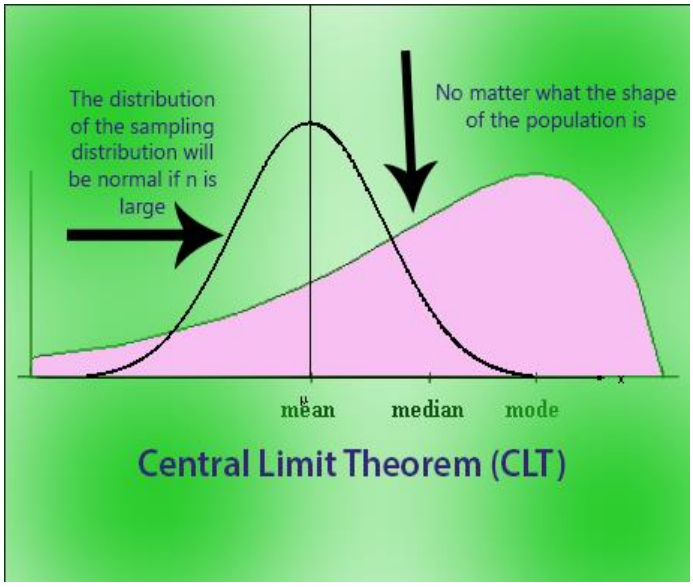
DETAILED DESCRIPTION OF WORK

During this project I implemented everything that I learnt on my projects.

Firstly, I learnt the basics of python, about python arrays, strings, dictionaries etc.

Then I learnt Statistics and Probability. In statistics and probability, I learnt about Central limit theorem and Hypothesis testing.

Central limit theorem: In probability theory, the central limit theorem (CLT) establishes that, in some situations, when independent random variables are added, their properly normalized sum tends toward a normal distribution (informally a bell curve) even if the original variables themselves are not normally distributed. The theorem is a key concept in probability theory because it implies that probabilistic and statistical methods that work for normal distributions can be applicable to many problems involving other types of distributions.



CLT

Hypothesis testing: Hypothesis testing is a form of **statistical inference** that uses data from a sample to draw conclusions about a population parameter or a population probability distribution. First, a tentative assumption is made about the parameter or distribution. This assumption is called the null hypothesis and is denoted by H0.

Then, I learnt as to how to clean the data and perform EDA based on that data. As nobody can directly put the raw data into the ML model. You have to clean the data and perform EDA.

EDA (Exploratory Data Analysis): It is an approach of doing data analysis.

EDA includes:

- Ask questions and get data
- Data Wrangling

1. Data Gathering
2. Data assessing
3. Data cleaning

- Draw conclusions
- Communicate

Based on the above learning I did a mini project on tmdb-movies dataset.

CODE and output are as follows:

```
In [1]: import pandas as pd

In [80]: df = pd.read_csv('tmdb-movies.csv')

In [81]: df.shape
Out[81]: (10866, 21)

In [82]: df.describe()
```

Out[82]:

	id	popularity	budget	revenue	runtime	vote_count	vote_average	release_year	budget_adj	revenue_adj
count	10866.000000	10866.000000	1.086600e+04	1.086600e+04	10866.000000	10866.000000	10866.000000	10866.000000	1.086600e+04	1.086600e+04
mean	66064.177434	0.646441	1.462570e+07	3.982332e+07	102.070863	217.389748	5.974922	2001.322658	1.755104e+07	5.136436e+07
std	92130.136561	1.000185	3.091321e+07	1.170035e+08	31.381405	575.619058	0.935142	12.812941	3.430616e+07	1.446325e+08
min	5.000000	0.000065	0.000000e+00	0.000000e+00	0.000000	10.000000	1.500000	1960.000000	0.000000e+00	0.000000e+00
25%	10596.250000	0.207583	0.000000e+00	0.000000e+00	90.000000	17.000000	5.400000	1995.000000	0.000000e+00	0.000000e+00
50%	20669.000000	0.383856	0.000000e+00	0.000000e+00	99.000000	38.000000	6.000000	2006.000000	0.000000e+00	0.000000e+00
75%	75610.000000	0.713817	1.500000e+07	2.400000e+07	111.000000	145.750000	6.600000	2011.000000	2.085325e+07	3.369710e+07
max	417859.000000	32.985763	4.250000e+08	2.781506e+09	900.000000	9767.000000	9.200000	2015.000000	4.250000e+08	2.827124e+09

```
In [83]: df.columns
Out[83]: Index(['id', 'imdb_id', 'popularity', 'budget', 'revenue', 'original_title',
       'cast', 'homepage', 'director', 'tagline', 'keywords', 'overview',
       'runtime', 'genres', 'production_companies', 'release_date',
       'vote_count', 'vote_average', 'release_year', 'budget_adj',
       'revenue_adj'],
```

```
In [84]: df = df[['budget','revenue','release_year','cast','genres','runtime','original_title','production_companies']]

In [85]: df.shape
Out[85]: (10866, 8)

In [86]: df = df[df['budget'] != 0]

In [87]: df = df[df['revenue'] != 0]

In [88]: df.shape
Out[88]: (3855, 8)

In [89]: df = df.dropna()

In [90]: df
```

Out[90]:

	budget	revenue	release_year	cast	genres	runtime	original_title	production_companies
0	150000000	1513528810	2015	Chris Pratt|Bryce Dallas Howard|Irrfan Khan|Vi...	Action|Adventure|Science Fiction|Thriller	124	Jurassic World	Universal Studios|Amblin Entertainment|Legenda...
1	150000000	378436354	2015	Tom Hardy|Charlize Theron|Hugh Keays-Byrne|Nic...	Action|Adventure|Science Fiction|Thriller	120	Mad Max: Fury Road	Village Roadshow Pictures|Kennedy Miller Produ...
2	110000000	295238201	2015	Shailene Woodley|Theo James|Kate Winslet|Ansel...	Adventure|Science Fiction|Thriller	119	Insurgent	Summit Entertainment|Mandeville Films|Red Wago...
3	200000000	2068178225	2015	Harrison Ford|Mark Hamill|Carrie Fisher|Adam D...	Action|Adventure|Science Fiction|Fantasy	136	Star Wars: The Force Awakens	Lucasfilm|Truenorth Productions|Bad Robot

File Edit View Insert Cell Kernel Widgets Help

Run Code

In [91]:
```
third_lowest = df.sort_values(['budget']).iloc[2]['original_title']
third_highest = df.sort_values(['budget']).iloc[-3]['original_title']
third_lowest, third_highest
```

Out[91]: ('Death Wish 2', "Pirates of the Caribbean: At World's End")

In [92]:
```
movies_between_2000_and_2005 = df[df['release_year'].isin([2000, 2001, 2002, 2003, 2004, 2005])]
```

In [93]:
```
no_of_words = 0
for i in range(movies_between_2000_and_2005.shape[0]):
    words_list = movies_between_2000_and_2005['original_title'].values[i].split(' ')
    no_of_words = no_of_words + len(words_list)

ans2 = no_of_words/movies_between_2000_and_2005.shape[0]
ans2
```

Out[93]: 2.681404421326398

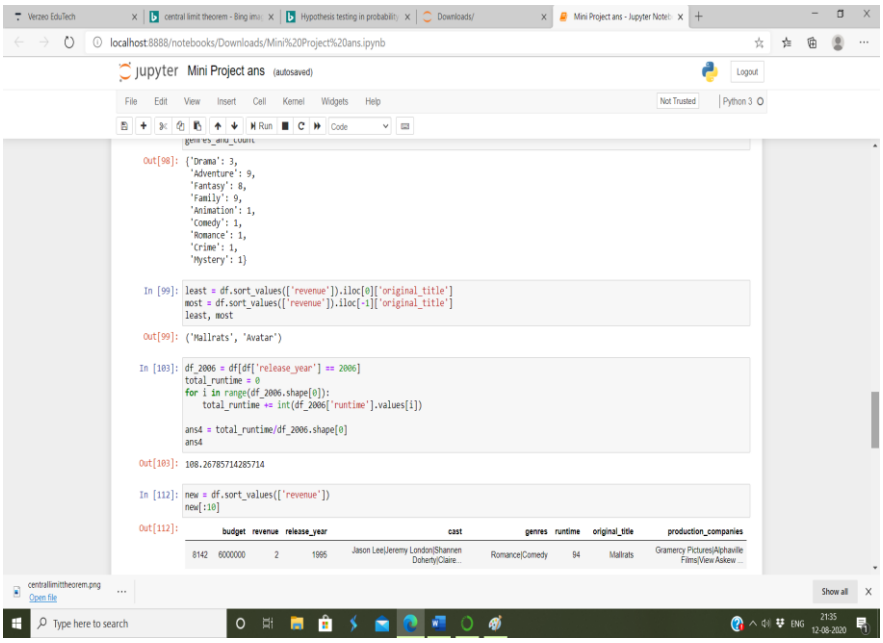
In [94]:
```
vin_diesel_df = df[df['cast'].str.contains('Vin Diesel')]
emma_watson_df = df[df['cast'].str.contains('Emma Watson')]
#for i in range(df.shape[0]):
```

In [96]:
```
genres_and_count = {}
for i in range(vin_diesel_df.shape[0]):
    genres = vin_diesel_df['genres'].values[i].split('|')
    for genre in genres:
        try:
            count = genres_and_count[genre]
            genres_and_count[genre] = count + 1
        except:
            genres_and_count[genre] = 1

genres_and_count
```

Out[96]:
```
{'Action': 14,
 'Crime': 7,
 'Thriller': 12,
 'Fantasy': 2,
 'Adventure': 5,
 'Science Fiction': 6,
 'Drama': 4,
 'Animation': 1,
 'Family': 2,
 'Comedy': 1}
```

In [98]:
```
genres_and_count = {}
for i in range(emma_watson_df.shape[0]):
    genres = emma_watson_df['genres'].values[i].split('|')
    for genre in genres:
        try:
            count = genres_and_count[genre]
            genres_and_count[genre] = count + 1
        except:
            genres_and_count[genre] = 1
```



Then, I learnt about Machine learning algorithms.

1. **Linear Regression: -** Linear Regression is a machine learning statistical method which can be used to quantify and make predictions based on relationships between numerical variables.

   The goal of regression is to find a line that fits our data points.

   The target variable of regression model is numeric

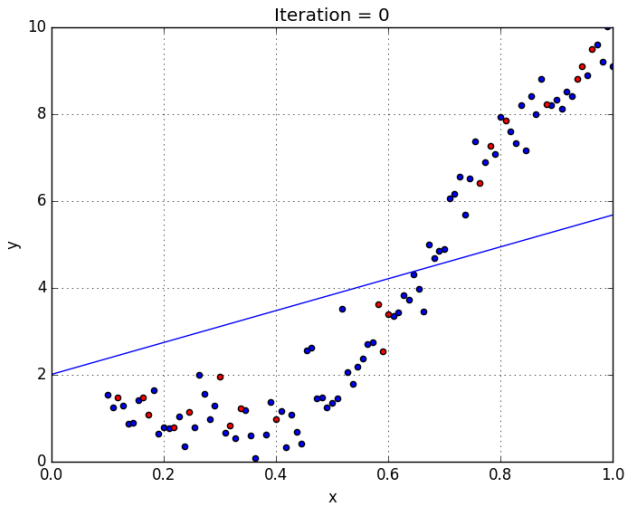
   Equation to remember is y = mx + b

   Y = mx + b

   b is the intercept -> where line crosses the Y axis

m is the slope -> give us the steep of the line

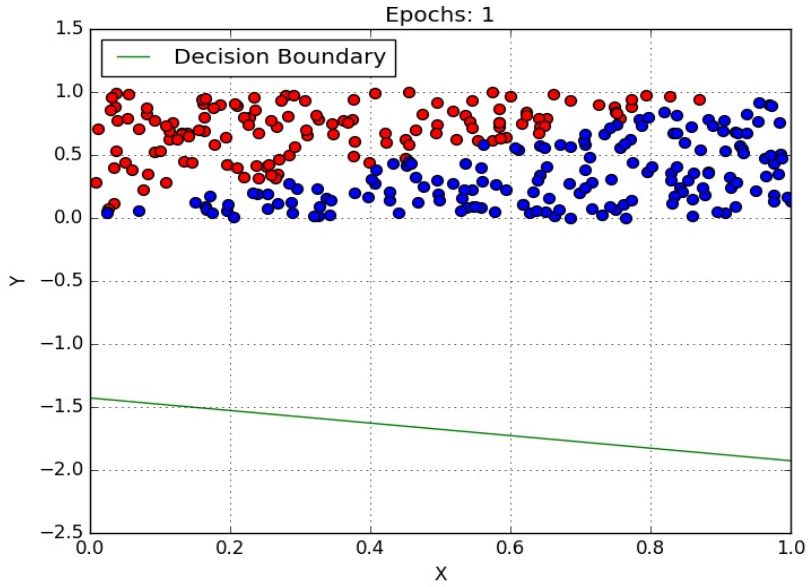
b = change in Y / change in X



LINEAR REGRESSION

2. **Logistic Regression:** Logistic regression is a machine learning statistical technique used to predict probability of binary response based on one or more independent variables

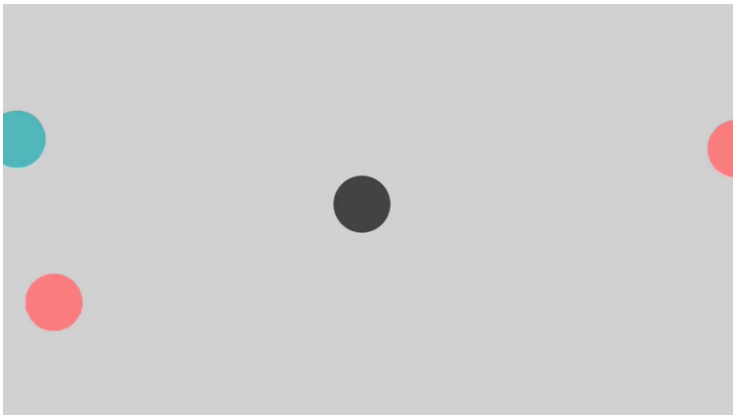
   Logistic regression predicts the probability of an event happening**.**



LOGISTIC REGRESSION

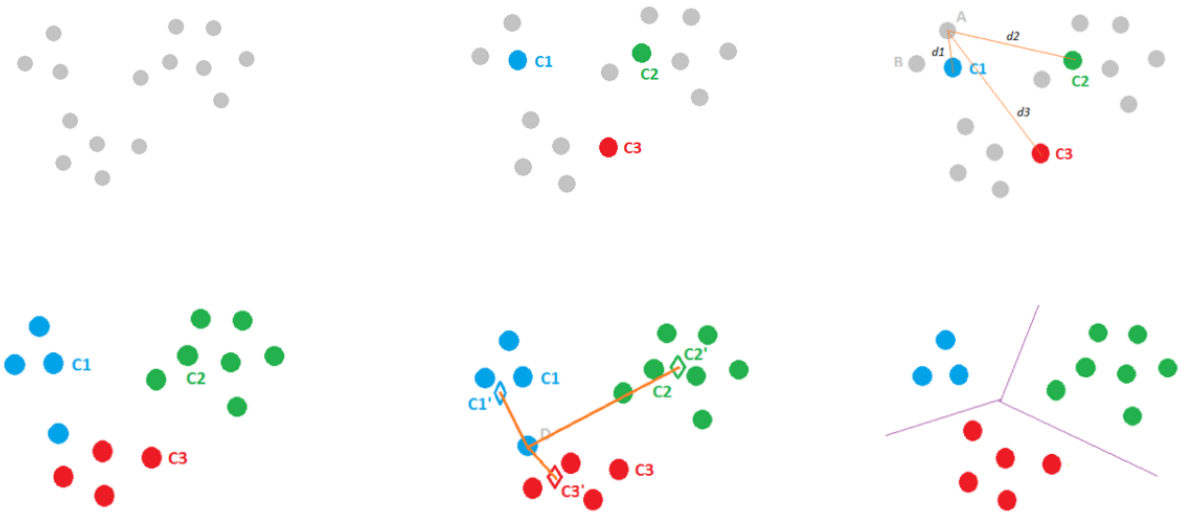
3. **KNN classification: -** K nearest neighbors is a machine learning algorithm that stores all available cases and classifies new cases based on a similarity measure. KNN is a lazy algorithm which means it does not use any training data points to make any generalizations.

   The target variable of KNN model can be numerical or categorical.



KNN MODEL

4. **K-means clustering**: K Means algorithm in an iterative algorithm that tries to partition the dataset into K predefined distinct non overlapping sub groups which are called as cluster.



K-means clustering

At, last in my major project, I coded all of these algorithms along with performing EDA on the dataset.

CONCLUSION:

Machine learning (**ML**) is the study of computer algorithms that improve automatically through experience. It is seen as a subset of artificial intelligence. Machine learning algorithms build a mathematical model based on sample data, known as "training data", in order to make predictions or decisions without being explicitly programmed to do so. Machine learning algorithms are used in a wide **variety of applications**, such as **email filtering and computer vision**, where it is difficult or infeasible to develop conventional algorithms to perform the needed tasks.

Machine learning is closely related to computational statistics, which focuses on making predictions using computers. The study of mathematical optimization delivers methods, theory and application domains to the field of machine learning. Data mining is a related field of study, focusing on exploratory data analysis through unsupervised learning. In its application across business problems, machine learning is also referred to as predictive analytics.

There are many applications for machine learning, including:

- Agriculture
- Anatomy
- Adaptive websites
- Affective computing
- Banking

- Bioinformatics
- Handwriting recognition
- Cheminformatics
- Sentiment analysis
- Search engines
- Medical diagnosis
- Marketing
- Economics
- Machine translation
- Sequence mining
- Theorem proving
- Robot locomotion
- General game playing
- Financial market analysis

  Etc..

APPENDICES

- www.google.com
- www.verzeo.in
- www.w3school.com

ANALYSIS OF VARIOUS ARTICLES ON EPIGENETICS OF ALZHEIMER'S DISEASE

Final Report

(15 May 2020 to 30 June 2020)

Submitted by

Anjali sharma(171505)

B.Tech in Bioinformatics(6 sem)

Name of Supervisor – Dr. Tiratha Raj Singh



BACHELOR OF TECHNOLOGY IN BIOINFORMATICS

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I take the opportunity to express profound sense of gratitude to **Prof. Tiratha Raj Singh**, without whom this project would not have been possible . He has been the pillar of strength , a source of great inspiration throughout our training period.

I also thank **Ph.D. Scholar Mr**. **Rohit Shukla** for his encouragement and constant support. I was lucky enough to have him who stood beside us and motivated us duringour studies and made this work possible.

I give my greatest acknowledgement to my **Parents** for all round support during studies. The endless sacrifices from my parents have made me what I am today.

CANDIDATE DECLARATION

I hereby declare that the work presented in this report entitled "Analysis of various articles on epigenetics of Alzheimer's diseases" in fulfilment of the requirement for the Summer Training submitted in department of Biotechnology,JUIT Waknaghat is an authentic record of our work carried out over a period from 15 May 2020 to 30 June 2020 under the supervision of Dr.Tiratha Raj Singh.

Anjali

Anjali Sharma

171505

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr.Tiratha Raj Singh

Associate Professor

Department of Biotechnology and Bioinformatics

Jaypee University Of Information Technology,Solan (HP)

CONTENTS

Sno.	Title	Page No.
1	Introduction	03-14
2	Materials and Methods	15-16
3	Results and Discussion	17-18
4	Conclusion	19
5	References	20-22

INTRODUCTION

Alzheimer's disease (AD) is a major form of senile dementia, characterized by progressive memory and neuronal loss combined with cognitive impairment.Alzheimer's disease and other dementias are a major and increasing global health challenge, with 40–50 million people currently living with dementia. 701 cases per 100 000 population in 1990 and 712 cases per 100 000 population in 2016, constituting an increase of 1·7%. However, because of population ageing and growth, the number of people affected by alzhiemers more than doubled since 1990 and almost 44 million prevalent cases were estimated globally in 2016. Age-standardised prevalence was 1·17 (1·17 –1·18) times higher in females than in male[1]. The AD is characterized by linguistic decline, irreversible and progressive cognitive impairment, memory loss and eventually cell death [2].

AD is characterized by the accumulation of extracellular senile plaques containg amyloid –β (Aβ) peptides and intracellular neurofibrillary tangles, which together with cerebral atrophy and neuronal cell death ,comprise the halmark features of the disease. The AD brain is also characterised by the presence of "inflammatory" response, even at prodormal stages. These responses result in actvation of astroglia and microglia cells, which can activate several signalling pathways(Wyss-Coray,2006;Avlia-Munoz and Arias,2014) to produce inflammatory signals such as cytokines and reactive oxygen species (ROS), leading to oxidative stress,which further leads to neuronal dysfunction .

Alzheimer's disease is multifactorial disorder that is determined by genetic and environmental factors as well as their interactions. Population-based prospective study is the major epidemiological approach to identifying influential factors for chronic multifactorial diseases. Age is the most powerful determinant of Alzheimer's disease, and gene mutations contribute to a small proportion of all cases. The strong association of Alzheimer's disease with increasing age may partially reflect the cumulative effect of different risk and protective factors over the lifespan, including the effect of complex interactions of genetic susceptibility, psychosocial factors, biological factors, and environmental exposures experienced over the lifespan. Evidence from epidemiological, neuroimaging, and neuropathological research, supports the role of

genetic, vascular, and psychosocial factors in the development of Alzheimer's disease, whereas evidence for the etiologic role of dietary or nutritional factors, occupational exposures, and inflammation is less clear.

GENETIC FACTORS

Mutations in amyloid precursor protein, presenilin-1, and presenilin-2 genes can cause early-onset familial Alzheimer's disease that account for no more than 5% of all cases. The majority of AD cases are sporadic, with considerable heterogeneity in their risk profiles and neuropathological features.

a) Apolipoprotein E ε4 (APOE ε4)

   The APOE ε4 allele is the only established susceptibility gene for both early- and late-onset Alzheimer's disease, and is a susceptibility gene, being neither necessary nor sufficient for the development of Alzheimer's disease

b) Family history

   Individuals who have a parent, brother or sister with Alzheimer's are more likely to develop the disease than those who do not have a first-degree relative with Alzheimer's.

c) Plasma lipid levels

BIOLOGICAL RISK FACTORS

Increasing age is a well-established risk factor for Alzheimer's disease. The incidence of Alzheimer's disease almost doubles with every 5 years of age . Female sex is often associated with an increased risk of AD, especially at the oldest-old age . Men seem to be at greater risk for vascular dementia than women.

VASCULAR DISORDERS AND RISK FACTORS

A number of vascular risk factors and disorders have been linked to Alzheimer's disease, but some factors may have a differential association with the risk of Alzheimer's disease depending on the age when the exposure is assessed.

a) Blood pressure
b) Cardiovascular diseases
c) Cerebrovascular diseases
d) Diabetes mellitus
e) Overweight and obesity
f) Hyperlipidaemia
g) The metabolic syndrome
h) Alcohol consumption
i) Cigarette smoking
j) Diet and nutrients

PSYCHOSOCIAL FACTORS

Psychological factors include social economic status, education attainment in early life, and work complexity in adult-life and leisure activities. Evidence from epidemiological research has been accumulating that some psychosocial factors and healthy lifestyle may postpone the onset of dementia, possibly by enhancing cognitive reserve.

a) Social economic status
b) High education
c) Physical activity
d) Mentally stimulating activity
e) Social network and social engagement
f) Depression

OTHER FACTORS

a) Inflammation
b) Hormone replacement therapy
c) Occupational exposures
d) Head trauma and traumatic brain injury

Factors	Systematic review	Results
Overweight and obesity	Meta-analysis of ten studies. Sixteen articles on 15 prospective studies with 3.2-36 years follow-up	Overweight: Dementia RR 1.26 (95% CI 1.10–1.44); Alzheimer's disease 1.35 (95% CI 1·19–1.54) Obesity: Dementia RR 1.64 (95% CI 1.34-2.00); Alzheimer's disease RR 2.04 (95% CI 1.59-2.62)
Smoking	Meta-analysis of four prospective studies with 2–25 years follow-up in over 17 000 people. In the four studies the dementia ORs were 3·17 (95% CI 1.37–7.35), 1.42 (1.07–1.89), 1.60 (1.00–2.57), and 1.63 (1.00–2.67)	Dementia RR 2.2 (95% CI 1.3–3.6)
Physical activity	13 prospective studies focusing on Alzheimer's disease, dementia, or both, with at least 150 000 participants	Dementia RR 0.72 (95% CI 0.60–0.86); Alzheimer's disease 0.55 (95% CI 0.36–0.84)
Cognitive reserve (intelligence, occupation, and education)	22 prospective studies with at least 29 000 participants followed up for a median of 7.1 years	Dementia OR 0.54 (95% CI 0.49–0.59)
Alcohol	15 longitudinal studies with 2–8 years follow-up and at least 14 000 participants	Dementia RR 0.74 (95% CI 0.61–0.91); Alzheimer's disease 0.72 (0.61–0.86)

Medical conditions

Midlife hypertension	At least 15 years follow-up in most studies, with at least 16 000 participants	Four of five longitudinal studies focusing on midlife hypertension suggested that it is a significant risk factor for incident dementia (RR 1.24–2.8 in different studies) The biggest differences were reported in studies using 160/95 mm Hg as the threshold for hypertension
Stroke	16 studies with at least 25 000 participants, mainly included patients aged 65 years and over	12 of 16 studies showed significant association between stroke and incident dementia, with overall doubling of incidence
Diabetes	15 prospective cohort studies	Dementia RR 1.47 (95% CI 1.25–1.73); Alzheimer's disease RR 1.39 (95% CI 1.16–1.66)

Factors	Systematic review	Results
Midlife hypercholesterolemia	18 studies, but only five assessed high cholesterol specifically in midlife. All five midlife studies had over 15 years follow-up and a total of over 15 000 participants	Four of five longitudinal studies in midlife suggested a significant positive association between high total cholesterol and incident dementia. For overall difference the RR was 1·4–3·1
Intervention studies		
Hypertension	12 091 participants between the three trials (SHEP, SYST-EUR, and SCOPE) with mean follow-up of 3·3 years. Only SYST-EUR reported significant benefit	OR 0.89 (95% CI 0.69–1.16) for incident dementia
Statins for prevention of dementia	26 340 participants between the two trials (PROSPER and HPS), with follow-up of 3·2 and 5 years. Cognition was measured with different instruments at different timepoints	Neither of the two trials reported significant benefit of statin therapy
Vitamins B12 or folate	Four trials in older people without existing cognitive impairment	Three trials showed no benefit. One trial (the only that selected participants based on increased homocysteine) reported benefit with respect to global function

RR=relative risk. OR=odds ratio. SHEP=Systolic Hypertension in the Elderly Program. SYST-EUR=Systolic Hypertension in Europe. SCOPE=Study on Cognition and Prognosis in the Elderly. PROSPER=PROspective Study of Pravastatin in the Elderly at Risk. HPS=Heart Protection Study.

Alzheimer disease is characterized by progressive cognitive decline usually beginning with impairment in the ability to form recent memories, but inevitably affecting all intellectual functions and leading to complete dependence for basic functions of daily life, and premature death. The pathological manifestations of Alzheimer disease include diffuse and neuritic extracellular amyloid plaques and intracellular neurofibrillary tangles accompanied by reactive microgliosis, dystrophic neurites, and loss of neurons and synapses.

National Institute of Neurological and Communicative Disorders and Stroke and the Alzheimer Disease and Related Disorders Association (NINCDSADRDA) developed a uniform set of criteria to enable clinicians and researchers to maintain consistency in the diagnosis. They included aspects of medical history, clinical examination,neuropsychological testing, and laboratory assessments which have been remarkably reliable and valid for the diagnosis of AD over the past three decades. Criteria recently been updated with major advances in

neuropsychological assessment, brain imaging and the neuropathological, biochemical and genetic understanding of this disease, revisions were considered a necessity.

The prevalence rates for AD also rise exponentially with age, increasing markedly after 65 years. There is almost a 15-fold increase in the prevalence of dementia, predominately Alzheimer disease, between the ages of 60 and 85 years . Countries like North America and Western Europe have at age 60 the highest prevalence of dementia (6.4 and 5.4% of the population at age 60), followed by Latin America (4.9%) and China and its developing western-Pacific neighbors (4.0%). The annual incidence rates (per 1000) for these countries were estimated at 10.5 for North America, 8.8 for Western Europe, 9.2 for Latin America and 8.0 for China and its developing western-Pacific neighbors, increasing exponentially with age in all countries, especially through the seventh and eighth decades of life.

ANTECEDENT RISK FACTORS THAT INCREASE THE RISK OF ALZHEIMER DISEASE

Table 1. Factors that modify the risk of Alzheimer disease

Antecedent	Direction	Possible mechanisms
Cardiovascular disease	Increased	Parenchymal destruction
		Strategic location
		↑ Aβ deposition
Smoking	Increased	Cerebrovascular effects
		Oxidative stress
Hypertension	Increased and decreased	Microvascular disease
Type II diabetes	Increased	Cerebrovascular effect
		Insulin and Aβ compete for clearance
Obesity	Increased	Increased risk of type II diabetes inflammatory
Traumatic head injury	Increased	↑Aβ and amyloid precursor protein deposition
Education	Decreased	Provides cognitive reserve
Leisure activity	Decreased	Improves lipid metabolism, mental stimulation
Mediterranean diet	Decreased	Antioxidant, anti-inflammatory
Physical activity	Decreased	Activates brain plasticity, promotes brain vascularization

Interventions toward Alzheimer's disease

Current evidence tends to support the notion that dementia onset may be postponed by implementing interventions toward the potential etiologic factors (both risk and protective

factors) (ie, primary prevention) and by early detection (ie, secondary prevention), whereas appropriate care and pharmacotherapy for patients with AD and dementia (ie, tertiary prevention) may help stabilize cognitive functions, reduce agitation, control neuropsychiatric symptoms, and improve the quality of life.

Interventions toward primary prevention

Primary intervention strategies

Theoretically, even if the mechanisms of vascular and psychosocial factors being involved in the pathogenesis and clinical expression of AD are still not fully understood, primary prevention seems possible as most vascular factors and disorders, psychosocial factors, and lifestyle factors are modifiable or amenable to management.38,175 One intervention strategy is to target vascular pathways, including management of midlife high blood pressure and obesity, high blood glucose level, and diabetes. In addition, preventing recurrent cerebrovascular disease and maintaining sufficient cerebral blood perfusion by adequately managing heart failure and avoiding very low blood pressure may help postpone clinical expression of the dementia syndrome, especially among very old people. The second strategy is to maintain the more active and socially integrated lifestyles by establishing extensive social networks and frequently participating in social, physical, and intellectually stimulating activities, which may reduce the risk or delay the onset of AD.38,132Taken together, the most effective strategy may be to encourage people implementing multiple preventive measures throughout the life course, including high educational attainment in childhood and early adulthood, active control of vascular factors and disorders over adulthood, and maintenance of mentally, physically, and socially active lifestyles during middle age and later in life.

Intervention trials toward primary prevention

The main clinical and intervention trials toward primary prevention by targeting the possible risk and protective factors for AD and dementia are summarized in Table II.160,161,176-182 Antihypertensive treatments in reducing the risk of dementia and AD have been tested in a few clinical trials. The pooling analysis of the 2007 Cochrane review, based essentially on three clinical trials (SHEP,183 Syst-Eur,184 and SCOPE185), found no convincing evidence that

blood pressure-lowering therapy among elderly individuals with hypertension could prevent dementia. However, in this review the SCOPE trial, which did not show any effect of blood pressure-lowering treatment by candesartan on the risk of dementia, was actually not a placebo-controlled trial due to ethical considerations. By contrast, the placebo-controlled PROGRESS trial among individuals with cerebrovascular disease (transient ischemic attacks and stroke), which did find a beneficial effect of antihypertensive therapy on cognitive function related to recurrent stroke, was not included.186 The cognition substudy of the double-blind placebo-controlled Hypertension in the Very Elderly Trial (HYVET-COG) among people 80+ years found a nonsignificant reduction in the risk of dementia related to antihypertensive treatment. Encouragingly, when data from this clinical trial were pooled together with those from three other doubleblind placebo-controlled trials (SHEP, Syst-Eur, and PROGRESS), antihypertensive treatment could reduce the risk of dementia by 13% (hazard ratio, 0.87; 95% CI, 0.76–1.00; P=0.045).177 It is worthwhile to notice that dementia or AD was the secondary end point in all major clinical trials of antihypertensive therapy, with a relatively short period of follow-up because the trials had to be terminated when benefits of the treatments were clearly shown in terms of primary end points (usually cardiac and cerebrovascular disease). In this context, if the beneficial effect of lowering blood pressure on dementia is not as strong as for cardiovascular disease, a longer period of observation is needed to demonstrate any significant beneficial effect. Estrogen therapy among postmenopausal women has been linked to a considerably lower risk of AD and dementia in numerous observational studies, but the large-scale clinical trial of the Women's Health Initiative Memory Study (WHI-MS) showed that estrogen therapy alone or in combination with progestin did not reduce incidence of probable dementia and mild cognitive impairment (MCI); instead, the active treatments with estrogen and estrogen plus progestin were found to be associated with a twofold increased risk for both dementia and MCI.178,179 It has been argued that in the WHI-MS hormone replacement therapy was given 10 to 15 years after the menopause when the "window of critical time" for putative beneficial effects of estrogen therapy may have been missed.187 Other major clinical trials of primary prevention against dementia, such as those with NSAIDs and vitamin E supplementation, have so far failed to confirm any efficacy against dementia and AD (Table II), while more clinical trials (eg, use of cholesterol-lowering drugs and blood glucose lowering drugs) are ongoing.188,189 The lack of

success in most primary prevention trials underscores the need of new strategies in future intervention studies.

Secondary prevention

Alzheimer's disease is characterized by a preclinical phase, possibly lasting years, during which progressive neurodegeneration in the brain is occurring before typical clinical symptoms (eg, cognitive deficits and subtle cognitive disturbances) become detectable.193 Theoretically, detection of AD at early stage may provide an opportunity for implementing therapeutic intervention to more effectively delay its progression to clinical dementia. However, there remains a challenge as to how to identify individuals during the preclinical phase of the disease, although some clinical markers, neuroimaging biomarkers, and biochemical markers have been investigated.194 First, numerous studies have suggested that deficits in specific cognitive domains such as episodic memory and verbal ability are conceivable up to 10 years before the dementia syndrome can be clinically diagnosed, with a more evident decline occurring over the final few years. The term "mild cognitive impairment" has been used in clinical settings to identify individuals with isolated memory loss (ie, "amnestic" type MCI), which is more likely to represent the preclinical phase of Alzheimer dementia. However, population-based followup studies have frequently shown that individuals with MCI represent a very heterogeneous group in terms of prognosis195,196; although elderly persons with MCI had increased risk of progressing to dementia, a substantial proportion remained stable or even reverted to normal during the next few years. Second, biochemical markers in serum and cerebrospinal fluid such as β-amyloid and τ-protein have been proposed for early detection of AD, but these markers are not sufficiently reliable in making diagnosis of AD in the presymptomatic phase.39,194 Finally, during the last decade neuroimaging has emerged as a useful tool to define AD at both preclinical and early clinical phases of the disease. For example, the amyloid positron emission tomography imaging tracer ligands offer opportunity for measuring β-amyloid in the brain in vivo, which provides the possibility for early diagnosis and for monitoring the course of antiamyloid therapy in AD.197,198 Furthermore, the medial-temporal lobe atrophy seen on volumetric MRI has been used in the identification of MCI and early AD as well as in the assessment of progression of MCI and early AD.199,200 Successful secondary prevention relies on both reliable detection of the disease at an early stage and availability of efficacious

interventions for slowing down progression of the disease. However, while efforts are being made to find ways to effectively counteract the course of AD, some methodological issues facing research on disease-modifying therapies and interventions remain a challenge.

Tertiary prevention

The tertiary prevention aims to avoid functional disability, and if possible, to improve quality of life for patients with AD. Cognitive training may help maintain cognitive function, slow down cognitive decline, and improve wellbeing for people with mild dementia. Current medications widely used for AD and dementia, including cholinesterase inhibitors (donepezil, rivastigmine, and galantamine) and the N-methyl-D-aspartate-receptor antagonist (memantine), are designed to target clinical symptoms of the disease such as cognitive and neuropsychiatric disturbances.201 The efficacy of antioxidant treatments in AD has not been proven. For example, the Cochrane review found no evidence of efficacy of vitamin E in the treatment of AD and in the prevention of progression of MCI to AD,203 although the randomized clinical trials of the Physicians' Health Study II suggested that a long-term β-carotene supplementation might provide cognitive benefits among men.204 Furthermore, high-dose B vitamin supplements did not slow down cognitive decline among individuals with mild to moderate AD.205 Intensive research is ongoing in an attempt to develop disease-modifying drugs by targeting the key neuropathological processes in AD such as β-amyloid protein.206

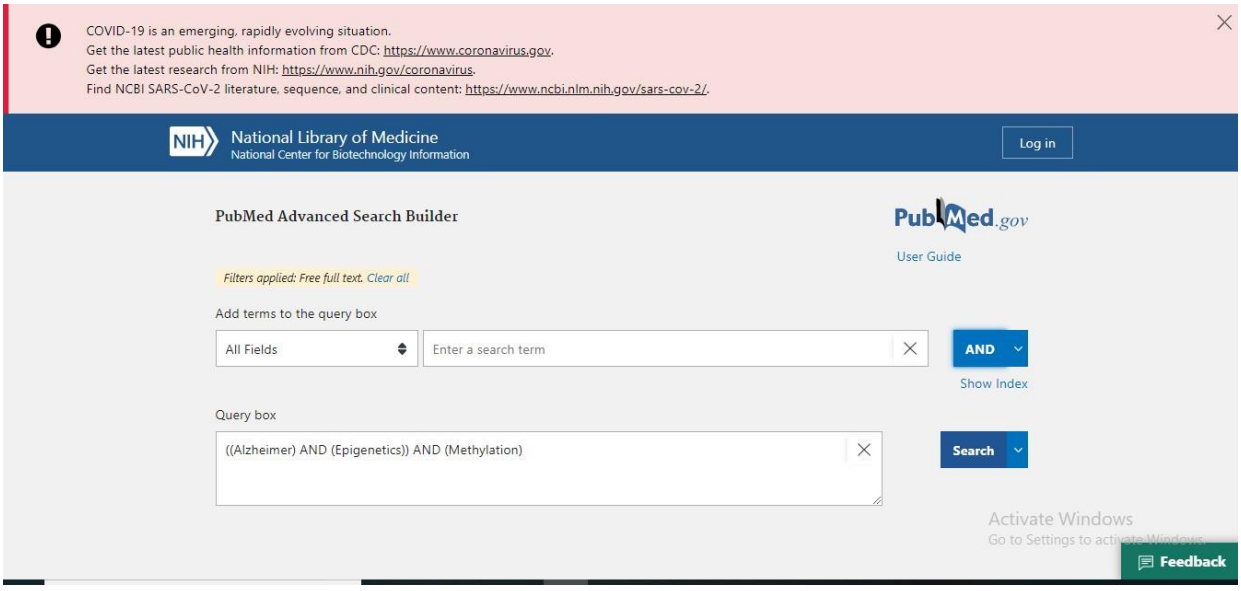
Materials and Methods

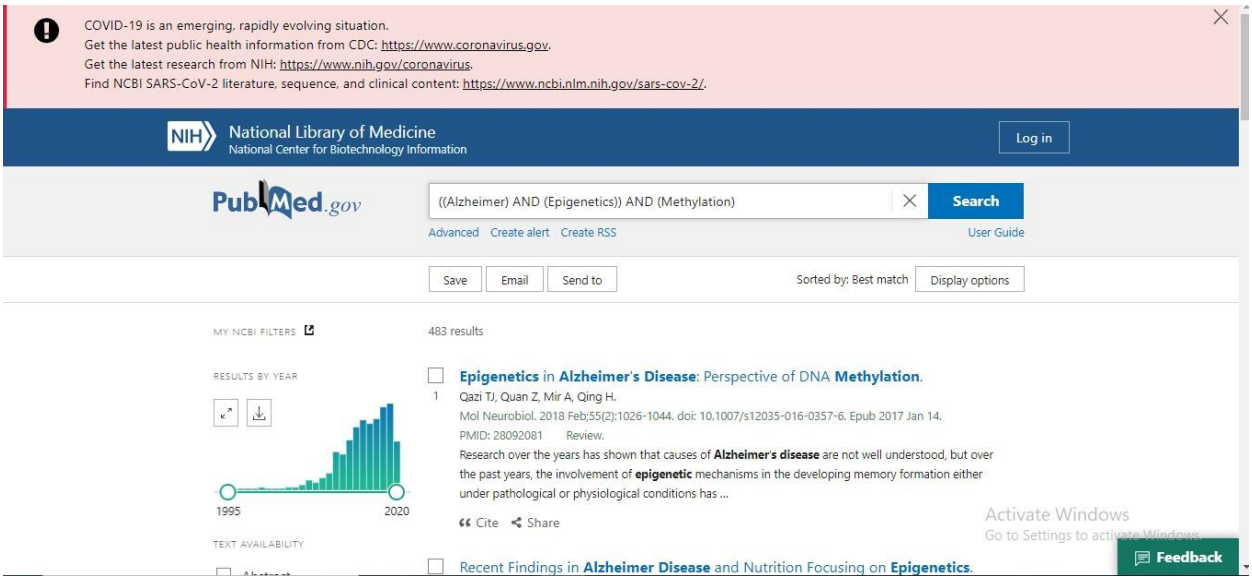
Retrieval of information for the database

A database is an organized collection of data, generally stored and accessed electronically from a computer system. In order to make a database on epigenetics of alzheimer disease, literature review was done. As in epigentics our main focus was on methylation,so the literature in which methylation was the main cause of alzheimer disease were studied. The articles are searched on the pubmed.

PubMed comprises more than 30 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites. **PubMed** is a free search engine accessing primarily the MEDLINE database of references and abstracts on life sciences and biomedical topics. The United States National Library of Medicine (NLM) at the National Institutes of Health maintain the database as part of the Entrez system of information retrieval.

Advance search on pubmed was done for reviewing the literature




COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: https://www.coronavirus.gov.
Get the latest research from NIH: https://www.nih.gov/coronavirus.
Find NCBI SARS-CoV-2 literature, sequence, and clinical content: https://www.ncbi.nlm.nih.gov/sars-cov-2/.
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483 results
RESULTS BY YEAR
1995
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Epigenetics in Alzheimer's Disease: Perspective of DNA Methylation.
1
Qazi TJ, Quan Z, Mir A, Qing H.
Mol Neurobiol. 2018 Feb;55(2):1026-1044. doi: 10.1007/s12035-016-0357-6. Epub 2017 Jan 14.
PMID: 28092081 Review.
Research over the years has shown that causes of Alzheimer's disease are not well understood, but over the past years, the involvement of epigenetic mechanisms in the developing memory formation either under pathological or physiological conditions has ...
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Recent Findings in Alzheimer Disease and Nutrition Focusing on Epigenetics.

Results and Discussion

By doing advance search in pubmed 483 results were obtained.

So from those 483 articles we collected information on how methylation is playing a role in epigenetics of alzheimer disease.

Following are the results obtained(here only 9 articles are mentioned,but this is done for 255 articles):

Sno.	NAME OF THE RESEARCH ARTICLE	Role of methylation	RELATION WITH METHYLATION
1	Recent Findings in Alzheimer Disease and Nutrition Focusing on Epigenetics	YES	The current review focuses on the epigenetic mechanisms of AD and how nutrition can influence the course of this disease through regulation of gene expression, according to the latest scientific findings. Epigenetics is becoming a very attractive subject for researchers because it can shed light on unknown aspects of complex diseases like AD. DNA methylation, histone modifications, and microRNAs are the principal epigenetic mechanisms involved in AD pathophysiology. Nutrition is an environmental factor that is related to AD through epigenetic pathways. Vitamin B-12, for instance, can alter the one-carbonmetabolismand thus interfere in the DNA methylation process.
2	Epigenetics and DNA methylomic profiling in Alzheimer's disease and other neurodegenerative diseases	YES	. This review discuss advances that have been made toward understanding the role of epigenetic processes in neurodegenerative disorders, with a particular focus on Alzheimer's disease. And also a brief overview of DNA modifications, followed by a summarization of studies of DNA modifications in Alzheimer's disease and other neurodegenerative diseases.
3	The epigenetics of aging and neurodegeneration	YES	They review current knowledge about the major epigenetic mechanisms, including DNA methylation and DNA demethylation, chromatin remodeling and noncoding RNAs, as well as the involvement of these mechanisms in normal aging and in the pathophysiology of the most common neurodegenerative diseases.
4	Role of Genetics and Epigenetics in the Pathogenesis of Alzheimer's Disease and Frontotemporal Dementia	YES	In this review, an overview of the current genetic and epigenetic progresses in AD and FTD is provided, with particular focus on 1) causative genes, 2) genetic risk factors and disease modifiers, and 3) epigenetics, including methylation, non-coding RNAs and chromatin remodeling.

5	DNA methylation analysis on purified neurons and glia dissects age and Alzheimer's disease-specific changes in the human cortex	YES	The current review focuses on how cell sorting strongly enhances the robust detection of disease-related DNA methylation changes even in a relatively small cohort. Numerous genes with cell-type-specific methylation signatures and document differential methylation dynamics associated with aging specifically in neurons such as CLU, SYNJ2 and NCOR2 or in glia RAI1,CXXC5 and INPP5A were identified
6	Could Alzheimer's Disease Originate in the Periphery and If So How So?		It is shown that the presence of the APOE ε4 allele, altered miRNA expression and epigenetic dysregulation in the promoter region and exon 1 of TREM2, as well as ANK1 hypermethylation and altered levels of histone post-translational methylation leading to increased transcription of TNFA, could variously explain increased levels of peripheral and central inflammation found in AD. In particular, as a result of increased activity of triggering receptor expressed on myeloid cells 2 (TREM-2), the presence of the apolipoprotein E4 (ApoE4) isoform, and changes in ANK1 expression, with subsequent changes in miR-486 leading to altered levels of protein kinase B (Akt), mechanistic (previously mammalian) target of rapamycin (mTOR) and signal transducer and activator of transcription 3 (STAT3), all of which play major roles in microglial activation, proliferation and survival, there is activation of microglia, leading to the subsequent (further) production of cytokines, chemokines, nitric oxide, prostaglandins, reactive oxygen species, inducible nitric oxide synthase and cyclooxygenase-2, and other mediators of inflammation and neurotoxicity. These changes are associated with the development of amyloid and tau pathology, mitochondrial dysfunction (including impaired activity of the electron transport chain, depleted basal mitochondrial potential and oxidative damage to key tricarboxylic acid enzymes), synaptic dysfunction, altered glycogen synthase kinase-3
			(GSK-3) activity, mTOR activation, impairment of autophagy, compromised ubiquitin-proteasome system, iron dyshomeostasis, changes in APP translation, amyloid plaque formation, tau hyperphosphorylation and neurofibrillary tangle formation.
7	Epigenetic Factors in Late-Onset Alzheimer's Disease: MTHFR and CTH Gene Polymorphisms, Metabolic Transsulfuration and Methylation Pathways, and B Vitamins	YES	DNA methylation and other epigenetic factors are important in the pathogenesis of late-onset Alzheimer's disease (LOAD). Methylenetetrahydrofolate reductase (MTHFR) gene mutations occur in most elderly patients with memory loss. MTHFR is critical for production of S-adenosyl-L-methionine (SAM), the principal methyl donor. A common mutation (1364T/T) of the cystathionine-γ-lyase (CTH) gene affects the enzyme that converts cystathionine to cysteine in the transsulfuration pathway causing plasma elevation of total homocysteine (tHcy) or hyperhomocysteinemia—a strong and independent risk factor for cognitive loss and AD.
8	Epigenetics and Pharmacology	YES	Epigenetic regulation of gene activity has been shown to be important in maintaining normal phenotypic activity of cells, as well as having a role in development and diseases such as cancer and neurodegenerative disorders such as Alzheimer's. Newer classes of drugs regulate epigenetic mechanisms to counteract disease states in humans. The reports in this issue describe some advances in epigenetic understanding that relate to human disease, and our ability to control these mechanisms by pharmacological means. Increasingly the importance of epigenetics is being uncovered - it is pharmacology that will have to keep pace.
9	Alzheimer's disease pathogenesis: Is there a role of folate?	YES	Epigenetic modifications, including changes in DNA methylation, have been implicated in a wide range of diseases including neurologicaldiseases such as Alzheimer's. The role of dietary folate in providing methyl groups required for maintenance and modulation of DNA methylation makes it a

Till now literature review of 255 articles were done out of 483.

Conclusion

In the present study an attempt has been made to analyze the role or effect of epigenetics on Alzhiemers's disease.Alzheimer disease is a chronic neurodegenerative disorder, and its complexity makes its cure an unsolved problem for the time being. A novel pathophysiologic aspect, that of epigenetics, promises the explanation of many medical mysteries including etiology and pathophysiology of AD. Epigenetic biomarkers can be a very helpful tool for the researchers to find the exact nutrients needed to create specific remedies, and maybe the same biomarkers can even be used in patient screening in the future. In this way, nutrition might grow to become a useful preventive and even a therapeutic alternative against AD, especially if combined with other antidementia interventions,such as acetylcholinesterase inhibitors, brain exercise, physical training, etc.

References

[1] Nichols, Emma, et al. "Global, regional, and national burden of Alzheimer's disease and other dementias, 1990–2016: a systematic analysis for the Global Burden of Disease Study 2016." The Lancet Neurology 18.1 (2019): 88-106.

[2] Blass, John P. "Alzheimer's disease and Alzheimer's dementia: distinct but overlapping entities." Neurobiology of aging 23.6 (2002): 1077-1084.

[3] Davies, Peter, and A. J. F. Maloney. "Selective loss of central cholinergic neurons in Alzheimer's disease." The Lancet 308.8000 (1976): 1403.

[4] De Jager, P.L.; Srivastava, G.; Lunnon, K.; Burgess, J.; Schalkwyk, L.C.; Yu, L.; Eaton, M.L.; Keenan, B.T.; Ernst, J.; McCabe, C.; et al. Alzheimer's disease: Early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nat. Neurosci. 2014, 17, 1156–1163. [CrossRef][PubMed]

[5]Lunnon,K.;Smith,R.;Hannon,E.;DeJager,P.L.;Srivastava,G.;Volta,M.;Troakes,C.;Al-Sarraj,S.;Burrage,J.; Macdonald, R.; et al. Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nat. Neurosci. 2014, 17, 1164–1170. [CrossRef]

[6] Shewale SJ, Huebinger RM, Allen MS, Barber RC. The potential role of epigenetics in Alzheimer's disease etiology. Biol Syst 2013;2:114.

[7] Balazs R. Epigenetic mechanisms in Alzheimer's disease. Degener Neurol Neuromuscul Dis 2014;4:85–102.

[8] Landgrave-Gómez J, Mercado-Gómez O, Guevara-Guzmán R. Epigenetic mechanisms in neurological and neurodegenerative diseases. Front Cell Neurosci 2015;9:58.

[9] Pezzi JC, Ens CM, Borba EM, Schumacher-Schuh AF, de Andrade FM, Chaves ML, Fiegenbaum M, Camozzato AL. DNA methyltransferase haplotype is associated with Alzheimer's disease. Neurosci Lett 2014;579:70–4.

[10] Chouliaras L, Mastroeni D, Delvaux E, Grover A, Kenis G, Hof PR, Steinbusch HW, Coleman PD, Rutten BP, van den Hove DL. Consistent decrease in global DNA methylation and hydroxymethylation in the hippocampus of Alzheimer's disease patients. Neurobiol Aging 2013;34:2091–9.

[11] Condliffe D, Wong A, Troakes C, Proitsi P, Patel Y, Chouliaras L, Fernandes C, Cooper J, Lovestone S, Schalkwyk L, et al. Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. Neurobiol Aging 2014;35:1850–4. 12. Wang J, Yu JT, Tan MS, Jiang T, Tan L. Epigenetic mechanisms in Alzheimer's disease: implications for pathogenesis and therapy. Ageing Res Rev 2013;12:1024–41.

[12] Fujiki R, Hashiba W, Sekine H, et al. GlcNAcylation of histone H2B facilitates its monoubiquitination. Nature. 2011; 480:557–60. [PubMed: 22121020]

[13] Xu Q, Yang C, Du Y, et al. AMPK regulates histone H2B O-GlcNAcylation. Nucleic Acids Res. 2014; 42:5594–604. [PubMed: 24692660]

[14] He Y, Roth C, Turkenburg JP, Davies GJ. Three-dimensional structure of a Streptomyces sviceus GNAT acetyltransferase with similarity to the C-terminal domain of the human GH84 OGlcNAcase. Acta Crystallogr D Biol Crystallogr. 2014; 70:186–95. [PubMed: 24419391]

[15] Zhang Q, Liu X, Gao W, et al. Differential regulation of the ten-eleven translocation (TET) family of dioxygenases by O-linked β-N-acetylglucosamine transferase (OGT). J Biol Chem. 2014; 289:5986–96. [PubMed: 24394411]

[16] Harwood KR, Hanover JA. Nutrient-driven O-GlcNAc cycling - think globally but act locally. J Cell Sci. 2014; 127:1857–67. [PubMed: 24762810]

[17] Myers SA, Panning B, Burlingame AL. Polycomb repressive complex 2 is necessary for the normal site-specific O-GlcNAc distribution in mouse embryonic stem cells. Proc Natl Acad Sci US A. 2011; 108:9490–5.

[18] Medford HM, Porter K, Marsh SA. Immediate effects of a single exercise bout on protein OGlcNAcylation and chromatin regulation of cardiac hypertrophy. Am J Physiol Heart Circ Physiol. 2013; 305:H114–23. [PubMed: 23624624]

[19] Cox EJ, Marsh SA. Exercise and diabetes have opposite effects on the assembly and O-GlcNAc modification of the mSin3A/HDAC1/2 complex in the heart. Cardiovasc Diabetol. 2013; 12:101. [PubMed: 23835259]

[20] Ito R, Katsura S, Shimada H, et al. TET3-OGT interaction increases the stability and the presence of OGT in chromatin. Genes Cells. 2014; 19:52–65. This paper demonstrates that the TET3-OGT interactions stabilize OGT on chromatin. [PubMed: 24304661]

SUMMER TRAINING ON DATA MINING IN BIOMEDICAL LITERATURE



Enrollment No.-171506
Name of the student- Vaibhav Gangta

Name of the supervisor- Dr. Tiratha Raj Singh

MAY-JUNE 2020

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS, JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT, SOLAN 173234, HIMACHAL PARDESH, INDIA

CANDIDATE'S DECLARATION

I hereby declare that the work presented in this report entitled "**Data Mining in Biomedical Literature"** in fulfilment of the requirement for the Summer Training submitted in the department of **Biotechnology and Bioinformatics, JUIT Waknaghat** is an authentic record of our own work carried out over a period from **16 May 2020 to 30 June 2020** under the supervision of **Dr. Tiratha Raj Singh**.



Vaibhav Gangta

171506

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr. Tiratha Raj Singh

Dated: 01/07/2020

ABSTRACT

Adaptation of information technology has leads to creation of several applications in health care informatics. Health care informatics is generating large amount of data. These data can be processed using data mining techniques to predict the diseases. Data mining is the process of analyzing, extracting data and furnishes the data as knowledge which forms the relationship within the available data. Some of the data mining techniques include association, clustering, classification and prediction. Various data mining tools are compared to analyze the performance of health care data and disease prediction.

High-throughput molecular analysis techniques nowadays yield datasets with a size and complexity at which they are no longer directly interpretable by humans. In recent years, pattern mining methods have become indispensable for life scientists to narrow down the search for relevant new knowledge instead of getting lost in the wealth of information. The term 'pattern mining' covers a wide variety of techniques that are all designed to transform complex datasets into something more manageable.

Association rule mining represents a data mining technique and its goal is to find interesting association or correlation relationships among a large set of data items. With massive amounts of data continuously being collected and stored in databases, many companies are becoming interested in mining association rules from their databases to increase their profits. Association rule mining has a wide range of applicability such market basket analysis, medical diagnosis/ research, Website navigation analysis, homeland security, education, financial and business domain and so on. In this paper we present an example of data mining technique represented by association rule mining known as market basket analysis. In the market basket analysis example the existing database was analyzed to identify potentially interesting patterns. For example, the discovery of interesting association relationships among huge amounts of business transaction records can help catalogue design, cross- marketing, loss leader analysis, and other business decision making processes. A typical example of association rule mining is market basket analysis. This process analyzes customer buying habits by finding associations between the different items that customers place in their "shopping baskets".

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(Vaibhav Gangta)

Dated: 01/07/2020

Sr. No.	TOPIC	Page No.
1.	CANDIDATE'S DECLARATION	2
2.	ABSTRACT	3
3.	ACKNOWLEDGEMENTS	4
4.	INTRODUCTION	6-10
5.	REVIEWOF LITERATURE	11-18
6.	CONCLUSION	19

INTRODUCTION

Data mining is concerned with the process of computationally extracting unknown knowledge from huge sets of data. Extraction of useful knowledge from the enormous data sets and providing decision-making results for the diagnosis and treatment of diseases is very important. Data mining can be used to extract knowledge by analyzing and predicting various diseases. Health care data mining has great potential to discover the hidden patterns in the data sets of the medical domain. Various data mining techniques are available with their suitability dependent on the health care data. Data mining applications in health care can have a wonderful potential and effectiveness. It automates the process of finding predictive information in huge databases.

Disease prediction plays an important role in data mining. Finding of a disease requires the performance of a number of tests on the patient. However, use of data mining techniques, can reduce the number of tests. This reduced test set plays significant role in performance and time. Health care data mining is an important task because it allows doctors to see which attributes are more important for diagnosis such as age, weight, symptoms etc. This will help the doctors diagnose the disease more efficiently.

Knowledge discovery in databases is the process of finding useful information and patterns in data. Knowledge discovery in databases can be done using data mining. It uses algorithms to extract the information and patterns derived by the knowledge discovery in databases process. Various stages of knowledge discovery in databases process is highlighted in **Fig.1**.

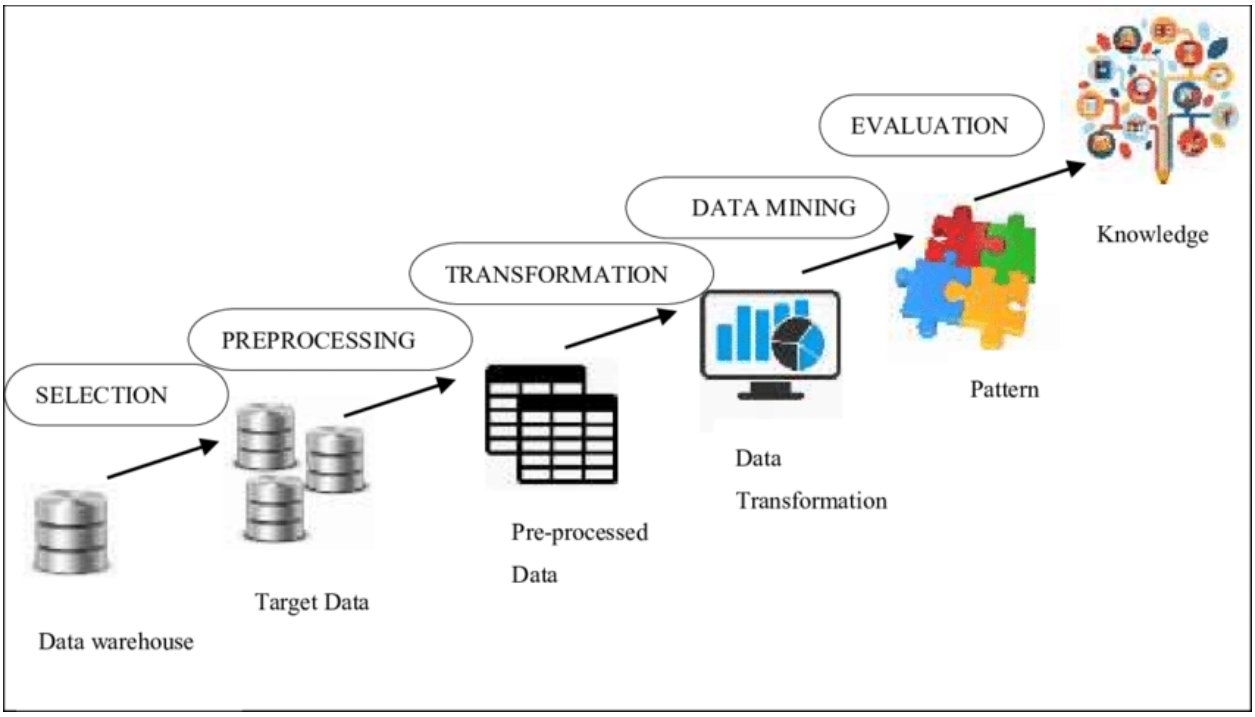

Fig.1: Healthcare Knowledge Discovery process:

The **Knowledge Discovery in database** (KDD) process is commonly defined with the stages in the figure above. In Selection stage, it obtains the data different resources. In preprocessing stage, it removes the unwanted missing and noisy data and furnished the clean data which can format to a common format in transformation stage. Then data mining techniques is applied to get desired output. Finally in the in the interpretation stage, it will present the result to end user in a meaningful manner.

Background

The manual extraction of patterns from data has occurred for centuries. Early methods of identifying patterns in data include Bayes' theorem (1700s) and regression analysis (1800s). The proliferation, ubiquity and increasing power of computer technology have dramatically increased data collection, storage, and manipulation ability. As data sets have grown in size and complexity, direct "hands-on" data analysis has increasingly been augmented with indirect, automated data processing, aided by other discoveries in computer science, especially in the field of machine learning, such as neural networks, cluster analysis, genetic algorithms (1950s), decision trees and decision rules (1960s), and support vector machines (1990s). Data mining is the process of applying these methods

with the intention of uncovering hidden patterns in large data sets. It bridges the gap from applied statistics and artificial intelligence (which usually provide the mathematical background) to database management by exploiting the way data is stored and indexed in databases to execute the actual learning and discovery algorithms more efficiently, allowing such methods to be applied to ever-larger data sets.

DATA MINING TECHNIQUES

Data mining is the process by which both the organizations and Data Scientists detect patterns in data for insights relevant to their needs. We have access to more data now than ever before. However, making sense of huge volumes of unstructured data to implement improvements can be extremely challenging because of the sheer amount of information. Therefore, use of Data Mining techniques in imperative. Some of the Data mining techniques like classification, clustering and association rules are widely used in disease data analysis.

Classification

Classification is a machine learning based data mining technique. Classification is used to classify each information in a set of data into one of predefined set of groups or classes. It makes use of mathematical techniques such as decision trees, linear programming, neural network and statistics to classify the data into different groups. Modern classification techniques provide more intelligent methods for effective prediction of diseases. Different types of classification techniques includes Support vector machine, discriminant analysis, naive based, decision trees, linear and non linear regression.

Clustering

Division of data into groups of similar objects is called Clustering. Certain fine details are lost by representing the data by fewer clusters but it achieves simplification. It models data by its clusters. Data modeling puts clustering in a historical perspective rooted in mathematics, statistics, and numerical analysis. According to machine learning perspective, clusters correspond to hidden patterns, the search for clusters is unsupervised learning, and the resulting system represents a data concept. From a practical perspective clustering plays an important role in data mining applications such as scientific data exploration, information retrieval and text mining, spatial database applications, Web analysis, CRM, marketing, medical diagnostics, computational biology, and many others.

Association rule mining

Association rule learning is a popular and well researched method for finding interesting relations between different data in large databases. It is intended to identify well built rules discovered in databases using different procedures of importance based on input data set. Association rule mining is the data mining process of finding the rules, finding frequent patterns, associations, correlations, or causal structures among sets of items that may govern associations and causal objects between sets of items. Understand customer buying habits by finding associations and correlations between the different items that customers place in their "shopping basket". The main applications of association rule mining includes basket data analysis, cross- marketing and catalog design. The above data mining techniques can be used in the diagnosis of diseases.

DATA MINING TOOLS

The development and application of data mining algorithms requires the use of powerful software tools. As the number of available tools continues to grow, the choice of the most suitable tool becomes increasingly difficult. Data mining tools like Weka, Rapidminer, Orange and Knime are used to perform various data mining techniques.

WEKA

The Waikato Environment for Knowledge Analysis (WEKA) is an open source software and machine learning toolkit introduced by Waikato University, New Zealand. WEKA supports several standard data mining tasks like data preprocessing, clustering, classification, regression, visualization and feature selection New algorithms can also be implemented using WEKA with existing data mining and machine learning techniques. WEKA provides various sources for loading data, including files, URLs and databases. It supports file formats include WEKA"s own ARFF format, CSV, Lib SVMs format, and C4.5's format. Many evaluation criteria are also provided in WEKA such as confusion matrix, precision, recall, true positive and false negative, etc. Some of the advantages of WEKA tool includes Open source, platform independent and portable, graphical user interface and contains very large collection of different data mining algorithms.

RAPIDMINER

RAPIDMINER (RM) is open source software which provides a good environment for data mining processes. It has the facility of drag-and-drop which is used to construct the dataflow. It support different file formats. Regression, classification and clustering tasks can be performed easily with different learning algorithms. Rapid Miner supports a large number of the classification and regression algorithms, decision trees, association rules, clustering algorithms, and many features are available for data pre- processing, normalization, filtering and data analysis. It can import data from different traditional and standard databases.

ORANGE

ORANGE is an open source data mining tool developed at the Bioinformatics Laboratory at the University of Ljubljana. Applications can be implemented using scripting and visual programming. Python library is available for data manipulation and widget alteration. Programming is performed by placing widgets on the canvas and connecting their inputs and outputs. This tool is suitable for machine learning and data mining algorithms. It can be easily used by both researchers of data mining and inexperienced users who want to develop and test their own algorithms. It gives advantage of reusing as much of the code as possible.

KNIME

KNIME (Konstanz Information Miner) is a general purpose open source data mining tool developed and maintained by the Swiss company. It is implemented on the Eclipse platform and has facility of data integration, processing, exploration, and analysis platform. KNIME can be integrated with other data mining tools such as R and WEKA.

REVIEW OF LITERATURE

ABOUT ARM

One of the most popular data mining techniques is association rule mining. The patterns discovered with this data mining technique can be represented in the form of *association rules*. *Rule support* and *confidence* are two measures of rule interestingness. Typically, association rules are considered interesting if they satisfy both a minimum support threshold and a minimum confidence threshold. Such thresholds can be set by users or domain experts.

Definition.

Let $I=\{I_1, I_2, ..., I_m\}$ be a set of items. Let D, the task relevant data, be a set of database transactions where each transaction T is a set of items such that $T \subseteq I$. Each transaction is associated with an identifier, called TID. Let A be a set of items. A transaction T is said to contain A if and only if $A \subseteq T$. An association rule is an implication of the form $A \Rightarrow B$, where $A \subset I$, $B \subset I$ and $A \cap B = \Phi$. The rule $A \Rightarrow B$ holds in the transaction set D with support s, where s is the percentage of transactions in D that contain $A \cup B$. The rule $A \Rightarrow B$ has confidence c. in the transaction set D if c is the percentage of transactions in D containing A which also contain B. That is, support($A \Rightarrow B$) = Prob{$A \cup B$} and confidence($A \Rightarrow B$) = Prob{B/A}.

Rules that satisfy both a minimum support threshold (minsup) and a minimum confidence threshold (minconf) are called *strong*. A set of items is referred to as an itemset. An itemset that contains k items is a k-itemset.

Apriori is an influential algorithm for mining frequent itemsets for Boolean association rules. The name of the algorithm is based on the fact that the algorithm uses prior knowledge of frequent itemset properties .

APRIORI ALGORITHM

Apriori is an algorithm for frequent item set mining and association rule learning over relational databases. It proceeds by identifying the frequent individual items in the database and extending them to larger and larger item sets as long as those item sets appear sufficiently often in the database. The frequent item sets determined by Apriori can be used to determine association rules which highlight general trends in the database: this has applications in domains such as market basket analysis.

Apriori uses a "bottom up" approach, where frequent subsets are extended one item at a time (a step known as *candidate generation*), and groups of candidates are tested against the data. The algorithm terminates when no further successful extensions are found. Apriori uses breadth-first search and a Hash tree structure to count candidate item sets efficiently. It generates candidate item sets of length *k* from item sets of length *k-1*. Then it prunes the candidates which have an infrequent sub pattern. After that, it scans the transaction database to determine frequent item sets among the candidates.

ALGORITHM 1: Apriori Algorithm.

$\text{Apriori}(T, \epsilon)$
$L_1 \leftarrow \{\text{large } 1-\text{itemsets}\}$
$k \leftarrow 2$
while $L_{k-1} \neq \emptyset$
$C_k \leftarrow \{c = a \cup \{b\} \mid a \in L_{k-1} \wedge b \notin a, \{s \subseteq c \mid |s| = k-1\} \subseteq L_{k-1}\}$
for transactions $t \in T$
$D_t \leftarrow \{c \in C_k \mid c \subseteq t\}$
for candidates $c \in D_t$
$count[c] \leftarrow count[c] + 1$
$L_k \leftarrow \{c \in C_k \mid count[c] \geq \epsilon\}$
$k \leftarrow k + 1$
return $\bigcup_k L_k$

PRIVACY PRESERVING TECHNIQUE (PPT)

Many real world applications of data mining with two or more participants require the sharing of sensitive data. Each participant has data related to different aspects. Each participant works with its own attribute set, but all participants have data about all the instances involved. Data mining requires the attributes of all the participants. Due to privacy concern, the participants may be reluctant to disclose their attribute values to other participants. This concept is known as privacy preserving vertically partition data mining, which allows the sharing of data among all the participants for the data mining results while at the same time values of the attributes remains private or confidential by the participants to whom it belongs. The challenge in such context is to protect the data privacy of all the participants as sharing of private data raises the privacy issues.

The following scenarios illustrate the situations in which this type of collaboration is interesting. For example,

(1) Association rule mining on health examination result and outpatient medical record gives the knowledge between abnormal test results and disease. It helps the physician as an additional reference during the examination of patients and diagnosis.

(2) Users are interested to know whether or not they have certain diseases by sharing their genome information with the health center. Due to privacy concern, users do not want to expose their genome information with the health center and health center does not want to disclose its gene biomarker information with users.

The digitalization in the healthcare with electronic health record (EHR) stores huge amount of records related to patient's background, diagnosis, and case history. Digital records related to patients gives the new direction to medical research in the area of data mining. Data mining helps to discover the knowledge related to diseases from the patient's data. Association rule mining on the integrated data of health examination reports and outpatient medical records helps to discover the correlations between disease and health examination reports. Distributed association rule mining in vertically partitioned data gives the results on integrated data. The integration of health examination reports and outpatient medical records requires the sharing of data with each other or to some trusted third party.

DATA PARTITION MODEL

In distributed environment, two major types of data partition model among all participants (Hospital with EHR systems), viz. ***Horizontal Partitioned*** and ***Vertical Partitioned*** data model are given. Some of the existing approaches towards privacy persevering distributed association rule mining of both kinds of data partitioning is being discussed. In the horizontally partitioned data, all the participants have the same schema, but each participant contains the records of different entities.

As shown in figure 2, all the EHR systems have the same schema but each EHR system contains the data of different patients. Some existing solutions for privacy preserving association rule mining with **horizontal partition data** are presented in. For example, in case of a heart disease research at the global level, many private hospitals with their local HER system data want to undertake the association rule mining. Each local HER system contains the data about the patients ID, sex, age, disease, treatment, duration etc. These hospitals are interested in a collaborative research for finding the relation among the sex, age, diagnosis and disease by the global dataset. As a result of the collaborative association rule mining, all the hospitals learn the rule, {*restecg = hypertrophy and type of chest pain = asymptomatic and slope = flat and thal = reversable*} => {*Heart Disease chance = Yes*} is true at the global level. However, to ensure the privacy of the patient and confidentiality of the local patterns, the hospitals would not want to share their local HER system data.

In case of the **vertically partitioned data**, each participant has different schema and it stores the data of the same set of entities. Privacy preserving association rule mining in vertically partition data. As shown in figure 3, Health examination data and outpatient data can be integrated based on common ID for discovering the correlations between abnormal test results and some disease. Medical researchers are interested in computing the association rule mining on the integrated data of the health examination record and outpatient record. Association rules discovered from this collaboration (e.g. *abnormal Rubella IgG test results carry a high risk of fetal damage*) helps to discover some correlations between some diseases and patient's attributes. Hence, Privacy preserving association rule mining in vertically partitioned healthcare data has received the substantial attention of medical researchers.

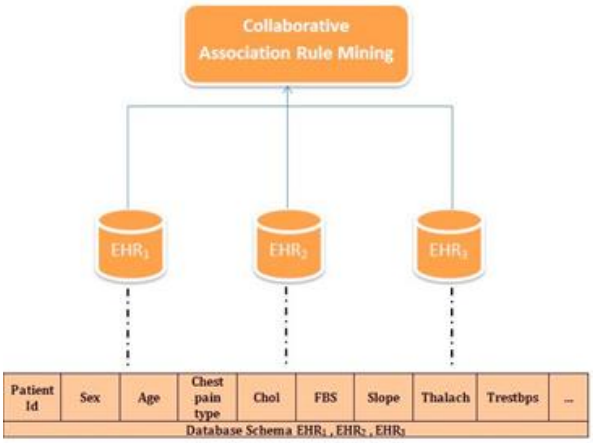

Fig. 2: Horizontal Partition Data Model.

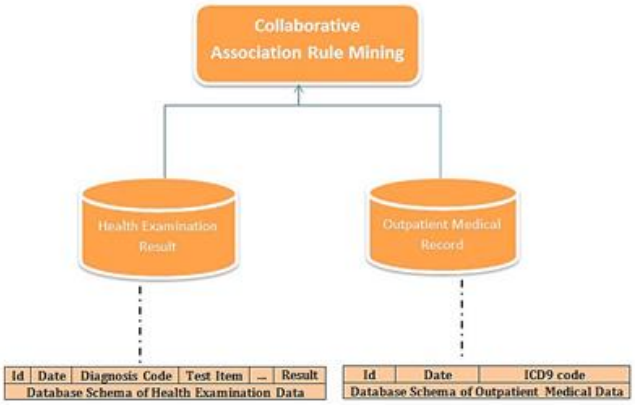

Fig. 3: Vertical Partition Data Model.

DISTRIBUTED ASSOCIATION RULE MINING (DARM)

Distributed association rule mining is a technique for a vertical partitioned data set across several sites. The aim of the **distributed association rule mining** is to discover all **rule**s with global support and global confidence greater than the user specified minimum support and confidence. The subsequent steps, utilizing the secure sum and secure set union methods described earlier are used. The basis of the algorithm is the Apriori algorithm, which use the (k-1) sized frequent item sets to generate the k sized frequent item sets.

The algorithm for finding the frequent itemset in vertically partitioned database is shown in algorithm. This algorithm begin with finding the *1-frequent itemset* L_1 from the database *D*. Step 3 of an algorithm generates the candidate itemset C_k from the frequent itemset L_{k-1} computed in the previous iteration. We can generate all the association rules once the algorithm gives frequent itemset and its counts. Step 1,3,11 and 14 require the sharing of information. Step 1, 3 and 14 do not disclose any private information to other participants, as the final set of frequent itemset $_k$ L_k is known to both participants. Our proposed approach shows the computation of step 11 for finding c_{count} without disclosing the private information.

Algorithm 2: DARM in vertically partitioned database:

1. $L1$= *find frequent 1- itemset(D)*
2. *for* ($k = 2; Lk-1 \_ \emptyset; k++$)
3. Ck= *apriori gen*($Lk-1$);
4. for *for each candidate* $c \in Ck$ do
5. *if*
6. *all the attributes of c are in A or B alone*
7. *c.count is calculated by that participant independently*
8. *else*
9. *Let c contains p attributes of A and q attributes of B*
10. *Participant A compute the* $\vec{X}$ *as* $xi = \Pi pj=1\ aj$ *and Participant B compute* $\vec{Y}$ *as* $yi = \Pi qj=1\ bj$
11. *collaboratively find the c.count*= $\vec{X} \cdot \vec{Y} = \Sigma ni=1\ xi \cdot yi$
12. *endif*
13. $Lk = \{c \in Ck\ |c.count \geq min\ sup\}$
14. *return* $L = \cup_k L_k$;

FREQUENT ITEMSETS

Itemset Mining- A frequent itemset mining is most commonly explained by market basket analysis. It attempts to identify associations, or patterns between the various items that have been chosen by a particular shopper and placed in their market basket. More specifically, the sets of products which has a higher frequency of buying together is predicted in this.

Let's assume that we have a set of items **I = {i1, i2, …, in}**. We also have a set of transactions **D** where each transaction **T** is a set of items such that T is a subset of I. Each T has an associated unique identifier called **TID**. Then:

- X -> Y is an association rule where X and Y are both subsets of I and not empty sets.
- X -> Y holds in D with confidence level c if at least c% of transactions in D containing X also contain Y.
- X -> Y has the support s if s% of transactions in D contain the intersection of X and Y.

Given a set of transactions D, we wish to generate all association rules X- > Y that have support and confidence greater than the user-specified minimum support and minimum confidence, respectively. We define the minimum support required for rules to be considered interesting. Starting with single item sets, we build new sets at each level if they continue to meet the minimum support.

BIOINFORMATICS APPLICATIONS

Frequent itemset mining can be used to tackle a broad range of bioinformatics problems. For the purpose of providing a representative overview of potential applications, we discuss six bioinformatics sub domains in which these techniques have been successfully used.

FREQUENT ANNOTATION MINING

Annotations of a molecular entity (such as a gene) describe certain properties (e.g. function or localization) by means of terms of a controlled vocabulary. They are crucial in many bioinformatics workflows. Frequent itemset mining can also be used to identify relationships between various existing ontologies. For example, cross-ontology association rule mining can connect the biological process, cellular compartment and protein function subtrees within the Gene Ontology.

STRUCTURAL MOTIF DISCOVERY

Structural patterns or motifs are frequently occurring combinations of structural properties in biomolecules (such as molecular sequences). Although these features are omnipresent and extremely diverse, the underlying conservation typically points to a functionally important role. As a consequence, motif discovery is an important and widely explored topic in bioinformatics. When structural features are trans- formed into transactions, frequent itemset mining can be used to discover combinations of structural features that occur more frequently than expected.

PATTERN DETECTION IN QUANTITATIVE 'OMICS' PROFILES

Association rule mining has been extensively used for the analysis of quantitative molecular profiles. A popular application is biclustering, which is the discovery of sets of submatrices within a larger matrix. The stereotypical use case of biclustering in bioinformatics is the analysis of co-expressed genes (with measured expression values) from a dataset under a (sub)set of conditions. High-throughput techniques for genome-wide expression profiling have resulted in the availability of many gene expression matrices.

FREQUENT ITEMSET-BASED EXPLORATION OF SNPs

Frequent itemset mining has also been used to identify strong associations between allelic combinations associated with diseases. An FP-based method was found to be suitable for the detection of strong inter- active effects. More recently, a scalable Apriori- based approach to identify discriminative patterns between high-order single-nucleotide polymorph- isms (SNPs) and disease phenotypes was proposed. Another method based on Apriori separates the search within the set attributes from the search between the set attributes, resulting in rules that were shown to be consistent with literature.

Millions of SNPs exist, with many of these showing correlated genotypes. This has led to the search for so- called tag SNPs that are subsets sufficient to infer the other SNPs from. Common methods suffer from various problems with larger chromosomes, thus becoming very memory-intensive and time-consuming.

CONCLUSION

Data mining techniques helps in finding the hidden knowledge in a group of disease data that can be used to analyze and predict the future behavior of diseases. Classification is one the data mining techniques which assigned a class label to a set of unclassified cases.

Data mining in healthcare is important to improve the medical industy standards. Piracy issues during the collaborative data mining for medical research are discussed here. To solve this, efficient approaches is introduced. An effective and efficient approach for privacy preserving association rule mining on vertically partition healthcare data. Association Rule mining has a wide range of applicability such market basket analysism medical diagnosis/ research, Website navigation, homeland security, education, financial and business domain and so on.

PROGRAMMING WITH PYTHON

(Creating a Fantasy Cricket team)

A report submitted in partial fulfillment of the requirements for the degree of

BACHELOR OF TECHNOLOGY

Internship with

INTERNSHALA

(22/05/2020 – 03/07/2020)

BY

Purvanshi Sharma

Batch- BI-61

Roll No. -171507



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

WAKNAGHAT, SOLAN - 173234

TABLE OF CONTENT

S.NO	Topics	Page No.
1.	Acknowledgement	0.1
2.	Student Declaration	0.2
3.	Introduction	1
4.	Description of Industry	2
5.	Description of Work	3
6.	Detailed Description of Work	4
7.	Conclusion	5
8.	Refrences	6

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I, Purvanshi Sharma would like to express our sincere gratitude to the TnP cell (Jaypee University of Information Technology, Solan, H.P). I would like to thank Dr. Sudhir Kumar Sayal, HOD Department of Biotechnology and Bioinformatics and the TnP cell; who has been a constant support through all my endeavors ; for providing me a wonderful opportunity for the fulfillment of requirements of the Internship (2020) with a report on

PROGRAMMING WITH PYTHON (Creating a Fantasy Cricket Team).

STUDENT DECLERATION

I, Purvanshi Sharma, hereby declare that the presented report of internship titled

"**PROGRAMMING WITH PYTHON (Creating a Fantasy Cricket Team)"** is uniquely prepared by me after the completion of 45 days' training at INTERNSHLA(online).

I also confirm that the report is only prepared for my academic requirement, not for any other purpose.

PURVANSHI SHARMA

Bachelor of Technology

Department of Biotechnology and Bioinformatics

Jaypee University of Information Technology

Wahnaghat, Solan-173234

INTRODUCTION

Basic Introduction to my Internship

The online training, Programming with **Python**, is a 6-week training program covering essential concepts on the building blocks of **Python**, object-oriented programming, the use of SQLite database and development of GUIs for **Python** applications.

Python is a popular programming language. It was created by Guido van Rossum, and released in **1991**.

It is used for:

- web development (server-side),
- software development,
- mathematics,
- system scripting.

Structure Query Language(**SQL**) is a **database** query language used for storing and managing data in Relational DBMS. **SQL** was the first commercial language **introduced** for E.F Codd's Relational model of **database**

DISCRIPTION OF INDUSTRY

Internshala is an internship and online training platform, based in Gurgaon, India. Founded by Sarvesh Agrawal, an IIT Madras alumnus, in 2010, the website helps students find internships with organisations in India.

The platform, which was founded in 2010, started out as a WordPress blog that aggregated internships across India and articles on education, technology and skill gap. Internshala launched its online trainings in 2014. As of 2018, the platform had 3.5 million students and 80,000 companies.

In August 2016, Telangana's not-for-profit organization, Telangana Academy for Skill and Knowledge (TASK) partnered with Internshala to help students with internship resources and career services.

In September 2016, Team Indus, Google XPRIZE shortlisted entity has partnered with Internshala for college outreach for its initiative, Lab2Moon

DESCRIPTION OF WORK

In my internship I was required to complete a total of 7 modules. Each module had a certain no. of video lectures, theory and assignments; after completion of a module I had to take a test pertaining to the content of the module**,** on which I was evaluated.

Overview of the Modules:

- **Introduction to Python** (getting acquainted to the basic syntax of python) My Score: 95%
- **Using Variables in Python**(detailed study of python variables) My Score: 90%
- **Basics of Programming**(Using functions and built in modules) My Score:93%
- **Principles of OOPs**(Using magic methods and operator overloading) My Score:90%
- **Connecting to SQLite database**(Connecting sql with python, creating records through python) My Score:53%
- **Developing a GUI with PYQT**(Converting a layout made in QT designer and converting it a python code) My Score: 100%
- **Applications of Python in various Disciplines**(A brief of various python applications) My Score:100%

After completion of all the modules, I had to give a final test, based on it's score I was awarded the final certificate. I scored 95% in the final test.

DETAILED DESCRIPTION OF WORK

During this course I, have completed the intermediate level of python which included Basics of python (IDLE, salient features of python, syntax), Various data types (strings, lists, tuples, dictionary), Construction of modules and packages, SQLite (Connecting to SQLite database through python, creation, insertion retrieval of records, error handling), Development of GUI using PYQT (using QT Designer).

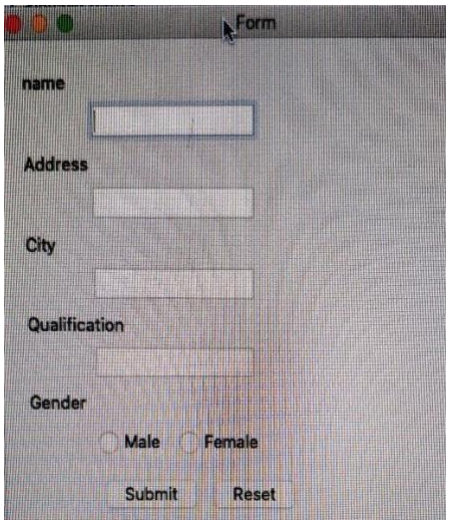
RESULTS:

CODE

```
from PyQt5 import QtCore, QtGui, QtWidgets


class Ui_t1(object):
    def setupUi(self, t1):
        t1.setObjectName("t1")
        t1.resize(400, 300)
        self.t1_2 = QtWidgets.QLabel(t1)
        self.t1_2.setGeometry(QtCore.QRect(10, 70, 54, 17))
        self.t1_2.setObjectName("t1_2")
        self.t2 = QtWidgets.QLabel(t1)
        self.t2.setGeometry(QtCore.QRect(10, 110, 54, 17))
        self.t2.setObjectName("t2")
        self.t3 = QtWidgets.QLabel(t1)
        self.t3.setGeometry(QtCore.QRect(10, 140, 54, 17))
        self.t3.setObjectName("t3")
        self.t4 = QtWidgets.QLabel(t1)
        self.t4.setGeometry(QtCore.QRect(10, 180, 54, 17))
        self.t4.setObjectName("t4")
        self.lineEdit = QtWidgets.QLineEdit(t1)
        self.lineEdit.setGeometry(QtCore.QRect(140, 50, 113, 33))
        self.lineEdit.setObjectName("lineEdit")
        self.lineEdit_2 = QtWidgets.QLineEdit(t1)
        self.lineEdit_2.setGeometry(QtCore.QRect(140, 90, 113, 33))
        self.lineEdit_2.setObjectName("lineEdit_2")
        self.lineEdit_3 = QtWidgets.QLineEdit(t1)
        self.lineEdit_3.setGeometry(QtCore.QRect(140, 130, 113, 33))
        self.lineEdit_3.setEchoMode(QtWidgets.QLineEdit.Password)
        self.lineEdit_3.setObjectName("lineEdit_3")
        self.lineEdit_4 = QtWidgets.QLineEdit(t1)
        self.lineEdit_4.setGeometry(QtCore.QRect(140, 170, 113, 33))
        self.lineEdit_4.setObjectName("lineEdit_4")
        self.t1.setValidator(QtGui.QIntValidator())
        self.retranslateUi(t1)
```

OUTPUT



CONCLUSION

Python an interpreted high level programming language, its design emphasizes on code readability with its notable use of significant white space. Its language constructs and object oriented approach helps us write clear, logical codes for small and large scale projects.

Is an easy to learn language, supports various databases like SQLite, MySQL, Oracle, DDl, etc.

It is also used to build server side web applications, it offers many frameworks from which to choose from including bottle.py, Flask, CherryPy, Pyramid, Django and web2py. Has a strong emphasis on readability which makes it a preferable language to be used for web development.

REFRENCES

- WWW.GOOGLE.COM
- WWW.INTERNSHALA.COM
- WWW.FREECAMPCODE.COMP
- WWW.W3SCHOOL.COM

SUMMER TRAINING ON STRUCTURAL BIOLOGY



DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS,
JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY,
WAKNAGHAT, SOLAN 173234, HIMACHAL PARDESH, INDIA

TOPIC: Structural analysis of SARS-CoV-2
(Structural Biology)

Enrollment No.-171508
Name of the student- Maharishi Kalla
Name of the guide -Dr. Narendra Kumar
MAY-JUNE 2020

CANDIDATE'S DECLARATION

I hereby declare that the work presented in this report entitled "**Structural analysis of SARS-CoV-2.**" in partial fulfilment of the requirements for the summer training submitted in the department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat is an authentic record of my own work carried out over a period from **16 May, 2020 to 30 June, 2020** under the supervision of **Dr.Narendra Kumar** (Assistant Professor).The matter embodied in the report has not been submitted for the award of any other training or internship.



Maharishi Kalla, 171508

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr.Narendra Kumar
Assistant Professor
Department of Biotechnology and Bioinformatics
Dated: 02-07-2020

ABSTRACT

A novel severe acute respiratory syndrome (SARS)-like coronavirus (SARS-CoV-2) recently emerged and is rapidly spreading in humans, causing COVID-19. **The sudden emergence and rapid spread of SARS-CoV-2 is endangering global health and economy.** SARS-CoV-2 has caused many more infections, deaths and economic disruptions than SARS-CoV in 2002–2003. Clinically approved vaccines or drugs that specifically target SARS-CoV-2 are also lacking..A key to tackling this pandemic is to understand the receptor recognition mechanism of the virus, which regulates its infectivity, pathogenesis and host range. SARS-CoV-2 and SARS-CoV recognize the same receptor—angiotensin-converting enzyme 2 (ACE2)—in humans. we studied the structure of structural basis of receptor recognition by SARS-CoV-2.

We studied about the structure recognition by SARS-CoV-2, structures showed that SARS-CoV RBD contains a core and a receptor-binding motif (RBM); the RBM mediates contacts with ACE2. The surface of ACE2 contains two virus-binding hotspots that are essential for SARS-CoV binding. Several naturally selected mutations in the SARS-CoV RBM surround these hotspots and regulate the infectivity, pathogenesis. the binding affinities between each of the three RBDs (SARS-CoV-2, chimeric and SARS-CoV) and ACE2.

Difference between the RBMs of SARS-CoV-2 and SARS-CoV **the conformation of the loops in the ACE2-binding ridge,** In both RBMs, one of the ridge loops contains an essential disulfide bond and the region between the disulfide-bond-forming cysteines is variable.

Various methods that were used by the researchers were explored.

This researchis very important in the present times as it helps to inform intervention strategies. First, neutralizing monoclonal antibodies that target the SARS-CoV-2 RBM can prevent the virus from binding to ACE2, and are therefore promising antiviral drugs. The structure has laid out all of the functionally important epitopes in the SARS-CoV-2 RBM that can potentially be targeted by neutralizing antibody drugs. Thus study can help to guide the development and optimization of these antibody drugs. Second, the RBD itself can function as a subunit vaccine.

INTRODUCTION

we studied the structure of structural basis of receptor recognition by SARS-CoV-2.SARS-CoV-2 and SARS-CoV recognize the same receptor—angiotensin-converting enzyme 2 (ACE2)—in humans. Here we determined the crystal structure of the receptor-binding domain (RBD) of the spike protein of SARS-CoV-2 (engineered to facilitate crystallization) in complex with ACE2. In comparison with the SARS-CoV RBD, an ACE2-binding ridge in SARS-CoV-2 RBD has a more compact conformation; moreover, several residue changes in the SARS-CoV-2 RBD stabilize two virus-binding hotspots at the RBD–ACE2 interface. These structural features of SARS-CoV-2 RBD increase its ACE2-binding affinity.

ABOUT

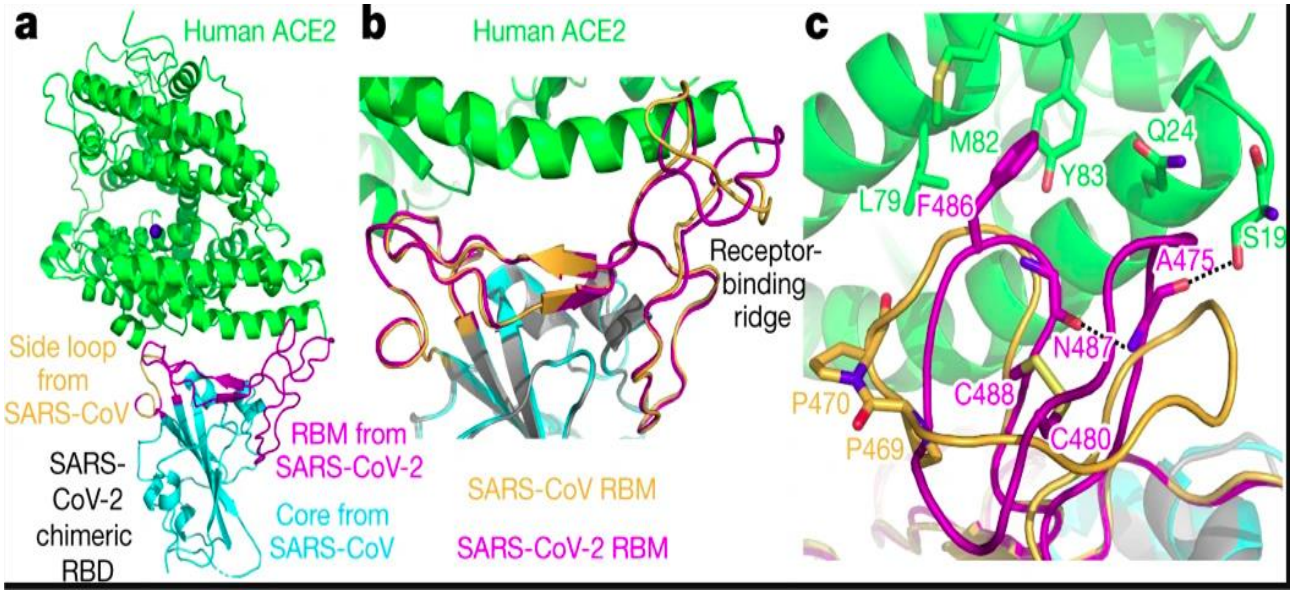
A novel severe acute respiratory syndrome (SARS)-like coronavirus (SARS-CoV-2) recently emerged and is rapidly spreading in humans, causing COVID-19. SARS-CoV-2 is a positive-sense single-stranded RNA virus that is contagiousin humans. As described by the U.S. National Institutes of Health, it is the successor to SARS-CoV-1 the strain that caused the 2002–2004 SARS outbreak. Taxonomically, SARS-CoV-2 is a strain of severe acute respiratory syndrome-related coronavirus (SARSr-CoV). It is believed to have zoonotic origins and has close genetic similarity to bat coronaviruses, suggesting it emerged from a bat-borne virus. There is no evidence yet to link an intermediate animal reservoir, such as a pangolin, to its introduction to humans. The virus shows little genetic diversity, indicating that the spillover event introducing SARS-CoV-2 to humans is likely to have occurred in late 2019

The sudden emergence and rapid spread of SARS-CoV-2 is endangering global health and economy. SARS-CoV-2 has caused many more infections, deaths and economic disruptions than SARS-CoV in 2002–2003. Clinically approved vaccines or drugs that specifically target SARS-CoV-2 are also lacking. Receptor recognition by coronaviruses is an important determinant of viral infectivity, pathogenesis and host range. Here we study the structural and biochemical mechanisms of receptor recognition by SARS-CoV-2.

Study of receptor recognition by SARS-CoV-2

A virus-surface spike protein mediates the entry of coronavirus into host cells. The spike protein of SARS-CoV contains a RBD that specifically recognizes ACE2 as its receptor. A series of crystal structures of the SARS-CoV RBD from different strains in complex with ACE2 from different hosts has previously been determined. The structures showed that SARS-CoV RBD contains a core and a receptor-binding motif (RBM); the RBM mediates contacts with ACE2. The surface of ACE2 contains two virus-binding hotspots that are essential for SARS-CoV binding. Several naturally

selected mutations in the SARS-CoV RBM surround these hotspots and regulate the infectivity, pathogenesis, and cross-species and human-to-human transmissions of SARS-CoV. Because of the sequence similarity between the spike proteins of SARS-CoV and SARS-CoV-2, it was recently predicted that SARS-CoV-2 also uses ACE2 as its receptor, which has been validated by other studies. Here we studied the structural basis of receptor recognition by SARS-CoV-2 and compared the ACE2-binding affinity among SARS-CoV-2, SARS-CoV and RaTG13. To understand the structural basis of ACE2 recognition by SARS-CoV-2, we studied crystallize the SARS-CoV-2 RBD–ACE2 complex.



a: Crystal structure of the SARS-CoV-2 chimeric RBD complexed with ACE2. ACE2 is shown in green. The RBD core is shown in cyan. The RBM is shown in magenta. A side loop in RBM is shown in orange. A zinc ion in ACE2 is shown in blue.

b: Comparison of the conformations of the ridge in SARS-CoV-2 RBM (magenta) and SARS-CoV RBM (orange).

c: Comparison of the conformations of the ridge from another viewing angle. In the SARS-CoV RBM, a proline-proline-alanine motif is shown. In the SARS-CoV-2 RBM, a newly formed hydrogen bond, Phe486, and some of the interactions of the ridge with the N-terminal helix of ACE2 are shown.

The overall structure of the chimeric RBD–ACE2 complex is similar to that of the SARS-CoV RBD–ACE2 complex. Similar to the SARS-CoV RBM, SARS-CoV-2 RBM forms a gently concave surface with a ridge on one side; it binds to the exposed outer surface of the claw-like structure of ACE2. The strong salt bridge between SARS-CoV RBD and ACE2 became a weaker (as judged by the longer

distance of the interaction), but still energetically favourable, N–O bridge between Arg439 of the chimeric RBD and Glu329 of ACE2.

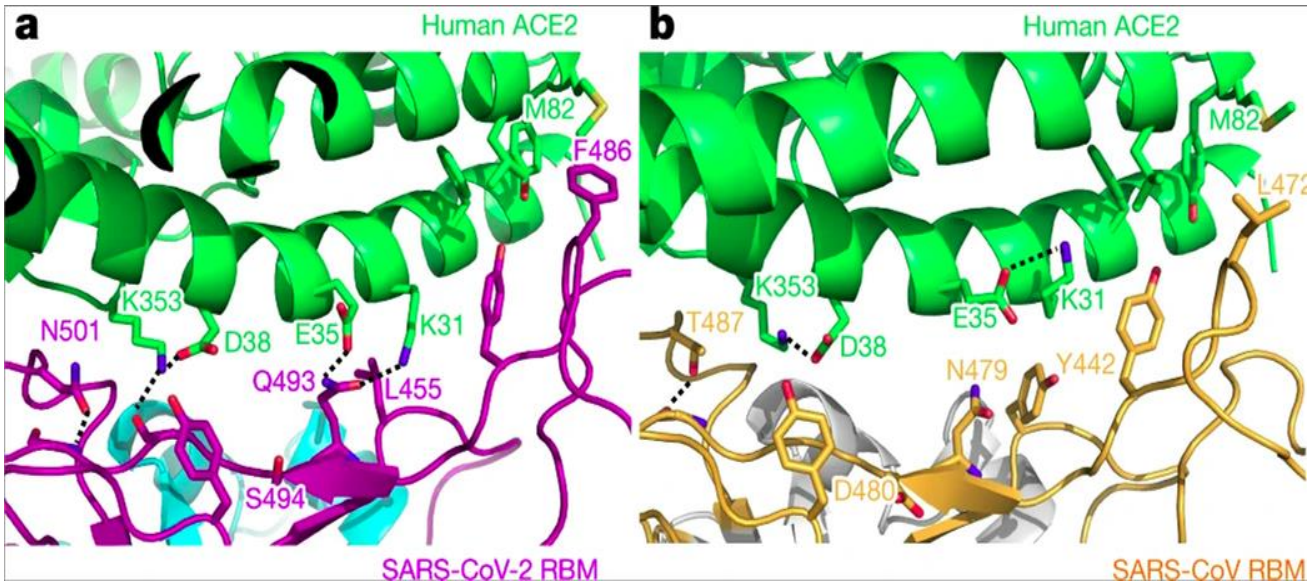
The overall structural similarity in ACE2 binding by SARS-CoV-2 and SARS-CoV supports a close evolutionary relationship between the two viruses.

Study of binding affinity

We studied the binding affinities between each of the three RBDs (SARS-CoV-2, chimeric and SARS-CoV) and ACE2. It found that the chimeric RBD has a higher ACE2-binding affinity than the SARS-CoV-2 RBD, consistent with the introduced N–O bridge between the chimeric RBD and ACE2. Both the chimeric and SARS-CoV-2 RBDs have significantly higher ACE2-binding affinities than the SARS-CoV RBD.

Difference between the RBMs of SARS-CoV-2 and SARS-CoV

the conformation of the loops in the ACE2-binding ridge, In both RBMs, one of the ridge loops contains an essential disulfide bond and the region between the disulfide-bond-forming cysteines is variable. Specifically, human and civet SARS-CoV strains and bat coronavirus Rs3367 all contain a three-residue motif proline-proline-alanine in this loop; the tandem prolines allow the loop to take a sharp turn. By contrast, SARS-CoV-2 and bat coronavirus RaTG13 both contain a four-residue motif glycine-valine/glutamine-glutamate/threonine-glycine; the two relatively bulky residues and two flexible glycines enable the loop to take a different conformation. Because of these structural differences, an additional main-chain hydrogen bond forms between Asn487 and Ala475 in the SARS-CoV-2 RBM, causing the ridge to take a more compact conformation and the loop containing Ala475 to move closer to ACE2 . As a consequence, the ridge in the SARS-CoV-2 RBM forms more contacts with the N-terminal helix of ACE2 . For example, the N-terminal residue Ser19 of ACE2 forms a new hydrogen bond with the main chain of Ala475 of the SARS-CoV-2 RBM, and Gln24 in the N-terminal helix of ACE2 also forms a new contact with the SARS-CoV-2 RBM . Moreover, compared with the corresponding Leu472 of the SARS-CoV RBM, Phe486 of the SARS-CoV-2 RBM points in a different direction and inserts into a hydrophobic pocket involving Met82, Leu79 and Tyr83 of ACE2 . In comparison to the SARS-CoV RBM, these structural changes in the SARS-CoV-2 RBM are more favourable for ACE2 binding.



a: The interface between the SARS-CoV-2 RBM and ACE2.

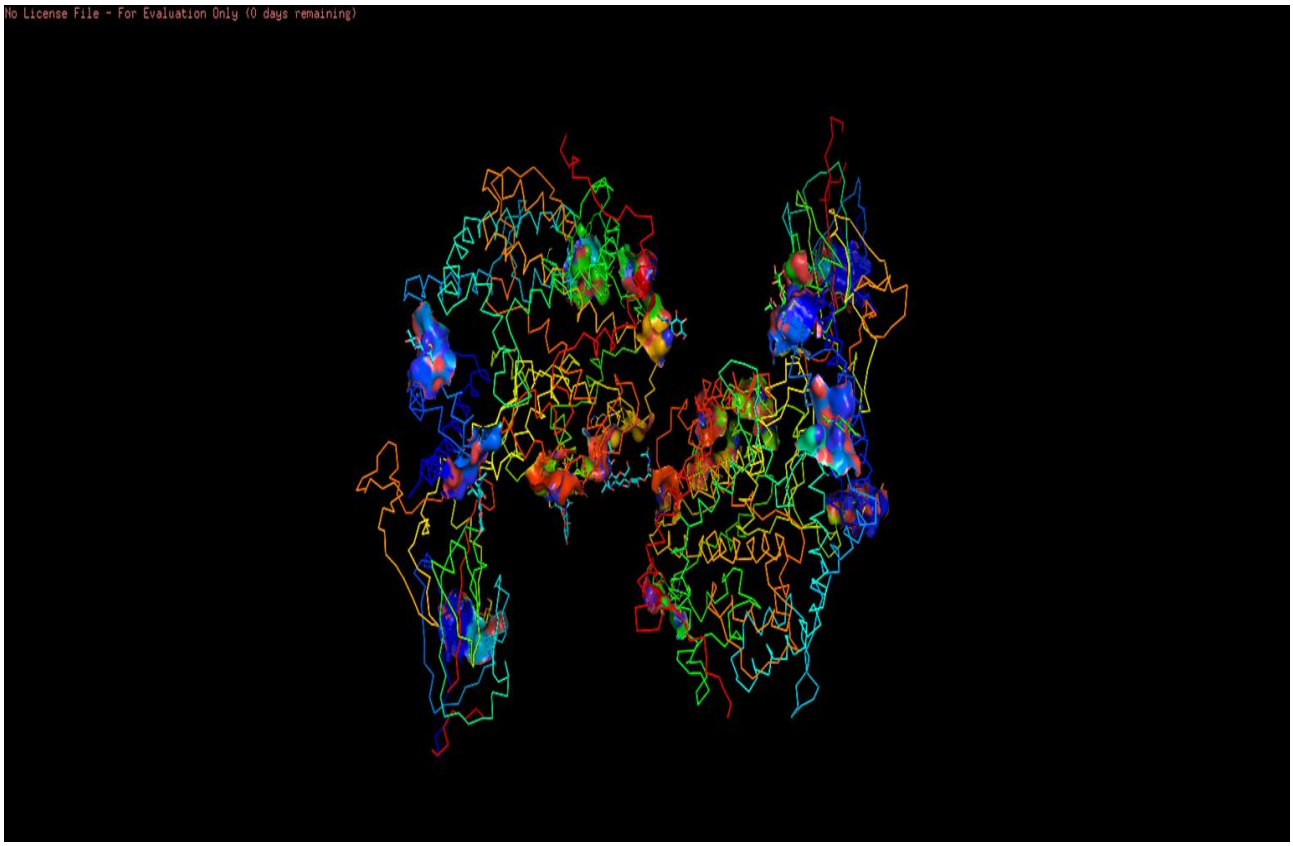
b: The interface between SARS-CoV RBM and ACE2.

SARS-CoV-2 recognizes ACE2 in comparison to SARS-CoV. We show that, compared with SARS-CoV, the SARS-CoV-2 RBM contains structural changes in the ACE2-binding ridge, largely caused by a four-residue motif (residues 482–485: Gly-Val-Glu-Gly). This structural change allows the ridge to become more compact and form better contacts with the N-terminal helix of ACE2.

The corresponding residue in the SARS-CoV RBM is a leucine, which probably forms a weaker contact with ACE2 owing to its smaller side chain. Finally, both virus-binding hotspots are more stabilized at the RBM–ACE2 interface through interactions with the SARS-CoV-2 RBM. As previous studies have shown11,12, these hotspots on ACE2 are important for coronavirus binding, because they involve two lysine residues that need to be accommodated properly in hydrophobic environments. Neutralizing the charges of the lysines is key to the binding of coronavirus RBDs to ACE2. The SARS-CoV-2 RBM has evolved strategies to stabilize the two hotspots: Gln493 and Leu455 stabilize hotspot 31, whereas Asn501 stabilizes hotspot 353

this study helps to inform intervention strategies. First, neutralizing monoclonal antibodies that target the SARS-CoV-2 RBM can prevent the virus from binding to ACE2, and are therefore promising antiviral drugs. Our structure has laid out all of the functionally important epitopes in the SARS-CoV-

2 RBM that can potentially be targeted by neutralizing antibody drugs. Thus, this study can help to guide the development and optimization of these antibody drugs. Second, the RBD itself can function as a subunit vaccine. The functionally important epitopes in the SARS-CoV-2 RBM that were identified in this study can guide structure-based design of highly efficacious RBD vaccines. Such a structure-based strategy for subunit vaccine design has previously been developed . This strategy may be helpful in designing SARS-CoV-2 RBD vaccines. Overall, this study can help to inform structure-based intervention strategies that target receptor recognition by SARS-CoV-2.



Structure of SARS-CoV-2 chimeric receptor-binding domain complexed with its receptor human ACE2

Methods used for these studies

Plasmid

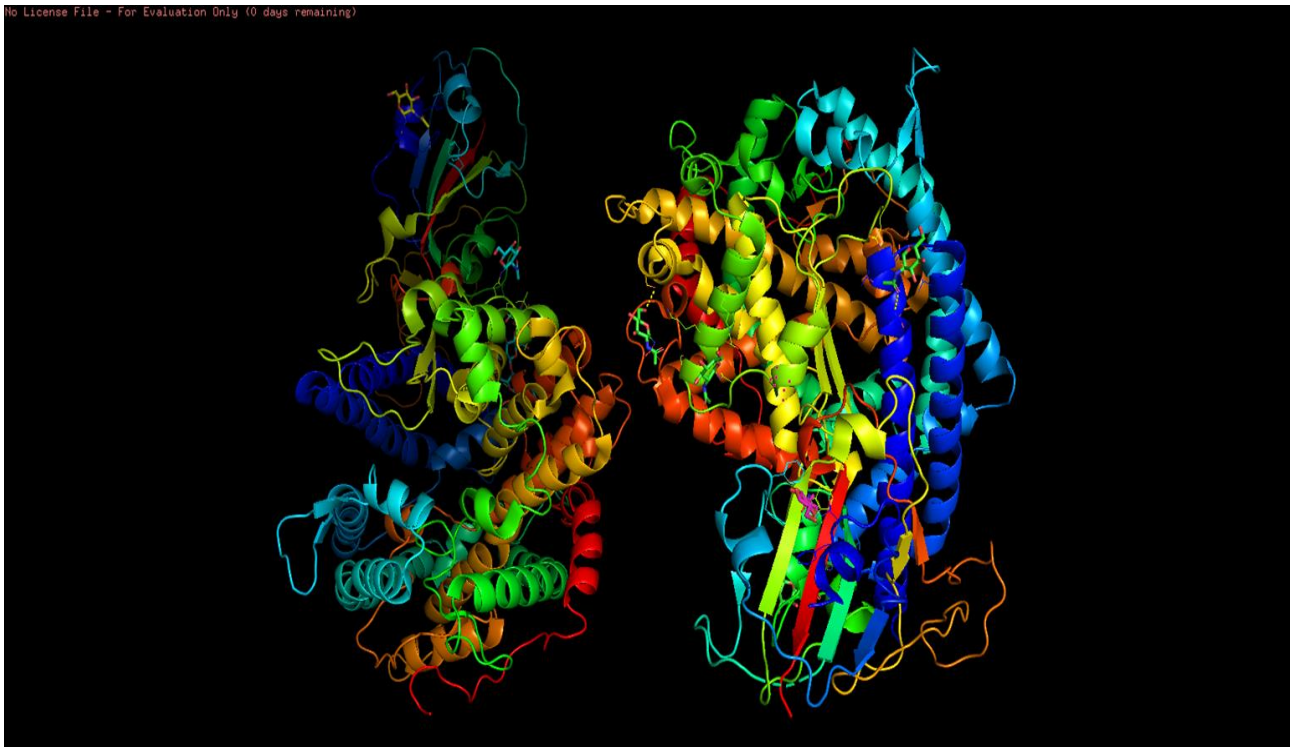
SARS-CoV-2 spike (GenBank accession number QHD43416.1), SARS-CoV spike (GenBank accession number AFR58740.1), RaTG13 spike (GenBank accession number QHR63300.2) and ACE2 (GenBank accession number NM_021804) were all synthesized. SARS-CoV-2, SARS-CoV, chimeric RBDs and ACE2 ectodomain were subcloned into pFastBac vector with a N-terminal honeybee melittin signal peptide and a C-terminal His6-tag.

Protein expression and purification

The proteins were prepared from Sf9 insect cells using the Bac-to-Bac system.

Crystallization and structure determination

X-ray diffraction data were collected at the Advanced Photon Source beamline 24-ID-E. The structure was determined by molecular replacement using the structure of SARS-CoV RBD complexed with ACE2 as the search template (Protein Data Bank (PDB) 2AJF).



Structure of SARS coronavirus spike receptor-binding domain complexed with its receptor

Protein–protein binding assay

Analyses of protein contact residues and protein buried surface areas

Protein contact residues were analysed using the LigPlot+ program.

Outcome

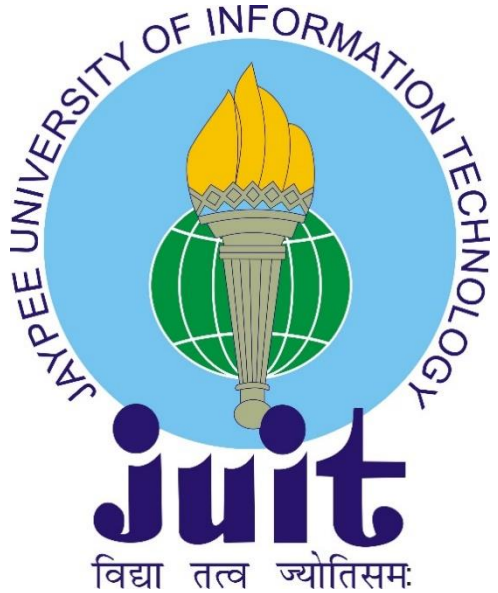
Finally, this study helps to inform intervention strategies. First, neutralizing monoclonal antibodies that target the SARS-CoV-2 RBM can prevent the virus from binding to ACE2, and are therefore promising antiviral drugs. The structure has laid out all of the functionally important epitopes in the SARS-CoV-2 RBM that can potentially be targeted by neutralizing antibody drugs. Thus study can help to guide the development and optimization of these antibody drugs. Second, the RBD itself can function as a subunit vaccine. The functionally important epitopes in the SARS-CoV-2 RBM that were identified in this study can guide structure-based design of highly efficacious RBD vaccines. Such a structure-based strategy for subunit vaccine design has previously been developed. This strategy may be helpful in designing SARS-CoV-2 RBD vaccines. Overall, this study can help to inform structure-based intervention strategies that target receptor recognition by SARS-CoV-2.

Summer Training on HealthCare Monitoring System Based Upon Features for CVD

Enrolment No- **171509**

Name of the student- **Aagam Mishra**

Name of Supervisor- **Dr. Tiratha Raj Singh**



June, 2020

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My sincere thanks goes to all the staff, professors and PhD scholars at JUIT, whose Kindness and friendly nature provided a very enjoyable research environment and a platform of excellence to do my dissertation.

Aagam Mishra

Candidate's Declaration

I hereby declare that the work presented in this report entitled "Healthcare Monitoring System Based Upon the Features for CVD" in the fulfilment of the requirements for the Summer Training submitted in the department of Biotechnology and Bioinformatics, Jaypee University of Information Technology Waknaghat is an record of my own work and carried out over a period from 16 May 2020 to 30 June 2020 under the supervision of Dr. Tiratha Raj Singh.



Aagam Mishra (171509)

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr. Tiratha Raj Singh

Dated: 01/07/2020

LIST OF FIGURES

Figure-01: Representation of proposed method
Figure-02: ANFIS Architecture
Figure-03: Association Rule representing heart disease
Figure-04: Representing correlation between gender and heart disease
Figure-05: Representing relation between age>45 and heart disease
Figure-06: Correlation between rural population and heart disease
Figure-07: Our proposed algorithm CBARBSN

LIST OF TABLES

Table-01: ANN Results

Table-02: Accuracy

TABLE OF CONTENTS

ABSTRACT

INTRODUCTION

Cardiovascular Disease and its Symptoms

Risk Factors for Coronary Heart Disease

DataMining in CVD

DataMining Algorithms

DataMining Tools

Association Rule Mining

Methodology

ANFIS Architecture

Result and Discussion

Conclusion

References

ABSTRACT

Heart disease is the single largest cause of death in developed countries and one of the main contributors to disease burden in developing countries. Mortality data from the registrar general of India shows that coronary heart disease (CHD) are a major cause of death in india.studies to determine the precise cause of death in rural areas of Andhra Pradesh have revealed that CHD cause about 30% death are in rural areas. Although significant progress has been made in the diagnosis and treatment of heart disease further investigation is still needed. Data mining techniques have been used in medical diagnosis for many years and have been known to be effective.

We will focus on Analysing Medical Data using Association Rule mining for Heart Attack Prediction. Association rule mining is one of the fundamental research topics in data mining and knowledge discovery that finds interesting association or correlation relation ship among a large set of data items and predicts the associative and correlative behaviors for new data. The Association rule mining algorithms must perform efficiently. In this project we will study about a new approach for association rule mining based on sequence number and clustering the transactional data base for heart attack prediction. Experimental results shows effectiveness of our proposed algorithm.

INTRODUCTION

Cardiovascular Disease and Its Symptoms:

The heart is one of the main organs of the human body. It pumps blood trough the blood vessels of the circulatory system. The circulatory system is extremely important because it transports blood, oxygen and other materials to the different organs of the body. Heart plays the most crucial role in circulatory system. If the heart does not function properly then it will lead to serious health conditions including death.

Heart diseases or cardiovascular diseases (CVD) are a class of diseases that involve the heart and blood vessels. Cardiovascular disease includes coronary artery diseases (CAD) like angina and myocardial infarction (commonly known as a heart attack).There is another heart disease, called coronary heart disease (CHD), in which a waxy substance called plaque develops inside the coronary arteries. These are the arteries which supply oxygen-rich blood to heart muscle. When plaque begins to build up in these arteries, the condition is called atherosclerosis. The development of plaque occurs over many years. With the passage of time, this plaque can harden or rupture (break open). Hardened plaque eventually narrows the coronary arteries which in turn reduces the flow of oxygen-rich blood to the heart. If this plaque ruptures, a blood clot can form on its surface. A large blood clot can most of the time completely block blood flow through a coronary artery [1]. Over time, the ruptured plaque also hardens and narrows the coronary arteries. If the stopped blood flow isn't restored quickly, the section of heart muscle begins to die. Without quick treatment, a heart attack can lead to serious health problems and even death. Heart attack is a common cause of death worldwide. Some of the common symptoms of heart attack are as follows.

1. *Chest pain*

   It is the most common symptom of heart attack. If someone has a blocked artery or is having a heart attack, he may feel pain, tightness or pressure in the chest.

2. *Nausea,Indigestion, Heartburn and Stomach Pain*

   These are some of the often overlooked symptoms of heart attack. Women tend to show these symptoms more than men.

3. *Pain in the Arms*

   The pain often starts in the chest and then moves towards the arms, especially in the left side.

4. *Feeling Dizzy and Light Headed*

   Things that lead to the loss of balance.

5. *Fatigue*

   Simple chores which begin to set a feeling of tiredness should not be ignored.

6. *Sweating*

Some other cardiovascular diseases which are quite common are stroke, heart failure, hypertensive heart disease, rheumatic heart disease, Cardiomyopathy, Cardiacarrhythmia, Congenital heart disease, Valvular heart disease, Aortic aneurysms, Peripheral artery disease and Venous thrombosis. Heart diseases may develop due to certain abnormalities in the functioning of the circulatory system or may be aggravated by certain lifestyle choices like smoking, certain eating habits, sedentary life and others. If the heart diseases are detected earlier then it can be treated properly and kept under control [2].

Risk factors for Coronary Heart Disease:

Over 300 risk factors have been associated with coronary heart disease and stroke. The major risk factors are classified into four categories.

A) Major modifiable risk factors:

1) High blood pressure 2) Tobacco use 3) physical inactivity 4) obesity 5) Unhealthy diets 6) Diabetes Mellitus

B) Other modifiable risk factors:

1) Low socio economic status 2) mental ill health 3) Psychosocial stress 4) Alcohol use 5) use of certain medication

C) Non modifiable risk factors:

1) Advancing Age 2) Gender 3) Heredity 4) Family history5) Ethnicity

D) Novel risk factors

1) Inflammation 2) Excess homo cysteine blood 3) Abnormal blood coagulation.

Comprehensive and integrated action is the means to prevent and control Cardio Vascular Diseases [3].

Data Mining in CVD:

Hospitals and clinics accumulate a huge amount of patient data over the years. These data provide a basis for analysis of risk factors for many diseases.we can predict the level of heart attack to find patterns associated with heart disease.one of the major topics in data mining research is the discovery of interesting patterns in data [4].

Data mining is a technology that blends traditional data analysis methods with sophisticated algorithms for processing large volumes of data. Data mining also known as knowledge discovery in data bases (KDD) is the process of automatically discovering useful information in large data repositories. it aims to extract interesting correlations, frequent patterns, associations among sets of items in transactional data bases or other data repositories.

Data Mining Algorithms:

Research on data mining has led to the formulation of several data mining algorithms. These algorithms can be directly used on a dataset for creating some models or to draw vital conclusions and inferences from that dataset. Some popular data mining algorithms are Decision tree, Naïve Bayes, k-means, artificial neural network etc. They are discussed as follows:

1. *Decision Tree*

A Decision tree is a decision support tool that uses a tree-like graph or model of decisions and their possible consequences including chance event outcomes and utility. It is one of the ways to display an algorithm. Decision trees are commonly used in operations research, specifically in decision analysis to help and identify a strategy that will most likely reach the goal. It is also a popular tool in machine learning. A Decision tree can easily be transformed to a set of rules by mapping from the root node to the leaf nodes one by one. Finally by following these rules, appropriate conclusions can be reached.

2. *C4.5*

It is a classifier in the form of a Decision tree. It is a supervised learning method which uses information gain and pruning for improved results. It is quite fast, popular and the output is easily interpretable.

3. *K-means Algorithm*

K-means creates k groups from a set of given objects so that the members of a group are more similar. Other than specifying the number of clusters, k-means also "learns" the clusters on its own without any information about which cluster a particular observation should belong to. That's why k-means can be called as semi-supervised learning method. K-means is specially effective over large datasets.

4. *ID3 Algorithm*

The ID3 algorithm (Quinlan86) is a Decision tree building algorithm which determines the classification of objects by testing the values of the properties. It builds the tree in a top down fashion, starting from a set of objects and the specification of properties. At each node of the tree, a property is tested and the results used to partition the object at that point are set. This process is recursively continued till the set in a given sub tree is homogeneous with respect to the classification criteria [5]. Then it becomes a leaf node. At each node, information gain is maximized and entropy is minimized. In simpler words, that property is tested which divides the candidate set in the most homogeneous subsets.

5. *Support Vector Machine(SVM)*

It is a supervised learning method which classifies data into two classes over a hyper plane. Support vector machine performs a similar task like C4.5 except that it doesn't use Decision trees at all. Support vector machine attempts to maximize the margin (distance between the hyper plane and the two closest data points from each respective class) to decrease any chance of misclassification. Some popular implementations of support vector machine are scikit-learn, MATLAB and of LIBSVM.

6. *Naive Bayes(NB)*

It is a simple technique for constructing classifiers. It is a probabilistic classifier based on Bayes' theorem. All Naive Bayes classifiers assume that the value of any particular feature is independent of the value of any other feature, given the class variable. Bayes theorem is given as follows: $P(C|X) = P(X|C) * P(C)/P(X)$, where X is the data tuple and C is the class such that P(X) is constant for all classes. Though it assumes an unrealistic condition that attribute values are conditionally independent, it performs surprisingly well on large datasets where this condition is assumed and holds [6].

Data Mining Tools:

Data mining tools provide ready to use implementation of the mining algorithms. Most of them are free open source software's so that researchers can easily use them. They have an easy to use interface. Some of the popular data mining tools are WEKA, RapidMiner, TANAGRA, MATLAB etc. Some of them are discussed as follows.

1. *WEKA*

It stands for Waikato Environment for Knowledge Learning. It is a computer program that was developed at the University of Waikato in New Zealand for the purpose of identifying information from raw data. WEKA supports different standard data mining tasks such as data pre-processing, classification, clustering, regression, visualization and feature selection. The basic premise of this application is to utilize a computer application that can be trained to perform machine learning capabilities and derive useful information in the form of trends and patterns. Originally written in C, the WEKA application was then completely rewritten in Java and is now compatible with almost every computing platform. Its user friendly graphical interface allows for quick set up and operation [7].

2. *RapidMiner*

Formerly called as YALE (Yet Another Learning Environment), is an environment for providing data mining and machine learning procedures including data loading and transformation (ETL), data preprocessing and visualization, modeling, evaluation and deployment. Rapid Miner is written in the Java programming language. Also, it can be used for text mining, multimedia mining, feature engineering, data stream mining etc.

3. *TANAGRA*

It is a free data mining software designed for academic and research purposes. It proposes several data mining methods such as exploratory data analysis, statistical learning and machine learning. TANAGRA comprises some paradigms and algorithms such as clustering, association rule, parametric and nonparametric statistics, factorial analysis, feature selection and construction algorithms.

4. *Apache Mahout*

It is a project of the Apache Software Foundation designed for free implementations of distributed or otherwise scalable machine learning algorithms that focus primarily in the areas of collaborative filtering, clustering and classification. Apache Hadoop is another open source, Java-based programming framework which supports the processing and storage of extremely large data sets in a distributed computing environment [8]. It is a part of the Apache project which is sponsored by the Apache Software Foundation.

5. *MATLAB*

It is the short form for matrix laboratory. It supports a multi-paradigm numerical computing environment. It is a fourth-generation programming language. MATLAB provides matrix manipulations, plotting of functions and data, algorithm implementations, creation of user interfaces and interfacing with programs written in other languages including C, C++,C#, Java, Fortran and Python.

Association Rule Mining:

Association rule mining were primarily proposed for market based analysis to understand consumer purchasing patterns in retailing industry. Since association rules are easy to understand and in widespread use, they have been successful in business applications, including finance, telecommunications and health care industry. Association rule is an unsupervised learning approach to discover the relationship or correlation among the items [9]. An Association Rule is an implication expression of the form X=>Y, Where X and Y are disjoint sets.i.e X_Y=Ø.

The strength of an association rule can be measured in terms of support and confidence. Both of them are in the form of percentage. Support determines how often a rule is applicable to a given data set ,while confidence determines how frequently items in Y appears in transactions that contain Y [10].

SUPPORT(X=>Y)=P(X_Y)

CONFIDENCE(X=>Y)=P(X_Y)/P(X)

Minimum support and minimum confidence are the two thresholds in association rule mining. These thresholds can be set by researchers or domain expert. The function of threshold in

mining tool is to help us to reduce minor rules efficiency. Association rule mining is decomposed into 2 major subtasks.

1) **Frequent item set generation**: to find all item sets that satisfy minimum support threshold. These item sets are called frequent item sets.

2) **Rule generation**: This subtask is to extract high confidence rules from the frequent item sets. Rules which satisfy minimum support and minimum confidence are said to be strong rules.

- **Quantitative Association Rules**:

  Association rules that contain continuous attributes are commonly known as Quantitative Association Rules. Mining the continuous attributes may reveal useful insights about data.

- **Boolean Matrix and Transactional Database:**

  a) **Transactional Database-** Let I={i1,i2,-----I n}be a set of items. Assume D is a set of transactions over I, called transaction database, in which a transaction is a set of items, that is subset of I.A transaction has associated unique identifier called transaction identifier (TID).

  b) **Boolean Matrix**

  The Boolean Matrix is a matrix with element values of "1" or "0".

  1 0 0 1

  0 0 0 1

  1 0 0 1

  1 1 1 0

- **Transforming Transactional Data Base into the Boolean Matrix**

  For any transaction data base D,suppose

F:D=>R

R=F(D)=(r ij)mXn`

And rij=1 Ii □Tj

0 Ii□Tj

Where J=1,2,--n

Data base D can be mapped on to the Boolean matrix R with the effect of F by scanning the database only once.

Transactional data

TID	ITEMS
1	1,2,3
2	4,5
3	3,4
4	1,4
5	1,3,5

Boolean matrix

1 0 0 1 0
1 0 0 1 0
0 0 1 1 0
0 0 0 1 1
1 0 1 0 1

METHODOLOGY

Algorithm: HAPBM (Heart Attack Prediction Using Matrix)

Input: Transactional Database D

Minimum Support S

Output: Frequent patterns to predict heart attack

Method: 1) Discretize the medical data

2) Transform the discretized medical data in Boolean matrix.

3) Calculate all one item set support Ci and all one transaction item support Ri.the on item support ci can be gotten by counting one transaction item support Ri.the one item support ci can be gotten by counting the column with value '1'and one transaction item sets Ri can be gotten by counting the rows with '1'.

4) Generate frequent 1 item sets. If one item support Ci is less than minimum support threshold S prune corresponding items.

5) Recompute Ri to generate frequent 2 item sets .if transaction item support Ri is less than 2 prune corresponding Transaction.

6) Generate k frequent item sets .Repeat the steps 4 and 5 till no frequent item sets are generated.

7) Generate the association rules from the frequent item sets.

Sample C Functions for Proposed Method.

1. **Checking the columns which do not satisfy the minimum support**

```
for(i=1;i<n;i++)//col
{
if(a[n][i]<=k)
{
continue;
}
col1++;
count=count+1;
//printf("%d\t%d\t",count,a[n][i]);
for(j=0;j<n;j++)//row
{
```

```
a1[j][col1]=a[j][ i];
}
}
```

2. **Finding the new row sum**

```
for(i=1;i<n;i++)
{
sum=0;
for(j=1;j<col1;j++)
{
sum=sum+a1[i][j];

}
a1[i][j]=sum;
//printf("s%d,i  %d,j  %d",a1[i][j],i,j);
}
```

3. **Checking the rows which do not satisfy the minimum support**

```
for(i=1;i<n;i++)//row
{
if(a1[i][col1]<rtre)
{
continue;
}
row1++;
for(j=0;j<col1+1;j++)
{
a2[row1][j]=a1[i][j];
}
```

1 frequent item sets are
{2,4,7,8,11,12,13,15,16,17,18,20}

2 frequent item set generation
check Ri for all the rows ,if ri<2,prune corresponding rows. Make the combinations of 1 itemsets,to get 2 itemsets and check support of 2 itemsets.if support of 2 item set<S prune the combination.

Frequent 2 item sets are
(2,8),(2,13),(2,16),(2,18),(4,8),(4,12),(4,13),(4,16),(4,17),(4,18)(7,8),(7,11),(7,12),(7,16),(7,17),(7,18),(8, 11), (8, 12),(8,15),(8,16),(8.17),(8,18),(8,20),(11,13),(11,16),(11,18),(11,20),(12,13),(12,16),(12,17),(12,18),(13,15),
(13,16),(13,17),(13,18),(13,20),(15,16),(15,18),(16,17),(16,18), (17,18),(18,20)

3- frequent item set generation
Check Ri for all the rows, if ri<3,prune corresponding row. Make the combinations of 2 itemsets,to get 3 item sets and check support of 3 item sets. if support of 3 item set<S prune the combination. The transactional data base will be shown in table 5

Frequent 3 item sets are
(2,8,13),(2,8,16),(2,13,16),(2,13,18),(2,16,18),(2,13,15),(4,8,11),(4,8,16),(4,8,18),(4,13,16),(4
,13,17),(4,13,18),
(4,16,18),(4,17,18),(7,8,16),(7,8,17),(7,8,18),(7,11,18),(7,11,13),(7,11,20),(7,16,17),(7,16,18)
,(7,17,18),(7,18,20),(8,11,12),(8,11,15),(8,11,18),(8,11,20),(8,11,13),(8,12,13),(8,12,16),(8,12
,18),(8,15,16),(8,15,18),(8,16,17),
(816,18),(8,17,18),(8,18,20),(11,13,16),(11,13,18),(11,16,18),(11,18,20),(12,13,16),(12,13,17
),(12,13,18),(12,13,20),(12,16,17),(12,16,18),(12,17,18),(13,15,16),(13,15,18),(13,16,17),(13,
16,18),(13,17,18),(13,18,20),(15,16,7),(16,17,18),(16,18,20)(17,18,20**)**

4- frequent item set generation
Check Ri for all the rows, if ri<4,prune corresponding row. Make the combinations of 3 itemsets,to get 4 item sets and check support of 4 item sets. If support of 4 item set<S prune the combination. The transactional data base will be shown in table 5
(2,8,13,16),(2,8,13,18),(4,13,16,18),(4,13,17,18),(7,8,16,17)(7,8,16,18),(7,16,17,18),(8,11,12,
18),(8,12,13,16),
(8,12,13,18),(8,12,16,18),(8,15,16,18),(8,15,17,18),(11,13,16,18),(11,16,18,20),(12,13,16,17)
,(12,16,17,18),
(13,15,16,17),(13,15,16,18),(13,15,16,20),(13,16,17,18),(13,17,18,20)

5 Frequent item set generation
Check Ri for all the rows, if ri<5,prune corresponding row. Make the combinations of 4 itemsets,to get 5 item sets and check support of 5 item sets. if support of 5 item set<S prune the combination.
5 frequent item sets are
1) (2, 8, 13, 16, 18),
2) (4, 13, 16, 17, 18)
3) (7, 8, 16, 17, 18)
4) (8, 12, 13, 16, 18)

6- **frequent item set generation**
Check Ri for all the rows, if ri<6, prune corresponding row. Make the combinations of 5 itemsets, to get 6- item sets and check support of 6 item sets. If support of 6 item set<S prune the combination. Here no combination will have support>minimum Support threshold. Hence algorithm will be terminated.
Above 5 frequent item sets implies rules like

1) **Age between 41-65 and Hyper Cholestremia=yes and smoking=yes and family history=No and**
   alcohol=yes
   =>Heart disease
2) **Person=male and smoking=yes and family history=No and Rural=yes alcohol=yes =>Heart**
   disease
3) **Hypertension=No and Hyper Cholestremia=yes and family history=No and Rural=yes alcohol=yes**
   =>Heart disease
4) **Hyper Cholestremia=yes and resting ECG>2 and smoking=yes and family history=No and alcohol=yes =>Heart disease**.

Algorithm: CBARBSN (Cluster Based Association Rule Mining Based On Sequence Number)

Input: D, a transactional database

Ms, The Minimum Support Threshold

Output: Frequent item sets

Method: 1) Scan the database **D** and partition the transaction table into equal no. of clusters using skipping Fragments. Cluster size should be well balanced in order to have same distribution of transaction fragments. Apply the method from step 2 to 6 on each cluster**.**

2) Find SN and SID of each item

3) The set of frequent 1 item sets say L1, can then be determined. It consists of candidate 1 Item. Sets which satisfy minimum support (**SID_ms**)

4) To discover the set of frequent 2- item sets say L2, Join **L1 ⋈ L2** and perform Logical AND .If Support of 2 -item sets is less than minimum Support **ms** prune 2 -item sets. Construct the Graph by Drawing Edge between each pair of 2 - Frequent item sets.

5) To determine frequent 3 item sets, traverse the graph as if there is a path among the nodes {i,j},{j,k}then the set {i,j,k}will be frequent 3 item sets.

6) The algorithm iterates to find upto n- frequent item sets

7) From each cluster find out the n-frequent item sets. These item sets are said to be local frequent Item sets

8) Intersect the set of frequent item sets from each cluster to get global frequent item sets (Item Sets which appear in both the Clusters are said to be global frequent item sets)

Algorithm: Adaptive Neuro Fuzzy Inference System (ANFIS) and Rule Extraction Algorithm

Method:

Step 1: Arrange the linguistic features in descending order with their weights.

Step 2: From that order select top N linguistic features for each class until each linguistic feature gets selected at least once.

Step 3: Count the frequency of linguistic features of each input feature.

Step 4: Keep the lower linguistic features separately and count the frequency in input feature.

Step 5: The input feature which has higher frequency is considered as more important than others. (If two input features are having same frequency then their top most linguistic feature weights determine the important one).

Step 6: Layered OR rules for classification are generated based on important input features, order of classes and top linguistic features in the following way. For all input features from most important to least important.

If f1 is lf1_1 then Class1_1

Else if f1 is lf1_2 then Class1_2 …….. Else if f1 is lf1_N then Class1_N …. ….

Else if f2 is lf2_1 then Class2_1 …. …. Else if f2 is lf2_N then Class2_N …. ….

Else if fn is lfn_1 then Classn_1 …. …. Else if fn is lfn_N then Classn_N

where fn represents nth input feature, lfn_N represents the Nth important linguistic feature of fn feature and Classn_N represents the class of Nth important linguistic feature of fn feature

Step 7: For all the input features

If all the rules of an input feature are found redundant in classification, the input feature is removed else step 10

Step 8: Layered OR rules for classification are generated order of classes and lowest linguistic features.

Step 9: if redundant, then input feature is removed else step 10.

Step 10: Rules of the remaining input features are the final rules.

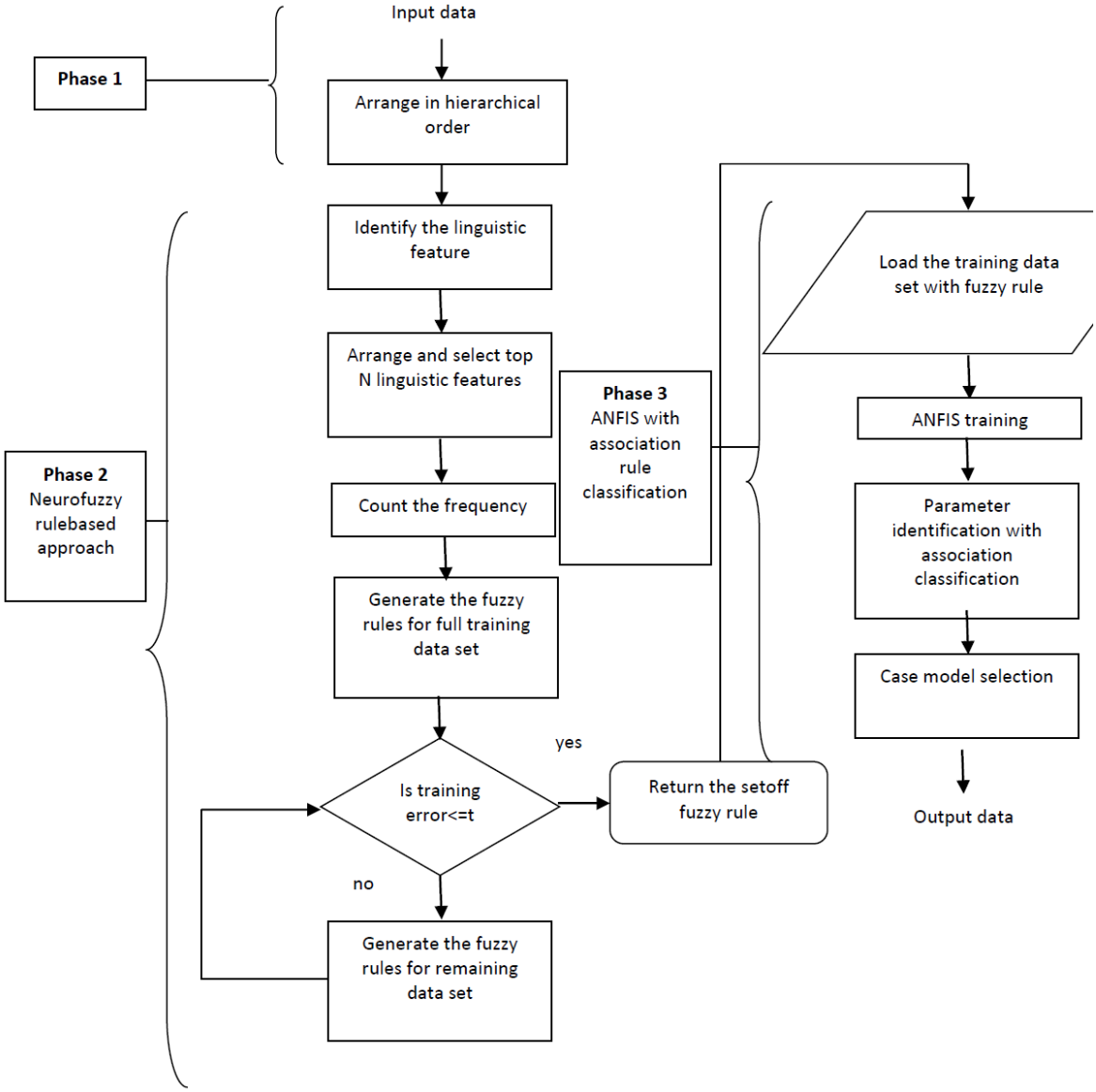


Figure-01: Representation of proposed method

ANFIS Architecture:

The fuzzy modeling and membership function reduces the human error to the greater extent[11]. The ANFIS Architecture for two input first order fuzzy model with two rules is shown in figure 2.

Layer 1: Fuzzification layer

Assume two inputs X and Y and one output Z.

Rule 1: if X is A1 and Y is B1, then f1= p1X+q1Y+r1

Rule 2: if X is A2 and Y is B2, then f2= p2X+q2Y+r2

Here every node i in this layer is an adaptive node with a node function,

Oi,1=μAi(x) for i=1,2 … (1)

Oi,1=μBi-2(x) for i=3, 4 … (2)

Layer 2: Rule antecedent layer

This layer includes the nodes which represents the antecedent part of association rule. The output of each node is given as

Oi=μAi(x) , μBi (x) for i=1,2 … (3)

Layer 3: Strengthen normalization layer

The weight obtained from the layer 2 is normalized by fixed nodes present in this layer. The output of the normalization layer is given as,

Oi= W-1=*wiw*1+*w*2 for i=1,2 … (4)

Layer 4: Consequent layer

The adaptive nodes included in this layer are the products of normalization strength in polynomial order.

Oi= W-1fi= W-1(ri(x) +s i(x)+t i) for i=1,2 …(5)

Layer 5: Inference Layer

The overall output is given as,

O =Σ1*i*=2*i*=1 W-1fi=ΣWifi*i*=2*i*=1ΣWi*i*=2*i*=1for i=1,2 … (6)

In layer 1 the eight modifiable parameters ci and σi where i=1,2,3,4. In layer 4 six modifiable parameters ri,si, and ti for i=1,2.

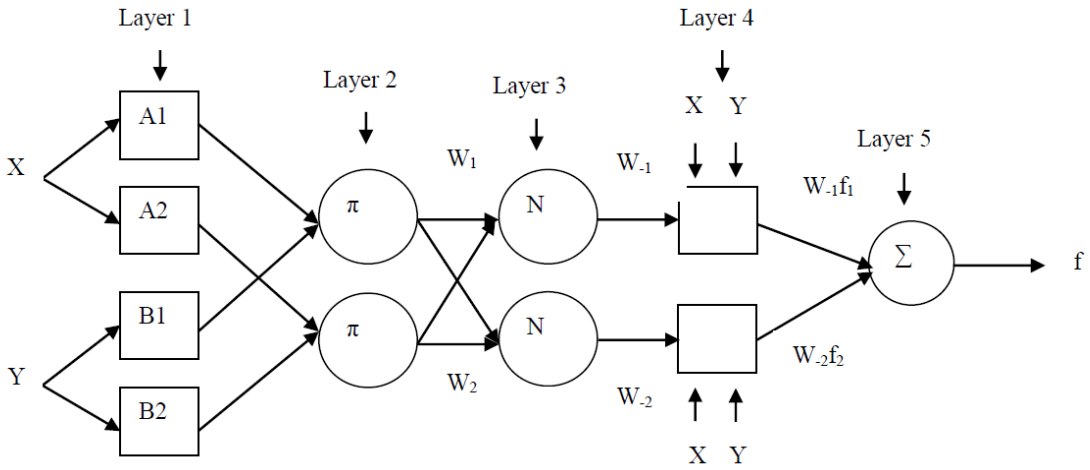


Figure-02: ANFIS Architecture

RESULT AND DISCUSSION

The following section describes different categories of association analysis for heart disease prediction.

A total of 70 patients records are collected from the cardio thoracic departments of various corporate hospitals in Andhra Pradesh. Based on the data collected, we analyzed medical data using our proposed approach. The patterns of CHD in Andhra Pradesh has been reported as follows.

- Out of 70 samples 52 rural population have associated with heart disease.
- Males are affected more than females
- 75% of population who had Hypertension are associate with heart disease.
- Population with age group >45 are correlated with heart disease.
- Smoking has been identified as a major risk factor.
- More than 50%of males who lives in rural are correlated with heart disease.
- Males with age group>45 and who have smoking habit are correlated with CHD.
- 20%of Diabetic patients are associated with heart disease.

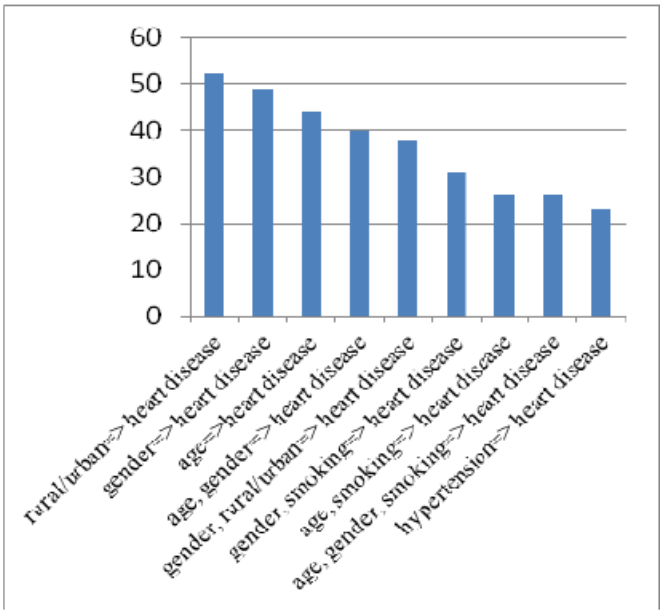


Figure-03: Association Rule representing heart disease

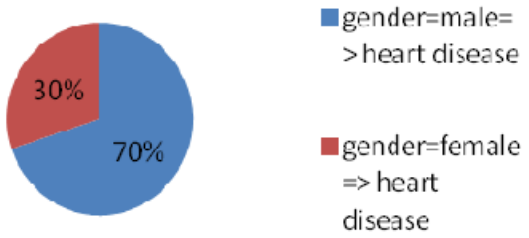


Figure-04: Representing correlation between gender and heart disease

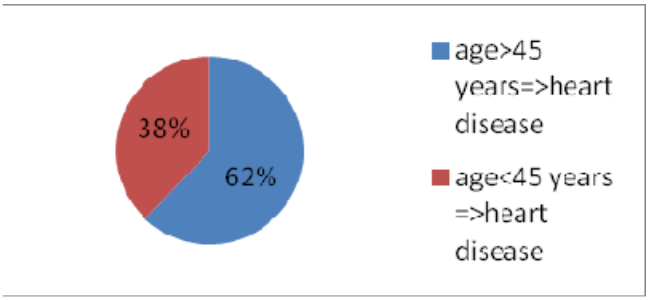


Figure-05: Representing relation between age>45 and heart disease

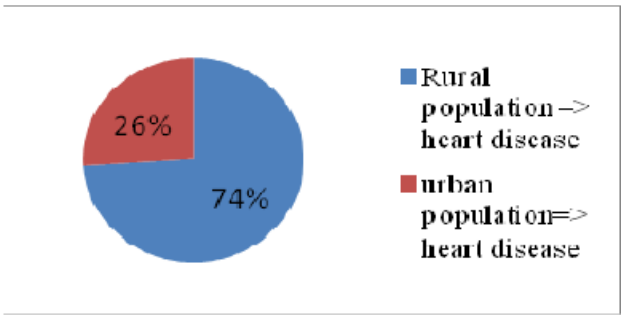


Figure-06: Correlation between rural population and heart disease

To assess the efficiency of the proposed method, we implemented the algorithm in C language on Pentium 4 processor. The fig shows the support vs. execution time in ms. The experimental results show that our algorithm performs better than the other algorithms.

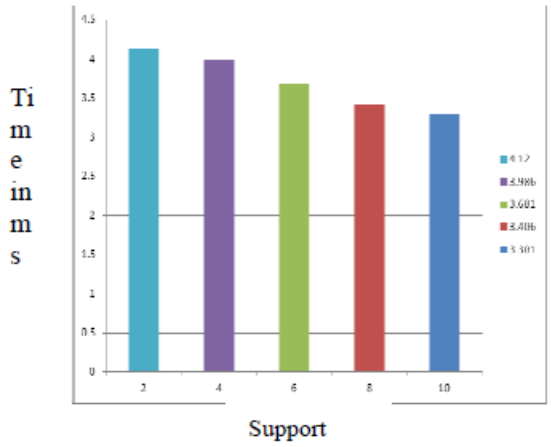


Figure-07: Our proposed algorithm CBARBSN

In figure 7 the execution time to mine association Rules is high and as the support increases execution Time slightly changes but in our proposed algorithm Execution time to mine association rules is less and as support increases execution time changes Drastically.

The Cleveland data set for heart disease is used for the evaluation. It consists of 303 instances with 14 medical attributes such as age: age in years ;sex: sex (1 = male; 0 = female) ; cp: chest pain type , Value 1: typical angina , Value 2: atypical angina ,Value 3: non-anginal pain ,Value 4: asymptomatic ;trestbps: resting blood pressure (in mm Hg on admission to the hospital) ;chol: serum cholestoral in mg/dl ;fbs: (fasting blood sugar > 120 mg/dl) (1 = true; 0 = false) ; restecg: resting electrocardiographic results , Value 0: normal ,Value 1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV) ,Value 2: showing probable or definite left ventricular hypertrophy by Estes' criteria ; thalach: maximum heart rate achieved ;exang: exercise induced angina (1 = yes; 0 = no) ; oldpeak = ST depression induced by exercise relative to rest ;slope: the slope of the peak exercise ST segment , Value 1: upsloping ,Value 2: flat, Value 3: downsloping ;ca: number of major vessels (0-3) colored by flourosopy ;thal: 3 = normal; 6 = fixed defect; 7 = reversable defect ;num: diagnosis of heart disease (angiographic disease status) ,Value 0: < 50% diameter narrowing ,Value 1: > 50% diameter narrowing .The programming language used for diagnosis heart disease is MATLAB which is an efficient tool for data analysis and visualization.

Two parameters are considered in training ANFIS system such as maximum number of epochs and number of hidden neurons. The number of epochs varies from 1000 to 5000 and hidden neuron ranges from 7 to 21. The results are shown in table 1. The system also has an additional module known as case-based module, where the user has to input values for 14 required attributes as specified by the Cleveland data set, in order to test the status of the patient whether heart disease is present or absent from that particular patient.

However the combination of 4000 epochs and 15 hidden neurons with an increment of 7 achieved the highest accuracy results as 93.12%. The system performs 5000 epochs with 21 hidden layers achieves 84.47%.

No.of epochs	No. of hidden neurons	Training data	Testing data	Case based classification
1000	7	77.11	76.54	Absent
1000	14	83.71	78.12	Absent
1000	21	84.45	87.56	Absent
2000	7	86.23	77.12	Absent
2000	14	85.89	86.54	Absent
2000	21	87.54	88.78	Absent
3000	7	84.52	81.64	Absent
3000	14	87.54	83.12	Absent
3000	21	87.47	88.81	Absent
4000	7	86.54	79.37	Absent
4000	14	84.32	**93.12**	Absent
4000	21	90.89	85.21	Absent
5000	7	87.12	86.54	Absent
5000	14	86.14	84.33	Absent
5000	21	83.58	84.47	Absent
Average results		85.5366	84.08	100% Absent

Table-01: ANN Results

So the system performs with large combinations. The system classifies the data that are "Absent" of heart disease, therefore the system is achieved 100% accuracy. In most systems, the testing data is very important and systems are evaluated on how best they can perform when receiving data from of someone who has not been trained earlier. Therefore, if considering this aspect, the combination of 5000 epochs and 15 hidden neurons is selected since it performs the highest using the testing data set.

Authors	**Method**	**Accuracy**	**Year**
Das et al[29]	Neural network ensemble	89.01%	2009
Anuj et al [30]	Weighted fuzzy rules	57.85%	2012
Samuel et al[26]	ANN and Fuzzy AHP	90.1%	2017
Bala et al[28]	Hadoop	86.2%	2016
Proposed method	ANFIS+ASSOCIATION RULE	**93.12%**	-

Table-02: Accuracy

In this model Receiver Operating Characteristic Curve is under the threshold 0.8 and error rate is 0.05. The sensitivity is measured. The decision support system ANN and fuzzy AHP achieved the accuracy of 90.1% by two steps. At first, the problem is represented in hierarchical structure. Second, decomposed into goal, attributes and alternatives. Then the fuzzy triangular membership function prior to the pair wise comparison is formed. The ANN and ANFIS approach of decision making achieved the accuracy of 90.74% by implementing three modules such as training, testing and case based module.

CONCLUSION

The objective of our work is to predict more accurately the presence of heart disease for Andhra Pradesh population. In our work we used matrix based approach to reduce no. of scans of data base. Our approach is simple and efficient for extracting significant patterns from the heart disease data for the efficient prediction of heart Disease in Andhra Pradesh. Our algorithm takes less time to generate patterns and reduces transactions at each stage thus reduces search space. The need to contain the epidemic of CHD as well as its combat its impact and minimize its toll on population of Andhra Pradesh is obvious and urgent. Strategies to meet the objective of prevention and control of CHD must be developed and efficiently implemented. In our future work we will try to incorporate to generate patterns using Advanced data mining techniques for heart disease prediction.

we proposed new algorithm to mine association rules from medical data based on digit sequence and clustering .The entire data base is divided into partitions of equal size, each partition will be called cluster. Each cluster is considered one at a time by loading the first cluster into memory and calculating frequent item sets. Then the second cluster is considered similarly and calculating frequent item sets .This approach reduces main memory requirement since it considers only a small cluster at a time and it is scalable and efficient.

The ANFIS with association rule approach in order to develop a Cardio Vascular disease diagnosis system. The table 2 clearly shows that the 93.2% accuracy is achieved using the training dataset. The ANFIS with association rule yields better results than the other method such as neural network ensemble, weighted fuzzy rules , ANN with Fuzzy AHP, Hadoop in cloud computing. This system can be used at hospital level by doctors and physicians to classify the patient's heart disease. Despite the promising results recorded by the proposed method, the optimal sets of hidden layer nodes and their respective weighted links still are a challenge. And as a result, the ANN classifiers in the study were trained and re-trained until the performance of the networks were relatively stable. The future work can be through applying Various ANFIS architecture with KNN.

REFERENCES

[1] P.-N. Tan, M. Steinbach, and V. Kumar, "Introduction to data mining, Pearson education," *Inc., New Delhi*, 2006.

[2] J. C. Principe, N. R. Euliano, and W. C. Lefebvre, *Neural and adaptive systems: fundamentals through simulations*, vol. 672. Wiley New York, 2000.

[3] W. Li, J. Han, and J. Pei, "CMAR: Accurate and efficient classification based on multiple class-association rules," in *Proceedings 2001 IEEE international conference on data mining*, 2001, pp. 369–376.

[4] A. G. Jardine, R. S. Gaston, B. C. Fellstrom, and H. Holdaas, "Prevention of cardiovascular disease in adult recipients of kidney transplants," *The Lancet*, vol. 378, no. 9800, pp. 1419–1427, 2011.

[5] R. R. Huxley and M. Woodward, "Cigarette smoking as a risk factor for coronary heart disease in women compared with men: a systematic review and meta-analysis of prospective cohort studies," *The Lancet*, vol. 378, no. 9799, pp. 1297–1305, 2011.

[6] S. A. Hannan, A. V. Mane, R. R. Manza, and R. J. Ramteke, "Prediction of heart disease medical prescription using radial basis function," in *2010 IEEE International Conference on Computational Intelligence and Computing Research*, 2010, pp. 1–6.

[7] J. Han, J. Pei, and M. Kamber, *Data mining: concepts and techniques*. Elsevier, 2011.

[8] A. H. Chen, S.-Y. Huang, P.-S. Hong, C.-H. Cheng, and E.-J. Lin, "HDPS: Heart disease prediction system," in *2011 computing in cardiology*, 2011, pp. 557–560.

[9] I. Bose and R. K. Mahapatra, "Business data mining—a machine learning perspective," *Information & management*, vol. 39, no. 3, pp. 211–225, 2001.

[10] W. A. AlZoubi, A. A. Bakar, and K. Omar, "Scalable and efficient method for mining association rules," in *2009 International Conference on Electrical Engineering and Informatics*, 2009, vol. 1, pp. 36–41.

[11] R. Agrawal, T. Imieliński, and A. Swami, "Mining association rules between sets of items in large databases," in *Proceedings of the 1993 ACM SIGMOD international conference on Management of data*, 1993, pp. 207–216.

INTERNSHIP REPORT

SUBJECT OF CHOICE: WEBSITE DEVELOPMENT



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY,

WAKNAGHAT, SOLAN 173234, HIMACHAL PRADESH

Name of Supervisor- Dr. Tiratha Raj Singh

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

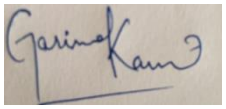
Enrollment No. : 171510

Submitted by: Garima Singh

CERTIFICATE

Candidate's Declaration

I hereby declare that the work presented in the report entitled "**Web Development"** is in fulfilment of the requirement for the summer training submitted in the department of Biotechnology and Bioinformatics, Waknaghat and is an authentic record of our own work carried out over a period from **16 May to 30th June , 2020** under the supervision of **Dr. Tiratha Raj Singh.**



Garima Singh

171510

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr. Tiratha Raj Singh (Supervisor)

Department of Biotechnology and Bioinformatics

Jaypee University of Information and Technology, Waknaghat

Dated on : 30.6.2020

ACKNOWLEDGEMENT

I take the opportunity to express profound sense of gratitude to my supervisor **Dr. Tiratha Raj Singh, Associate Professor, Jaypee University of Information Technology, Waknaghat, Solan** without whom this report would not have been possible. He has been a great inspiration throughout the internship period.

I extend my sincere thanks to **Dr. Tiratha Raj Singh** for giving me the opportunity to work in my area of interest and help me to enhance my skills. Also his continuous guidance, efforts, and invertible suggestion throughout the duration of the internship were like a blessing in disguise.

CONTENT

Chapters	Content	Page Number
Chapter 1	Abstract	5
Chapter 2	Introduction	6
Chapter 3	Information and Implementation	7-20
Chapter 4	Material and Methods	21-23
Chapter 8	Scope of website development	24
Chapter 7	References	25

Chapter 1 Abstract

A website development tool provides companies with a podium for this necessary web presence and allows them to get in touch with millions of web surfers all over the world, widening the range of their potential customers. This doesn't just make the companies accessible, but accessible to the global population. It also gives businesses the chance to portray themselves in the ways they want to be seen, with a platform that's built on their terms and can effectively market the services or products that they offer. In addition, a website will make businesses look more reliable if they're represented in a professional way. To develop a website in accordance with specific criteria, the business can either hire a developer or do it themselves by choosing from the best web development software, which will assist in creating polished websites.

Website development can include anything from simply programming the data of a website to adding client liaison, content, network security and web server configuration, e-commerce development and more. It usually ranges from creating the simplest, plain text to the most difficult web-based applications, social network services and electronic business. Some website developers incorporate design into their web building, while others leave it strictly at coding and writing mark-up. It should go without saying that the better a website looks, the more visitors it will attract, so it's worthwhile to focus on the design aspects as well as the coding when developing your website. The content should accurately depict what your service provides and be geared towards enticing the site's visitors, in order to keep them engaged.

I have learnt certain components of website development and have tried to implement the same with multiple websites and atom editor is used for the same.

Chapter 2 Introduction

The design of your website can either make or break the business you are trying to deliver. It actually makes a difference on how your target audience views your business or company and potentially turn them into your customers. As such, developing a website design that has an impressive user interface will result in a much better conversion rate, which leads to better business and revenue.

And in order to be a full stack developer (front-end) developer, the job is to provide the company a website that somehow acts as asset to the company. During the course of my internship I learnt various concepts, standards ,languages and libraries and their significance in order to design a website.

HTML5 is the latest evolution of the standard that defines HTML. The term represents two different concepts. It is a new version of the language HTML, with new elements, attributes, and behaviours, and a larger set of technologies that allows the building of more diverse and powerful Web sites and applications.

Cascading Style Sheets is a style sheet language used for describing the presentation of a document written in a markup language like HTML.

Bootstrap help in Quickly design and customize responsive mobile-first sites with Bootstrap, the world's most popular front-end open source toolkit, featuring Sass variables and mixins, responsive grid system, extensive prebuilt components, and powerful JavaScript plugins.

JavaScript, often abbreviated as JS, is a programming language that conforms to the ECMAScript specification. It has curly-bracket syntax, dynamic typing, prototype-based object-orientation, and first-class functions.

Chapter 3 Information and Implementation

3.1 Website Development Lifecycle:

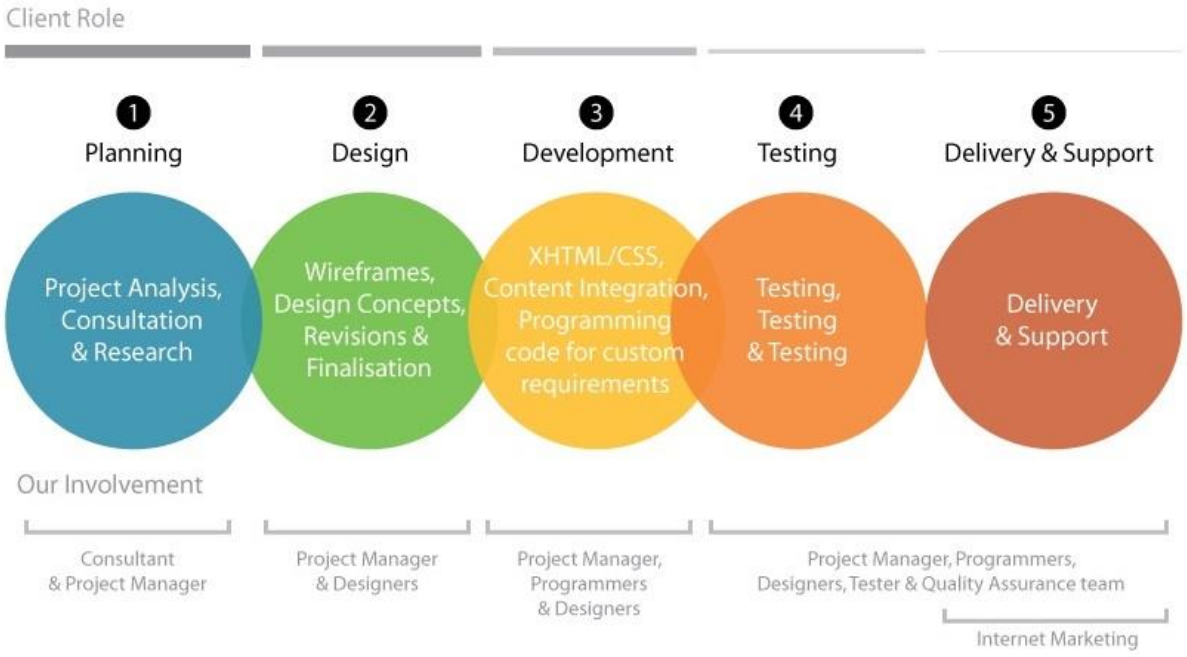


Fig 3.1 Web Development Life Cycle

- **Gathering Information: Purpose, Main Goals, and Target Audience**

This stage, the stage of discovering and researching, determines how the subsequent steps will look like. The most important task at this point is to get a clear understanding of your future website purposes, the main goals you wish to get, and the target audience you want to attract to your site. Such kind of a website development questionnaire helps to develop the best strategy for further project management.

News portal differs from the entertainment websites, and online resources for teenagers look different than sites for adults. Different types of websites provide visitors with different functionality, which means that different technologies should be used according to purposes. A well-described and detailed plan based on this pre-development data can protect you from spending extra resources on solving the unexpected issues such as design changing or adding the functionality that wasn't initially planned.

- **Planning: Sitemap and Wireframe Creation**

At this stage of the website development cycle, the developer creates the data that allows a customer to judge how the entire site will look like. Sometimes, before you start to code or even work on a design, there's a necessity to get approval from a customer that everything looks fine so you can begin the next phase of developing. In this case, a wireframe or mock-up is created. A wireframe is a visual representation of the user interface that you're going to create.

- **Design: Page Layouts, Review, and Approval Cycle**

During the design phase, your website takes shape. All the visual content, such as images, photos, and videos is created at this step. Once again, all the info that was gathered through the first phase is crucial. The customer and target audience must be kept in mind while you work on a design.

The website layout is the result of a designer's work. It can be a graphic sketch or an actual graphic design. The primary function of the layout is to represent the information structure, visualize the content, and demonstrate the basic

functionality. Layouts contain colors, logos, images and can give a general understanding of the future product.

- **Content Writing and Assembly**

Content writing and compiling usually overlaps with other stages of website creation, and its role can't be underestimated. At this step, it is necessary to put in writing the very essence you'd like to communicate to the audience of your website and add calls-to-action. Content writing also involves the creation of catching headlines, text editing, writing new text, compiling the existing text, etc., which takes time and effort. As a rule, the client undertakes to provide website content ready to migrate to the site. It is better when all website content is provided before or during website coding.

- **Coding**

At this step, you can finally start creating the website itself. Graphic elements that have been designed during the previous stages should be used to create an actual website. Usually, the home page is created first, and then all sub-pages are added, according to the website hierarchy that was previously created in the form of a sitemap. Frameworks and CMS should be implemented to make sure that the server can handle the installation and set-up smoothly.

All static web page elements that were designed during the mock-up and layout creation should be created and tested. Then, special features and interactivity should be added. A deep understanding of every website development technology that you're going to use is crucial at this phase.

- **Testing, Review, and Launch**

Testing is probably the most routine part of a process. Every single link should be tested to make sure that there are no broken ones among them. You should check every form, every script, run a spell-checking software to find possible typos. Use code validators to check if your code follows the current web standards. Valid code is necessary, for example, if cross-browser compatibility is crucial for you.

- **Maintenance: Opinion Monitoring and Regular Updating**

What's important to remember is that a website is more of a service than a product. It's not enough to "deliver" a website to a user. You should also make sure that everything works fine, and everybody is satisfied and always be prepared to make changes in another case.

The feedback system added to the site will allow you to detect possible problems the end-users face. The highest priority task, in this case, is to fix the problem as fast as you can. If you won't, you may find one day that your users prefer to use another website rather than put up with the inconvenience.

3.2. Technologies/Scripting languages/elements used for building a website:

3.2.1 HTML-5:

HTML (HyperText Markup Language) is the most basic building block of the Web. It defines the meaning and structure of web content. "HyperText" refers to links that connect web pages to one another, either within a single website or between websites. Links are a fundamental aspect of the Web. By uploading

content to the Internet and linking it to pages created by other people, you become an active participant in the World Wide Web.

HTML uses "markup" to annotate text, images, and other content for display in a Web browser. HTML markup includes special "elements" such as <head>, <title>, <body>, <header>, <footer>, <article>, <section>, <p>, , , <img>, <aside>, <audio>, <canvas>, <datalist>, <details>, <embed>, <nav>, <output>, <progress>, <video> and many others.

Tags in HTML are case insensitive. That is, they can be written in uppercase, lowercase, or a mixture. Example <title> tag can be written as <Title>,<TITLE> or in any other way.

- Introduction to HTML

  It sets the stage, getting you used to important concepts and syntax such as looking at applying HTML to text, how to create hyperlinks, and how to use HTML to structure a web page.

- Multimedia and embedding

  This explores how to use HTML to include multimedia in your web pages, including the different ways that images can be included, and how to embed video, audio, and even entire other webpages.

- HTML tables

  Representing tabular data on a webpage in an understandable, accessible way can be a challenge. This module covers basic table markup, along with more complex features such as implementing captions and summaries.

- HTML forms

Forms are a very important part of the Web — these provide much of the functionality you need for interacting with websites, e.g. registering and logging in, sending feedback, buying products, and more. This module gets you started with creating the client-side/front-end parts of forms.

- Use HTML to solve common problems

Provides links to sections of content explaining how to use HTML to solve very common problems when creating a web page: dealing with titles, adding images or videos, emphasizing content, creating a basic form, etc.

Using this basic HTML I designed a webpage "my personal site/CV". And here is the link of the same:

https://garima-kanwar.github.io/CV/



Fig 3.2.1.1 Only HTML and its elements are used for designing this.

3.2.2 CSS:

CSS (Cascading Style Sheets) is a declarative language that controls how webpages look in the browser. The browser applies CSS style declarations to selected

elements to display them properly. A style declaration contains the properties and their values, which determine how a webpage looks.

CSS is one of the three core Web technologies, along with HTML and JavaScript. CSS usually styles HTML elements, but can be also used with other markup languages like SVG or XML.

Syntax:

```
selectorlist {
  property: value;
  [more property:value; pairs]
}
```

... where selectorlist is: selector[:pseudo-class] [::pseudo-element] [, more selectorlists]

- **CSS first steps:**

  CSS (Cascading Style Sheets) is used to style and layout web pages — for example, to alter the font, color, size, and spacing of your content, split it into multiple columns, or add animations and other decorative features. This module provides a gentle beginning to your path towards CSS mastery with the basics of how it works, what the syntax looks like, and how you can start using it to add styling to HTML.

- **CSS building blocks**

  This module carries on where CSS first steps left off — now you've gained familiarity with the language and its syntax, and got some basic experience with using it, it’s time to dive a bit deeper. This module looks at the cascade

and inheritance, all the selector types we have available, units, sizing, styling backgrounds and borders, debugging, and lots more.

- **Styling text**

  With the basics of the CSS language covered, the next CSS topic for you to concentrate on is styling text — one of the most common things you'll do with CSS. Here we look at text styling fundamentals, including setting font, boldness, italics, line and letter spacing, drop shadows, and other text features. We round off the module by looking at applying custom fonts to your page, and styling lists and links.

- **CSS layout**

  At this point we've already looked at CSS fundamentals, how to style text, and how to style and manipulate the boxes that your content sits inside. It focuses on how to place your boxes in the right place concerning the viewport, and one another. We have covered the necessary prerequisites so we can now dive deep into CSS layout, looking at different display settings, modern layout tools like flexbox, CSS grid, and positioning, and some of the legacy techniques you might still want to know about.

  Using Html and CSS I designed another website, by mimicking http://seanhalpin.io/ website.

  Link: https://garima-kanwar.github.io/My_website/.



Fig 3.2.2.1 (a)

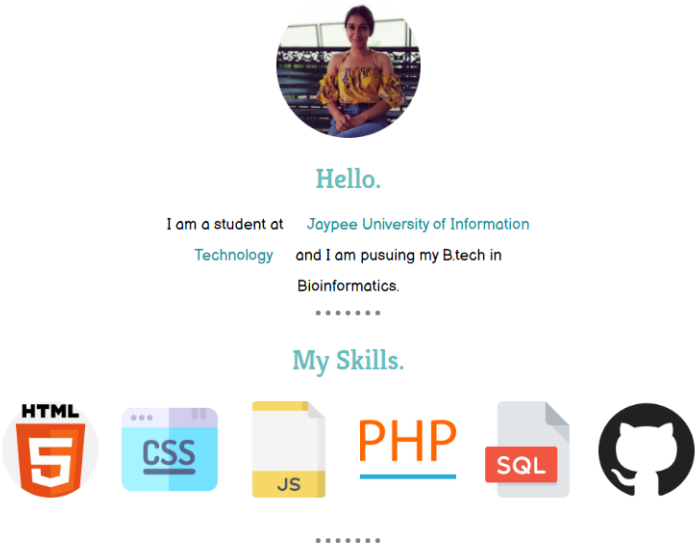
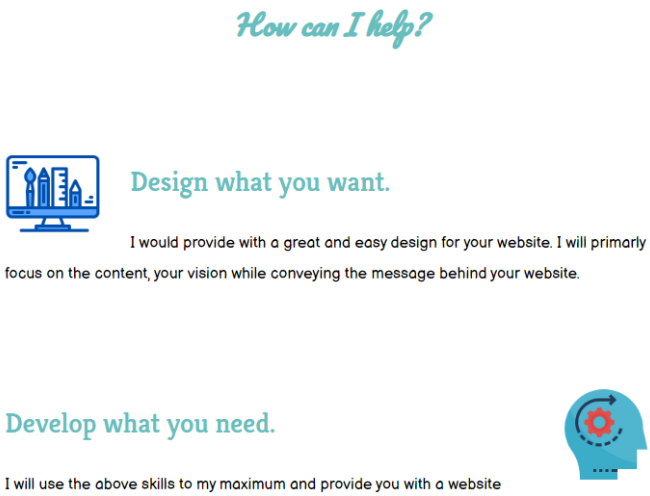


Fig 3.2.2.1 (b)



.Fig 3.2.21 (c)

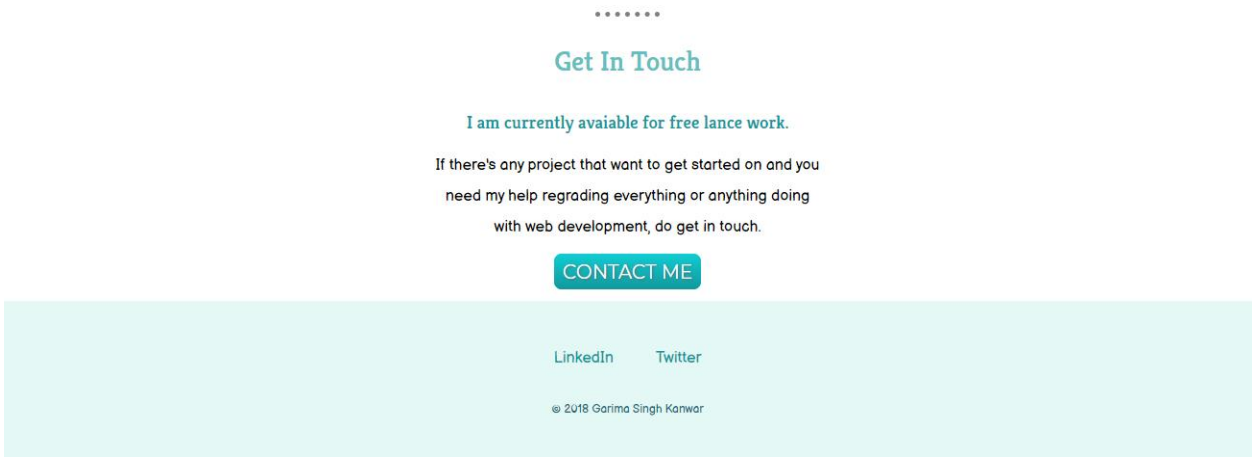


Fig 3.2.2.1 (d)

Fig 3.2.2.1 (a), (b), (c), (d) are the parts of the website that was created by using only HTML and CSS

3.2.3 BOOTSTRAP:

Bootstrap is a free, open source HTML, CSS, and JavaScript framework for quickly building responsive websites.

Initially, Bootstrap was called Twitter Blueprint and was developed by a team working at Twitter. It supports responsive design and features predefined design templates that you can use out of the box, or customize for your needs with your code. You don't need to worry about compatibility with other browsers either, as Bootstrap is compatible with all modern browsers and newer versions of Internet Explore.

- **Preprocessors**

Bootstrap ships with vanilla CSS, but its source code utilizes the two most popular CSS preprocessors, Less and Sass. It will help you to quickly get started with precompiled CSS or build on the source.

- **One framework, every device**

Bootstrap easily and efficiently scales your websites and applications with a single code base, from phones to tablets to desktops with CSS media queries.

- **Full of features**

With Bootstrap, you get extensive and beautiful documentation for common HTML elements, dozens of custom HTML and CSS components, and awesome jQuery plugins.

Using Bootstrap, html and CSS I designed another website

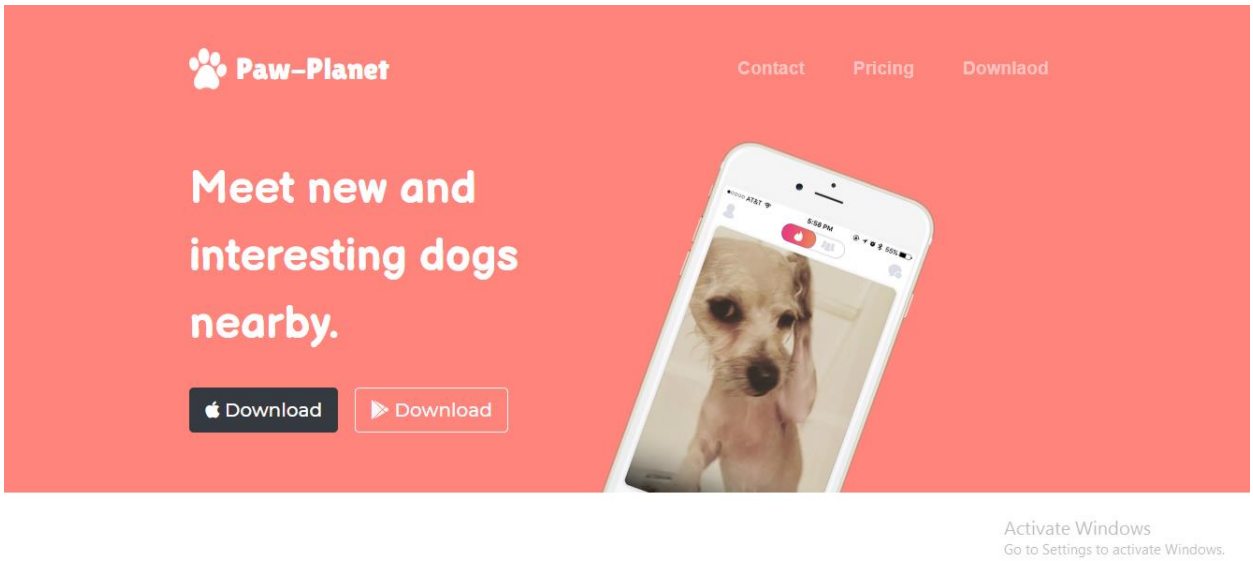


Fig 3.3.3.1 (a)

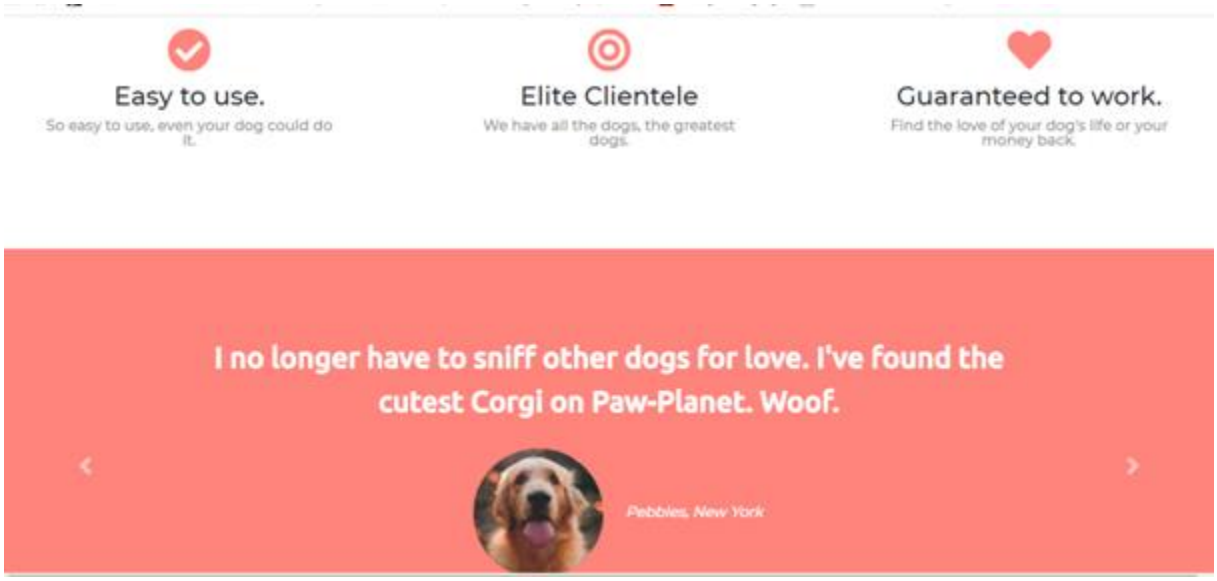


Fig 3.3.3.1 (b)

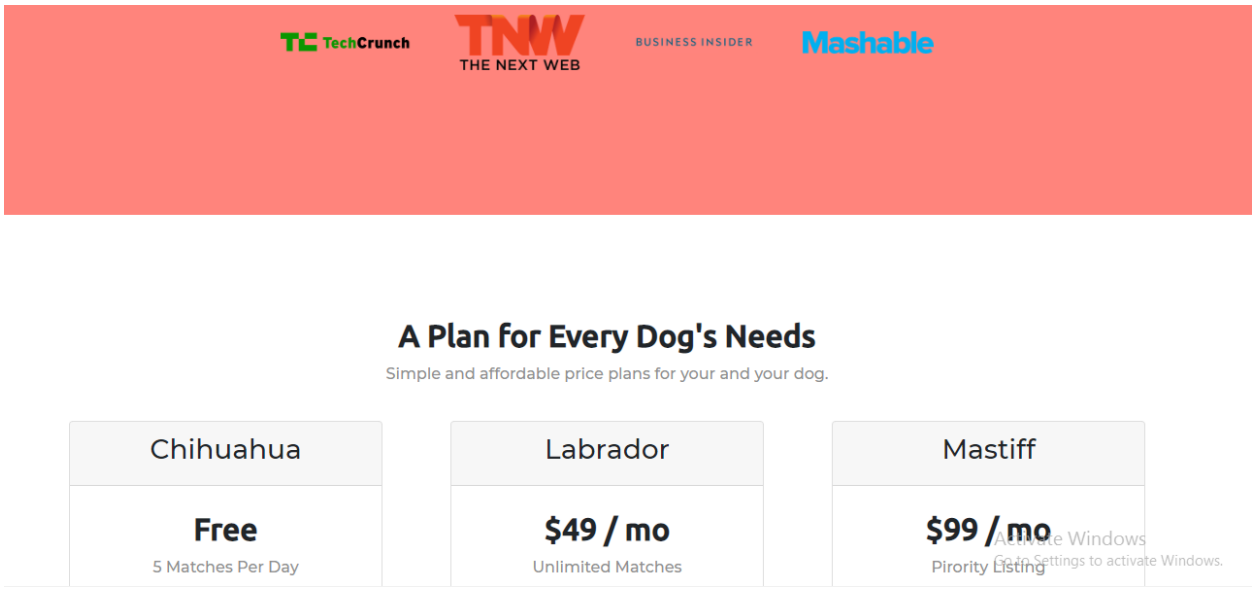


Fig 3.3.3.1 (c)

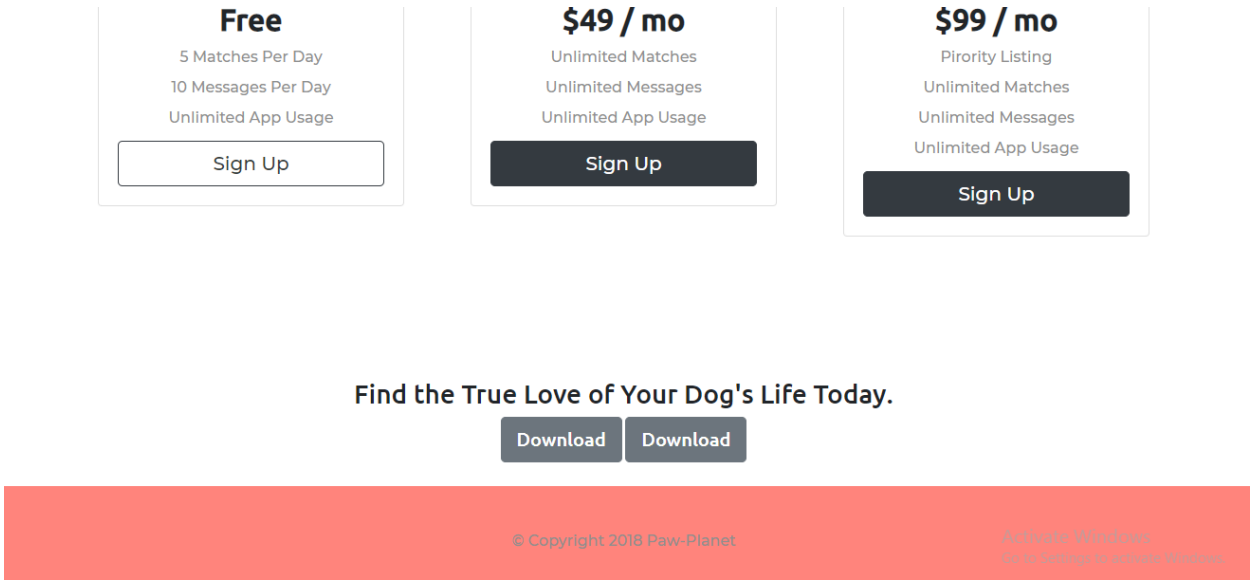


Fig 3.3.3.1 (d)

Fig 3.3.3.1 (a), (b), (c), (d) displays the images of the website desgined using bootstrap.

3.3.4 JavaScript:

JavaScript (or "JS") is a programming language used most often for dynamic client-side scripts on webpages, but it is also often used on the server-side, using a runtime such as Node.js.

JavaScript **should not** be confused with the Java programming language. Although *"Java"* and *"JavaScript"* are trademarks (or registered trademarks) of Oracle in the U.S. and other countries, the two programming languages are significantly different in their syntax, semantics, and use cases.

JavaScript is mostly used in the browser, enabling developers to manipulate webpage content through the DOM, manipulate data with AJAX and IndexedDB, draw graphics with canvas, interact with the device running the browser through various APIs, and more. JavaScript is one of the world's most commonly-used languages, owing to the recent growth and performance improvement of APIs available in browsers.

Chapter 4 Material and Methods

The editor that I used was Atom.

4.1 Atom:

Atom is a free and open-source text and source code editor for macOS, Linux, and Microsoft Windows with support for plug-ins written in Node.js, and embedded Git Control, developed by GitHub. Atom is a desktop application built using web technologies. Most of the extending packages have free software licenses and are community-built and maintained. Atom is based on Electron (formerly known as Atom Shell), a framework that enables cross-platform desktop applications using Chromium and Node.js. It is written in CoffeeScript and Less.

Atom was released from beta, as version 1.0, on 25 June 2015. Its developers call it a "hackable text editor for the 21st Century". It is fully customizable in HTML, CSS, and JavaScript.

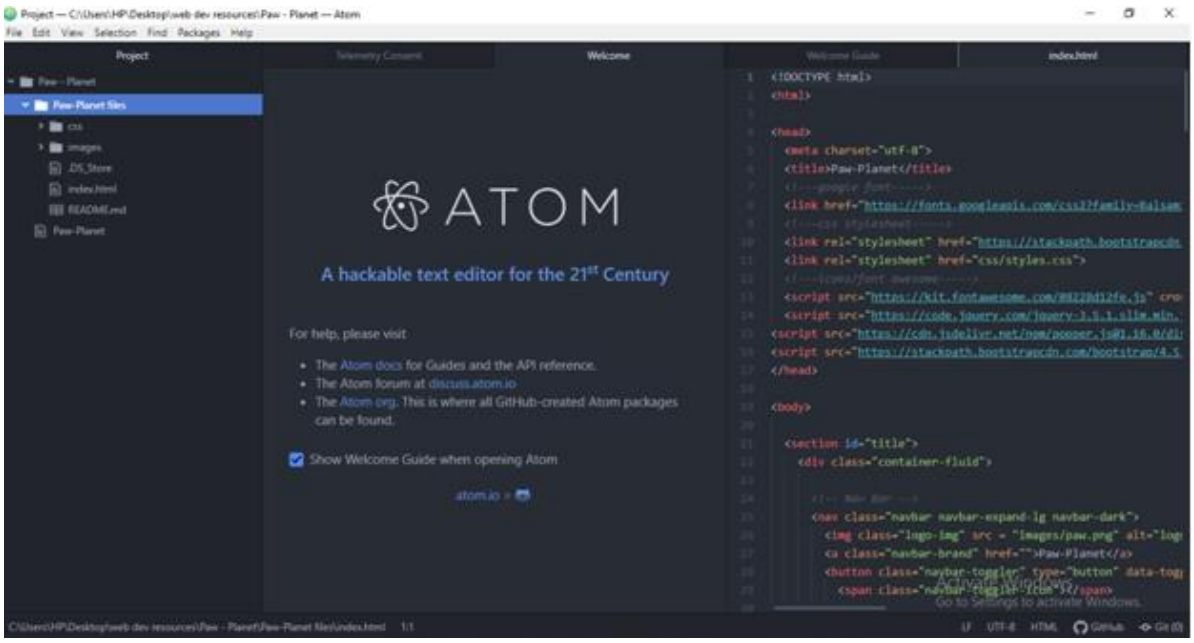


Fig 4.1.1 Atom Editor

Other technologies that were used or referred to :

4.2. Favicon.io generator:

A **favicon** (pronounced "fave-icon") is a small, iconic image that represents your website. **Favicons** are most often found in the address bar of your web browser, but they can also be **used** in lists of bookmarks in web browsers and feed aggregators.

Link: https://favicon.io/

4.3 Balsamiq: Wireframing Tool :

It helps one to quickly mock up and wireframe layouts, create UI elements, and define user flowcharts, navigational structure, and information architecture — all in one design tool. When you're ready, share links to your clickable and interactive wireframes to get everyone on the same page early in the design process.

Link : https://balsamiq.com/

4.4 Flat icon:

It helps to discover free flat vector icons used for a lot of purposes and to provide an additional touch to the website and enhance the text understanding.

Link : https://www.flaticon.com/

4.5 Google fonts:

Google Fonts is a library of 992 free licensed font families, an interactive web directory for browsing the library, and APIs for conveniently using the fonts via CSS and Android.

Link : https://fonts.google.com/

4.6

4.6 CSS Button Generator:

It helps to generate a button with any desired specification and parameters and generated code can be directly used in the css file using the similar class.

Link : https://www.bestcssbuttongenerator.com/

4.7 Toggle Pesticide:

This extension inserts the **Pesticide** CSS into the current page, outlining each element to better see placement on the page.

Link : http://pesticide.io/

Chapter 5 Scope of Website Development

Web designing or web development is a short term professional job oriented course. There are huge opportunities available for the students who want to work in this field. Many private and public organizations hires web designer for their online work and website development. With the rapid advent of online industry, the demand of web development professionals is increasing and this has created a huge job opportunities for the aspirants in the upcoming days.

Also an experienced person in this field can also work as a freelancer; there are many online companies which provide online projects to the individuals.

The major career fields in this field include:

Front end Developer: The front end developer generally works at client side dealing with the web page design, graphics that is accessible to the user.

Back end Developer: The back end developer is a person who is responsible for the back end development that interacts with the server. This type of web developer specializes in the languages like Php, ruby, ASP.Net, Java, Cold Fusion, and Perl.

You can also work in education industry.

The job profiles for the web developer includes:

- Front end web developer
- Back end web developer
- Web application developer
- Design and layout analyst
- Senior web analyst
- Web marketing analyst

Chapter 6 References

- Mdn Documentation

  https://developer.mozilla.org/en-US/

- Dev API Documentation

  https://devdocs.io/

- W3schools

  https://www.w3schools.com/

- Bootsrap Documentation

  https://getbootstrap.com/

- Javascript documentation

  https://devdocs.io/javascript/

- Jquery

  https://jquery.com/

- https://javascript.info/

PROGRAMMING WITH PYTHON

FINAL REPORT

(15 MAY 2020 TO 26 JUNE 2020)

Submitted by

Prerna tiwari(171511)

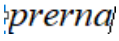
B-Tech in bioinformatics(6 sem)

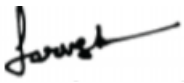
Supervisor name –Sarvesh Agrawal



BACHELOR OF TECHNOLOGY IN BIOINFORMATICS DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS, JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT, SOLAN 173234, HIMACHAL PRADESH, INDIA

Student signature **supervisor signature**





ACKNOWLEDGEMENT

I take the opportunity to express profound sense of gratitude to my training supervisor Sarvesh Agrawal , without whom this training would not have been possible . He has been the pillar of strength , a source of great inspiration throughout my training period.

I was lucky enough to have him who stood beside me and motivated me during the entire training period and made me understand each and every concept clearly in depth and also resolved my doubts .

I give my greatest acknowledgement to my Parents for all round support during studies. The endless sacrifices from my parents have made me what I am today.

CONTENTS

S.NO	TITLE
1	Introduction to python
2	Using variables in python
3	Basic programming in python
4	Principles of oops
5	Connecting to SQLite databases
6	Developing a GUI with PYQT
7	Application of python in various disciplines

Declaration

I hereby declare the work presented in this training report titled “programming with python “in partial fulfilment in requirement for the degree of bachelor of technology in Bio Informatics submitted in the department of Bio informatics

Jaypee university of information and technology waknaghat is an authentic record of my own work carried out over a period from 15 may 2020 to 26 june 2020 under the company internshala.

The matter embodied in the report has not been submitted for the award of any other degree or diploma .

Name of the student-Prerna Tiwari

Roll no.-171511

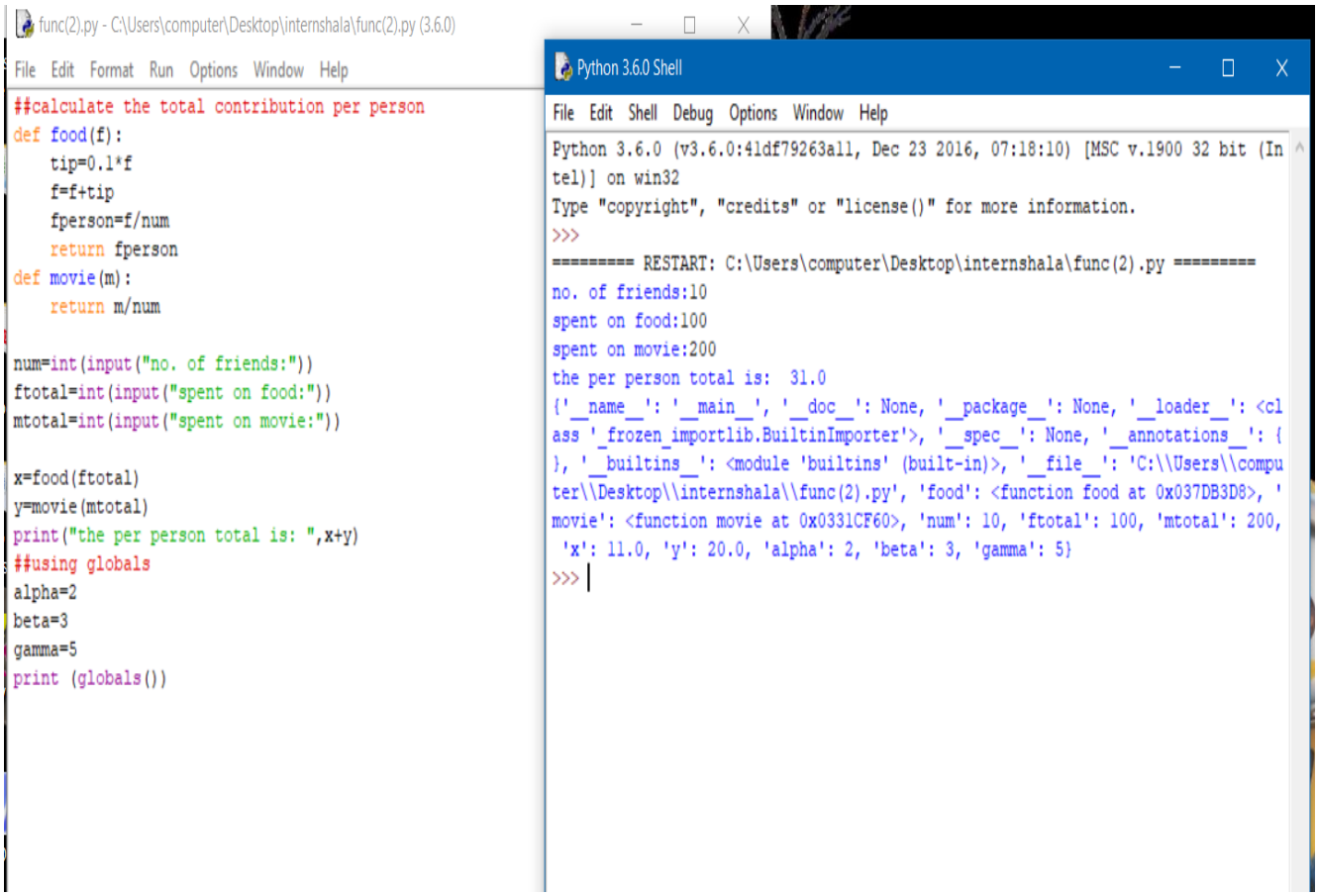
INTRODUCTION

The purpose of six weeks training is to master the language python along with all its concepts in detail and learn how to combine all this knowledge gained in the entire training session and buld a fully functional databse using python language .

Python is a language used in various disciplines such as data science ,machine learning , artificial intelligence etc. Python can be used on asever to create web applications and also can be used for rapid prototyping or the production ready software development

Python works on different platforms and has a simple syntax and allows programmers to write codes in fewer lines unlike other languages python program runs on an interpreter meaning code can be executed as soon as its written.it can be treated in object oriented or functional way.

Python was designed for readability and uses lines to complete a command unlike other languages which uses semicolons or parentheses and relies on indentation,whitespace such as scopes of loops function and classes other languages use curly brackets for this purpose .



Python is a interpreted programming language that means as a developer we write (.py) files in text editor and put those files into the interpreter to be executed .String in python are array of bytes representing Unicode characters .Square brackets can be used to access element of the string .

Python is a high-level interpreted ,interactive language .python is a beginners language.....python is a beginners language-python is a great language for the beginner-level programmers and supports the development of a wide range of applications from simple text processing to WWW browser to games.

Python uses code modules that are interchangeable instead of a long list of instructions that was standard for functional programming languages the standard implementation of python is called “cpython”

INDUSTRY DESCRIPTION

Internshala is an internship and online training platform based in Gurugram India found by Sarvesh Agrawal an IIT Madras alumunus ,in 2010 .The website helps students find internships within organizations in India.

The platform which was founded in 2010 started out as a WordPress blog that aggregated internships across India and articles on education ,technology and skill gap. Internshala launched its online trainings in 2014 . As of 2018 the platform had 3.5 million registered student and 80,000 companies .

The python training was prepared and conducted by Malhar Lathkar who is a senior educator with 25 years of work experience as a programming technology trainer also a published technical author and E-learning content writer .

WORK DESCRIPTION

Python programming is a 6-week online training program that gives a comprehensive description about the language and how it becomes an essential part in data science ,development of databases ,machine learning ,artificial intelligence etc.

In this training i thoroughly learnt about the concepts of creating functions ,understanding data types ,using and constructing modules packages and built in functions .

A detailed overview about the concepts of oops and how to create class and objects in python was given in the training process understanding and implementing inheritance and using magic methods was taught in the training .

The training also made me learn about SQL and how to create a database using SQL link and access SQL database using python .After which i was able to design and develop a gui using PYQT designer also learnt about the concepts of layout managers and event driven programs within it in detail .

At the end of the 5 week i was able to design a fully functional menu system using python as programming language .along with all the concepts learnt earlier in the previous topics .

```
def menufunction(self, action):
        txt= (action.text())
        no=int(self.t1.text())
        print (txt, no)
        if txt =='Square':
            self.t2.setText(str(no*no))
        if txt =='Cube':
            self.t2.setText(str(no*no*no))
        if txt =='SqrRoot':
            self.t2.setText(str(math.sqrt(no)))
        if txt=='CubeRoot':
            self.t2.setText(str(math.pow(no,1/3)))
```

Event handler for File Menu - Statement in the setupUI method

self.menuFile.triggered[QtWidgets.QAction].connect(self.menufunction)

At the end of the sixth week applications of python was explained carried along with a module test on the basis of which certificate was awarded.

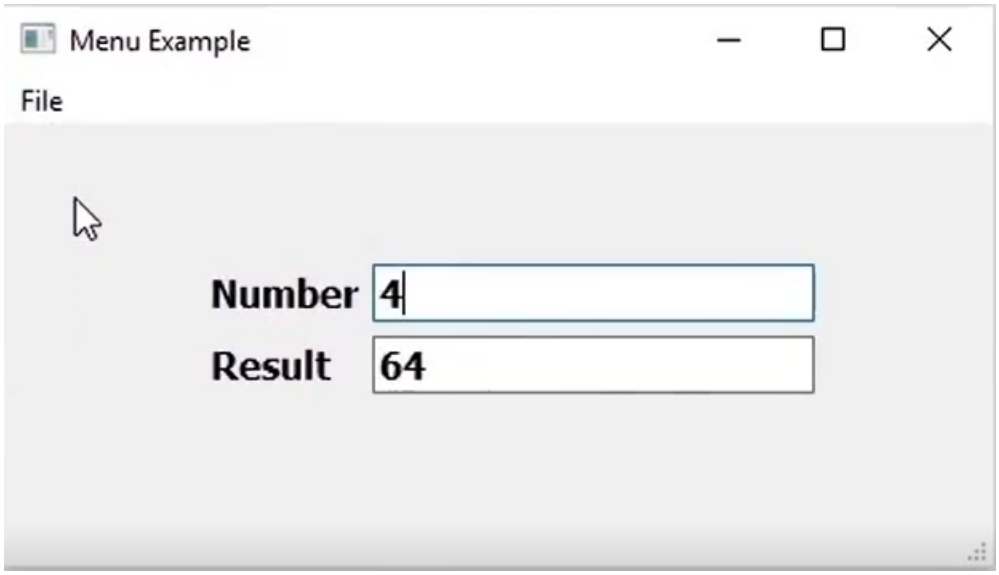
PROJECT DESCRIPTION

Building a menu system with the following functionalities :-

->creating menus in QT designer.

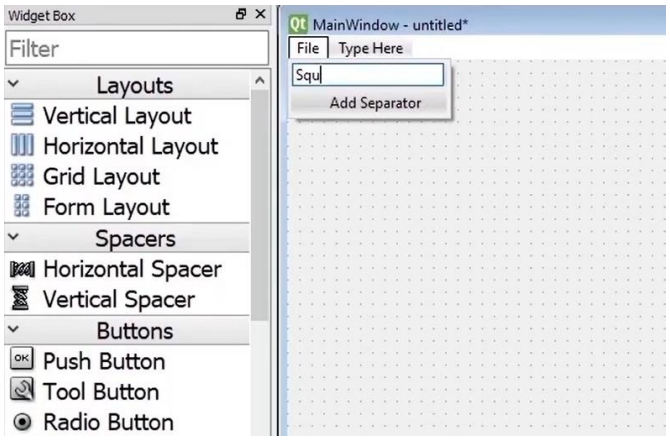
->using qmenu object in qt designer to create menus .

->using qaction to implement event handler .

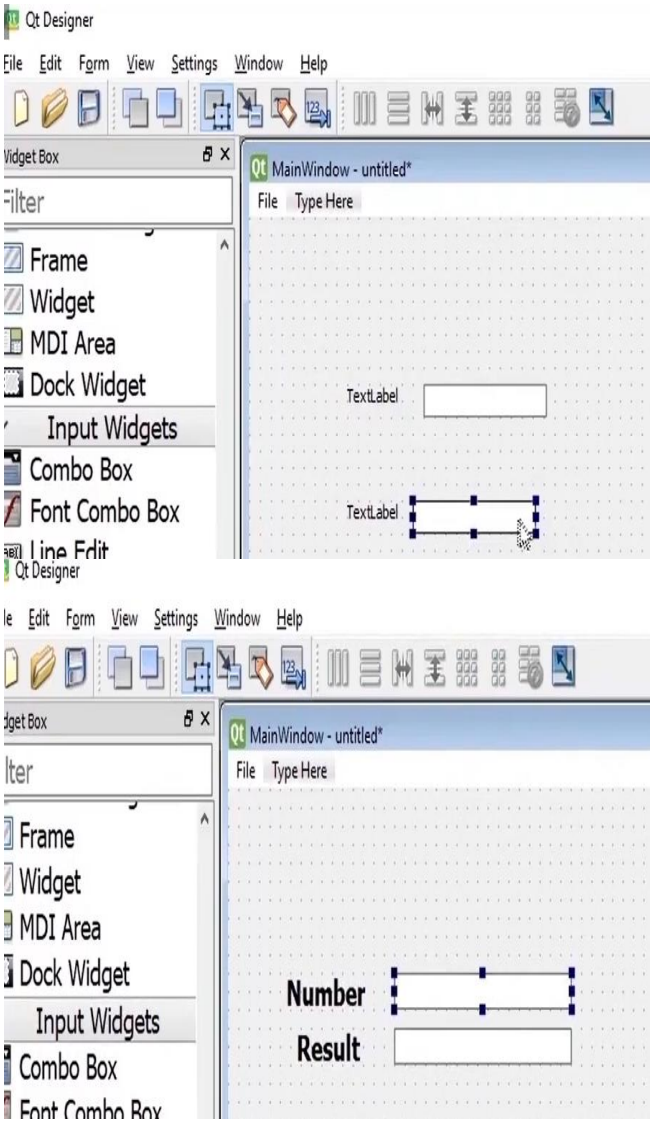


Steps-:

1.create form in the main window template.



2. Adding labels and widgets and changing the boxes to number and result.

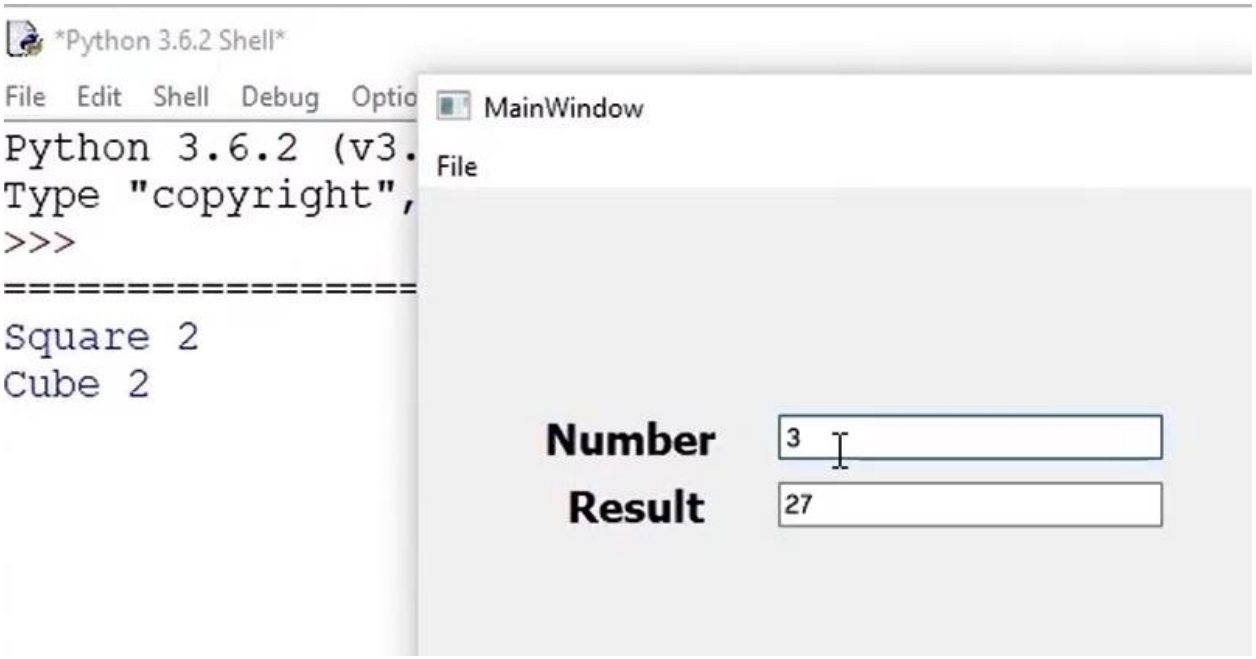


3.creating a pyuic5 file by saving this .

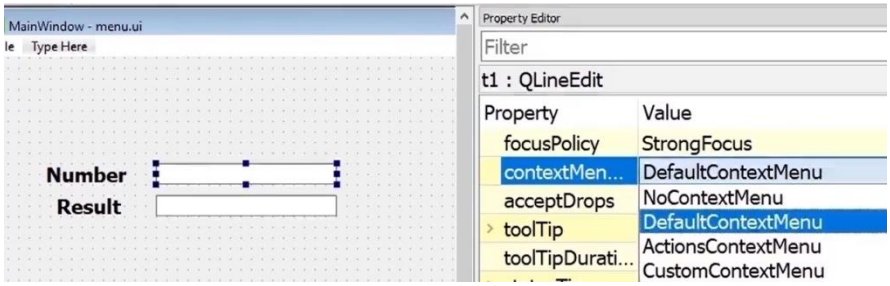
```
from PyQt5 import QtCore, QtGui, QtWidgets

class Ui_MainWindow(object):
    def setupUi(self, MainWindow):
        MainWindow.setObjectName("MainWindow")
        MainWindow.resize(800, 600)
        self.centralwidget = QtWidgets.QWidget(MainWindow)
        self.centralwidget.setObjectName("centralwidget")
        self.label = QtWidgets.QLabel(self.centralwidget)
        self.label.setGeometry(QtCore.QRect(56, 100, 91, 20))
        font = QtGui.QFont()
        font.setPointSize(14)
        font.setBold(True)
        font.setWeight(75)
        self.label.setFont(font)
        self.label.setObjectName("label")
```

4.adding menu function in the setup ui method and import math and here is our fully function menu system .



5.Adding context menu at the end of the menu system in the setupui file.



CONCLUSION

In the conclusion i was successful in learning the concepts of python ,oops and designing a database combined together to build a fully functional menu system with the help of QTdesigner and PYQT5.

I am looking forward to use this knowledge and develop more databases.

REFERENCES

Training received from

https://internshala.com/

->all content of report from:

https://www.wikipedia.org/

https://www.simplilearn.com/

SUMMER TRAINING ON SYSTEMS BIOLOGY



TOPIC: Exploring HMDB and drugbank

with reference to metabolomics

Enrollment No.-171512

Name of the student- Riya Dhiman

Name of the guide -Dr. Narendra Kumar

MAY-JUNE 2020

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS,

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY,

WAKNAGHAT, SOLAN 173234, HIMACHAL PARDESH, INDIA

CANDIDATE'S DECLARATION

I hereby declare that the work presented in this report entitled "**SYSTEMS BIOLOGY:Exlploring HMDB and DrugBank with reference to metabolomics**." in partial fulfilment of the requirements for the summer training submitted in the department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat is an authentic record of my own work carried out over a period from **16 May, 2020 to 30 June, 2020** under the supervision of **Dr.Narendra Kumar** (Assistant Professor).The matter embodied in the report has not been submitted for the award of any other training or internship.



Riya Dhiman, 171512

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr.Narendra Kumar
Assistant Professor
Department of Biotechnology and Bioinformatics
Dated: 02-07-2020

ABSTRACT

Systems biology is increasingly popular, but to many biologists it remains unclear what this new discipline actually encompasses. Systems biology, being a holistic approach involves modeling and analysis of metabolic pathways, regulatory and signal transduction networks for understanding cellular behavior.

Metabolomics, which is defined as the comprehensive analysis of metabolites in a biological specimen, is an emerging technology that holds promise to inform the practice of precision medicine. Historically, small numbers of metabolites have been used to diagnose complex metabolic diseases as well as monogenic disorders such as inborn errors of metabolism. Current metabolomic technologies go well beyond the scope of standard clinical chemistry techniques and are capable of precise analyses of hundreds to thousands of metabolites. Consequently, metabolomics affords detailed characterization of metabolic phenotypes and can enable precision medicine at a number of levels, including the characterization of metabolic derangements that underlie disease, discovery of new therapeutic targets, and discovery of biomarkers that may be used to either diagnose disease or monitor activity of therapeutics.

First described in 2007, the HMDB is now considered the standard metabolomic resource for human metabolic studies. Over the past decade the HMDB has continued to grow and evolve in response to emerging needs for metabolomics researchers and continuing changes in web standards. The number of experimental spectra has grown by almost fourfold and the number of illustrated metabolic pathways has grown by a factor of almost 60. Significant improvements have also been made to the HMDB's chemical taxonomy, chemical ontology, spectral viewing, and spectral/text searching tools. **HMDB primarily covers the endogenous Human metabolome**.

The performance of the HMDB website have been made and these should greatly enhance its ease of use and its potential applications in nutrition, biochemistry, clinical chemistry, clinical genetics, medicine, and metabolomics science.

DrugBank is a richly annotated resource that combines detailed drug data with comprehensive drug target and drug action information. Since its first release in 2006, DrugBank has been widely used to facilitate in silico drug target discovery, drug design, drug docking or screening, drug metabolism prediction, drug interaction prediction and general pharmaceutical education. DrugBank has also significantly improved the power and simplicity of its structure query and text query searches.**DrugBank covers the exogenous human metabolome.**

INTRODUCTION

Systems biology is an approach in biomedical research to understand the larger picture—be it at the level of the organism, tissue, or cell—by putting its pieces together. It is collaborative, integrating many scientific disciplines – biology, computer science, engineering, bioinformatics, physics and others – to predict how these systems change over time and under varying conditions, and to develop solutions to the world's most pressing health and environmental issues.

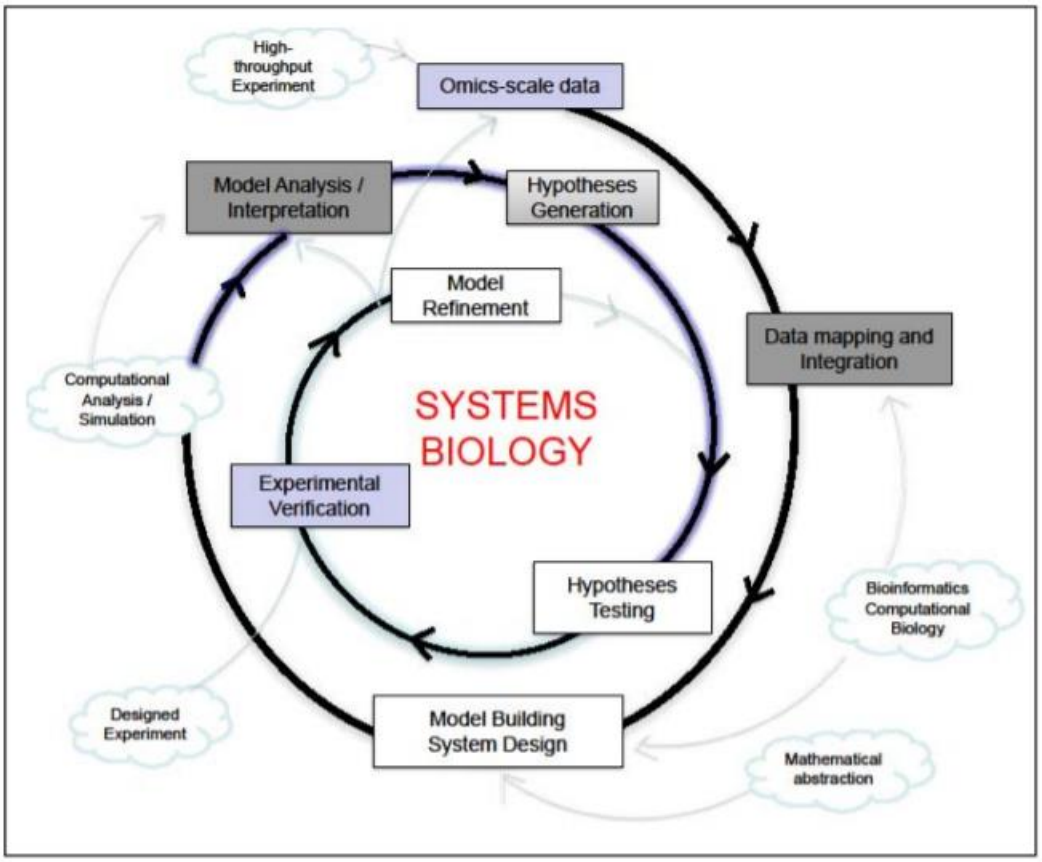


Figure 1. Worflow of system biology

Systems biology is based on the understanding that the whole is greater than the sum of the parts. The organization and integration of biological systems has long been of interest to scientists. Systems biology as a formal, organized field of study, however, emerged from the genomics revolution, which was catalyzed by the Human Genome Project (HGP; 1990–2003) and the availability to biologists of the DNA sequences of the genomes of humans and many other organisms. The establishment of the field was also influenced heavily by the general recognition that organisms, cells, and other biological entities have an inherently high degree of complexity.

Two dominant themes of modern biology are rooted in that new outlook: first, the view that biology is fundamentally an informational science—biological systems, cells, and organisms store and transfer information as their most-fundamental processes—and second, the emergence of new technologies and approaches for studying biological complexity.

Systems are defined and abstracted at different levels, which are simulated and analysed using different types of mathematical and computational techniques. Insights obtained from systems level studies readily lend to their use in several applications in biotechnology and drug discovery, making it even more important to study systems as a whole.

HMDB

The Human Metabolome Database (HMDB) is currently the most complete and comprehensive curated collection of human metabolite and human metabolism data in the world. It contains records for more than 2180 endogenous metabolites with information gathered from thousands of books, journal articles and electronic databases. In addition to its comprehensive literature-derived data, the HMDB also contains an extensive collection of experimental metabolite concentration data compiled from hundreds of mass spectra (MS) and Nuclear Magnetic resonance (NMR) metabolomic analyses performed on urine, blood and cerebrospinal fluid samples.

It is Created by the Human Metabolome Project funded by Genome Canada. One of the first dedicated metabolomics databases, the HMDB facilitates human metabolomics research, including the identification and characterization of human metabolites using NMR spectroscopy, GC-MS spectrometry and LC/MS spectrometry.

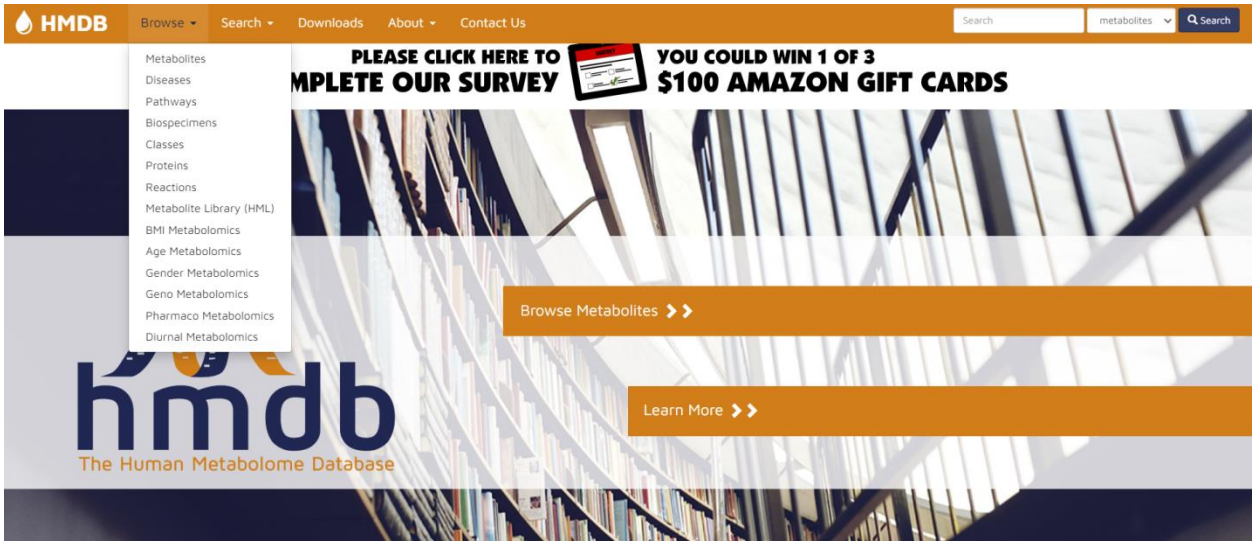


Figure 2. Webpage of HMDB

Each metabolite entry in the HMDB contains an average of 90 separate data fields including a comprehensive compound description, names and synonyms, structural information, physico-chemical data, reference NMR and MS spectra, biofluid concentrations, disease associations, pathway information, enzyme data, gene sequence data, SNP and mutation data as well as extensive links to images, references and other public databases.

A key feature that distinguishes the HMDB from other metabolic resources is its extensive support for higher level database searching and selecting functions. The HMDB's structure similarity search tool (ChemQuery) is the equivalent to BLAST for chemical structures.

HMDB contains 3 kinds of data:

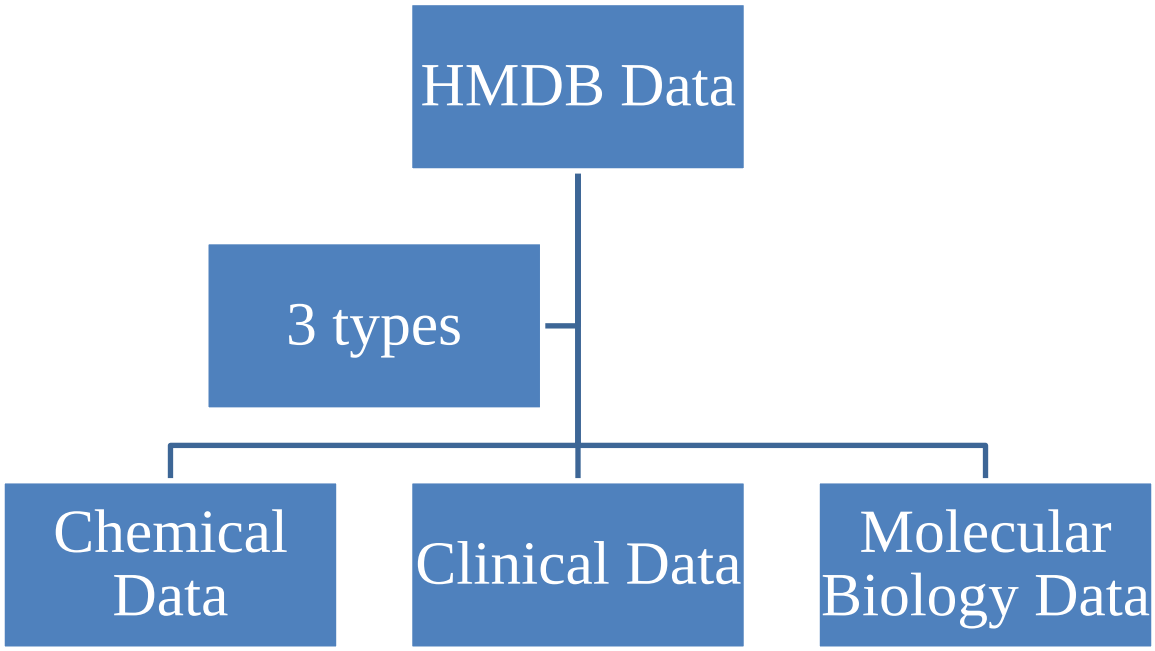


Figure 3. Representation of type of data in HMDB

Downloading data from HMDB supports different formats:

Protein/Gene sequences- FASTA FORMAT

Structures- SDF FORMAT

Metabolite and Protein data- XML FORMAT

And different links are available for Spectra search

METABOLOMICS

Metabolomics is a newly emerging field of ‘omics’ research concerned with the high-throughput identification, quantification and characterization of the small molecule metabolites in the metabolome . The metabolome can be defined as the complete complement of all small molecule (<1500 Da) metabolites found in a specific cell, organ or organism. It is a close counterpart to the genome, the transcriptome and the proteome. Together these four ‘omes’ constitute the building blocks of systems biology.

Metabolomics in conjunction with other system biology approaches has great potential to advance our understanding of human diseases and hence rapidly gaining importance as a powerful tool for biomarker discovery and likely to have a huge impact on understanding of disease onset and progression and can thus augment the development of clinical diagnostics

The foundation to all metabolomics research lies in the work done by hundreds of metabolic biochemists and clinical chemists over the past 70 years. The pathways, reactions and reactants that were identified by these scientists are now available in many excellent on-line metabolic pathway databases such as KEGG , BioCyc and Reactome . More recently, information about the genes and diseases that are associated with perturbations to these pathways has come on-line through such outstanding resources as OMMBID and OMIM .

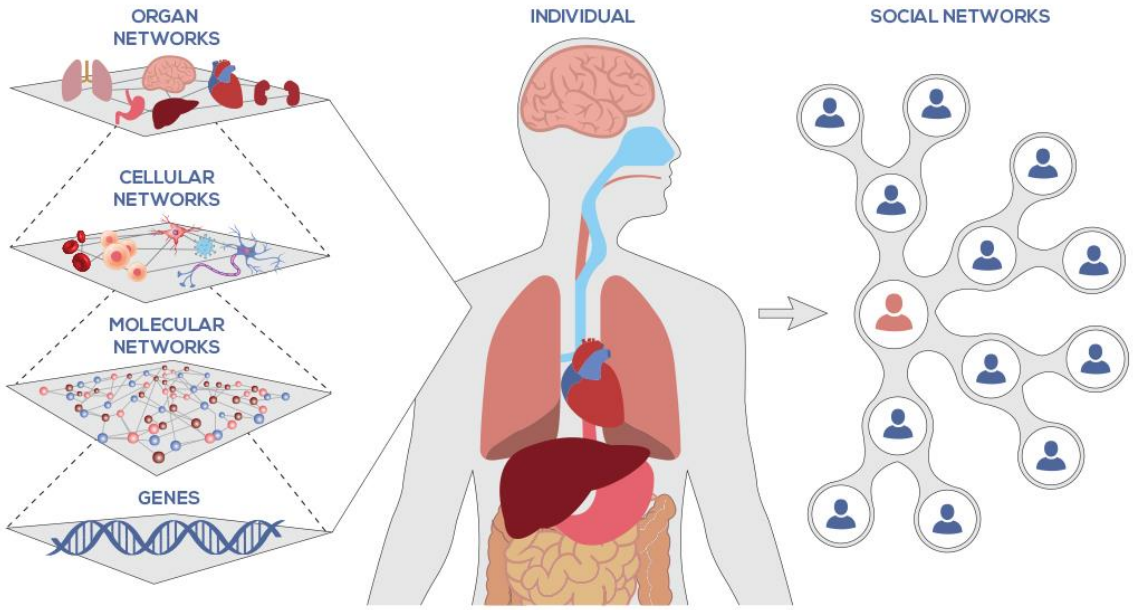


Figure 4

Metabolomics databases require information not only about compounds and reactions but also data about compound concentrations, biofluid or tissue locations, subcellular locations, physical properties, known disease associations, nomenclature, descriptions, enzyme data, mutation data and characteristic MS or NMR spectra. These data need to be readily available, experimentally validated, fully referenced, easily searched, readily interpreted and they need to cover as much of the human metabolome as possible. In other words, metabolomics researchers need a metabolic equivalent to GenBank or SwissProt. To address these needs, and to serve as a potential model for other metabolomic resources, databases like HMDB have been developed .

HMDB Metabolite Library

The Human Metabolome Library (HML) is a chemical resource with the power to help confirm, validate or quantify suspected metabolites in tissues or biospecimens. The Human Metabolome Library has been developed through the efforts of the Human Metabolome Project. Each of the HML's 1019 in-stock compounds were acquired through purchase, custom synthesis or purification. Researchers interested in HML may contact The Metabolomics Innovation Centre for further information.

IDENTIFICATION of DISEASES realated metabolites using HMDB source

Metabolites disrupted by abnormal state of human body are deemed as the effect of diseases. In comparison with the cause of diseases like genes, these markers are easier to be captured for the prevention and diagnosis of metabolic diseases. Currently, a large number of metabolic markers of diseases need to be explored. metabolite-disease associations were extracted from Human Metabolome Database (HMDB) using a text mining tool NCBO annotator as priori knowledge.

HUMAN SERUM METABOLOME:

So far found out to be the most abundant. lood is composed of two parts: a cellular component consisting of red and white blood cells and platelets, and a liquid carrier, called plasma. Plasma is the straw-colored liquid in which blood cells are suspended, which accounts for approximately 50–55% of blood volume, with blood cells (erythrocytes, leukocytes and platelets) accounting for the remaining portion . Plasma is obtained from a blood sample, if anti-coagulants are introduced, by simply centrifuging the sample and removing or decanting the most buoyant (non-cellular) portion. If no anticoagulant is added and the blood is allowed to clot, the supernatant fluid is called the serum, which is less viscous than plasma and lacks fibrinogen, prothrombin and other clotting proteins . Both plasma and serum are aqueous solutions (about 95% water) containing a variety of substances including proteins and peptides (such as albumins, globulins, lipoproteins, enzymes and hormones), nutrients (such as carbohydrates, lipids and amino acids), electrolytes, organic wastes and variety of other small organic molecules suspended or dissolved in them.

In terms of small molecules, the compositions of plasma and serum appear to be very similar.However, to improve readability of the manuscript, the term “serum” is used when referring to the liquid portion of blood.

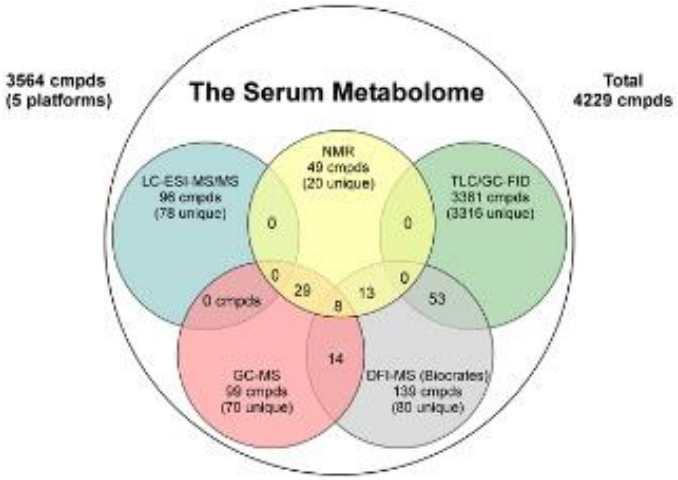


Figure 5

DRUGBANK

The latest version of DrugBank (release 2.0) has been expanded significantly over the previous release. With ~4900 drug entries, it now contains 60% more FDA-approved small molecule and biotech drugs including 10% more ‘experimental’ drugs. Significantly, more protein target data has also been added to the database, with the latest version of DrugBank containing three times as many non-redundant protein or drug target sequences as before (1565 versus 524). Each DrugCard entry now contains more than 100 data fields with half of the information being devoted to drug/chemical data and the other half devoted to pharmacological, pharmacogenomic and molecular biological data.

There are essentially two kinds of online drug resources:

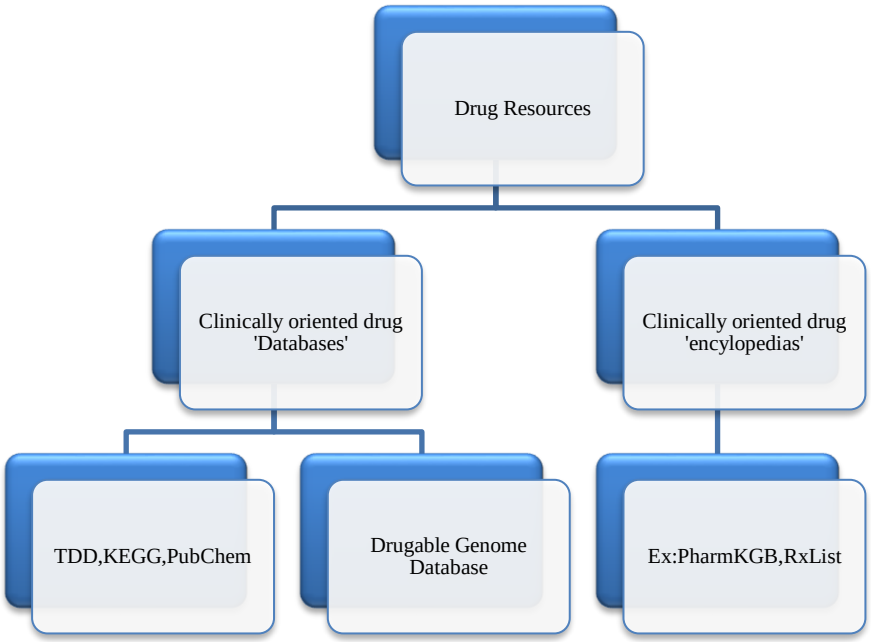


Figure 6

The HMDB database supports extensive text, sequence, chemical structure and relational query searches. Four additional databases, DrugBank, T3DB, SMPDB and FooDB are also part of the HMDB suite of databases. DrugBank contains equivalent information on ~2280 drug and drug metabolites as in HMDB.

DrugBank and Human Metabolome Database (HMDB) are resources of curated chemistry-to-protein relationships widely used in the chemogenomic arena.

DRUGBANK AND HMDB

DrugBank collates target and mechanism-of-action information. HMDB collates detailed chemical, clinical and biochemical data on human metabolites. These are linked to other databases including enzymes involved in the transformations.Like HMDB, Drugbank also supports a wide variety of text,chemical formula, mass,chemical structures and sequence searches.In addition, DrugBank provides number of general browsing tools for more specific tasks. (PharmaBrowse and GenoBrowse).

Also,DrugBank has a number of data fields that are not found in HMDB such as mechanism of action,absorption and pharmacokinetic data.On the other hand biofluid concenteration is included in HMDB and not in the DrugBank.The HMDB is a clearly a rich resource for drug and drug metabolite.Currently the HMDB’s collection of spectral data on drug metabolites is still quite sparse.As with drugbank,the HMDB still lacks pathway diagrams for most of its drug metabolites.

CONCLUSION

HMDB used for applications in metabolomics, clinical chemistry, biomarker discovery and general education. Over the past 10 years the HMDB has grown from a small, somewhat specialized chemical database to the largest, most comprehensive, organism-specific metabolomic 'knowledgebase' in the world. Throughout this evolution it has strived to maintain the highest quality and currency of data, to continuously improve the quality of its user interface, and to attentively listen to all members of the metabolomics community.

Just like GenBank during the 1990s, the HMDB is going through a rapid phase of growth with constant additions and corrections being made and the release of different database 'builds' every two months. Other kinds of 'metabo-omic' data such as pharmacometabolomic data and geno-metabolomic data have also been added to make the HMDB much more compatible with the increasing number of multi-omic or systems biology studies that are being undertaken.

Metabolomics is already a powerful tool in drug discovery and development and in metabolic engineering.While maintaining these strengths, the field promises to play a heightened role in systems biology research, which is transforming the practice of medicine and our ability to engineer living organisms.

Protein Interaction Network Analysis

Summer Internship Report

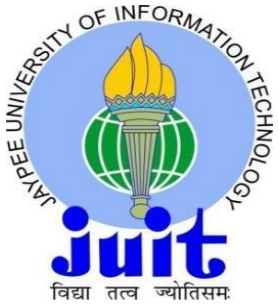
Under the supervision of

Dr. Narendra Kumar
(Assistant professor)

By

Kritika Sharma
(171513)

To



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

WAKNAGHAT, SOLAN – 173 234

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TABLE OF CONTENT

Sr. No.	Content	Page No.
1	Abstract	3
2	Introduction	4-5
3	Materials and Methods	6
4	Result	7-9
5	Discussion	10
6	Conclusion	11
7	References	12

Abstract

The study of the interactome –the totality of the protein-protein interactions taking place in a cell has experienced an enormous growth in the last few years. Biological networks representation and analysis has become an everyday tool for many biologists and bioinformatics, as these interaction graphs allow us to map and characterize signaling pathways and predict the function of unknown proteins. However, given the size and complexity of interacting datasets, extracting meaningful information from interaction networks can be a daunting task. Many different tools and approaches can be used to build, represent and analyses biological networks. Cytoscape provides core functionality to load, visualize, search, filter and save networks, and hundreds of Apps extend this functionality to address specific research needs. Esophageal adenocarcinoma (EAC) is one of the most lethal tumors in the world with a helpless anticipation. Recognizable proof of sub-atomic demonstrative methods is a significant objective. Since protein-protein interaction (PPI) network analysis is an appropriate technique for molecular assessment, in the present research a PPI network related to EAC was targeted. Among 182 EAC-related proteins which were distinguished, 129 were included for a principle associated part. Proteins based on centrality analysis of characteristics, for example, degree, betweenness, closeness and stress were screened and key nodes were presented. Two bunches were resolved of which just one was huge measurably. Quality cosmology uncovered 50 terms in three gatherings related with EAC. The discoveries demonstrate nine crucial proteins could frame a competitor biomarker panel for EAC. Moreover, a significant group with 27 proteins identified with the sickness was recognized. Gene ontology analysis of this cluster demonstrated fundamental related terms to closely correspond with those for colorectal cancer.

Introduction

Cytoscape is an open source, publicly available network visualization and analysis tool(www.cytoscape.org). Cytoscape is one of the most popular open-source software tools for the visual exploration of biomedical networks composed of protein, gene and other types of interactions. It offers researchers a versatile and interactive visualization interface for exploring complex biological interconnections supported by diverse annotation and experimental data, thereby facilitating research tasks such as predicting gene function and pathway construction. Cytoscape provides core functionality to load, visualize, search, filter and save networks, and hundreds of Apps extend this functionality to address specific research needs.

Cytoscape is widely used in biological network analysis and it supports many use cases in molecular and systems biology, genomics and proteomics:

- It can import and load molecular and genetic interaction datasets in several formats.
- It can make effective use of several visual features that can effectively highlight key aspects of the elements of the network. This can be saved in the form of visual styles, exported and imported for re-use.
- It can project and integrate global datasets and functional annotations.
- It has a wide variety of advanced analysis and modeling tools in the form of plug-in that can be easily installed and applied to different approaches.
- It allows visualization and analysis of human-curated pathway datasets such as Reactome or KEGG[1].

Esophageal adenocarcinoma is one of the most widely recognized malignancies on the planet with a helpless anticipation. EAC positioned as the 6th driving reason for malignancy passing in the world . In 2012, it is assessed that 455,800 esophageal malignancy cases and 400,200 passing's are happened in the word. In view of chosen vaults, the most noteworthy esophageal malignant growth occurrence rates are in Malawi, South Africa, and Iran .

The occurrence of esophageal adenocarcinoma has been expanded significantly in the course of recent years and it maybe speaks to a genuine ascent in ailment trouble . It has been accounted for the quick increment in the rate of EAC among white men. EAC is the 6th most regular disease among guys and ninth most basic malignant growth among females comprehensively. Henan area of northern china has the most elevated occurrence and mortality of EAC in the world. The majority of EAC patients present with advanced metastatic disease upon diagnosis [2].

It is important to understand the molecular mechanism in the tumor invasion process to assist finding new biomarkers for early diagnosis and prognostic evaluation . There has been a lack of systematic analysis of the molecular markers that characterize protein of EAC. Attempts to clarify the mechanism underlying esophageal cancer by searching for novel proteins and proteins interactions are attractive recently. Understanding a network containing proteins, and generalized an existing computational methods were used to identify related disease proteins simultaneously [3].

PPI network analysis as an attracting method is used for molecular assessment of many diseases .In this method, many proteins implicated to a certain disease are retrieved and attributed in an interactive structure (PPI network) .

Crucial nodes of the network are the important proteins related to the studied disease. These key proteins interact with the large numbers of the nodes of network and considerable types of their connections are as shortest length paths so they are called hub-bottleneck proteins [4].Quality cosmology investigation can be utilized to decide fundamental natural procedures, subatomic capacity, cell part and biochemical pathways comparative with the proteins. These discoveries can be utilized in understanding of assumed jobs of the proteins in beginning and improvement of any maladies .

In this study, we intended to explain protein-protein cooperation's of EAC by arranging investigation. It can prompt a board of useful biomarkers explicit to esophageal adenocarcinoma.

Materials and Methods

Since the significant proteins related to a certain disease are selected and collected in the string data base and this data bank is up dated periodically, a number of 200 possible proteins correlated to esophageal adenocarcinoma were retrieved from disease query of STRING DB [5].

This database is one of the Cytoscape programming applications that gives cooperation data from three unique boards including ailment question, protein inquiry, and PubMed question. The strength of protein corporations can be fitted for system development. The proteins were broken down through the undirected edges strategies by Cytoscape programming.

The fundamental associated segment of PPI organized was format by degree esteems. Force law is a line that connects the quantity of the hubs as a component of degree esteems. The reasonable fitted force law is related to scale free system .The developed system was without scale organization. The top 10% of the hubs dependent on degree esteem were chosen as center point hubs.

Degree, betweenness, closeness, stress circulations were accommodated all the more screening of the acquainted center point hubs due to recognize powerful center point qualities. Anyway gathering of the center hubs is led to determine super center point hubs and the other intense center point qualities (the top strong center hubs are presented as supercenter qualities.

Furthermore, the obtained cluster as a sub-network was analyzed and the contributing nodes were classified regarding degree values. The top center point proteins of the group and the principle associated segment were thought about and the major candidate biomarker board was presented. The associations of the proteins of board were illustrated.

Result

Various 200 potential related proteins for esophageal adenocarcinoma were looked at by means of the STRING database however just 182 proteins were found in the database and remembered for study.

The protein-protein association system of infection was developed with 182 proteins. The quantity of 50 hubs were secluded and one segment of three associated hubs were shaped. The principle associated segment including 129 hubs and 562 edges was built (see Figure 1).

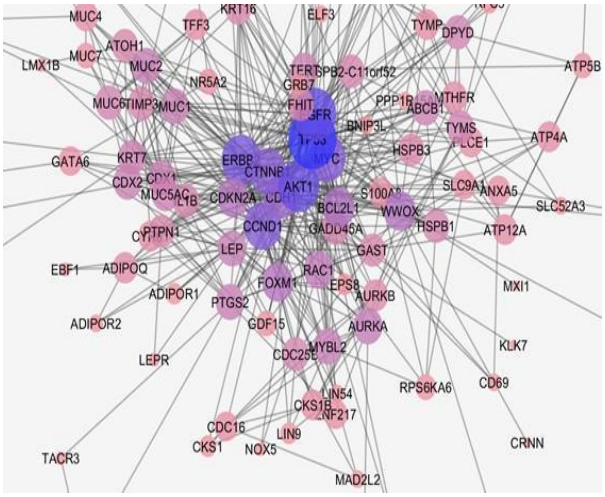
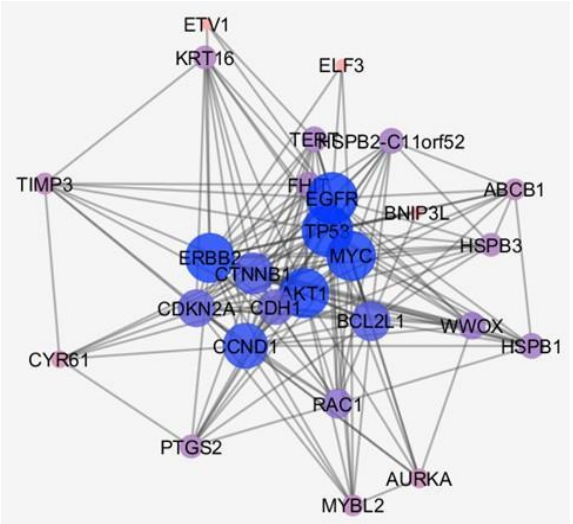


Figure 1. Main Connected Component of protein-protein interaction network of esophageal adenocarcinoma. The component includes 129 nodes and 562 edges. The network is layout by degree value of the nodes. The bigger size of the node corresponds to a higher value of degree. The color change from orange to blue indicates increment of degree value.

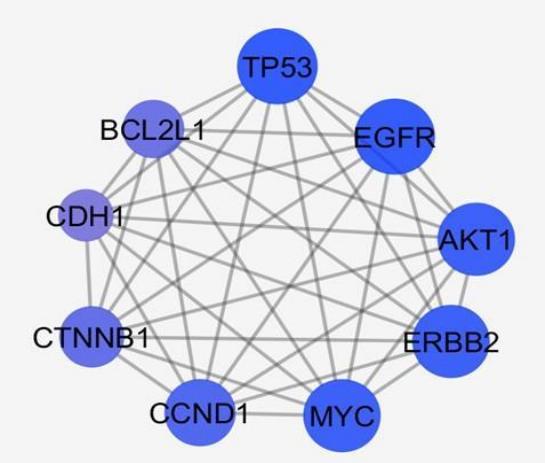
As it appeared in Figure 1 every hub is recognizable from different hubs dependent on degree esteem. The system was examined and the hubs were arranged by degree esteem. The top 10% of the hubs (counting 13 proteins) were chosen as center point hubs. The trademark properties of the center hubs dependent on examination of the system are classified in (Table 1). These properties include degree, betweenness, closeness, stress, disease score and average shortest path length (ASPL).

Table 1. The Top 10% of the Nodes (Including 13 Proteins) Based on Degree Value were Selected as Hub Nodes. The top eight genes are introduced as related biomarkers to EAC. D, BC, CC, S, DS and ASPL correspond to degree, betweenness centrality, closeness centrality, stress, disease score and average shortest paths length respectively.

R	name	Description	D	BC	CC	S	DS	ASPL
1	TP53	tumor protein p53	58	0.26	0.6	15192	1.83	1.67
2	EGFR	epidermal growth factor receptor	45	0.12	0.55	9250	1.21	1.83
3	AKT1	v-akt murine thymoma viral oncogene homolog 1	43	0.1	0.53	7606	0.84	1.88
4	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	39	0.06	0.52	5894	1.55	1.91
5	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	35	0.08	0.51	5902	1.27	1.95
6	CCND1	cyclin D1	35	0.06	0.52	5630	1.14	1.92
7	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	34	0.07	0.53	5986	1.04	1.89
8	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	29	0.06	0.51	4596	1.04	1.96
9	BCL2L1	BCL2-like 1	23	0.03	0.47	2464	0.69	2.11
10	WWOX	WW domain containing oxidoreductase	22	0.06	0.46	4504	1.32	2.16
11	FOXM1	forkhead box M1	21	0.05	0.46	4318	0.78	2.16
12	CDKN2A	cyclin-dependent kinase inhibitor 2A	21	0.01	0.47	1082	1.37	2.12
13	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	18	0.04	0.46	2826	0.71	2.17



The Sub- Network Corresponds to the Significant Cluster. The sub-network includes 27 nodes and 179 edges. This cluster was determined by cluster ONE application of Cytoscape software. The cluster identification was restricted by the presence of at least 10 nodes in the cluster ($p<0.001$).



Final Candidate Biomarker Panel Related to Esophageal Adenocarcinoma Including Proteins and Their Interactions. The size and color of the nodes are layout by degree value. The bigger size and highlighted color corresponds to a higher value of degree. All of the nodes are connected to each other.

Discussion

Protein molecules play a major role in different diseases and stress conditions that their expression contributes to the onset and advances of diseases [6]. These related proteins to a specific sort of sickness or condition are available in an entire communicating framework (PPI), that value further examination for deciphering centrality jobs .Such that, the related proteins are screened and positioned as such lastly among many starting proteins a couple of proteins will be introduced as featured proteins .These key proteins can be conceivably differential biomarkers. In this examination, 200 proteins identified with throat adenocarcinoma from STRING DB were recovered; notwithstanding, just 182 proteins were removed. Finally, the developed PPI system of EAC was by 182 proteins. The system contains 50 disengaged proteins, a triple associated hub and a principal associated part. The fundamental part contains 129 hubs and 562 edges (see Figure 1). In this part (organize), the hubs are distincted depending on the job of the hubs in the system. This job is dependent on the focal properties of the hubs in the system. Degree, betweenness, closeness and stress are four significant focal boundaries in the system examination.

The system was broken down and focal boundaries of the hubs were resolved. These boundaries were arranged dependent on degree esteem and the top10% of the hubs (counting 13 hubs) were chosen as center point hubs and organized in Table 1. Normally, a set number of proteins can be considered as an intriguing board for a particular ailment. Along these lines, it is attempted to confine the quantity of the center hubs.

Every protein is associated with the other eight proteins. Since every single key hub is normal between the fundamental system and bunch 1, quality metaphysics of the components of cluster-1 can give valuable data about related organic procedures to EAC. Quality cosmology findings showed that the hubs of bunch 1 assume key jobs in esophageal adenocarcinoma harm.

It is a powerful affirmation for the discoveries of the broken down system. In this way, it is a novel mix and positioned quality set that is presented as a biomarker board of EAC. A dense part of a network including some nodes that are closely connected together is called cluster [7].

Conclusion

In conclusion, it can be concluded that there is a cluster including 27 proteins identified with esophageal adenocarcinoma disease. By consider the elements of cluster-1 and the key proteins in the Protein Interaction network of this disease, a board including TP53, EGFR, AKT1, ERBB2, MYC, CCND1, CTNNB1, CDH1, AND BCL2L1 was presented as a candidate biomarker panel for esophageal adenocarcinoma . Still, more investigation in the field is required for approval of these discoveries.

References

1. Su, G., Morris, J. H., Demchak, B., & Bader, G. D. (2014). Biological network exploration with Cytoscape 3. *Current protocols in bioinformatics*, *47*(1), 8-13.

2. Greenwald, B. D. (2000). Photodynamic therapy for esophageal cancer. Update. *Chest Surgery Clinics of North America*, *10*(3), 625-637.

3. Gao, Y. F., Yuan, F., Liu, J., Li, L. P., He, Y. C., Gao, R. J., ... & Jiang, Y. (2015). Identification of new candidate genes and chemicals related to esophageal cancer using a hybrid interaction network of chemicals and proteins. *PloS one*, *10*(6), e0129474.

4. Goh, K. I., Cusick, M. E., Valle, D., Childs, B., Vidal, M., & Barabási, A. L. (2007). The human disease network. *Proceedings of the National Academy of Sciences*, *104*(21), 8685-8690.

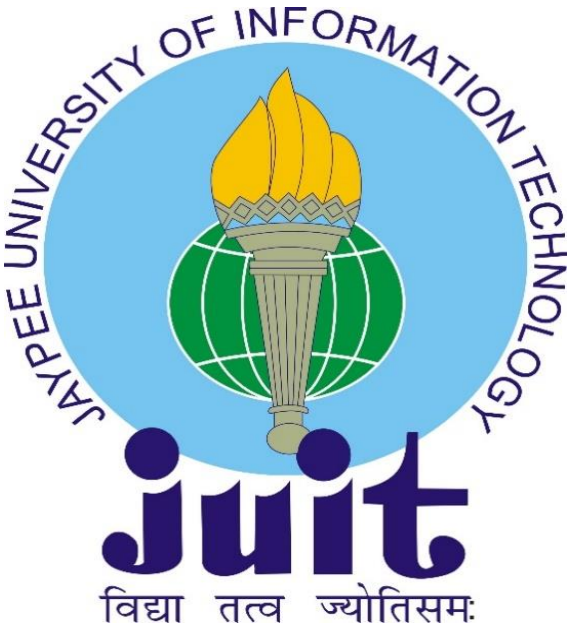
5. https://string-db.org/

6. Zamanian–Azodi, M., Rezaei-Tavirani, M., Rahmati-Rad, S., & Tavirani, M. R. (2016). Ethanol and cancer induce similar changes on protein expression pattern of human fibroblast cell. *Iranian journal of pharmaceutical research: IJPR*, *15*(Suppl), 175.

7. Milenković, T., & Pržulj, N. (2008). Uncovering biological network function via graphlet degree signatures. *Cancer informatics*, *6*, CIN-S680.

SUMMER INTERNSHIP ON DATA MINING

TITLE: TEXT MINING IN BIOMEDICAL LITERATURE



Enrolment No- **171514**

Name of the student- **Apurva Garg**

Name of Supervisor- **Dr. Tiratha Raj Singh**

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Certificate

Candidate's Declaration

I hereby declare that the work presented in this report entitled "Text Mining In Biomedical Literature" in fulfilment of the requirement for the Summer Training submitted in the department of Biotechnology and Bioinformatics , is an authentic record of our own work carried out over a period from 16 May 2020 to 30 June 2020 under the supervision of Dr. Tiratha Raj Singh.



Apurva Garg
171514

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr. Tiratha Raj Singh
Dated: 30-06-2020

ACKNOWLEDGEMENT

I would like to begin by thanking my supervisor Dr. Tiratha Raj Singh, Associate Professor at the department of Biotechnology and Bioinformatics in Jaypee University of Information Technology, for giving me the opportunity to work with him. His immense understanding and curiosity in research allowed me to learn many things. His guidance and encouragement were indispensable in completing this dissertation.

I would like to thank all the researchers and scholars partially involved in the process of successful completion of my project.

My sincere thanks goes to all the staff, professors and PhD scholars at JUIT, whose Kindness and friendly nature provided a very enjoyable research environment and a platform of excellence to do my dissertation.

Apurva Garg

TABLE OF CONTENTS

Chapters	Content	Page Number
Chapter 1	Abstract	5
Chapter 2	Introduction	6
Chapter 3	Literature Review	7-11
Chapter 4	Methodology	11-15
Chapter 6	Conclusion	16
Chapter 7	References	17

LIST OF FIGURES:

Fig1.1 Decision Tree Example
Fig1.2 SVM Example

Chapter 1 ABSTRACT

Researchers are systematically tackling gene functions and complex regulatory processes by studying organisms at different levels of organization, from genomes, transcriptomes and proteomes to metabolomes and interactomes. To fully realize the value of such high-throughput data requires advanced bioinformatics for integration, mining, comparative analysis, and functional interpretation. Furthermore, with an ever-increasing volume of biomedical literature now available electronically, there is both a pressing need and a great opportunity to fully utilize text mining tools for knowledge extraction. However, despite recent advancements, text mining tools are not being broadly used by biologists. Such a gap is partly due to the lack of close interactions between the text mining and the biological user communities. The goal of this application is to develop a digital research infrastructure that links text mining with data mining in the systems biology context for biomedical knowledge discovery, with a special focus on the utility and usability of the system for real world scientific applications. Building upon the bioinformatics framework we have already developed, as well as our close interactions with the biomedical research community, the specific aims are to: (i) integrate existing text mining tools to identify and extract protein and network information from scientific literature, (ii) connect text mining and data mining with omics data integration and web interface to capture and visualize network knowledge, and (iii) conduct user studies, develop scientific use cases, provide training and outreach, and disseminate the system to the broad biomedical user community.

Chapter 2 INTRODUCTION

Biomedical text mining (including **biomedical natural language processing** or **BioNLP**) refers to the methods and study of how text mining may be applied to texts and literature of the biomedical and molecular biology domains. The strategies developed through studies in this field are frequently applied to the biomedical and molecular biology literature available through services such as PubMed.

Text mining, also referred to as text data mining, roughly equivalent to text analytics, is the process of deriving high-quality information from text. High-quality information is typically derived through the devising of patterns and trends through means such as statistical pattern learning. Text mining usually involves the process of structuring the input text (usually parsing, along with the addition of some derived linguistic features and the removal of others, and subsequent insertion into a database), deriving patterns within the structured data and finally evaluation and interpretation of the output.

Like other text documents, biomedical documents contain unstructured data. Research publications follow different formats, contain different types of information, and are interspersed with figures, tables, and other non-text content. Both unstructured text and semi-structured document elements, such as tables, may contain important information that should be text mined . Clinical documents may vary in structure and language between departments and locations. Other types of biomedical text, such as drug labels, may follow general structural guidelines but lack further details.

Text mining employs many computational technologies, such as machine learning, natural language processing, biostatistics, information technology, and pattern recognition, to find new exciting outcomes hidden in unstructured biomedical text. There are many applications of cancer-related text mining, such as identifying malignant tumor related biomedical mentions (genes, proteins, etc.), finding relationships among biomedical entities (protein–protein, gene–disease, etc.), extracting knowledge from text and generating hypotheses, and constructing or improving pathways.

Chapter 3 LITERATURE REVIEW

Biomedical literature is one of the major sources of current biomedical knowledge. One of the largest sources of biomedical literature is the MEDLINE database, created in 1965 and accessible through PubMed. This database contains over 23 million references to journal articles in the life sciences, and more than 860,000 entries were added in 2016.

Automatic methods for Information Extraction (IE) aim at obtaining useful information from large datasets, where manual methods would be unfeasible. Text mining aims at using IE methods to process text documents. The main challenge of text mining is in developing algorithms that can be applied to unstructured text to obtain useful structured information. Biomedical literature is particularly challenging to text mining algorithms for several reasons. The writing style differs from other types of literature since it is more formal and complex.

More recently, bioinformatics databases have adopted text mining tools to more efficiently identify new entries. **MirTarBase** is a database of experimentally validated miRNA-target interactions published in journal papers. The curators of this database use a text mining system to identify new candidate entries for the database, which are then manually validated. This system was necessary due to the important role miRNAs have been found to play in human diseases over the last decade, leading to a high number of papers published about this subject. The introduction of the system as part of the workflow has led to a 7-fold increase in the number of interactions added to the database.

Natural Language Processing (NLP) has been the focus of many researchers since the 1950s. The main difference between NLP and text mining is the objective of the tasks. While NLP techniques aim at making sense of the text, for example, determining its structure or sentiment, the objective of text mining tasks is to obtain concrete structured knowledge from text. However, there is overlap between the two fields, and text mining tools usually make use of NLP concepts and tasks.

The following list defines NLP concepts relevant to text mining.

- Token: a sequence of characters with some meaning, such as a word, number or symbol. The NLP task of identifying the tokens of a text is known as tokenization. It is of particular importance to text mining since most algorithms will not consider elements smaller than tokens.

- Part-of-speech (POS): the lexical category of each token, for example, noun, adjective, or punctuation. The category imparts additional semantics to the tokens. Part-of-speech tagging is an NLP task that consists in classifying each token automatically.
- Lemma and stem: the base form of a word. The lemma represents the canonical form of the word, corresponding to a real word. The stem does not always correspond to a real word, but only to the fragment of a word that never changes. For example, the lemma of the word "induces"is "induce"while the stem is "induc-".
- Sentence splitting: the NLP task consisting of identifying the sentence boundaries of a text. The methods used to accomplish this task should consider the difference between a period at the end of a sentence, and at the end of an acronym or abbreviation. It is desirable to break a document into sentences because they represent unique ideas.
- Entity: a segment of text with relevance to a specific domain. An entity may be composed of one or more tokens. Entity types relevant to biomedicine include genes, proteins, chemicals, cell lines, species, and biological processes.

TEXT MINING TASKS:

- **Topic modelling**: the classification of documents according to their topics or themes. The objective of this task is to organize a set of documents to identify which documents are more relevant to a given topic. Related tasks include document triage and document clustering.
- **Named Entity Recognition (NER):** consists of identifying entities that are mentioned in the text. In most cases, the exact location of each entity in the text is required, given by the offset of its first and last character. In some cases, discontinuous entities may be considered, therefore requiring multiple offset pairs. The classification of entity properties such as its type (e.g., protein, cell line, chemical) can be included in this task.

  Current biomedical named entity recognition technique falls into three major categories: dictionary-based approaches, rule-based approaches and machine learning approaches . However, dictionary-based approaches tends to miss undefined terms that are not mentioned in the dictionary , rule-based approaches require rules that identify terms from text, and the resulting rules are often not effective in all cases . Machine learning approaches generally require standard annotated training data sets which usually takes tremendous human efforts to build . Moreover, most

machine learning approaches tend to be data-driven and application domain-oriented and precision, recall rate, and F_1 rate are often used to evaluate the performance of the recognition, as follows:

- Precision : True Positive/True Positive+False Positive
- Recall: True Positive/False Negative+True Positive
- F1 Score: 2 *(precision*recall)/(precision+recall)

For example, when we identify a gene term, true positive refers to a gene term is correctly identified as a gene; false positive indicates a non-gene term is incorrectly identified as a gene, and false negative incorrectly identifies a gene term as non-gene term.

- **Normalization:** consists of matching each entity to an identifier belonging to a knowledge base that unequivocally represents its concept. For example, a protein may be mentioned by its full name or by an acronym; in this case, the normalization process should assign the same identifier to both occurrences. The identifiers can be provided by an external database or ontology Related tasks include named entity disambiguation entity linking, and harmonization.
- **Relationship Extraction (RE):** the identification of entities that participate in a relationship described in the text. Most tools consider relations between two entities in the same sentence. Biomedical relations commonly extracted are protein-protein and drug-drug interactions.

  Presently, the best F_1 rates for biomedical named entity recognition systems are not as good as the results from general purpose ones. Researchers have tried many methods to improve the performance, by combining different approaches and proposing hybrid approaches , conducting post-processing after machine learning, and adding biomedical domain knowledge. Conventional relationship extraction is focused on investigating biomedical relation extraction (e.g., protein–protein interaction and gene–disease relation) from biomedical terms (e.g., genes, proteins, diseases, or drugs). Many researchers have done much work on relationship extraction. The system developed by Ben Abacha et al. is able to identify the correct semantic relationship between each pair of entities using MetaMap to identify medical substances while a linguistic patterns approach determines the semantic relationship between each pair. The systems developed by Chun et al. could extract

gene–disease relations from Medline. They used a machine learning-based named entity recognition system to remove incorrect disease and gene names caused by dictionary matching-based term recognition. They found that improving the terms recognition performance could also improve the relationship extraction precision.

- **Event extraction:** can be considered an extension of the relationship extraction task, where the label of the relationship and role of each participant is specified. The events extracted should represent the mechanisms described in the text Related task: slot-filling.

In addition, researchers are focusing on the relationship between genes and other biomedical entities, as well as the relationship between proteins and other biomedical entities, such as gene–disease relationships and protein sub-cellular relationships.

TEXT MINING TOOLKITS:

One of the most widely used text mining toolkits is Stanford CoreNLP ,which aggregates various tools developed by the Stanford NLP team for processing text data. Biomedical text mining tools may use Stanford CoreNLP to pre-process the data (e.g., for sentence splitting, tokenization and co-reference resolution) and to generate features for machine learning classifiers (e.g., for POS tagging, lemmatization, and dependency parsing).

- NLTK, another NLP toolkit, was implemented as a Python library. This toolkit provides interfaces to various NLP resources, such as Word-Net, tokenizers, stopwords lists, and datasets from community challenges. It is often used by developers who are getting started in text mining, due to its well-designed API, and to the availability of various online tutorials for this toolkit. More recently, another Python-based toolkit was released, spaCy, which is more focused on computational perfor- mance, using state-of-the-art algorithms.
- ClearTK is a text mining toolkit based on machine learning and the Apache Unstructured Information Management Architecture (UIMA). This framework provides interfaces to several machine learning libraries and feature extractors.
- GATE is one of the few text mining toolkits which has features specially designed for biomedical text mining. This toolkit provides plugins for bioinformatics resources such as Linked Life Data and other ontologies, and specialized biomedical NLP tools.

Furthermore, a graphical user interface is available to visualize and edit the data and system architecture.

Relationship and Event Extraction:

- For RE, most tools use ML algorithms to classify which pairs of entities mentioned in the text constitute a relationship. In this task, kernel methods and Support Vector Machines are popular. jSRE uses a shallow linguistic kernel which takes into account the tokens, POS, and lemmas around each entity of the pair. It has been used for various problems, including drug- drug interaction extraction.
- Distant supervision has become particularly relevant to RE tasks because it is more expensive to develop a corpus annotated with relation developed an approach to gene RE using DeepDive, a general purpose system for training distantly supervised RE models. They applied this approach to a corpus of full-text documents from three journals, using the BioGRID and Negatome databases as reference. Another DS-based tool, IBRel, uses TransmiR, a database of miRNA-gene associations, to extract the same type of relationships from text.
- Biomedical event extraction is a complex task, but some tools have been developed. Turku Event Extraction System (TEES) identifies complex events based on trigger words and graph methods. This system has been evaluated on multiple community challenges, on event extraction and RE tasks, such as the BioNLP-ST 2011 event extraction task. In the 2016 edition of BioNLP-ST, presented VERSE, a system for extracting relationships and events from text, and evaluated it on three different subtasks. This system is based on ML algorithms, and has the advantage of being able to extract relationships between entities in different sentences.
- **Textpresso** is a system for biomedical information extraction based on regular expressions and ontologies. This system has been applied to various domains, and a portal to search the results obtained on each domain is provided in the web interface.

TEXT MINING PROCESS:

1. Search and Retrieval of documents.
2. Pre-processing of documents.
3. Term document matrix.
4. Natural Language Processing.

Chapter 4 METHODOLOGY

Data mining algorithms:

Before applying data mining algorithms to medical data, researchers must understand what kind of data mining algorithms exists and how they function. Generally, data mining algorithms are classified into two categories: descriptive (or unsupervised learning) and predictive (or supervised learning) Descriptive data mining clusters data by measuring the similarity between objects (or records) and discovers unknown patterns or relationships in data so that users can readily understand a huge amount of data. Descriptive data mining is exploratory in nature. This type of data mining includes clustering, association, summarization, and sequence discovery. Prediction data mining infers prediction rules (a.k.a. classification/prediction models) from (training) data and applies the rules to unpredicted/unclassified data. Prediction data mining includes classification, regression, time series analysis, and prediction.

To help researchers understand the importance of data mining, and application of data mining techniques, three of the most widely-used data mining algorithms (classification, clustering, and association) will be discussed below along with guidelines for their respective use.

- **Classification:** Classification is used to classify data into predefined categorical class labels. “Class” in classification, is the attribute or feature in a data set, in which users are most interested. It is defined as the dependent variable in statistics. To classify data (or records), a classification algorithm creates a classification model consisting of classification rules.
- **Naive Bayesian classifier:** A naive (or simple) Bayesian classifier based on Bayes’ theorem is a probabilistic statistical classifier. Here, the term “naïve” indicates conditional independence among features or attributes. The “naïve” assumption greatly reduces computation complexity to a simple multiplication of probabilities. The major advantage of the naïve Bayesian classifier is its rapidity of use. This rapidity occurs because it is the simplest algorithm among classification algorithms. Because of this simplicity, it can readily handle a data set with many attributes. In addition, the naïve Bayesian classifier needs only small set of training data to develop

accurate parameter estimations because it requires only the calculation of the frequencies of attributes and attribute- outcome pair(s) in the training data set.

- **Neural network:** Neural Network (NN), as the name indicates, attempts to mimic the neurological functions of the brain (i.e., neural networks). NN consists of computational nodes that emulate the functions of the neurons in the brain. Each node/neuron as a simple processor is interconnected with other nodes via links with adjustable weights. The link weights are adjusted when the NN is learning or being trained. The nodes are classified into two categories (Input and Output layers) or three categories (Input, Hidden and Output layers).However, the input layer is not considered or counted when neural network algorithms are classified because the input layer is simply used to take the input values and pass them to the next layer. For example, a neural network algorithm having input, hidden, and output layers is called a two (or multi)-layer neural network.
- **Decision tree:** Ross Quinlan introduced a decision tree algorithm (known as Iterative Dichotomiser (ID)3) in 1979,as a successor of ID3, is the most widely-used decision tree algorithm. Decision tree classifiers construct a flowchart-like tree structure,in a top- down, recursive, divide-and-conquer, manner. The Attribute Selection Method (ASM) is the key process in the construction of a decision tree. The ASM selects a splitting criterion (attribute) that best splits the given records into each of the class labels. In other words, this method seeks an attribute whose sorting result is closest to the pure partitions by the class in terms of class values. Selected attributes become nodes in a decision tree. For example (as seen in Fig. 1),Family_History_of_Lung_Cancer is the first attribute (or the root node) selected by ASM. Decision trees which consist of IF-THEN rules are classification models. In other words, constructing a decision tree is the training step of classification.

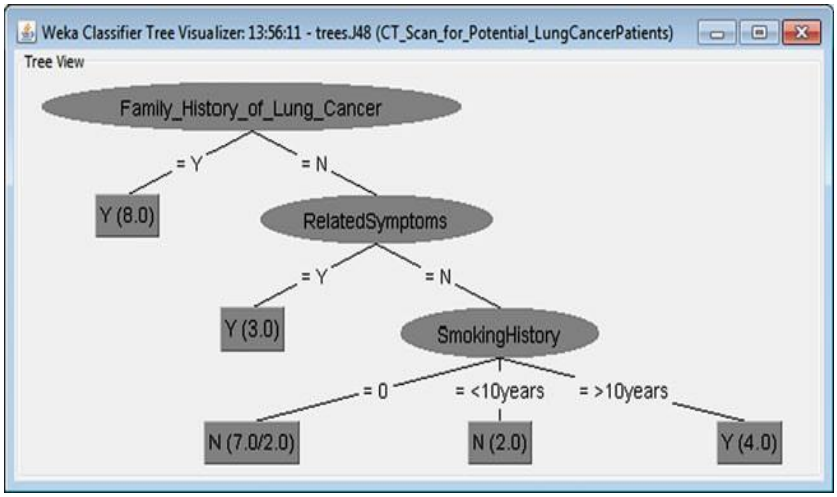


Fig1.1 Decision Tree Example

- **Support Vector Machine:** The fundamental strategy used by SVM is that, when a dataset is represented in a high dimensional feature space, it searches for the (linear) optimal separating hyperplane where the margin between two different objects (or records) is maximal (see Fig.1.2where, for simplicity's sake, there are only two dimensions (attributes) represented: blood pressure and cholesterol). Hyperplanes are actually decision boundaries between two different sets of objects (e.g., in Fig1.2, the safe objects and the risky objects). To find the hyperplane with the maximal margin, the SVM uses support vectors (in Fig.1.2 the support vectors are the two double- lined objects) and the margin is determined using the two support vectors.

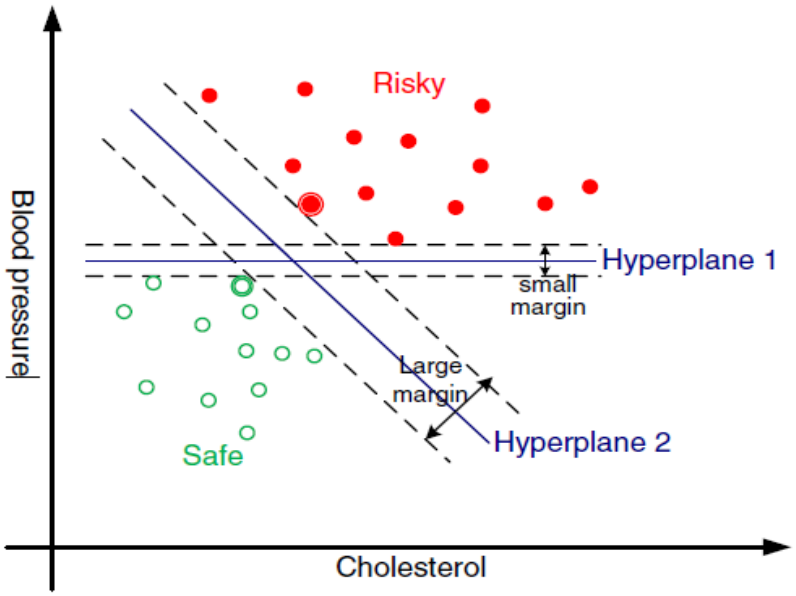


Fig1.2: SVM Example

- **Clustering:** Clustering is defined as unsupervised learning that occurs by observing only independent variables (unlike supervised learning analyzing both independent variables and a dependent variable). In order words, unlike classification, clustering does not use “class”. In fact, this is the main difference between classification and clustering. For this reason, clustering may be best used for studies of an exploratory nature, especially if those studies encompass large amount of data, but very little is known about data (such as the mass of data typically generated by microarray analysis).Clustering is used to group objects (records) into a specific number of clusters so that the objects within a cluster have very high similarity and objects from different clusters have very low similarity. Similarities between two objects are measured using their attribute values.
- **Hierarchical clustering algorithms:** Hierarchical clustering algorithms successively merge the most similar two groups of objects based on the pairwise distances between two groups of objects until a termination condition holds, so that objects are hierarchically grouped. A main advantage of the use of hierarchical clustering algorithms is the visualization capability that shows how much objects in the data set are similar one another. In addition, with the utilization of a dendrogram, researchers can reasonably guess the number of clusters. This is a distinguishing feature of hierarchical algorithms because other clustering algorithms cannot provide this very useful feature, especially when there is no additional information available about the data itself.
- **Partitional clustering algorithms:** Unlike hierarchical clustering algorithms, partitional clustering algorithms require a user to input *k,* (which is the number of clusters). Generally, partitional algorithms directly relocate objects to *k* clusters. Partitional algorithms are categorized according to how they relocate objects, how they select a cluster centroid (or representative) among objects within a (incomplete) cluster, and how they measure similarities between objects and cluster centroids. For example, K-means, the most widely-used partitional algorithm, first randomly selects *k* centroids (objects), and then decomposes objects into *k* disjoint groups by iteratively relocating objects based on the similarity between the centroids and the objects. In K-means, a cluster centroid is the mean value of objects in the cluster. In many cases, the cluster centroids are not actual cluster objects. Unlike K- means, K-

medoids, selects the nearest object to the mean value of objects in a cluster. The major advantages of partitional clustering algorithms over other methods, is their superior clustering accuracy as compared with hierarchal clustering algorithms that is the result of their global optimization strategy (i.e., the recursive relocations of objects).

Chapter 5 CONCLUSION

In this, we first discussed the background, definition, and process of data mining, the major differences between statistics and data mining, and the uniqueness of data mining in biomedical and healthcare fields. Various data mining algorithms in classification, clustering, and association and their advantages and drawbacks were outlined. Guidelines on how to use data mining algorithms in each area of classification, clustering, and association were provided. Three data mining applications in the healthcare industry were introduced. Finally, the application of data mining technologies that have been used for research purposes in the biomedical and healthcare fields was discussed.Data mining has been widely used in the biomedical and healthcare fields because of its descriptive and predictive power. Using data mining technologies, healthcare professionals can predict health insurance fraud, under-diagnosed patients, healthcare cost, disease prognosis, disease diagnosis, and the length of stay (LOS) in a hospital. In addition, they can obtain frequent patterns from biomedical and healthcare databases, such as relationships between health conditions and a disease, relationships among diseases, and relationships among drugs.

Currently, data mining has several problems that hamper its clinical usage by health professionals. First, data mining algorithms usually require user parameter(s) mainly because each data mining algorithm has its own theoretical assumptions. End-users usually do not have sufficient information about the parameters and their selection. To make the problem worse, data mining results are usually very sensitive to the parameters. Second, data mining accuracy is normally not high enough to be used in a clinical environment. The generally low quality of patient data contributes to the problem given that hospital information systems are usually designed for financial/billing purposes.

Biomedical text mining systems are not as golden standard tools of biomedical researchers as retrieval systems and sequencing tools. The next important mission of text mining for us is to develop applications that are really helpful to biomedical research, so that researchers can get more productive and make more progress in the information rapid growing ear. To achieve the goal, more concerns should be put on helping biological biomedical scientists to remove the obstacles that block the development rather than discussions that are not related with actual demands. One of the hottest topics of text mining is to coordinate and cooperate with multiple subjects. That is, biomedical text mining, coupled with other data and means, should yield consistent, measurable, and testable results.

Chapter 6 REFERENCES

- A.M. Cohen, W.R. Hersh A survey of current work in biomedical text mining Brief Bioinform, 6 (2005).
- World Health OrganizationWorld health statistics 2009 World Health Organization, Geneva (2009)
- S. Ananiadou, S. Pyysalo, J. Tsujii, D.B. KellEvent extraction for systems biology by text mining the literature Trends Biotechnol, 28 (2010)
- The Technology Review Ten, MIT Technology Review (January/ February 2001).
- Larose, D. T., Discovering knowledge in data: an introduction to data mining. Wiley, 2004.
- Hand, D., Mannila, H., Smyth, P., Principles of data mining. MIT, 2001.
- Fayyad, U., Piatetsky-Shapiro, G., and Smyth, P., The KDD process of extracting useful knowledge from volumes of data. Commun. ACM 39, 1996.
- Berger, A., and Berger, C., Data mining as a tool for research and knowledge development in nursing. Comput. Inform. Nurs., 2004.
- Shearer, C., The CRISP-DM model: the new blueprint for data mining. J Data Warehouse , 2000.
- Fayyad, U., Piatetsky-Shapiro, G., and Smyth, P., From data mining to knowledge discovery in databases. Commun. ACM 39 , 1996.
- D. Maier, W. Kalus, M. Wolff, S.G. Kalko, J. Roca, I. Marin de Mas, *et al.*Knowledge management for systems biology a general and visually driven framework applied to translational medicine BMC Syst Biol, 5 (2011)

SUMMER TRAINING

Report submitted in partial fulfillment of the requirements for the degree of

BACHELOR OF TECHNOLOGY

Under the supervision of

Prof. Narendra Kumar

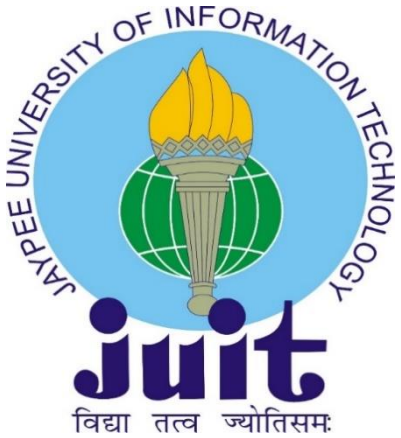
ASSISTANT

PROFESSOR DEPT. OF

BIOINFORMATICS

By

Sarvjeet Kaur (171515)



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, SOLAN, H.P.

Title : IMGT DATABASE

Introduction

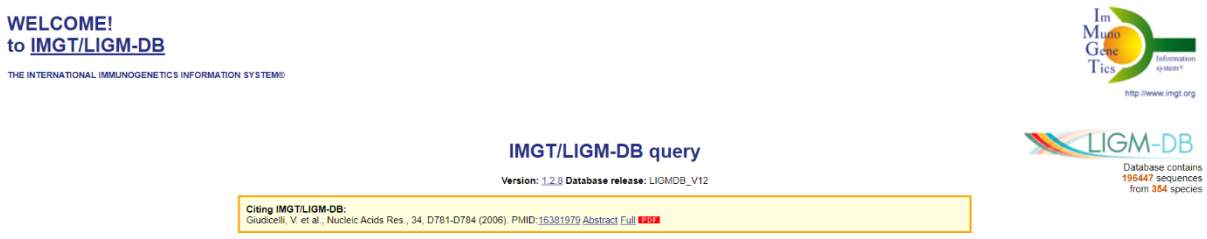
IMGT®, the international ImMunoGeneTics information system® http://www.imgt.org, is the global reference in immunogenetics and immunoinformatics, created in 1989 by Marie-PauleLefranc (Université de Montpellier and CNRS). IMGT® is a high-quality integrated knowledge resource specialized in the immunoglobulins (IG) or antibodies, T cell receptors (TR), major histocompatibility (MH) of human and other vertebrate species, and in the immunoglobulin superfamily (IgSF), MH superfamily (MhSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates. IMGT® provides a common access to sequence, genome and structure Immunogenetics data, based on the concepts of IMGT-ONTOLOGY and on the IMGT Scientific chart rules. IMGT® works in close collaboration with EBI (Europe), DDBJ (Japan) and NCBI (USA). IMGT® consists of sequence databases, genome database, structure database, and monoclonal antibodies database, Web resources and interactive tools.

About

IMGT databases

1. **IMGT/LIGM-DB (doc) LIGM, Montpellier, France**
   Nucleotide sequences of IG and TR from 354 species (196 447 entries)

   Is the first database of IMGT®, the international ImMunoGeneTics information system®, the high-quality integrated database specializing in Immunoglobulins (IG), T cell Receptors (TR) and Major Histocompatibility Complex (MHC) molecules of all vertebrate species, created in 1989 by Marie-Paule Lefranc (LIGM, Université Montpellier II, CNRS and on the web since July 1995.



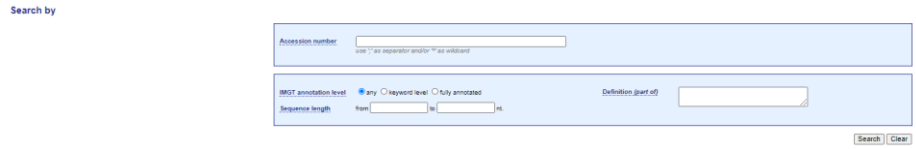
Searches by:

1.1.Search by Accession number

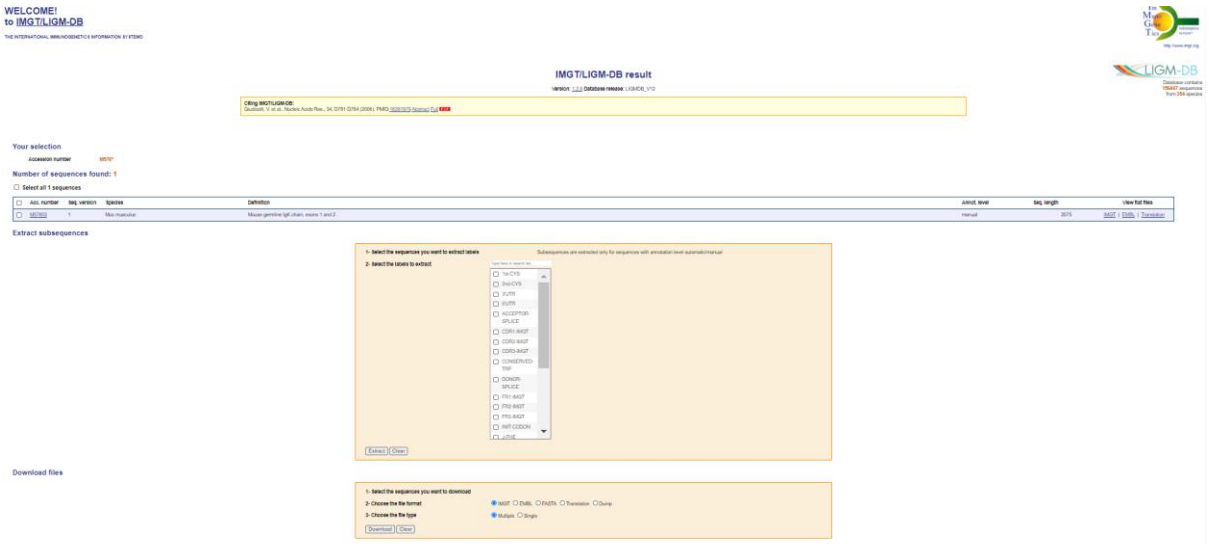
Accession number is identical to EMBL accession number. Accession number field is case sensitive, use upper case.
You can search for:

- a single accession number (ex: M94115)
- a range of accession numbers starting with a common prefix using '*' as wildcard (ex: M941*)
- several accession numbers using ';' as separator (ex: M94115; M94116; M94117)

- the combination of the two cases cited above (ex: M941*; M94349)



For example

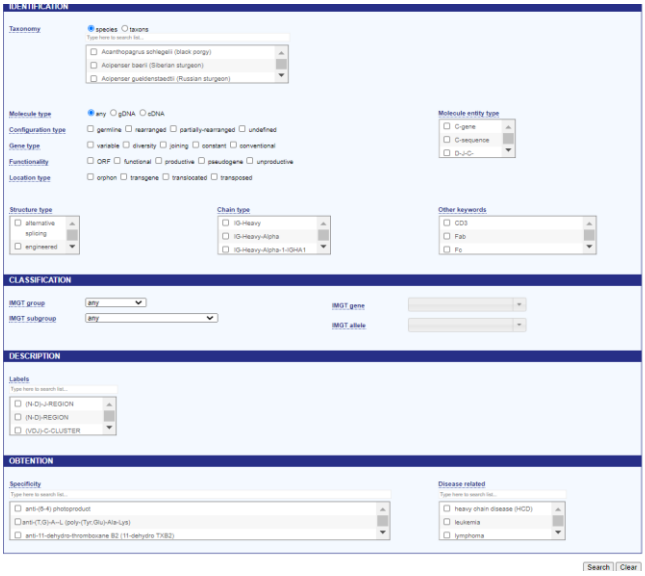


1.2.Search by IMGT-ONTOLOGY concepts

An **ontology** is a concise and non ambiguous description of the more significant and relevant **concepts** in an application domain.

IMGT-ONTOLOGY, is the first ontology which allows the management of the immunogenetics knowledge for all vertebrate species with jaws (*gnathostomata*).

The molecular synthesis and genetics of the immunoglobulin (IG) and T cell receptor (TR) chains and the polymorphism of the MH are particularly complex, and therefore one of the first tasks of IMGT-ONTOLOGY comprises a formal specification of the terms to be used in the domain of immunogenetics and bioinformatics, of the rules for IMGT gene nomenclature and for the numbering of amino acids and codons.



1.3.Search by bibliographical references

Author Sequences can be retrieved by the name of the author of their associate Author field is not case sensitive.

Check "first author only" option to restrict your **search** on on first author only. This option is available only if an author name is entered in author field.

Type Select 'any' to not restrict your **search** on one reference type.

Journal This field is shown only if Type field above is set on 'Journal'.

PMID Sequences can be retrieved by their associated reference's PMID, you can enter several PMIDs using ';' as separator

Year Sequences can be retrieved by their associated reference's year. Sequences in **IMGT**/LIGM-DB are linked to **references** from 1971 to now.

2. Title *(part of)* Sequences can be retrieved by the exact title or a part of the title of their associated **references**. The title field is not case sensitive.



3. **IMGT/MH-DB ANRI, BPRC, hosted at EBI**
Sequences of the human MH (HLA) is the global reference in immunogenetics and immunoinformatics, created in 1989 by Marie-Paule Lefranc (Université de Montpellier and CNRS). IMGT® is a high-quality integrated knowledge resource specialized in the immunoglobulins (IG) or antibodies, T cell receptors (TR), major histocompatibility (MH) of human and other vertebrate species, and in the

immunoglobulin superfamily (IgSF), MH superfamily (MhSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates. IMGT® provides a common access to sequence, genome and structure Immunogenetics data, based on the concepts of IMGT-ONTOLOGY and on the IMGT Scientific chart rules.



4. **IMGT/PRIMER-DB (doc) LIGM, Montpellier, France**
   Oligonucleotides (primers) of IG and TR from 11 species (1 864 entries)
   An IMGT/PRIMER-DB primer is an oligonucleotide defined, classified and described by comparison to an IMGT/LIGM-DB reference sequence.

- This provides the following advantages for the data standardization:
  - IMGT/PRIMER-DB primers can easily be compared to data from the other IMGT databases (IMGT/LIGM-DB, IMGT/GENE-DB, IMGT/3Dstructure-DB), IMGT Web resources (IMGT Repertoire) and tools (IMGT/V-QUEST, IMGT/PhyloGene). These data are described according to the standardized rules of the IMGT Scientific chart, based on IMGT-ONTOLOGY.
  - IMGT/PRIMER-DB primer definition, classification and description are independent from the experimental conditions, from DNA sources and from the different combinations (sets and couples) in which the primer can be used. That means that (i) the specificity of a primer (subgroup, gene or allele specific) which is either described experimentally or deduced from sequence comparison is not used for the primer classification, although these data are provided in the IMGT/PRIMER-DB Primer card in Classification comments and specificity, (ii) the sequences resulting from the PCR amplifications are uniquely associated to the couples.
- An IMGT/PRIMER-DB set consists of IMGT/PRIMER-DB primers sharing identical properties (species, group and orientation). An IMGT/PRIMER-DB set may be composed of only one IMGT/PRIMER-DB primer.
- An IMGT/PRIMER-DB couple consists of sets of opposite orientation for which IMGT/LIGM-DB sequences are known (or expected). An IMGT/PRIMER-DB couple comprises a Sense IMGT/PRIMER-DB set and an Antisense IMGT/PRIMER-DB set. For example, an IMGT/PRIMER-DB couple may consists of Sense IMGT/PRIMER-DB sets of V regions associated to Antisense IMGT/PRIMER-DB sets of C regions.



Search by:

4.1. Search by accession number:

4.1.1. **IMGT/PRIMER-DB Primer accession number**(IPP) Unique identifier of each primer in IMGT/PRIMER-DB.
Consists of 3 letters "IPP" (for IMGT/PRIMER-DB Primer) and 6 numbers.

4.1.2. **IMGT/PRIMER-DB Set accession number**(IPS) Unique identifier of each set in IMGT/PRIMER-DB.
Consists of 3 letters "IPS" (for IMGT/PRIMER-DB Set) and 6 numbers.

4.1.3. **IMGT/PRIMER-DB Couple accession number**(IPC) Unique identifier of each couple in IMGT/PRIMER-DB.
Consists of 3 letters "IPC" (for IMGT/PRIMER-DB Couple) and 6 numbers.

4.2.Or select IMGT/PRIMER-DB primers according to criteria:



4.3.Or select IMGT/PRIMER-DB sets: consists of IMGT/PRIMER-DB primers sharing identical properties (species, group and orientation). An IMGT/PRIMER-DB set may be composed of only one IMGT/PRIMER-DB primer.



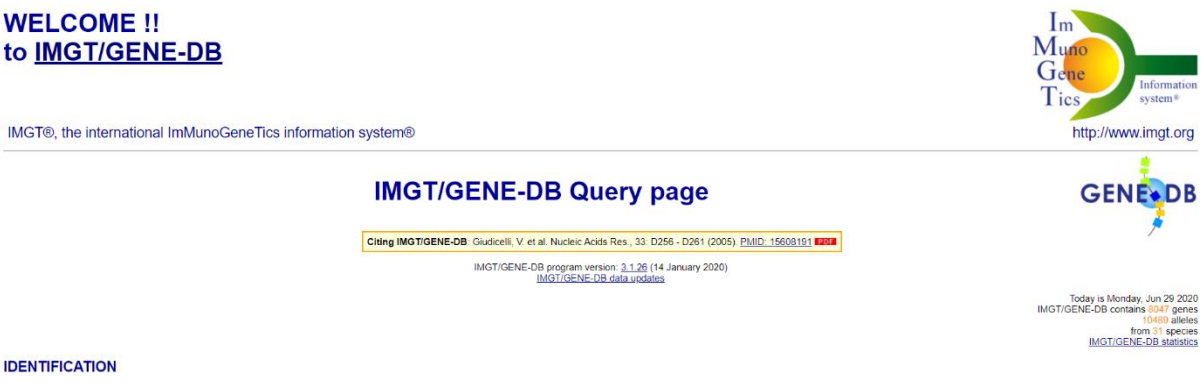
5. IMGT/CLL-DB (bylaws) LIGM, Montpellier, France
G sequences from CLL, an initiative of the IMGT/CLL-DB group

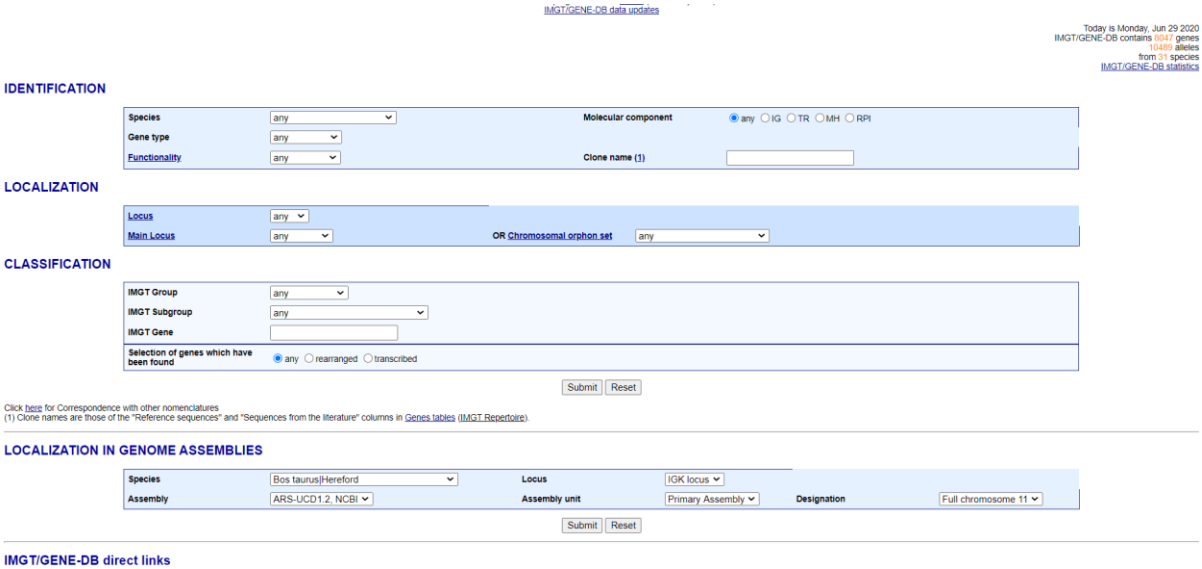


IMGT/CLL- DB GROUP

About us:
The **IMGT/CLL-DB group** is a joint academic initiative between IMGT® and ERIC, The European Research Initiative on CLL (http://www.ericll.org/), devoid of any commercial interest. Its primary aim is to develop and maintain a database with immunogenetic data from patients with Chronic Lymphocytic Leukemia (CLL) attended at academic institutions, to foster high-quality collaborative research on CLL and related disorders. The database system specifications fulfill the storage requirements in order to efficiently manage the continuously increasing amount of data collected and stored into the database. The main outlet for the IMGT/CLL-DB is a purpose-built interactive platform providing all data, information and knowledge to members in a user-friendly yet robust way.

6. **IMGT/GENE-DB (doc) LIGM, Montpellier, France**
   International nomenclature for IG and TR genes from human, mouse, rat and rabbit (8 047 genes, 10 489 alleles) MGT/GENE-DB is the IMGT genome database for IG and TR genes from human, mouse and other vertebrates, on the Web since February 2003. IMGT/GENE-DB provides a full characterization of the genes and of their alleles: IMGT gene name and definition, chromosomal localization, number of alleles, and for each allele, the IMGT allele functionality, and the IMGT reference sequences and other sequences from the literature. IMGT/GENE-DB allele reference sequences are available in FASTA format (nucleotide and amino acid sequences with IMGT gaps according to the IMGT unique numbering, or without gaps). IMGT/GENE-DB includes links to the IMGT Repertoire standardized resources (Chromosomal localization, Locus representation, Tables of alleles, Alignments of alleles, IMGT Protein displays, IMGT Colliers de Perles, etc.), to the IMGT/LIGM-DB and IMGT/3Dstructure-DB structures and IMGT/2Dstructure-DB IMGT databases.





IDENTIFICATION

Species:
only species for which genes have been entered in IMGT/GENE-DB are available.
MolecularComponent:
IG or TR.
GeneType:
allows the selection on one of the gene types.
Functionality:
allows the selection on IG and TR functionality.
Clone name:
enter a clone name or the first letters of a clone name. Clone names are those of the "Reference sequences" and "Sequences from the literature" columns in Genes tables.

CLASSIFICATION

IMGT group:
allows the selection on IMGT groups.
IMGT subgroup:
allows the selection on IMGT subgroups.
IMGT gene:
enter an IMGT gene name, for example IGHV1-2 (List of human genes according to the IMGT nomenclature).

Note that the search is case sensitive and that UPPERcase is the rule.

You can also enter only the first letters of the IMGT gene name: for example the selection of IGHV will list in the next page all genes which have an IMGT gene name beginning with IGHV.

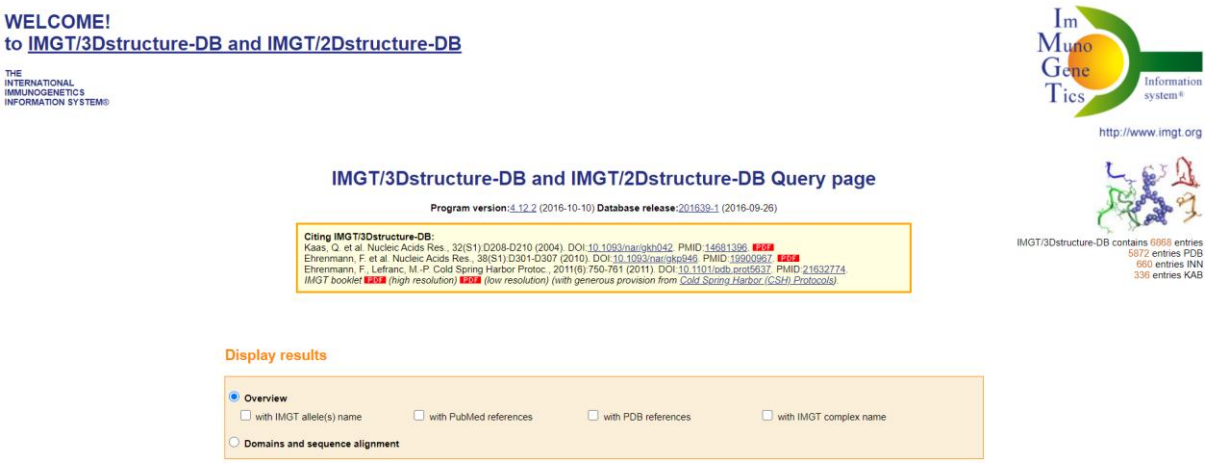
LOCALIZATION

Locus:
allows the selection on IG and TR loci (includes main loci and chromosomal orphon sets).
Main Locus:
allows the selection on a main IG or TR locus.
Chromosomal orphon set:

allows the selection on IG or TR genes which are outside the main loci or Chromosomal orphon set.

As Main Locus may contain RPI genes, a selection on 'Molecular component' 'IG' or 'TR' prior to the request will allow to only retrieve IG or TR genes.

7. **IMGT/3Dstructure-DB and IMGT/2Dstructure-DB (doc) LIGM, Montpellier, France**
   3D structures (IMGT Colliers de Perles) of IG antibodies, TR, MH and RPI (6 868 entries)
   Source: PDB, INN, Kabat
   The IMGT/3Dstructure-DB Query page shows, at the top of the page, the status of the database (Current date, the total number of entries and its decomposition (PDB, INN) and the date of the last update) and at the bottom of the page, the last entries and the access to the IMGT tools (IMGT/DomainDisplay, IMGT/Collier-de-Perles, IMGT/DomainGapAlign, IMGT/DomainSuperimpose and IMGT/mAb-DB).



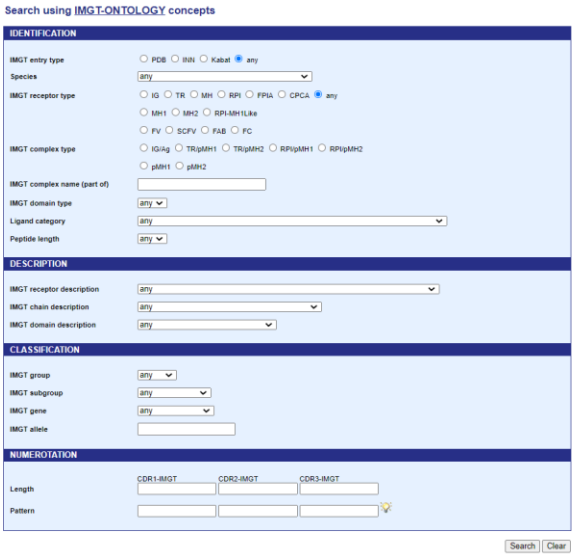
7.1.Search by Entry code or Molecule name(receptor or ligand)

The IMGT/3Dstructure-DB entry code (ID) is identical to the PDB code, INN code or PROTEIN code. PDB code is an alphanumeric code (Ex : 1ao7), INN code is a numeric code (Ex: 7637) while PROTEIN code is an alphanumeric code which lenght is equals to 6 (Ex : p00054).

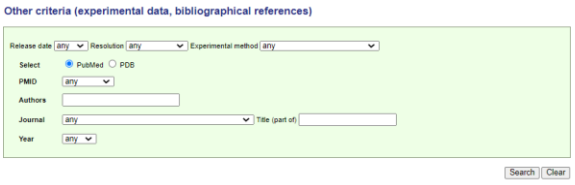
An AutoComplete behavior is available for this field. AutoComplete works in the following manner: as you type in the beginning of a PDB code previous entries are pulled from a storage area and you may elect to simply select one of these entries. By selecting an entry, you no longer have to input the string because AutoComplete finishes entering the string for you.

7.2.Search using IMGT-ONTOLOGY concepts

This section allows users to search entries using the IMGT-ONTOLOGY concepts (IDENTIFICATION, DESCRIPTION, CLASSIFICATION and NUMEROTATION) for each type of IMGT entry. This kind of search uses linked select elements. Linked select elements are two or more selects, where choosing a value in one changes the available values in some of the rest. For example, selecting an IMGT receptor type will updates the 'IMGT receptor description' select to only contain receptor description from the IMGT receptor type selected. In the same way, selecting an IMGT group will updates the 'IMGT subgroup' select to only contain subgroup(s) from the IMGT group selected.
Choose an **IMGT entry type** and then a: Species (also includes Camelized, Chimeric, Humanized, Caninized and Synthetic), IMGT receptor type (IG, TR, MH, RPI, FPIA or Any), IMGT receptor description, IMGT chain description, IMGT group, IMGT subgroup, IMGT gene or IMGT allele.



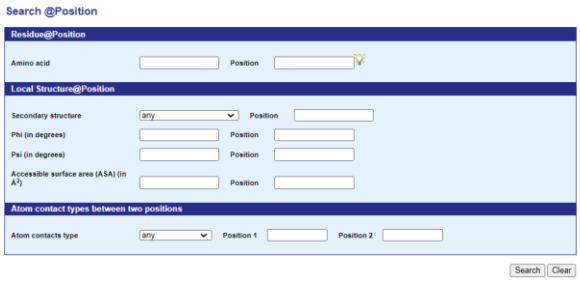
7.3.Other criteria (experimental data, bibliographical references)



7.4.Search @position

The form allows an easy search by the following criteria:

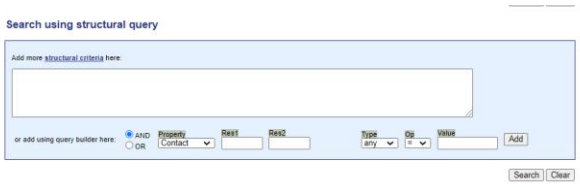
- Residue@Position, that is presence of a given amino acid at a given position. Position is according to the IMGT unique numbering
- Local Structure@Position, with the following criteria:
  - Secondary structure (alpha helix, 3-10 helix, PI-helix, extended conformation, isolated bridge, turn or coil)
  - Phi and Psi angles (in degrees)
  - Accessible surface area (ASA) in angstrom^2 (Å^2)
- Atom contact type between two positions



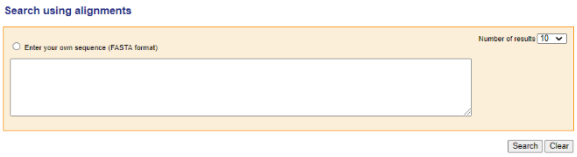
7.5.Search using structural query

A complex query can be performed. It is made up of a list of structural criteria coordinated by parentheses and boolean operator (AND and OR).
The query can be entered in the text area, either manually, or with the Javascript helper tool (available below the text area). The selection of a structural criteria in the scrolling list of the helper tool will show the corresponding fields to be filled in. A 'Quick Help' is available for each criterion.
The different criteria currently implemented are:

- *Contact*: Atom contact type between two positions. Example: 'contact(111V,108V,HB)>0' will query for IMGT/3Dstructure-DB entries which contain an hydrogen bond between position 111 and 108 in a V type domain (111V,108V)
- *HB*: Hydrogen bond between two amino acids (STRIDE hydrogen bonds). Example: 'HB(111V,108V)' will query for IMGT/3Dstructure-DB entries which contain an hydrogen bond between position 111 and 108 in a V type domain (111V,108V) as determined using the algorithm STRIDE
- *SS*: Secondary structure of a given residue. Example: 'SS(112V)=H' will query for IMGT/3Dstructure-DB entries which contain at position 112 in a V type domain (112V) a residue in the phi/psi helix conformation
- *Phi* and *Psi*: Amino acid φ and ψ angles in degrees
- *ASA*: Accessible surface area (in square angstroms, $Å^2$)
- *AA*: Amino acid type is in the one letter abbreviation. Example: 'aa(89V)=M' will query for IMGT/3Dstructure-DB entries which contain at position 89 in a V type domain (89V) a methionine (=M)
- *Length* and *Pattern*: CDR-IMGT length (only available for the V type domain)
- *Pattern*: Amino acid pattern in a CDR-IMGT. As an example '[GSE]..L..Y' will query for IMGT/3Dstructure-DB entries which contain sequences with a CDR-IMGT pattern starting with an G,S or E, the fourth amino acid being a leucine and the seventh amino acid being a tyrosine
- *Description*: IMGT domain description
- *Species*: Species here includes humanized, camelized, chimeric and synthetic
- *Group*: Structure's gene group
- *Gene*: Wanted gene name



7.6.Search using alignments



New or updated entries:

New or updated entries

1CDH 1HH6 1G9M 1FG9 1EZV 1EKU 1AU1
1P84 1NBP 1KB9 1M47 1QVN 1M48 1M49
1M4A 1M4B 1M4C 1HIG 1PW6 1PY2 1KYO
2H3N 2CR3 2O6Q 2IBZ 2ZNX 2RCJ 2H32
3G9V 3MJ6 3MJ7 3MJ9 3WD5 3DJ9 3BES
3WHE 3CXH 3NN8 3RA7 3INK 3VI3 3VI4
3TWI 3BJ9 3DIF 3QB1 3G3A 3SE3 3REV
3MOD 3JZ7 3M18 3M19 4YAQ 4G6M 4FHB
4RRP 4ZS7 4YDL 4K5U 4NEJ 4NEM 4G3Y
4ZUS 4ZUT 4ZUU 4ZUV 4ZUW 4YPG 4LLD
5D7K 5D7L 5DR5 5DT1 5JUE 5L88 5LGH
5HI3 5HI4 5HI5 5AYU 5FFL 5FYJ 5IRO
5FYK 5FYL 5KN5 5DXW 5L9D 5FTT 5FTU
5KVF 5KVG 5EOR 5KZC 5E03 6739 7559
8114 8448 8824 9226 9590 10035 10194
10195 10208 10213 10262 10263 10273 3E6J
5E94

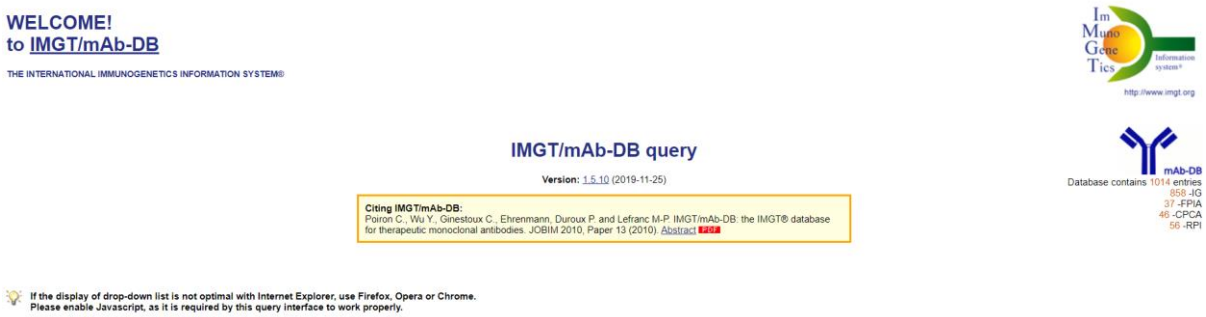
Related other IMGT® resources

Related other IMGT® resources

- IMGT/DomainDisplay
- IMGT/DomainSuperimpose tool
- IMGT/Collier-de-Perles
- IMGT/mAb-DB
- IMGT/DomainGapAlign

8. **IMGT/mAb-DB (doc) LIGM, Montpellier, France**
   Monoclonal antibodies (IG, mAb), fusion proteins for immune applications (FPIA), composite proteins for clinical applications (CPCA), and related proteins (RPI) of therapeutic interest (1 014 entries)

   Is part of IMGT®, the international ImMunoGeneTics information system®, the high-quality integrated information system specialized in immunoglobulins (IG), T cell receptors (TR), major histocompatibility complex (MHC) of human and other vertebrates species, immunoglobulin superfamily (IgSF), MHC superfamily (MhcSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates species, created in 1989 by Marie-Paule Lefranc (Laboratoire d'ImmunoGénétique Moléculaire, LIGM, Université Montpellier 2 and CNRS) and on the Web since July 1995. IMGT/mAb-DB is the IMGT® monoclonal antibodies (mAb) database. IMGT/mAb-DB provides a unique expertised resource on monoclonal antibodies (mAbs) with diagnostic or therapeutic indications, fusion proteins for immune applications (FPIA), composite proteins for clinical applications (CPCA) and relative proteins of the immune system (RPI) with clinical indications.



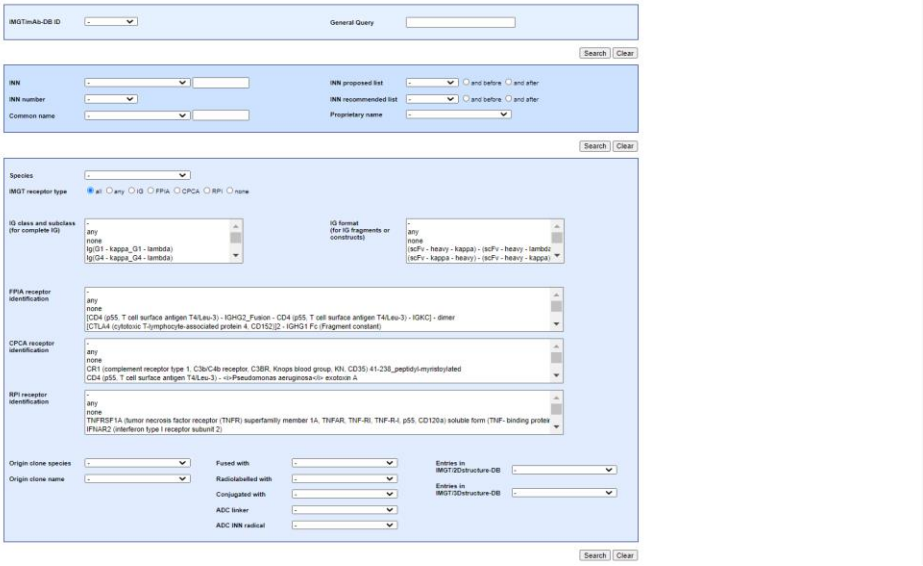
Search by:

Allows to query IMGT/mAb-DB by:

- **IMGT/mAb-DB ID** which has been defined in order to identify the IMGT/mAb-DB entries by numeric code.
- **IMGT/mAb-DB General Query** allows you to make requests on multiple fields (Currently : INN Name, common name, proprietary name, IG format, PMID, author name, publication title), even with just a part of the information.

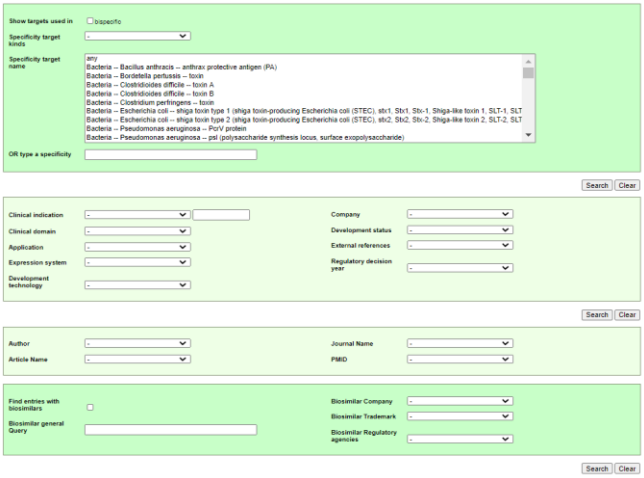
Allows to query IMGT/mAb-DB by:

- **INN (International Nonproprietary Name)** provided by WHO/INN (World Health Organization).
  The search by INN is case insensitive . A selection on INN is also possible in a drop-down list.
- **INN number**
- **INN proposed list** as published by WHO/INN.
  - **'and before' and 'and after':** allows a search of mAb published before a proposed (or recommended) list.
- **INN recommended list** as published by WHO/INN.
- **Common name** includes name found in the literature. The search by Common name is case insensitive.
- **Proprietary name** includes antibody registered trademark, usually identified by symbol ™ (not yet registered) and ® (registered). The search by Proprietary name is case insensitive.

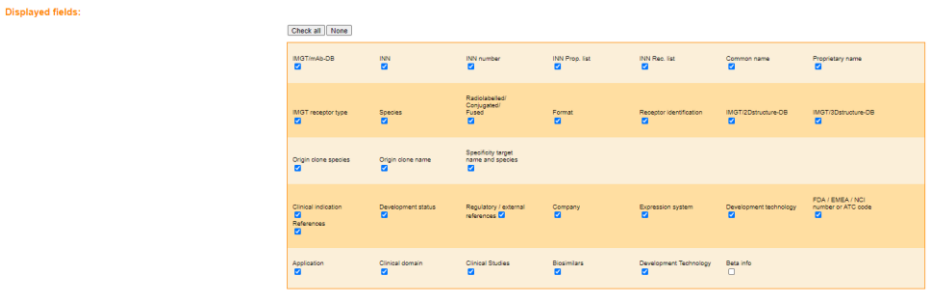


Allows to query IMGT/mAb-DB by:

- **Show** : Allows to filter the specificities by their species : human / non human
- **Specificity target species** : Allows to filter the specificities by species
- **Specificity target name**: A bispecific antibody is an antibody with two different variable domain binding sites (Fv), each binding to a different antigen. By keeping the "shift" key pressed, it's possible to select several specificity.
- **Type a specificity** : This field can be used as a wildcarded query in mAb specificities



Displayed fields: Allows to select fields to be displayed in the result of the query. Selecting criteria may force the display of corresponding fields.



IMGT Web resources

IMGT Repertoire (IG and TR, MH and RPI)
IMGT Scientific chart (Sequence and 3D structure identification and description, Numbering, Nomenclature, Representation rules)
IMGT Index (FactsBook,IMGT-NC reports,IUIS-NC,IMGT-ONTOLOGY, Sequence submission,Taxonomy...)
IMGT Bloc-notes (Interesting links, PubMed, Meeting announcements, Postdoctoral positions and jobs, Messages, Search engines...)
IMGT Education (IMGT Lexique, Aide-mémoire, Tutorials, Questions and answers, Enseignements...)
IMGT Posters and diaporama
The IMGT Medical page
The IMGT Veterinary page

The IMGT Biotechnology page
The IMGT Immunoinformatics page

IMGT tools

IMGT/V-QUEST (doc) (sequence alignment software for IG and TR)
IMGT/HighV-QUEST (doc) (NGS High-Throughput analysis of IG and TR)
IMGT/StatClonotype (doc) (Statistical analysis from IMGT/HighV-QUEST output)
IMGT/JunctionAnalysis (doc) (for human and mouse IG and TR)
IMGT/Allele-Align
IMGT/PhyloGene (doc)
IMGT/DomainDisplay (doc) (Amino acid sequences)
IMGT/LocusView, IMGT/GeneView, IMGT/GeneSearch, IMGT/CloneSearch (doc) (for human IGK, IGL, IGH, TRA/TRD, TRB, TRG, mouse TRA/TRD and human MH)
IMGT/GeneInfo (doc) (TIMC and ICH, Grenoble; LIGM, Montpellier)
IMGT/GeneFrequency (doc)
IMGT/DomainGapAlign (doc)
IMGT/Collier-de-Perles (doc)
IMGT/DomainSuperimpose (doc)
IMGT/StructuralQuery (doc)

IMGT other accesses

Compare your sequence against IMGT (BLAST, FASTA)
IMGT/LIGM-DB Sequence submission
IMGT downloads

IMGT Latest news

UPDATE 2020: Sheep (Ovisaries) TRA/TRD in IMGT/GENE-DB, IMGT/LIGM-DB and IMGT Web resources (Thu, 25 Jun 2020 12:12:36 +0200)
CREATION 2020: Arabian camel (Camelusdromedarius) IGK in IMGT/GENE-DB, IMGT/LIGM-DB and IMGT Web resources (Thu, 11 Jun 2020 11:12:05 +0200)
UPDATE 2020: Bovine (Bostaurus) TRA/TRD in IMGT/GENE-DB, IMGT/LIGM-DB and IMGT Web resources (Mon, 08 Jun 2020 12:14:56 +0200)
New version of IMGT/HighV-QUEST (version 1.7.2) (Thu, 07 May 2020 15:13:01 +0200)

SUMMER TRAINING

Report submitted in partial fulfillment of the requirements for the degree of

BACHELOR OF TECHNOLOGY

Under the supervision of

Prof. Narendra Kumar

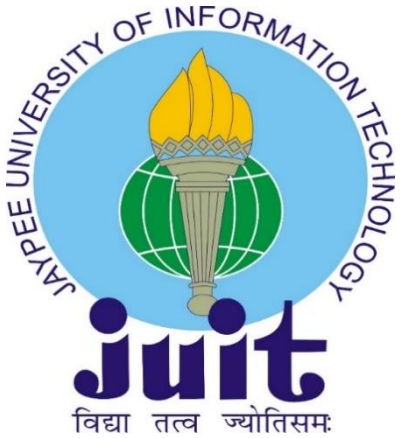
ASSISTANT

PROFESSOR DEPT. OF

BIOINFORMATICS

By

Srishti Thakur_171516



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, SOLAN, H.P.

Title : IMGT DATABASE

Introduction

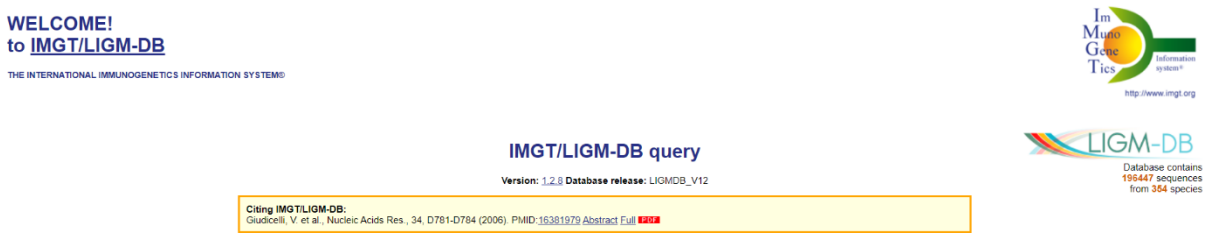
IMGT®, the international ImMunoGeneTics information system® http://www.imgt.org, is the global reference in immunogenetics and immunoinformatics, created in 1989 by Marie-PauleLefranc (Université de Montpellier and CNRS). IMGT® is a high-quality integrated knowledge resource specialized in the immunoglobulins (IG) or antibodies, T cell receptors (TR), major histocompatibility (MH) of human and other vertebrate species, and in the immunoglobulin superfamily (IgSF), MH superfamily (MhSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates. IMGT® provides a common access to sequence, genome and structure Immunogenetics data, based on the concepts of IMGT-ONTOLOGY and on the IMGT Scientific chart rules. IMGT® works in close collaboration with EBI (Europe), DDBJ (Japan) and NCBI (USA). IMGT® consists of sequence databases, genome database, structure database, and monoclonal antibodies database, Web resources and interactive tools.

About

IMGT databases

1. **IMGT/LIGM-DB (doc) LIGM, Montpellier, France**
   Nucleotide sequences of IG and TR from 354 species (196 447 entries)

   Is the first database of IMGT®, the international ImMunoGeneTics information system®, the high-quality integrated database specializing in Immunoglobulins (IG), T cell Receptors (TR) and Major Histocompatibility Complex (MHC) molecules of all vertebrate species, created in 1989 by Marie-Paule Lefranc (LIGM, Université Montpellier II, CNRS and on the web since July 1995.



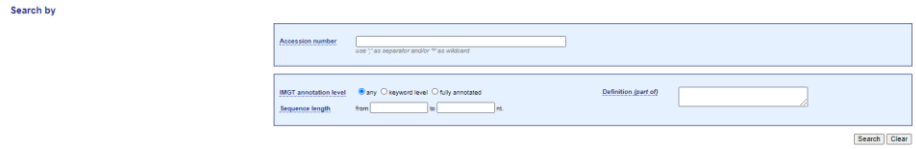
Searches by:

1.1.Search by Accession number

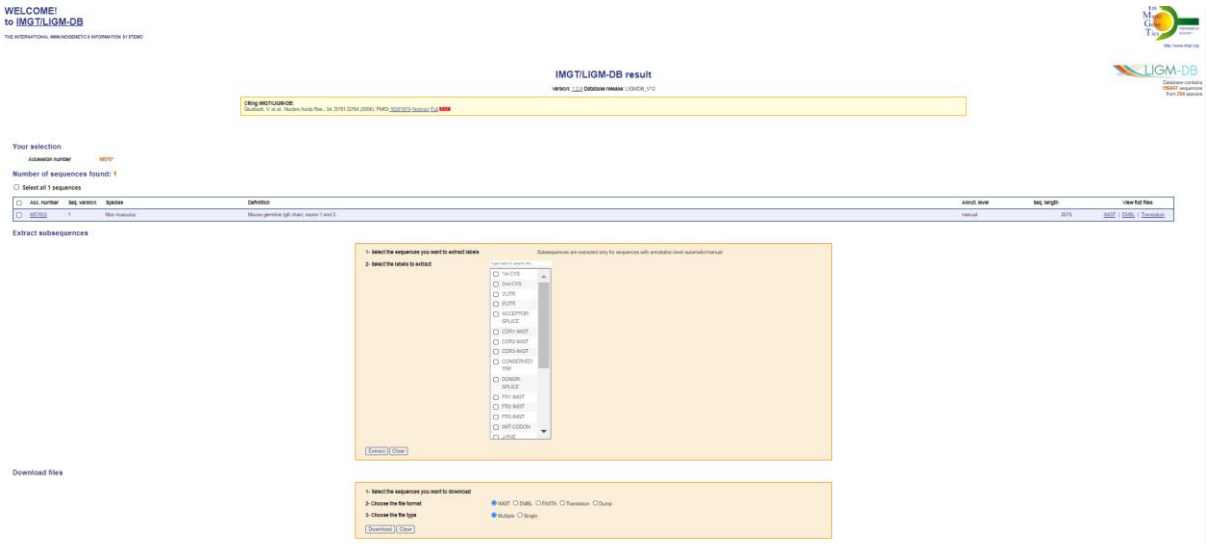
Accession number is identical to EMBL accession number. Accession number field is case sensitive, use upper case.
You can search for:

- a single accession number (ex: M94115)
- a range of accession numbers starting with a common prefix using '*' as wildcard (ex: M941*)
- several accession numbers using ';' as separator (ex: M94115; M94116; M94117)

- the combination of the two cases cited above (ex: M941*; M94349)



For example

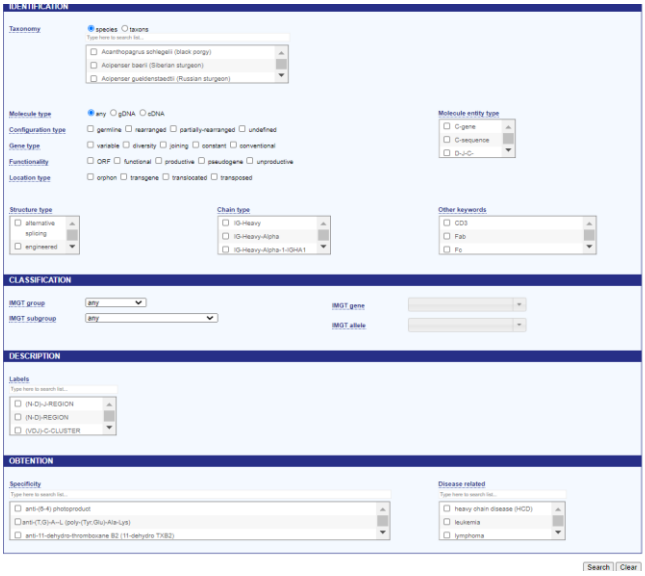


1.2.Search by IMGT-ONTOLOGY concepts

An **ontology** is a concise and non ambiguous description of the more significant and relevant **concepts** in an application domain.

IMGT-ONTOLOGY, is the first ontology which allows the management of the immunogenetics knowledge for all vertebrate species with jaws (*gnathostomata*).

The molecular synthesis and genetics of the immunoglobulin (IG) and T cell receptor (TR) chains and the polymorphism of the MH are particularly complex, and therefore one of the first tasks of IMGT-ONTOLOGY comprises a formal specification of the terms to be used in the domain of immunogenetics and bioinformatics, of the rules for IMGT gene nomenclature and for the numbering of amino acids and codons.



1.3.Search by bibliographical references

Author Sequences can be retrieved by the name of the author of their associate Author field is not case sensitive.

Check "first author only" option to restrict your **search** on on first author only. This option is available only if an author name is entered in author field.

Type Select 'any' to not restrict your **search** on one reference type.

Journal This field is shown only if Type field above is set on 'Journal'.

PMID Sequences can be retrieved by their associated reference's PMID, you can enter several PMIDs using ';' as separator

Year Sequences can be retrieved by their associated reference's year. Sequences in **IMGT**/LIGM-DB are linked to **references** from 1971 to now.

2. Title *(part of)* Sequences can be retrieved by the exact title or a part of the title of their associated **references**. The title field is not case sensitive.



3. **IMGT/MH-DB ANRI, BPRC, hosted at EBI**
Sequences of the human MH (HLA) is the global reference in immunogenetics and immunoinformatics, created in 1989 by Marie-Paule Lefranc (Université de Montpellier and CNRS). IMGT® is a high-quality integrated knowledge resource specialized in the immunoglobulins (IG) or antibodies, T cell receptors (TR), major histocompatibility (MH) of human and other vertebrate species, and in the

immunoglobulin superfamily (IgSF), MH superfamily (MhSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates. IMGT® provides a common access to sequence, genome and structure Immunogenetics data, based on the concepts of IMGT-ONTOLOGY and on the IMGT Scientific chart rules.



4. **IMGT/PRIMER-DB (doc) LIGM, Montpellier, France**
   Oligonucleotides (primers) of IG and TR from 11 species (1 864 entries)
   An IMGT/PRIMER-DB primer is an oligonucleotide defined, classified and described by comparison to an IMGT/LIGM-DB reference sequence.

- This provides the following advantages for the data standardization:
  - IMGT/PRIMER-DB primers can easily be compared to data from the other IMGT databases (IMGT/LIGM-DB, IMGT/GENE-DB, IMGT/3Dstructure-DB), IMGT Web resources (IMGT Repertoire) and tools (IMGT/V-QUEST, IMGT/PhyloGene). These data are described according to the standardized rules of the IMGT Scientific chart, based on IMGT-ONTOLOGY.
  - IMGT/PRIMER-DB primer definition, classification and description are independent from the experimental conditions, from DNA sources and from the different combinations (sets and couples) in which the primer can be used. That means that (i) the specificity of a primer (subgroup, gene or allele specific) which is either described experimentally or deduced from sequence comparison is not used for the primer classification, although these data are provided in the IMGT/PRIMER-DB Primer card in Classification comments and specificity, (ii) the sequences resulting from the PCR amplifications are uniquely associated to the couples.
- An IMGT/PRIMER-DB set consists of IMGT/PRIMER-DB primers sharing identical properties (species, group and orientation). An IMGT/PRIMER-DB set may be composed of only one IMGT/PRIMER-DB primer.
- An IMGT/PRIMER-DB couple consists of sets of opposite orientation for which IMGT/LIGM-DB sequences are known (or expected). An IMGT/PRIMER-DB couple comprises a Sense IMGT/PRIMER-DB set and an Antisense IMGT/PRIMER-DB set. For example, an IMGT/PRIMER-DB couple may consists of Sense IMGT/PRIMER-DB sets of V regions associated to Antisense IMGT/PRIMER-DB sets of C regions.



Search by:

4.1. Search by accession number:

4.1.1. **IMGT/PRIMER-DB Primer accession number**(IPP) Unique identifier of each primer in IMGT/PRIMER-DB.
Consists of 3 letters "IPP" (for IMGT/PRIMER-DB Primer) and 6 numbers.

4.1.2. **IMGT/PRIMER-DB Set accession number**(IPS) Unique identifier of each set in IMGT/PRIMER-DB.
Consists of 3 letters "IPS" (for IMGT/PRIMER-DB Set) and 6 numbers.

4.1.3. **IMGT/PRIMER-DB Couple accession number**(IPC) Unique identifier of each couple in IMGT/PRIMER-DB.
Consists of 3 letters "IPC" (for IMGT/PRIMER-DB Couple) and 6 numbers.

4.2.Or select IMGT/PRIMER-DB primers according to criteria:



4.3.Or select IMGT/PRIMER-DB sets: consists of IMGT/PRIMER-DB primers sharing identical properties (species, group and orientation). An IMGT/PRIMER-DB set may be composed of only one IMGT/PRIMER-DB primer.



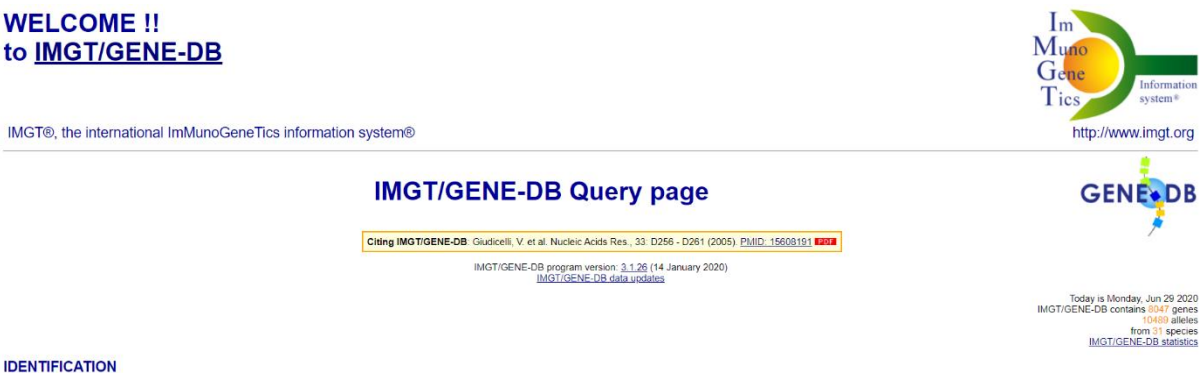
5. IMGT/CLL-DB (bylaws) LIGM, Montpellier, France
G sequences from CLL, an initiative of the IMGT/CLL-DB group

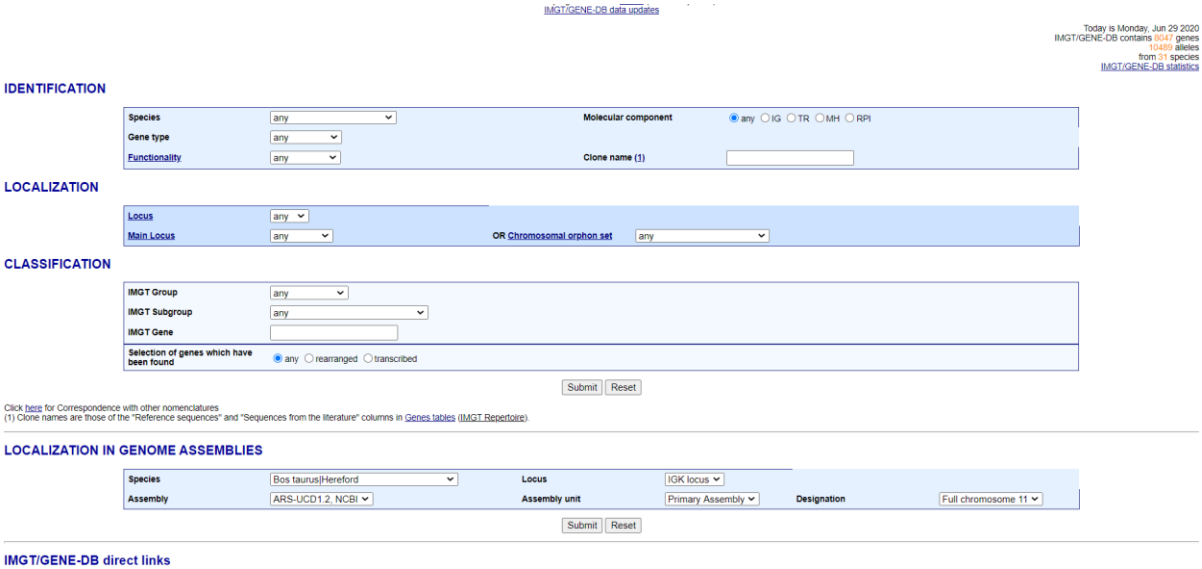


IMGT/CLL- DB GROUP

About us:
The **IMGT/CLL-DB group** is a joint academic initiative between IMGT® and ERIC, The European Research Initiative on CLL (http://www.ericll.org/), devoid of any commercial interest. Its primary aim is to develop and maintain a database with immunogenetic data from patients with Chronic Lymphocytic Leukemia (CLL) attended at academic institutions, to foster high-quality collaborative research on CLL and related disorders. The database system specifications fulfill the storage requirements in order to efficiently manage the continuously increasing amount of data collected and stored into the database. The main outlet for the IMGT/CLL-DB is a purpose-built interactive platform providing all data, information and knowledge to members in a user-friendly yet robust way.

6. **IMGT/GENE-DB (doc) LIGM, Montpellier, France**
   International nomenclature for IG and TR genes from human, mouse, rat and rabbit (8 047 genes, 10 489 alleles) MGT/GENE-DB is the IMGT genome database for IG and TR genes from human, mouse and other vertebrates, on the Web since February 2003. IMGT/GENE-DB provides a full characterization of the genes and of their alleles: IMGT gene name and definition, chromosomal localization, number of alleles, and for each allele, the IMGT allele functionality, and the IMGT reference sequences and other sequences from the literature. IMGT/GENE-DB allele reference sequences are available in FASTA format (nucleotide and amino acid sequences with IMGT gaps according to the IMGT unique numbering, or without gaps). IMGT/GENE-DB includes links to the IMGT Repertoire standardized resources (Chromosomal localization, Locus representation, Tables of alleles, Alignments of alleles, IMGT Protein displays, IMGT Colliers de Perles, etc.), to the IMGT/LIGM-DB and IMGT/3Dstructure-DB structures and IMGT/2Dstructure-DB IMGT databases.





IDENTIFICATION

Species:
only species for which genes have been entered in IMGT/GENE-DB are available.
MolecularComponent:
IG or TR.
GeneType:
allows the selection on one of the gene types.
Functionality:
allows the selection on IG and TR functionality.
Clone name:
enter a clone name or the first letters of a clone name. Clone names are those of the "Reference sequences" and "Sequences from the literature" columns in Genes tables.

CLASSIFICATION

IMGT group:
allows the selection on IMGT groups.
IMGT subgroup:
allows the selection on IMGT subgroups.
IMGT gene:
enter an IMGT gene name, for example IGHV1-2 (List of human genes according to the IMGT nomenclature).

Note that the search is case sensitive and that UPPERcase is the rule.

You can also enter only the first letters of the IMGT gene name: for example the selection of IGHV will list in the next page all genes which have an IMGT gene name beginning with IGHV.

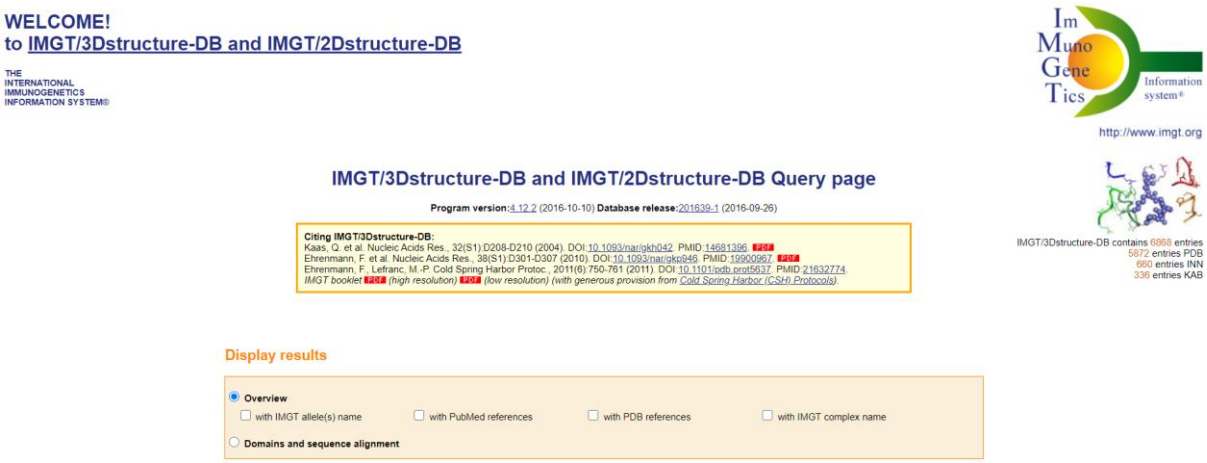
LOCALIZATION

Locus:
allows the selection on IG and TR loci (includes main loci and chromosomal orphon sets).
Main Locus:
allows the selection on a main IG or TR locus.
Chromosomal orphon set:

allows the selection on IG or TR genes which are outside the main loci or Chromosomal orphon set.

As Main Locus may contain RPI genes, a selection on 'Molecular component' 'IG' or 'TR' prior to the request will allow to only retrieve IG or TR genes.

7. **IMGT/3Dstructure-DB and IMGT/2Dstructure-DB (doc) LIGM, Montpellier, France**
   3D structures (IMGT Colliers de Perles) of IG antibodies, TR, MH and RPI (6 868 entries)
   Source: PDB, INN, Kabat
   The IMGT/3Dstructure-DB Query page shows, at the top of the page, the status of the database (Current date, the total number of entries and its decomposition (PDB, INN) and the date of the last update) and at the bottom of the page, the last entries and the access to the IMGT tools (IMGT/DomainDisplay, IMGT/Collier-de-Perles, IMGT/DomainGapAlign, IMGT/DomainSuperimpose and IMGT/mAb-DB).



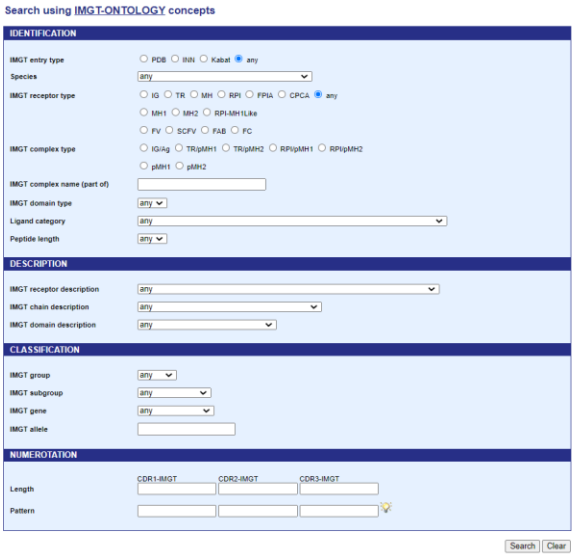
7.1.Search by Entry code or Molecule name(receptor or ligand)

The IMGT/3Dstructure-DB entry code (ID) is identical to the PDB code, INN code or PROTEIN code. PDB code is an alphanumeric code (Ex : 1ao7), INN code is a numeric code (Ex: 7637) while PROTEIN code is an alphanumeric code which lenght is equals to 6 (Ex : p00054).

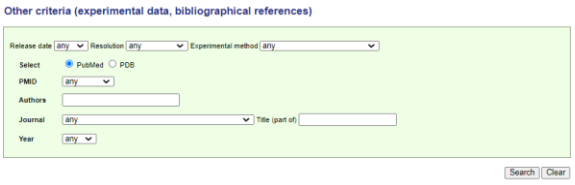
An AutoComplete behavior is available for this field. AutoComplete works in the following manner: as you type in the beginning of a PDB code previous entries are pulled from a storage area and you may elect to simply select one of these entries. By selecting an entry, you no longer have to input the string because AutoComplete finishes entering the string for you.

7.2.Search using IMGT-ONTOLOGY concepts

This section allows users to search entries using the IMGT-ONTOLOGY concepts (IDENTIFICATION, DESCRIPTION, CLASSIFICATION and NUMEROTATION) for each type of IMGT entry. This kind of search uses linked select elements. Linked select elements are two or more selects, where choosing a value in one changes the available values in some of the rest. For example, selecting an IMGT receptor type will updates the 'IMGT receptor description' select to only contain receptor description from the IMGT receptor type selected. In the same way, selecting an IMGT group will updates the 'IMGT subgroup' select to only contain subgroup(s) from the IMGT group selected.
Choose an **IMGT entry type** and then a: Species (also includes Camelized, Chimeric, Humanized, Caninized and Synthetic), IMGT receptor type (IG, TR, MH, RPI, FPIA or Any), IMGT receptor description, IMGT chain description, IMGT group, IMGT subgroup, IMGT gene or IMGT allele.



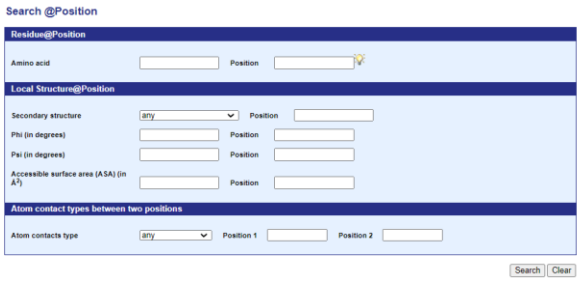
7.3.Other criteria (experimental data, bibliographical references)



7.4.Search @position

The form allows an easy search by the following criteria:

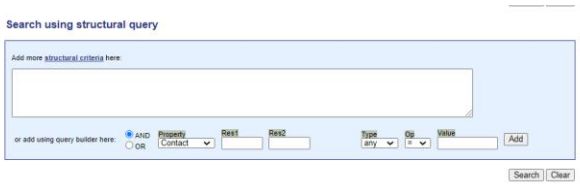
- Residue@Position, that is presence of a given amino acid at a given position. Position is according to the IMGT unique numbering
- Local Structure@Position, with the following criteria:
  - Secondary structure (alpha helix, 3-10 helix, PI-helix, extended conformation, isolated bridge, turn or coil)
  - Phi and Psi angles (in degrees)
  - Accessible surface area (ASA) in angstrom^2 (Å^2)
- Atom contact type between two positions



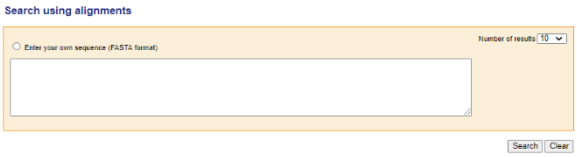
7.5.Search using structural query

A complex query can be performed. It is made up of a list of structural criteria coordinated by parentheses and boolean operator (AND and OR).
The query can be entered in the text area, either manually, or with the Javascript helper tool (available below the text area). The selection of a structural criteria in the scrolling list of the helper tool will show the corresponding fields to be filled in. A 'Quick Help' is available for each criterion.
The different criteria currently implemented are:

- *Contact*: Atom contact type between two positions. Example: 'contact(111V,108V,HB)>0' will query for IMGT/3Dstructure-DB entries which contain an hydrogen bond between position 111 and 108 in a V type domain (111V,108V)
- *HB*: Hydrogen bond between two amino acids (STRIDE hydrogen bonds). Example: 'HB(111V,108V)' will query for IMGT/3Dstructure-DB entries which contain an hydrogen bond between position 111 and 108 in a V type domain (111V,108V) as determined using the algorithm STRIDE
- *SS*: Secondary structure of a given residue. Example: 'SS(112V)=H' will query for IMGT/3Dstructure-DB entries which contain at position 112 in a V type domain (112V) a residue in the phi/psi helix conformation
- *Phi* and *Psi*: Amino acid φ and ψ angles in degrees
- *ASA*: Accessible surface area (in square angstroms, $Å^2$)
- *AA*: Amino acid type is in the one letter abbreviation. Example: 'aa(89V)=M' will query for IMGT/3Dstructure-DB entries which contain at position 89 in a V type domain (89V) a methionine (=M)
- *Length* and *Pattern*: CDR-IMGT length (only available for the V type domain)
- *Pattern*: Amino acid pattern in a CDR-IMGT. As an example '[GSE]..L..Y' will query for IMGT/3Dstructure-DB entries which contain sequences with a CDR-IMGT pattern starting with an G,S or E, the fourth amino acid being a leucine and the seventh amino acid being a tyrosine
- *Description*: IMGT domain description
- *Species*: Species here includes humanized, camelized, chimeric and synthetic
- *Group*: Structure's gene group
- *Gene*: Wanted gene name



7.6.Search using alignments



New or updated entries:

New or updated entries

1CDH 1HH6 1G9M 1FG9 1EZV 1EKU 1AU1
1P84 1NBP 1KB9 1M47 1QVN 1M48 1M49
1M4A 1M4B 1M4C 1HIG 1PW6 1PY2 1KYO
2H3N 2CR3 2O6Q 2IBZ 2ZNX 2RCJ 2H32
3G9V 3MJ6 3MJ7 3MJ9 3WD5 3DJ9 3BES
3WHE 3CXH 3NN8 3RA7 3INK 3VI3 3VI4
3TWI 3BJ9 3DIF 3QB1 3G3A 3SE3 3REV
3MOD 3JZ7 3M18 3M19 4YAQ 4G6M 4FHB
4RRP 4ZS7 4YDL 4K5U 4NEJ 4NEM 4G3Y
4ZUS 4ZUT 4ZUU 4ZUV 4ZUW 4YPG 4LLD
5D7K 5D7L 5DR5 5DT1 5JUE 5L88 5LGH
5HI3 5HI4 5HI5 5AYU 5FFL 5FYJ 5IRO
5FYK 5FYL 5KN5 5DXW 5L9D 5FTT 5FTU
5KVF 5KVG 5EOR 5KZC 5E03 6739 7559
8114 8448 8824 9226 9590 10035 10194
10195 10208 10213 10262 10263 10273 3E6J
5E94

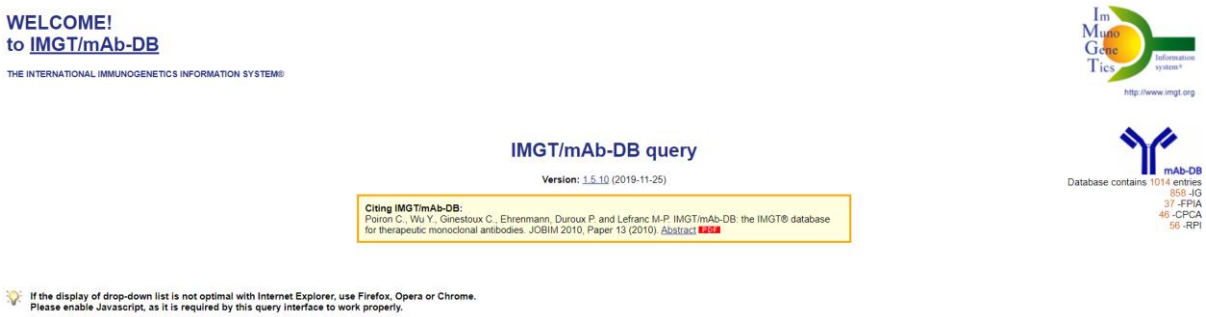
Related other IMGT® resources

Related other IMGT® resources

- IMGT/DomainDisplay
- IMGT/DomainSuperimpose tool
- IMGT/Collier-de-Perles
- IMGT/mAb-DB
- IMGT/DomainGapAlign

8. **IMGT/mAb-DB (doc) LIGM, Montpellier, France**
   Monoclonal antibodies (IG, mAb), fusion proteins for immune applications (FPIA), composite proteins for clinical applications (CPCA), and related proteins (RPI) of therapeutic interest (1 014 entries)

   Is part of IMGT®, the international ImMunoGeneTics information system®, the high-quality integrated information system specialized in immunoglobulins (IG), T cell receptors (TR), major histocompatibility complex (MHC) of human and other vertebrates species, immunoglobulin superfamily (IgSF), MHC superfamily (MhcSF) and related proteins of the immune system (RPI) of vertebrates and invertebrates species, created in 1989 by Marie-Paule Lefranc (Laboratoire d'ImmunoGénétique Moléculaire, LIGM, Université Montpellier 2 and CNRS) and on the Web since July 1995. IMGT/mAb-DB is the IMGT® monoclonal antibodies (mAb) database. IMGT/mAb-DB provides a unique expertised resource on monoclonal antibodies (mAbs) with diagnostic or therapeutic indications, fusion proteins for immune applications (FPIA), composite proteins for clinical applications (CPCA) and relative proteins of the immune system (RPI) with clinical indications.



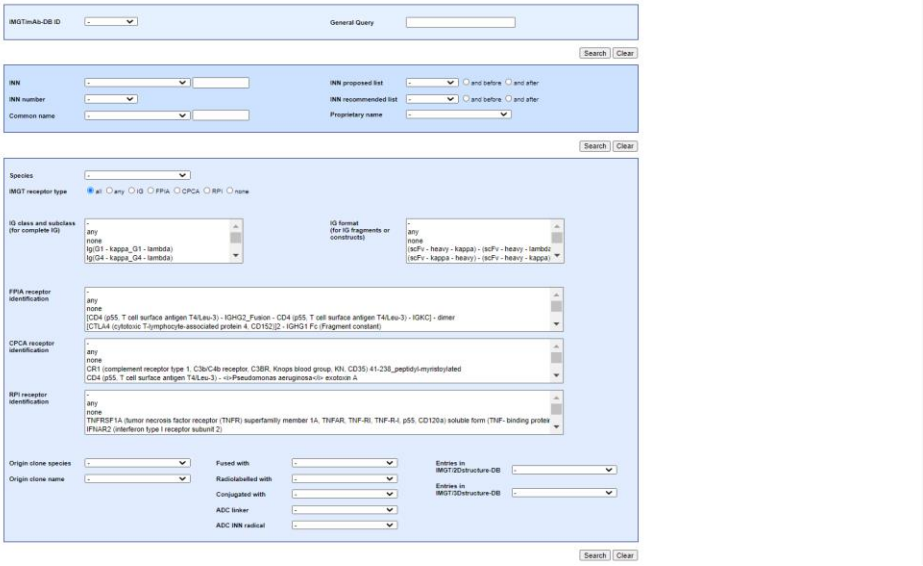
Search by:

Allows to query IMGT/mAb-DB by:

- **IMGT/mAb-DB ID** which has been defined in order to identify the IMGT/mAb-DB entries by numeric code.
- **IMGT/mAb-DB General Query** allows you to make requests on multiple fields (Currently : INN Name, common name, proprietary name, IG format, PMID, author name, publication title), even with just a part of the information.

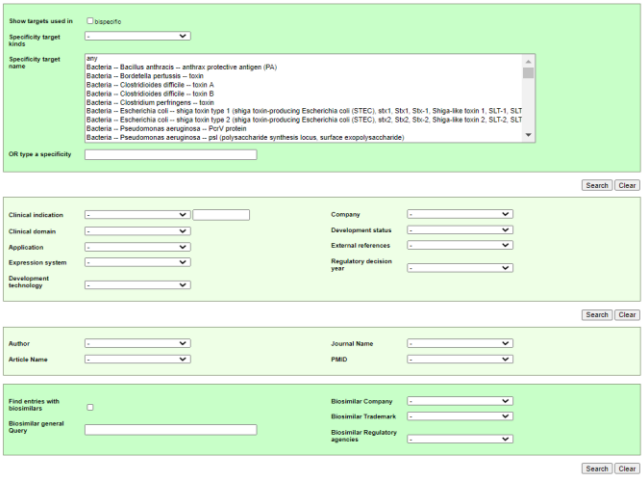
Allows to query IMGT/mAb-DB by:

- **INN (International Nonproprietary Name)** provided by WHO/INN (World Health Organization).
  The search by INN is case insensitive . A selection on INN is also possible in a drop-down list.
- **INN number**
- **INN proposed list** as published by WHO/INN.
  - **'and before' and 'and after':** allows a search of mAb published before a proposed (or recommended) list.
- **INN recommended list** as published by WHO/INN.
- **Common name** includes name found in the literature. The search by Common name is case insensitive.
- **Proprietary name** includes antibody registered trademark, usually identified by symbol ™ (not yet registered) and ® (registered). The search by Proprietary name is case insensitive.

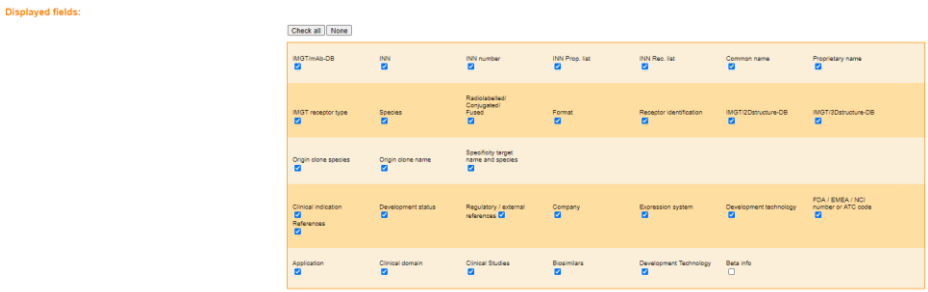


Allows to query IMGT/mAb-DB by:

- **Show** : Allows to filter the specificities by their species : human / non human
- **Specificity target species** : Allows to filter the specificities by species
- **Specificity target name**: A bispecific antibody is an antibody with two different variable domain binding sites (Fv), each binding to a different antigen. By keeping the "shift" key pressed, it's possible to select several specificity.
- **Type a specificity** : This field can be used as a wildcarded query in mAb specificities



Displayed fields: Allows to select fields to be displayed in the result of the query. Selecting criteria may force the display of corresponding fields.



IMGT Web resources

IMGT Repertoire (IG and TR, MH and RPI)
IMGT Scientific chart (Sequence and 3D structure identification and description, Numbering, Nomenclature, Representation rules)
IMGT Index (FactsBook,IMGT-NC reports,IUIS-NC,IMGT-ONTOLOGY, Sequence submission,Taxonomy...)
IMGT Bloc-notes (Interesting links, PubMed, Meeting announcements, Postdoctoral positions and jobs, Messages, Search engines...)
IMGT Education (IMGT Lexique, Aide-mémoire, Tutorials, Questions and answers, Enseignements...)
IMGT Posters and diaporama
The IMGT Medical page
The IMGT Veterinary page

The IMGT Biotechnology page
The IMGT Immunoinformatics page

IMGT tools

IMGT/V-QUEST (doc) (sequence alignment software for IG and TR)
IMGT/HighV-QUEST (doc) (NGS High-Throughput analysis of IG and TR)
IMGT/StatClonotype (doc) (Statistical analysis from IMGT/HighV-QUEST output)
IMGT/JunctionAnalysis (doc) (for human and mouse IG and TR)
IMGT/Allele-Align
IMGT/PhyloGene (doc)
IMGT/DomainDisplay (doc) (Amino acid sequences)
IMGT/LocusView, IMGT/GeneView, IMGT/GeneSearch, IMGT/CloneSearch (doc) (for human IGK, IGL, IGH, TRA/TRD, TRB, TRG, mouse TRA/TRD and human MH)
IMGT/GeneInfo (doc) (TIMC and ICH, Grenoble; LIGM, Montpellier)
IMGT/GeneFrequency (doc)
IMGT/DomainGapAlign (doc)
IMGT/Collier-de-Perles (doc)
IMGT/DomainSuperimpose (doc)
IMGT/StructuralQuery (doc)

IMGT other accesses

Compare your sequence against IMGT (BLAST, FASTA)
IMGT/LIGM-DB Sequence submission
IMGT downloads

IMGT Latest news

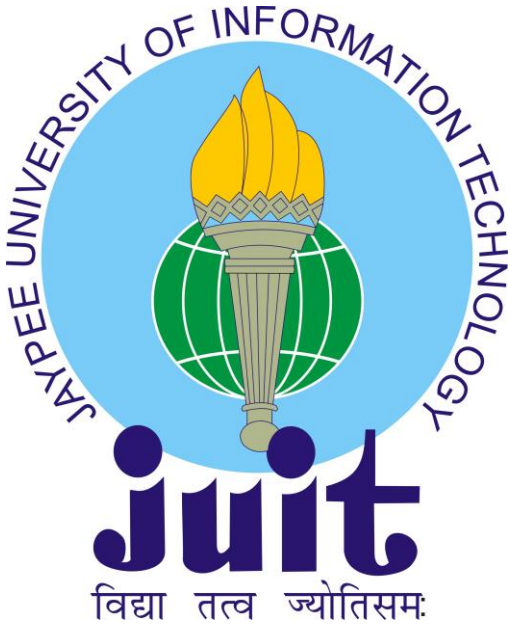
UPDATE 2020: Sheep (Ovisaries) TRA/TRD in IMGT/GENE-DB, IMGT/LIGM-DB and IMGT Web resources (Thu, 25 Jun 2020 12:12:36 +0200)
CREATION 2020: Arabian camel (Camelusdromedarius) IGK in IMGT/GENE-DB, IMGT/LIGM-DB and IMGT Web resources (Thu, 11 Jun 2020 11:12:05 +0200)
UPDATE 2020: Bovine (Bostaurus) TRA/TRD in IMGT/GENE-DB, IMGT/LIGM-DB and IMGT Web resources (Mon, 08 Jun 2020 12:14:56 +0200)
New version of IMGT/HighV-QUEST (version 1.7.2) (Thu, 07 May 2020 15:13:01 +0200)

Automated Personality Classification Using Data Mining Techniques

Enrolment No. - **171517**

Name of the student – **Aakanksha Gautam**

Name of Supervisor – **Dr. Tiratha Raj Singh**



June, 2020

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS,

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY,

WAKNAGHAT, SOLAN 173234, HIMACHAL PRADESH, INDIA

ACKNOWLEDGEMENT

I would like to begin by thanking my supervisor Dr. Tiratha Raj Singh, Associate Professor at the Department of Biotechnology and Bioinformatics in Jaypee University of Information Technology, for giving me the opportunity to work with him. His immense understanding and curiosity in research allowed me to learn many things. His guidance and encouragement were indispensable in completing this dissertation.

Aakanksha Gautam

Candidate's Declaration

I hereby declare that the work presented in this report entitled "Automated Personality Classification using Data Mining Techniques" in the partial fulfilment of the requirement for the Summer Training submitted in the department of Biotechnology and Bioinformatics, Jaypee University of Information Technology Waknaghat is an record of my own work and carried out over a period from 16 May 2020 to 30 June 2020 under the supervision of Dr. Tiratha Raj Singh.



Aakanksha Gautam(171517)

This is to certify that the above statement made by the candidate is true to the best of my knowledge.



Dr. Tiratha Raj Singh

Dated: 30/062020

TABLE OF CONTENTS

ABSTRACT

INTRODUCTION

LITERATURE REVIEW

Novel approaches to automated personality classification: Ideas and their potentials

Using Twitter Content to predict Psychopathy

Educational Game (Detecting personality of players in an educational game)

System for Personality and Happiness Detection

Predicting Personality with Social Media

An examination of online learning effectiveness using data mining

PROPOSED WORK

Naïve Bayes Algorithm

Support Vector Machine

Big Five Personality Traits

RESULT ANALYSIS

CONCLUSION

FUTURE OUTCOMES

REFRENCES

ABSTRACT

Personality is one feature that determines how people interact with the outside world. Personality can be defined as a necessary element of a person's behaviour. The way people interact with other people determines their personality. This paper covers the topic of Automated Personality Classification – a system that analyses the personality of a user based on certain features using Data Mining Algorithms. In this paper, we propose a system which analyses the personality of an applicant. This system will be helpful for organizations as well as other agencies who would be recruiting applicants based on their personality rather than their technical knowledge. The personality prediction results are based on Big Five Personality traits and the classification is done using Naïve Bayes Algorithm and Support Vector Machine.

• INTRODUCTION

Personality classification has been one of the most researched topics in the recent past. Personality is a combination of an individual's behaviour and characteristics features that determines how he/she reacts under different situations. Personality can influence what all choices a person makes regarding various things like books, clothes, music and films [1]. Personality can also affect his/her interaction with the outside world and his/her environment. Personality can also be used as an additional feature during recruitment process, career counselling, health counselling, etc.

Predicting personality by analyzing the behaviour of the person is an old technique. This manual method of personality prediction required a lot of time and resources. Analyzing personality based on one's nature was a tedious task and a lot of human effort would be required to do such analysis. This traditional method of predicting personality would require a lot of time and was very limited in scale. Also, this manual analysis did not give accurate results while analyzing the personality of a user from their nature and behaviour. Since analysis was done manually, it affected the accuracy of the results as humans are prone to biases and prejudices.

Data mining techniques are therefore used to study and analyze data and then identify any hidden patterns or information from a large data set. These techniques are used to mine user characteristics and then train the model accordingly to predict the personality of other users in the future. Using these techniques, we can analyze the personality of an applicant applying for a job in an organization which gives priority to one's behaviour and personality rather than technical knowledge. Also, the applicant gets to know what all personality traits are in him/her and what all traits are missing. Thus, we can then guide him/her to develop those traits or to strengthen the other traits accordingly.

The main objective of this paper is to overview the data mining algorithms which are used to predict the personality of the user. In this paper, we focus on an online test which would be given by the applicant and then his/her personality would be predicted accordingly based on the Big Five Personality traits. In this way, we can filter out candidates applying for a specific position in the organization. Thus, it would save the resources of the organization and they would then interview only those candidates which would be most suitable for the job.

- # LITERATURE REVIEW

1. Novel approaches to automated personality classification: Ideas and their potentials

This paper [2] has proposed various new researches regarding the concept of Automated Personality Classification. Firstly, all the possible solutions are examined and what all improvements can be made to the existing problems of Automated Personality Classification. Then the extension of the Automated Personality Classification [APC] problem such as the Dynamic APC is considered and how to remove inconsistency in textual data. This entire research was carried out in the context of social networks and related data mining mechanisms.

2. Using Twitter Content to predict Psychopathy

Twitter, a micro blogging site, is used by a number of users to share their experiences and thoughts about their day-to-day life. Although researchers have often discarded the method of predicting personality by analyzing the tweets because they are of the view that it contains very little content to predict significant information, but these tweets can be combined to make a larger picture of the user who is posting them. Select RUSBoost [3], a new form of ensemble learning has been used to predict psychopathy using Twitter, which uses four classification learners and four feature selection techniques.

3. Educational Game (Detecting personality of players in an educational game)

Education Data Mining [4] aims at developing methods for modeling student behavior based on data such as chat conversations, discussions in class, etc. However, methods like Intelligent Tutoring System (ITS) and Educational Data Mining (EDM) used individual's behavior and personality for analysis purpose. Thus, a user adaptable system is developed which analyses student's behavior during their interaction using methods like Intelligent Tutoring System and Educational Data Mining.

4. System for Personality and Happiness Detection

This [5] work proposed a system for predicting the personality and happiness of a user. According to Eysenck's theory of human personality, the authors built a system wherein they would collect the text messages from social media such as Facebook and Twitter and then classify them into various personality types. Although a clear link between personality features and happiness cannot be established, however some correlation does exist between them which could be found in the coming future.

5. Predicting Personality with Social Media

Social media [6] is a place where the users tend to present themselves to the outside world, sharing their personal details and giving insights to other people into their lives. Personality plays an important part in many types of interactions among people; it can be used to predict the job satisfaction, professional as well as romantic relationship success. Until now, in order to accurately predict user's personality, they needed to take a personality test. However, this was highly impractical while collecting data from social media platforms and hence correct analysis of personality was a problem.

6. An examination of online learning effectiveness using data mining

Online learning [7] has become highly popular because of technological advancement that makes it possible to have discussions even from a distance. Most studies that have been conducted report how effective online learning has helped students to improve their learning power while assessing the learning process simultaneously. It is possible by applying data mining technique wherein we can assess the students' online learning experiences on the basis of their log files. However, students need to spend more effort to be a successful silent learner as is suggested by the produced predictive model.

- # PROPOSED WORK

To counter the problems of the existing system, we have proposed an Automatic Personality Classification system which uses Data Mining techniques to classify the personality of the applicants. The system uses algorithms like Naïve Bayes, Support Vector Machine and Big Five Model along with advanced data mining to mine user characteristics data and learn from the patterns. This learning can now be used to classify/predict user personality based on past classifications. The system analyses vast user characteristics and behaviours and based on the patterns observed, it stores its own user characteristics patterns in the database. The system now predicts new user personality based on personality data stored by classification of previous user data. This system is useful for predicting personality of applicants applying for various roles in an organization. We have designed an Automatic Personality Classification system in which every applicant is given a separate user name and password. Each applicant logins the test using his/her user name and password and then takes the survey. The survey consists of 30 questions, where each question determines one of the Big Five Personality traits. Once the applicant takes the survey of 30 questions, he/she can see the result of his/her personality. The survey analyses the personality of the applicant based on the Big Five Personality traits. We have also displayed a graph based on various qualifications specified by the applicants in the registration page. The graph then predicts which all candidates are suitable for a particular job opening in an organization. The algorithms like Naïve Bayes and Support Vector Machine groups the qualities of the applicants of different streams and a graph is shown which depicts the which set of candidates would be most suitable for a particular post in the organization. This type of graph will be helpful in screening the candidates and would save the resources of the organization. The organization, on seeing the graph, can call only those applicants belonging to a particular stream whose scores are greater than the score of applicants of other streams. Thus, this type of system would be cost effective for an organization as well as provide accurate results for choosing applicants for a particular job.

- ***Naïve Bayes Algorithm***

Naïve Bayes Algorithm, which is a type of an inductive learning algorithm, is considered to be one of the most efficient and effective algorithms that is widely used in data mining. The performance of Naïve Bayes Algorithm in classifying data is quite accurate because the conditional independence assumption on which the entire algorithm is set up is rarely true for the real world applications. The application of Bayes theorem forms the basis of Naïve Bayes Algorithm [8]. A variation of Naïve Bayes Algorithm is Multinomial Naïve Bayes Algorithm which is also designed for classification purposes. The Multinomial Naïve Bayes Algorithm uses multinomial distribution in which it considers the either the number of times a particular word occurred or the weight of that particular word as a classification feature. The Naïve Bayes algorithm combines both efficiencies i.e. optimal time performances with reasonable accuracy. The only theoretical drawback of the Naïve Bayes Method is that it assumes conditional independence to be within the linguistic features. However, even if the Naïve Bayes Algorithm produces an oversimplified model, the classification results which it produces are surprisingly accurate. In our system datasets, the results are either stored in the form of accurate or inaccurate. Hence the entire working of the system depends on the corresponding probabilities of either accurate or inaccurate. The steps involved in the Naïve Bayes Algorithm are:

- The dataset is converted into a frequency table.
- Likelihood table is created by finding the probabilities of each and every question.
- Naïve Bayesian equations are then used to calculate the posterior probability of each class. The class with highest probability is then the outcome of the prediction.

2. Support Vector Machine

Support Vector Machine which is a type of supervised learning algorithm analyses the data and recognizes pattern for classification purposes [8]. A set of training data is taken and then it is marked as a part of category to predict whether the test document is a member of an existing class or not. The Support Vector Machine models represent the data set in the form of a point in space which is divided by either a line or hyperplane. The main idea behind the support vector machine algorithm is that if a classifier performs well at the most challenging comparisons, then it will definitely perform even better at the easiest comparisons. Support Vector Machine which is a nonlinear classifier often produces superior classification results than other classifier methods. Support Vector Machine is based on non-linearly mapping the input data to some high dimensional space where the data is separated linearly, thus giving accurate classification results. The steps involved in Support Vector Machine are:

- Create vectors for given question answers.
- Then calculate the weights of the vectors.
- Get the vectors with highest value and find value of personality
- Finally predict personality type

3.Big Five Personality Traits

The Big Five Personality traits are the five dimensions or the domains of personality that can be used to analyze or predict the personality of a user [9]. The Big Five Factors are:

- Openness to Experience or Imagination Capability
- Agreeableness
- Extraversion
- Neuroticism or Emotional Stability
- Conscientiousness

The Big Five Personality Model is the most widely accepted and researched model for predicting the personality of a user. The Big Five Personality traits are found in a variety of people of different ages, locations and cultures. The Big Five Personality results are very accurate and predict the true personality of a user to a large extent.

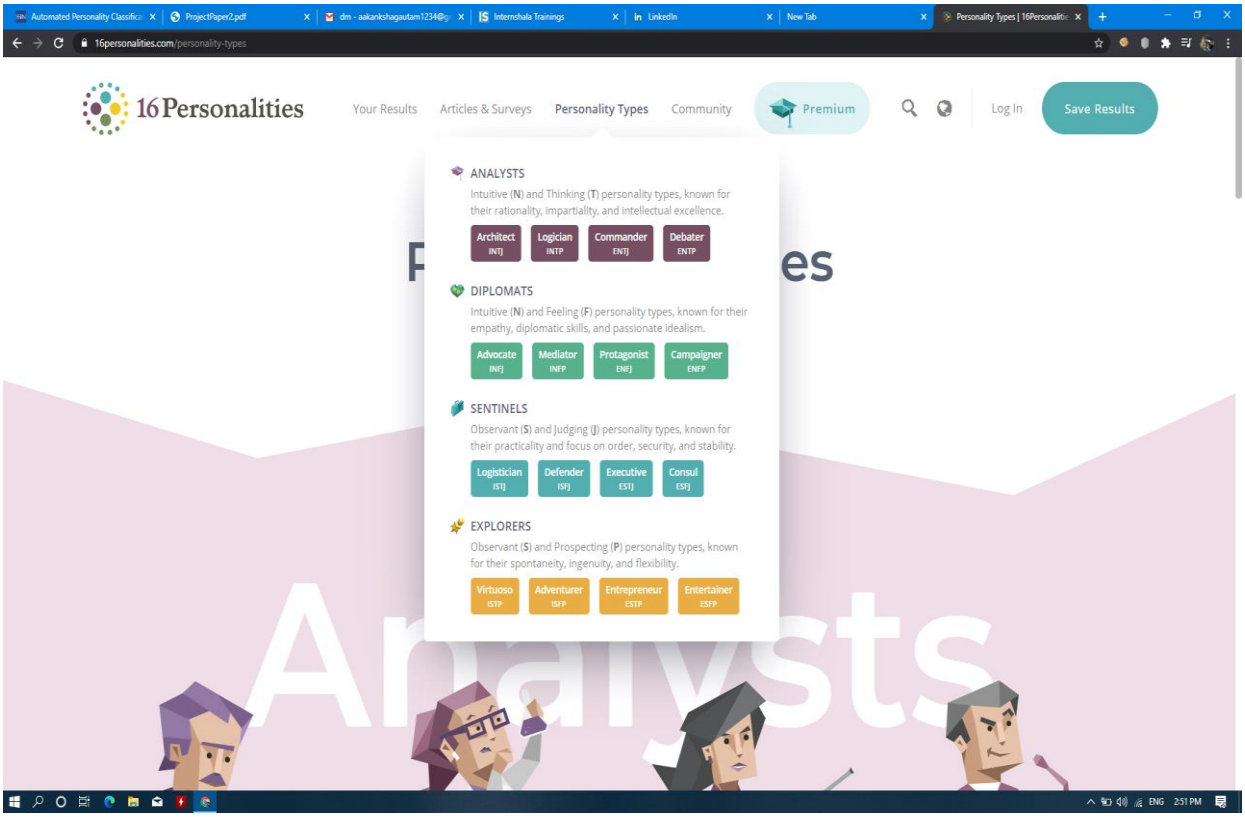


Fig01: 16 Personalities Types

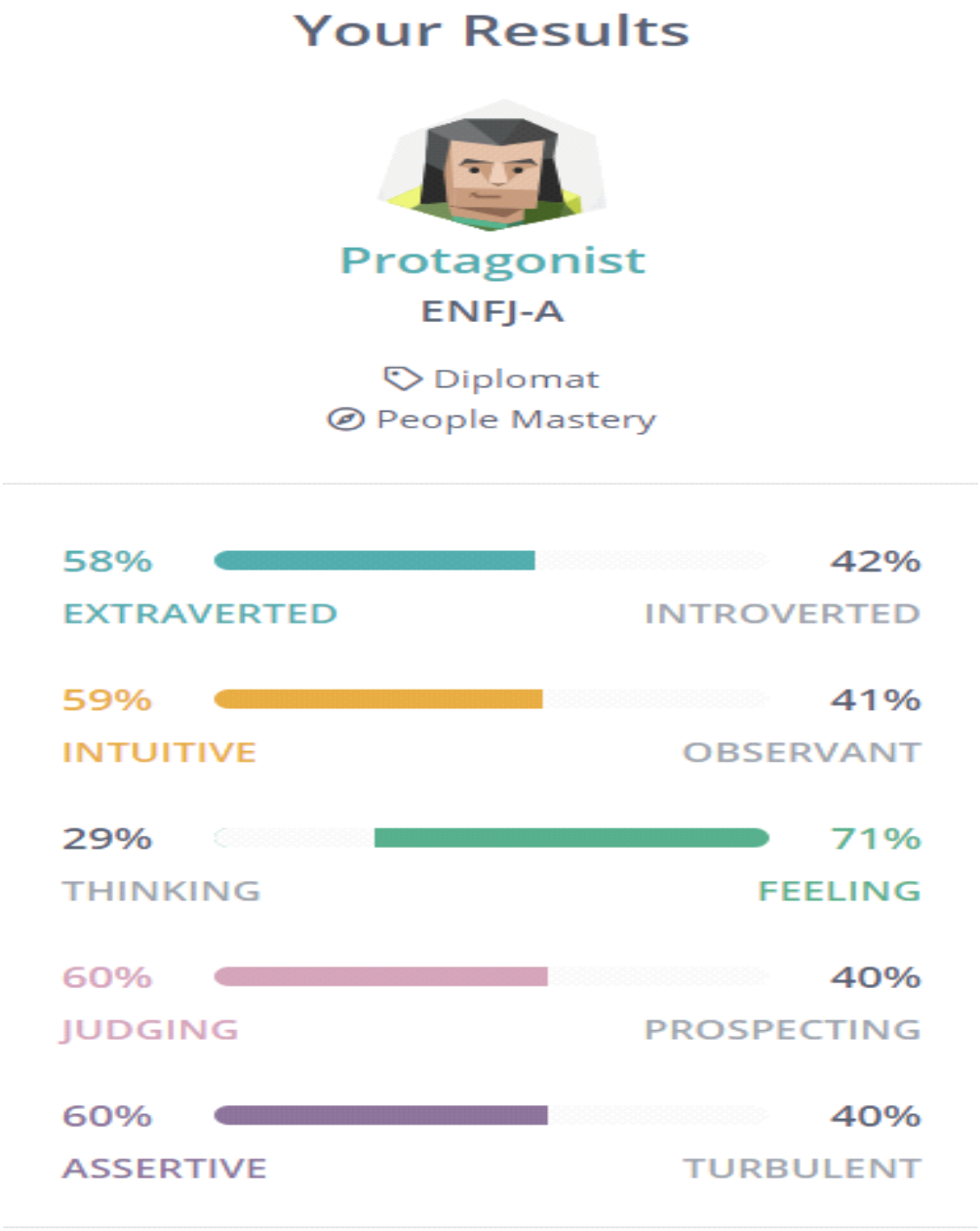


Fig02: The result obtained after running algorithm to find out the Personality type

- # RESULT ANALYSIS

Analysis on Advanced Naïve Bayes and SVM

Naive Bayes comes under the class of generative models for classification. It models the posterior probability from the class conditional densities. So the output is a probability of belonging to a class. SVM on the other hand is based on a discriminant function given by $y = w.x+b$. Here the weights w and bias parameter b are estimated from the training data. It tries to find a hyperplane that maximizes the margin and there is optimization function in this regard. Performance wise SVMs using the radial basis function kernel are more likely to perform better as they can handle non-linearities in the data. Naive Bayes performs when the features are independent of each other which does not happen in real, but still its performance is good in that case as well.

- # CONCLUSION

Social network analysis has increased tremendously in recent times. To extract the personality of the authors on the social networking websites is very useful for much application in various domain like including job success, attractiveness, marital satisfaction and happiness. Personality detection from text means to extract the behavior characteristics of authors written the text. This paper presents state-of-art review of the emerging field i.e. personality detection from text. This paper discusses the state-of-art methods for personality detection; In addition, state-of-art publicly available dataset is discussed. Two types of techniques have been employed for detection of personality from the text i.e. machine learning based approach based on social network activities and second is based on the linguistic properties present in the text.

• FUTURE OUTCOMES

Apart from the work done towards this system, future work mainly comprises of the following objectives:

- For future work, we want to include an extended experiment of the methods proposed in current research to sentiment analysis, opinion mining, as well as emotion detection in other domains. Also, we want to extend the method in this work to apply in Big-Five personality detection.
- This would test the proposed approach on a larger dataset of Facebook profile pictures.
- There can be module where user will be provided with career guidance which matches his personality. · For example: if a user has the ability to speak well and able to convince opposite person. So, this user will be good in marketing field.

• REFERENCES

[1] I. Cantandir, I. Fernandez-Tobiaz, A. Belllogin(2013). Relating personality types with user preferences in multiple entertainment domains, EMPIRE 1st Workshop on Emotions and Personality in Personalized Services.

[2] Aleksandar Kartelj, Vladimir Filipović, Veljko Milutinović(2012). Novel approaches to automated personality classification: Ideas and their potentials, Proceedings of 35th International convention MIPRO, IEEE.

[3] Randall Wald, Taghi M. Khoshgoftaar , Amri Napolitano, Chris Sumner (2012). Using Twitter Content to Predict Psychopathy, 11th International conference on Machine Learningand Applications,IEEE.

[4] Fazel Keshtkar, Candice Burkett, Haiying Li and Arthur C Graesser(2014). Using Data Mining Techniques to Detect the Personality of Players in an Educational Game,Springer International Publishing.

[5] Educational Game Yago Saez, Carlos Navarro, Asuncion Mochon and Pedro Isasi(2014). A system for personality and happiness detection, International Journal of Interactive Multimedia and Artificial Intelligence.

[6] J. Golbeck, C. Robles, K.Turner(2011). Predicting personality with social media, In CHI'11 Extended Abstracts on Human Factors in Computing Systems,pp. 253-262.

[7] Nurbiha A Shukora , Zaidatun Tasira, Henny Vander Meijden(2015). An Examination of Online Learning Effectiveness using Data Mining, Science Direct - Procedia - Social and Behavioral Sciences 172, 555 – 562.

[8] C.D. Manning, P. Raghavan, H. Schutze (2008). Introduction to Information Retrieval. Cambridge University Press, ISBN: 978-0-521-86571-5

[9] P.T. Costa, R.R. McCrae (1992). Revised NEO personality inventory (NEO-PI-R) and NEO five-factor inventory (NEOFFI), Psychological Assessment Resources.



TARGETING SARS-COV-2 MAIN PROTEASE FOR COVID-19

REPORT FOR SUMMER TRAINING 2020
(3RD YEAR)
DURATION : 15 MAY – 30 JUNE , 2020
SUBMITTED TO : DR. RAJ KUMAR
SUBMITTED BY : CHHAVI THAKUR
(171518)

TARGERTING SARS-CoV-2 MAIN PROTEASE FOR COVID-19

A Report

Submitted in fulfilment of the requirements for the internship in the degree of

BACHELOR OF TECHNOLOGY
IN
BIOINFORMATICS

Under the supervision of

Dr. Raj Kumar
Assistant professor

BY

CHHAVI THAKUR

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TO



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Chhavi thakur

(171518)

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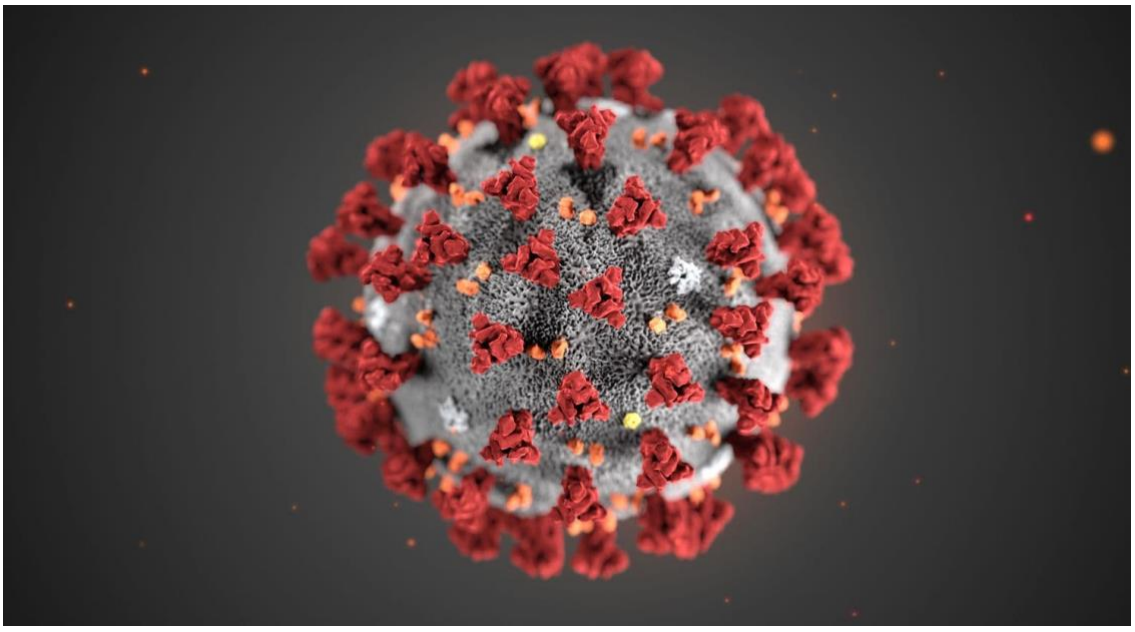
OUTLINE

S.NO	TOPIC	PAGE NO.
1	ABSTRACT	4
2	INTRODUCTION	5
3	METHODOLOGY	9
4	LITERATURE REVIEW	25
5	CONCLUSION	28
6	FUTURE SCOPE	29
7	REFERENCES	30

ABSTRACT

Science has emerged today as the most revolutionary co-operative activity of mankind, Computer-aided drug design (CADD) has been playing essential roles in modern drug discovery and development. The COVID-19 pandemic has sparked an unprecedented wave of research. Novel coronavirus, 2019-nCoV, has been identified as the cause of an outbreak of respiratory illness that originated in Wuhan, China, and which has spread to several other countries around the world.

It can infect humans and multiple species of animals, causing a wide spectrum of diseases. The coronavirus main protease (Mpro), which plays a pivotal role in viral gene expression and replication through the proteolytic processing of replicase polyproteins, is an attractive target for anti CoV drug design.The main protease of SARS-CoV-2 (M^{pro}) is a critical target for designing potent antiviral agents against COVID-19.This project aims at analysing binding properties of existing inhibitors of other viral proteases like **zika virus protease** against SARS-CoV-2 main protease (M^{pro}).



INTRODUCTION

General

The recent outbreak of a novel corona virus disease (COVID-19), occurring from a severe acute respiratory syndrome (SARS), which is now considered as a global pandemic. WHO, on 30 January 2020, declared this outbreak as Public Health Emergency of International Concern and later on 11 February 2020 named it as COVID-19. According to the data of WHO currently (as on July 4, 2020), more than 11,206,722 COVID-19 cases have been confirmed globally, and the number of death toll rose to 5, 29,403 which are increasing exponentially. To date no specific medications have been developed, and therefore considering the risk factors associated with this disease, there is an urgent need for a treatment method to treat this disease in order to limit the transmission.

Drug-Repurposing

It is also known as drug repositioning, is a drug development strategy predicated on the reuse of existing licensed drugs for new medical indications. Among all the treatment strategies, the uses of already known viral medications have great advantages as the pharmacokinetics, pharmacodynamics, and safety profiles of these drugs have already been established. This drug repurposing strategy has gained significance as they are expected to be faster with less investment.

Protease Inhibitors

Preliminary studies revealed Lopinavir/ritonavir combined therapy as a potential inhibitor of the virus. Along with these two drugs, many other antiviral drugs have also been screened. Recently, anti-malarial drug chloroquine (and hydroxychloroquine have been reported to have certain curative effect on COVID-19. Numerous reports to identify the potential inhibitors of novel corona virus (COVID-19) have recently been published using computational methods .The transcription of the genomic RNA inside the cell generates a polypeptide which is proteolytically cleaved by the main protease (MPro which is also known as 3CLPro or chymotrypsin-like protease) at 11 different sites to produce proteins necessary for the replication of the virus. Inhibition of the activity of the main protease is expected to block the viral replication as no human proteases are known having similar cleavage specificity. Therefore MPro is one of the most explored drug targets among the corona viruses that plays a major role in the translation and replication of new generation viruses from the viral genomic.

Why it is called 3CL^{pro} or M^{pro}

The functional polypeptides are released from the polyproteins by extensive proteolytic processing. This is primarily achieved by 33.1-kD HCoV 229E main proteinase (M^{pro}), which is frequently also called 3C-like proteinase (3CL^{pro}) to indicate a similarity of its cleavage-site specificity to that observed for picoronavirus 3C proteinases.

Structure

SARS-CoV-2 was found to be a positive-sense, single-stranded RNA virus belonging to the genus Betacoronavirus. Phylogenetic analysis revealed that SARS-CoV-2 is closely related (88–89% similarity) to two bat-derived SARS-like corona viruses, namely bat-SL-CoVZC45 (GenBank accession no. **MG772933.1**) and bat-SL-CoVZXC21 (GenBank accession no. **MG772934.1**), but it is more distant from SARS-CoV (~79% similarity) and Middle East respiratory syndrome corona virus (MERS-CoV) (~50% similarity). RNA-based metagenomic next-generation sequencing approach was applied to identify a human coronavirus from two pneumonia cases during the Wuhan outbreak in 2019. Its entire genome was 29 881 bp in length. Phylogenetic analysis indicates that SARS-CoV-2 is similar to the corona virus circulating in *Rhinolophus* (horseshoe bats), with 98.7% nucleotide similarity to the partial RNA-dependent RNA polymerase (*RdRp*) gene of the bat corona virus strain BtCoV/4991 (GenBank **KP876546**, 370 bp sequence of *RdRp*) and 87.9% nucleotide similarity to bat corona virus strain bat-SL-CoVZC45 and bat-SL-CoVZXC21. Evolutionary analysis based on ORF1a/1b, S and N genes suggests that SARS-CoV-2 is more likely a novel corona virus that was independently introduced from animals to humans. Based on the findings of genomic investigations and the presence of some bats and live animals in the seafood market in Wuhan, SARS-CoV-2 may have originated from bats or bat droppings associated with contaminated materials in the market or surrounding region. At this time, there are no specific vaccines or treatments for COVID-19. However, there are many ongoing clinical trials evaluating potential treatments.

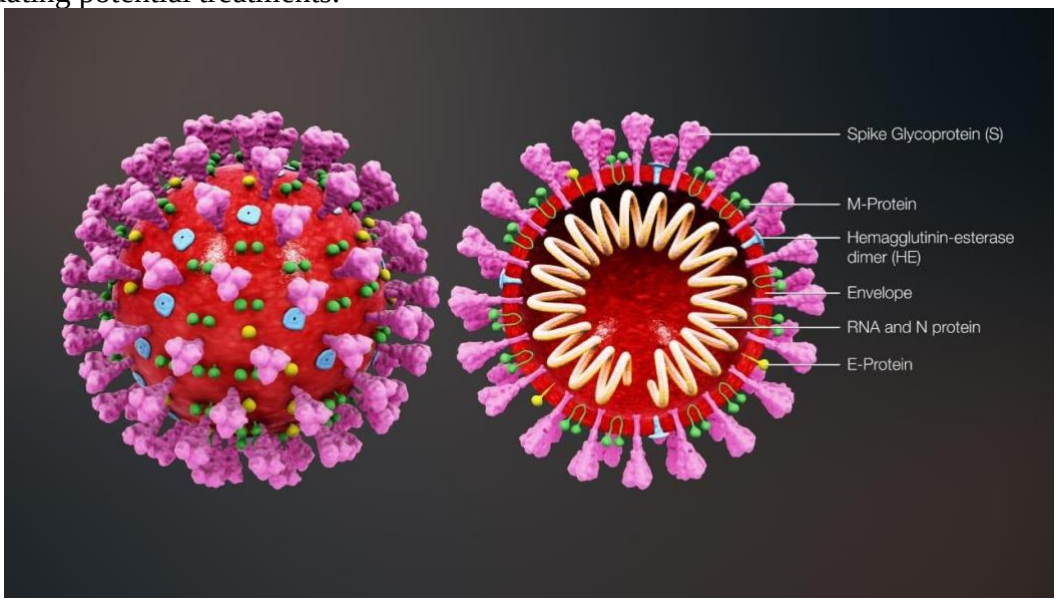


Fig1: Structure of COVID-19

Domains of SARS-CoV 3CL^{pro} or M^{pro}

The 3DstructureofSARS-CoV-2Mpro (PDB ID. 6Y2G), is made up of three domains, where domain I, II and III spans across 8-101, 102-184 and 201-306 amino acid residues, respectively. Domain I and II mainly consists of b-barrels while domain III mainly consists of a-helices. The substrate/active site of binding is located at the cleft of domain I and II, which consists of two catalytic residues, namely, HIS41 and CYS145.

It has following features:

- SARS-CoV M^{pro} and SARS-CoV-2 M^{pro} share more than 96% similarity
- Therefore, their 3D structures are highly similar
- Substrate/inhibitors bind to the same binding site
- Substrate/inhibitor binding site lies between domain-I and domain-II

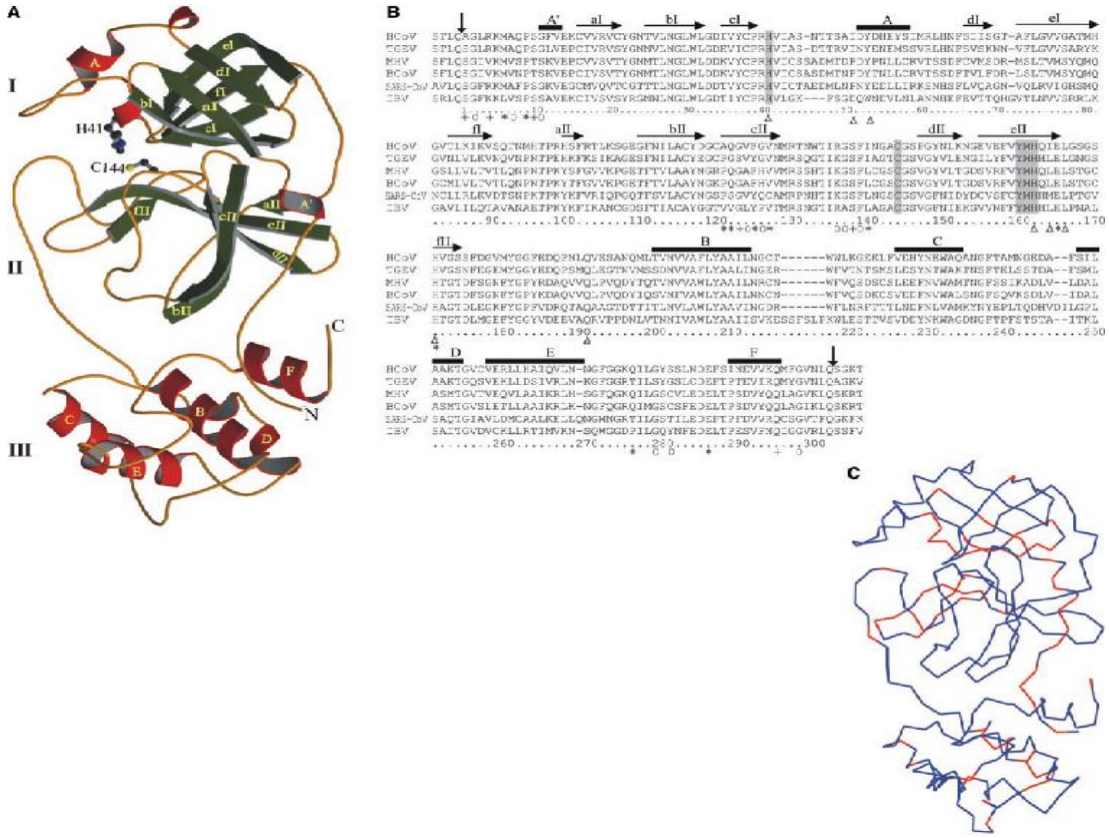


Fig2: Domain

SARS-CoV-2 M^{pro} is a dimer

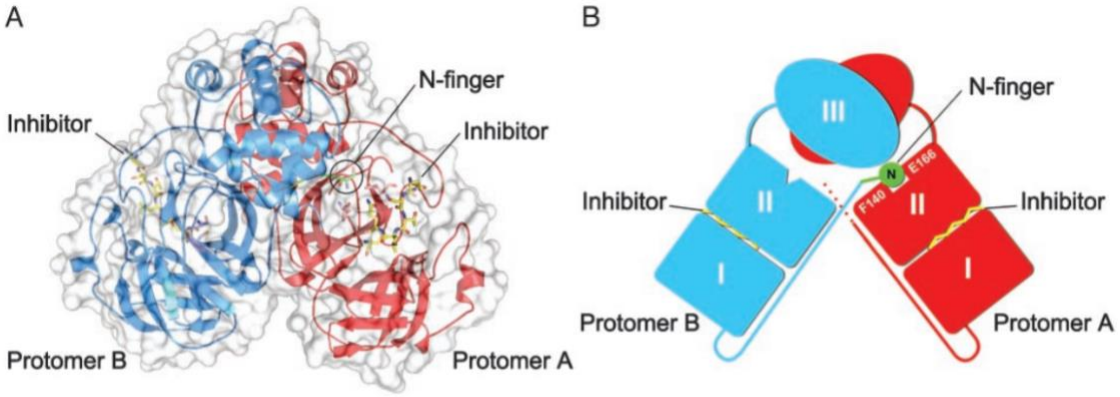


Fig. 1. The SARS-CoV M^{pro} dimer structure complexed with a substrate-analogue hexapeptidyl CMK inhibitor. (*A*) The SARS-CoV M^{pro} dimer structure is presented as ribbons, and inhibitor molecules are shown as ball-and-stick models. Protomer A (the catalytically competent enzyme) is red, protomer B (the inactive enzyme) is blue, and the inhibitor molecules are yellow. The N-finger residues of protomer B are green. The molecular surface of the dimer is superimposed. (*B*) A cartoon diagram illustrating the important role of the N-finger in both dimerization and maintenance of the active form of the enzyme. Fig3: Dimer

METHODOLOGY

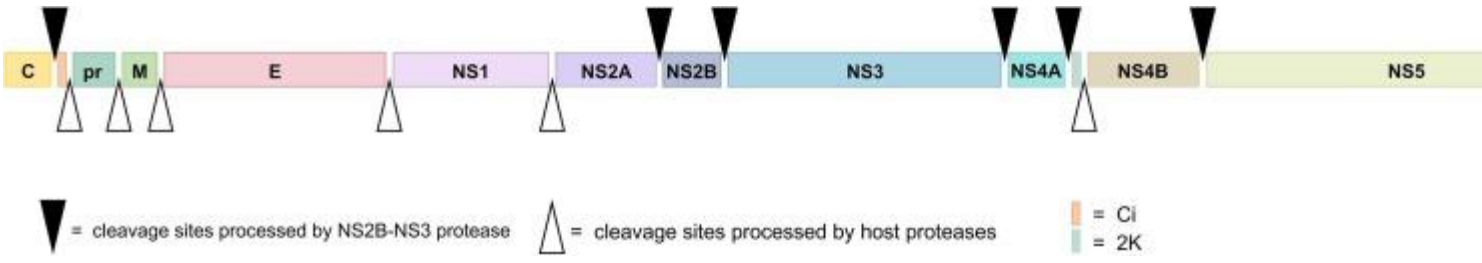
- **STEP1 - Finding existing inhibitors (clinically tested) each of: Zika virus protease**

ABOUT ZIKA VIRUS PROTEASE

In recent years, the Zika virus has emerged from a neglected flavivirus to a health-threatening pathogen that causes epidemic outbreaks associated with neurological disorders and congenital malformations. In addition to vaccine development, the discovery of specific antiviral agents has been pursued intensely. The Zika virus protease NS2B-NS3 catalyses the processing of the viral precursor polyprotein as an essential step during viral replication.

- **Zika virus protease NS2B-NS3 as drug target**

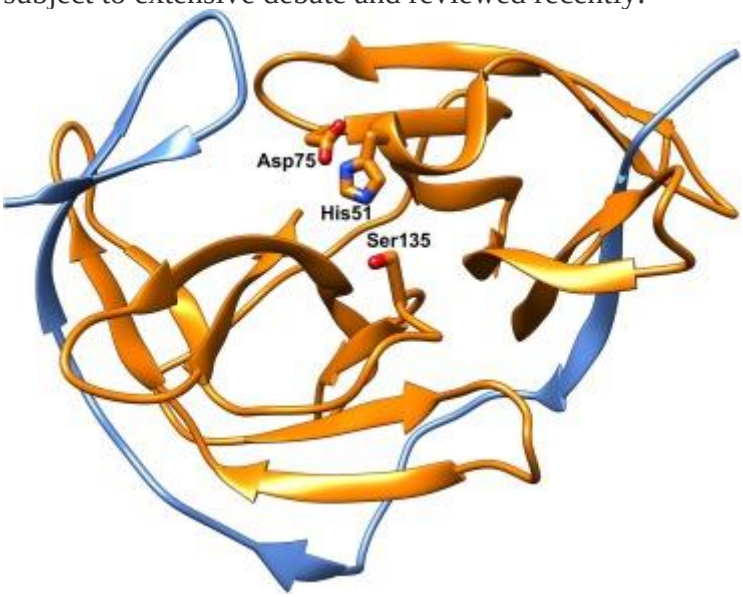
The biochemistry and structural biology of NS2B-NS3 and its prospects as drug target have recently been reviewed from various angles.Like other flaviviruses, the Zika virus contains a single-stranded RNA genome that is translated by the host cell ribosomal system into a non-functional polyprotein. Co– and post-translational processing by host-cell proteases and the ZIKV protease NS2B-NS3 at specific cleavage sites generate the structural and non-structural (NS) proteins necessary for viral replication . The crucial function of proteases in viral pathogenesis has been exploited to develop drugs against chronical viral infectious diseases caused by HCV or HIV, where protease inhibitors are essential therapeutics.



Flavivirus polyprotein and protease cleavage sites. Co- and post-translationally, the viral polyprotein is cleaved into structural (C, capsid; prM, pre-membrane; E, envelope) and non-structural (NS1-NS5) proteins by host proteases (mainly by the signal peptidase complex; the protease responsible for cleaving the NS1/NS2A junction remains unknown) and the viral protease NS2B-NS3 at the membrane of the endoplasmatic reticulum (ER).

Ci is a small part of the polyprotein that remains in the ER membrane after release of C and prM by proteolysis. At a later stage, prM is further processed to the mature membrane (M) protein by furin at the Golgi apparatus.NS1 has been reported to be involved in immune invasion and formation of the viral particle complex. The hydrophilic core region of NS2B serves as cofactor of the protease domain located in the N-terminal part of NS3. The C-terminal segment of NS3 contains an ATP-dependent helicase essential for viral RNA unwinding.NS5 comprises an RNA-dependent RNA polymerase and a methyltransferase in its C- and N-terminal segments, respectively.The roles of NS2A, NS4A and NS4B are subject of ongoing research.

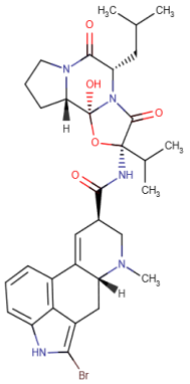
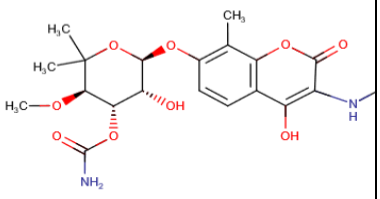
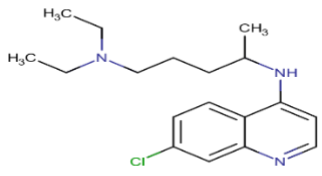
NS3 is a serine protease that comprises a catalytic triad of serine, histidine and aspartate in its active site. It requires a small hydrophilic proportion of NS2B as cofactor domain (major parts of NS2B serve as hydrophobic membrane anchors). In its catalytically active form, the C-terminal β-hairpin of NS2B wraps around the active site of NS3 . The relevance of conformational dynamics of this C-terminal domain of NS2B, which can result in open and closed states of the substrate binding site, has been subject to extensive debate and reviewed recently.

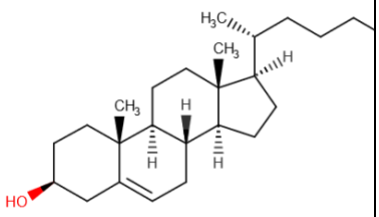
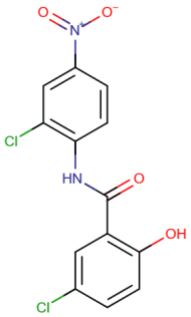
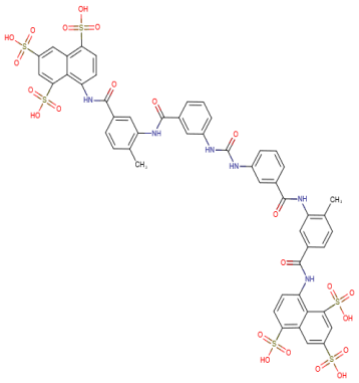


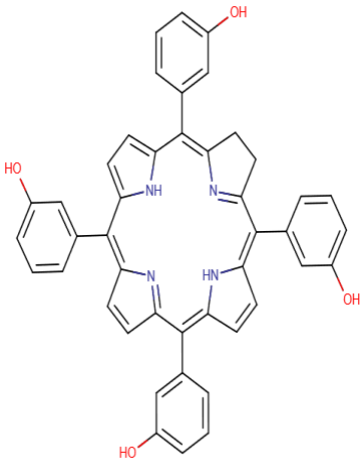
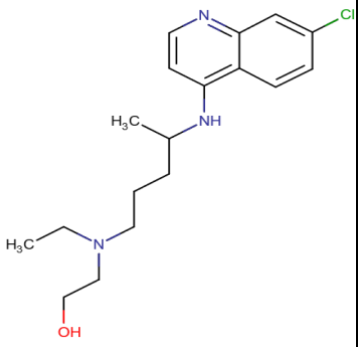
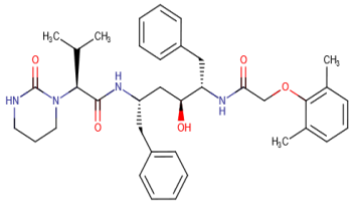
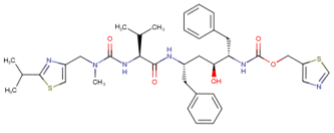
X-ray crystal structure of the Zika virus protease NS2B-NS3 in its catalytically active conformation (PDB code: 5LC0). The co-crystallised ligand 1 is not shown. NS2B is shown in blue, NS3 is orange. Residues of the catalytic triad are highlighted.

Following the nomenclature for protease sub-sites introduced by Schechter and Berger,flavivirus proteases share a strong preference for dibasic substrate residues in P_1 and P_2. As arginine and lysine side chains are both positively charged at physiological pH, this has challenged drug discovery campaigns based on substrate analogues. A comprehensive analysis of ZIKV polyprotein sequences from human isolates undertaken for this article reveals full conservation for arginine in P_1 and tolerance for arginine, lysine and glutamine in P_2 amongst all sites cleaved by NS2B-NS3 . Within the prime site, the important P_1' residue shows high conservation for small residues, either serine or glycine, informing the design of substrate-derived inhibitors. With respect to individual cleavage sites, the data demonstrate high conservation for residues ranging from P_4-P_4', except for the non-prime site of the C/Ci cleavage site .

TABLE OF INHIBITORS

S. no	INHIBITOR	DESCRIPTION	CLINICAL TRIAL	STRUTURE	CITATION
1.	**BROMOCRIPTINE**	Bromocriptine, a dopamine D2/D3 agonist used in the treatment of Parkinson's disease and galactorrhea, inhibits ZIKV NS2B-NS3 and shows anti-ZIKV activity in cell-based assays	PHASE 4 COMPLETED		J. Lei, G. Hansen, C. Nitsche, C.D. Klein, L. Zhang, R. Hilgenfeld
2.	**NOVOBIOCIN**	Novobiocin, an aminocoumarin antibiotic, inhibited protease activity by highly stable binding with ZIKV NS2B-NS3 protease to diminish its catalytic efficiency It can inhibit ZIKV replication with an IC_{50} of 26.12 ± 0.33 µg/ml and CC_{50} of 850.50 µg/ml in Vero cells and an IC_{50} of 38.14 ± 4.53 µg/ml and CC_{50} of 1103.18 µg/ml in Huh-7 cells .	PHASE 4 COMPLETED		Kirby et al., 1956; Yuan et al., 2017
3.	**CHLOROQUINE AND 25-HYDROXYCHOL-ESTROL**	Chloroquine and 25-hydroxycholesterol de monstrated their ability to inhibit ZIKV internalization *in vitro.*	PHASE 4		Li et al., 2017a

			PHASE 0		
4.	**NICLOSAMIDE**	Niclosamide is an FDA-approved drug broadly used in the treatment of intestinal helminthiasis . It can prevent endosomal acidification, but the mechanism is not fully elucidated	PHASE 4 COMPLETED		Fonseca et al., 2012; Jurgeit et al., 2012
3	**SURAMIN**	Suramin , an approved polyanion antiparasitic drug, can be a potential inhibitor of Zika virus complex NS2B/NS3 proteinase with IC_{50} of 47 μM	PHASE 3 COMPLETED		Coronado et al., 2018

4	**Temoporfin**	The photosensitiser temoporfin was the most potent non-competitive ZIKV NS2B-NS3 inhibitor, decreased flaviviral titers and RNA copies in cell culture and showed protection of mice against lethal challenge.	PHASE 2 COMPLETED		Z. Li, M. Brecher, Y.Q. Deng, *et al.*
5	**Hydroxychloroquine**	Hydroxychloroquine , a drug already approved and used in pregnancy, can inhibit the bZiPro construct of NS2B-NS3 protease activity with an inhibition constant (Ki) of 92.34 ± 11.91 µM	PHASE 4 COMPLETED		Kumar et al., 2018
6	**lopinavir**	Lopinavir-ritonavir can inhibit protease activity of ZIKV replication with an IC_{50} of 4.78 ± 0.41 µg/ml and CC_{50} of 30.00 µg/ml in Vero cells and an IC_{50} of 3.31 ± 0.36 µg/ml CC_{50} of 32.12 µg/ml in Huh-7 cells	PHASE 4 COMPLETED		Yuan et al., 2017
7	**ritonavir**	Mentioned above.	Phase 4 COMPLETED		Yuan et al., 2017

ZIKA VIRUS PEPTIDE INHIBITORS

Inhibitor	Sequence	Testing model	Cell lines	IC_{50} (μM)	CC_{50} (μM)	References
Peptide Z2	MAVLGDTAWDF GSVGGALNSLG KGIHQIFGAAF	*in vitro*	BHK21 cells Vero cells	1.75 ± 0.13 3.69 ± 0.27	–	Yu et al. (2017)
P5	GQASNGVFVIH WGKFDSFGIAV	*in vitro*	Vero cells	3.27	–	Chen et al. (2017)
Ev37	GLINEKKVQQYLDE KLPNGVVKGALKSL VHKAAKNQNLCAF NVDTVGMCDADCK RQGKAKGVCHGT KCKCDVELSYKK	*in vitro*	Huh-7 cells	–	–	Li et al. (2019)
Aprotinin	–	*in vitro*	–	0.07 ± 0.012	–	Shiryaev et al. (2017)
Acyl-KR-aldehyde	–	–	–	0.208	–	Li et al. (2017d)
AH-D peptide	SGSWLRDVWDWIC TVLTDFKTWLQSKL	*in vivo*	In mouse	0.0119	–	Cho et al. (2009), Jackman et al. (2018)
FFAAP	FFAAP	*in vitro*	Human JEG-3 cells Vero cells		–	Margueron and Reinberg (2011), Di Croce and Helin (2013), Kim et al. (2015), Vasireddi et al. (2019)
ZMP STE24	–	*in vitro*	T98-G cells	–	–	Fu et al. (2017)

Peptide derivatives

1. Early drug discovery campaigns targeting the HIV aspartyl protease capitalised on substrate-derived peptides that were further developed into lead compounds.

2. Most peptide-based active-site inhibitors that target ZIKV NS2B-NS3 were also derived from the protease's substrate (**1**–**6**).

3. All of them contain at least two basic side chain residues (arginine, lysine or mimetic) to address the dibasic substrate recognition motif, which is a major reason for their lack of drug-likeness and developability.

4. The first reported inhibitor of ZIKV NS2B-NS3 was the small **dipeptide** 1 that contains a C-terminal boronic acid for covalent-reversible modification of Ser135. The presence of the **boronic-acid** warhead boosts inhibition by more than three orders of magnitude compared with a C-terminal carboxylate.[5]The binding interactions of peptide **1** with ZIKV NS2B-NS3 have been studied by X-ray crystallography, confirming the covalent attachment of the boronate to Ser135 and occupation of the critical S_1 and S_2 pockets by the arginine and the benzylamine side chains, respectively. Mainly due to these critical basic and reactive groups, peptide **1** displays poor antiviral activity in cell-based dengue and West Nile assays and lacks off-target selectivity as it is also a strong inhibitor of thrombin and trypsin, limiting its prospects as lead compound.

5. **Dipeptide** 2 is a very similar analogue with a C-terminal aldehyde warhead. Covalent-reversible hemiacetal formation of **2** with Ser135 was also confirmed by X-ray crystallography. A stabilising salt bridge between P_2 of the inhibitor and Asp83 of NS2B observed in the co-crystal structures of ZIKV NS2B-NS3 with dipeptides **1** and **2** is a unique feature that is not conserved amongst flaviviruses. Compounds **1** and **2** were also very useful to study conformational dynamics and protein-ligand interactions by NMR spectroscopy.

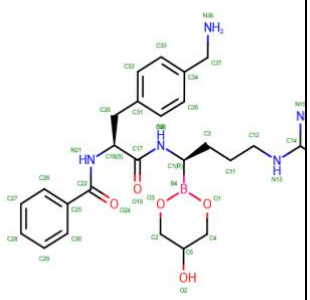
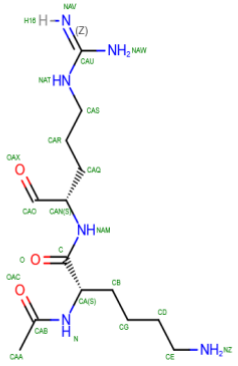
6. **Peptide** 3 demonstrates that a covalent modifier is not necessarily a requirement to achieve high affinity to the active site, as proven by X-ray crystallography. Due to the presence of four guanidine and one benzamide groups, however, **3** is a highly charged molecule, illustrating the dilemma that high affinity against flavivirus proteases often correlates with undesirable physiochemical properties. Despite being a strong pan-flaviviral NS2B-NS3 protease inhibitor, its lack of activity against West Nile and dengue viruses in cell-based assays and off-target inhibition of furin disqualify **3** as a promising lead compound.

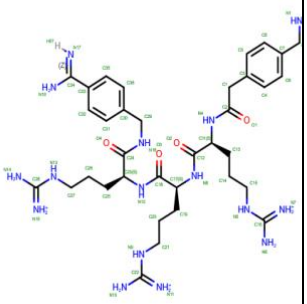
7. **Compound** 4 is a biotinylated ZIKV NS2B-NS3 probe that binds irreversibly to S135 by phosphonate formation. Sufficient labelling of ZIKV NS2B-NS3 occurs at nanomolar concentration after only one minute of incubation.

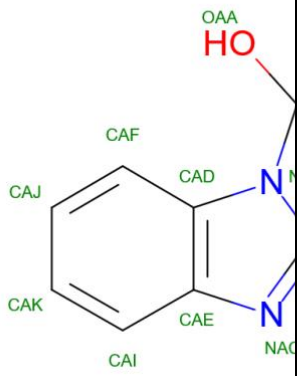
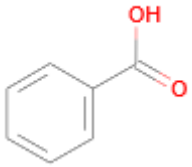
8. Recently, **peptide** 5 was reported as the first macrocyclic compound that binds to the active site of ZIKV NS2B-NS3. It is a cyclised version of the substrate sequence covering residues from P_4-P_1'. Substrate cyclisation significantly increases the proteolytic stability from below one minute to over

20 h and the proteolytic cleavage product remains bound to the active site as demonstrated by X-ray crystallography . Interactions with NS2B-NS3 are dominated by P_1 lysine and P_2 arginine; P_3 lysine is rather exposed, indicating limited importance for future inhibitor design. The latter point is supported by the pronounced tolerance for glycine in P_3

9. **Compound** 6 is part of a series of metallopeptides that can irreversibly inactivate NS2B-NS3 by oxidative damage using the copper-binding ATCUN motif fused to an NS2B-NS3 recognition motif. After competitive binding to NS2B-NS3, modification occurs by activating the copper redox cycle with hydrogen peroxide or ascorbate. Modifications of His51 (part of the catalytic triad) and Thr53 in the active site were associated with the inactivation mechanism.

S.NO	INHIBITOR	STRUCTURE	CITATION	COMMENTS
1.	**Boronate inhibitor (5LC0)**		**Lei, J.**, **Hansen, G.**, **Nitsche, C.**, **Klein, C.D.**, **Zhang, L.**, **Hilgenfeld, R.** (2016) Science **353**: 503-505	**Classification: HYDROLASE** **Organism(s):** Zika virus **Global Symmetry**: Cyclic - C2 **Global Stoichiometry**: Homo 2-mer - A2
2.	**DIPEPTIDE INHIBITOR (5H6V)**		Structural Dynamics of Zika Virus NS2B-NS3 Protease Binding to Dipeptide Inhibitors **Li, Y.**, **Zhang, Z.**, **Phoo, W.W.**, **Loh, Y.R.**, **Wang, W.**, **Liu, S.**, **Chen, M.W.**, **Hung, A.W.**, **Keller, T.H.**, **Luo, D.**, **Kang, C.**	Structure of Zika virus protease in complex with a dipeptide inhibitor **Classification: VIRAL PROTEIN/INHIBITOR** **Organism(s):** Zika virus **Expression System:** Escherichia coli **Global Symmetry**: Asymmetric - C1 **Global Stoichiometry**: Hetero 2-mer - A1B

			(2017) Structure **25**: 1242-1250.e3	
3.	***Crystal structure of Zika NS3 protease with 4-guanidinomethyl-phenylacetyl-Arg-Arg-Arg-4-amidinobenzylamide*** **(5ZOB)**		**Peptide-like** / **Enzyme inhibitor** Structures of Zika virus NS2B-NS3 protease in complex with peptidomimetic inhibitors. **Phoo, W.W.**, **Zhang, Z.**, **Wirawan, M.**, **Chew, E.J.C.**, **Chew, A.B.L.**, **Kouretova, J.**, **Steinmetzer, T.**, **Luo, D.** (2018) Antiviral Res **160**: 17-24	**Classification: HYDROLASE/ HYDROLASE INHIBITOR** **Organism(s):** Zika virus, synthetic construct **Expression System:** Escherichia coli **Global Symmetry**: Asymmetric - C1 **Global Stoichiometry**: Hetero 5-mer - A2BC1
4.	**6JPW** ***Crystal structure of Zika NS2B-NS3 protease with compound 1C***	NA	**Nitsche, C.**, **Onagi, H.**, **Quek, J.P.**, **Otting, G.**, **Luo, D.**, **Huber, T.** (2019) Org Lett **21**: 4709-4712	**Classification: VIRAL PROTEIN** **Organism(s):** Zika virus, synthetic construct **Expression System:** Escherichia coli **Global Symmetry**: Asymmetric - C1

				Global Stoichiometry: Hetero 2-mer - A1B
5.	**5H4I** ***Unlinked NS2B-NS3 Protease from Zika Virus in complex with a compound fragment***		Crystal structure of unlinked NS2B-NS3 protease from Zika virus **Zhang, Z., Li, Y., Loh, Y.R., Phoo, W.W., Hung, A.W., Kang, C., Luo, D.** (2016) Science **354**: 1597-1600	**Classification: VIRAL PROTEIN** **Organism(s):** Zika virus **Expression System:** Escherichia coli **Global Symmetry**: Asymmetric - C1 **Global Stoichiometry**: Hetero 2-mer - A1B
6.	**5YOD** ***Crystal structure of zika virus NS3 protease in complex with a small molecule inhibitor***		Structural Insights into the Inhibition of Zika Virus NS2B-NS3 Protease by a Small-Molecule Inhibitor **Li, Y., Zhang, Z., Phoo, W.W., Loh, Y.R., Li, R., Yang, H.Y., Jansson, A.E., Hill, J., Keller, T.H., Nacro, K., Luo, D., Kang, C.**	**Classification: VIRAL PROTEIN/INHIBITOR** **Organism(s):** Zika virus **Expression System:** Escherichia coli **Global Symmetry**: Asymmetric - C1 **Global Stoichiometry**: Hetero 2-mer - A1B

			(2018) Structure **26**: 555-564.e3	

- Using these inhibitors to check their binding with SARS-CoV-2 M^{pro} using molecular docking.

STEP -2 LIGAND PREPARATION

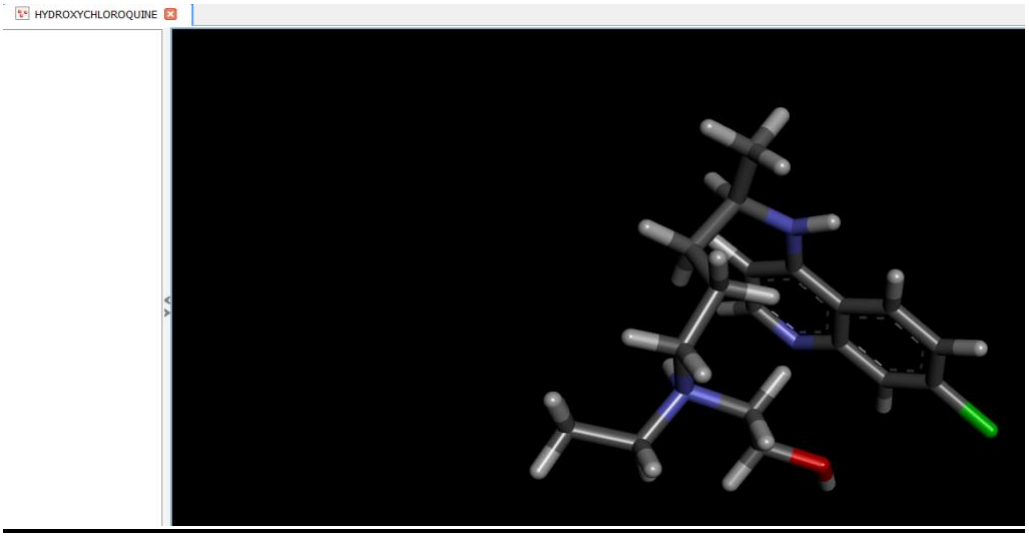
- **For 2D Structures**

1. Open UCSF Chimera
2. Open PubChem in the browser and type inhibitor name.
3. Get the SMILES string
4. Go to UCSF Chimera Tools -> Structure Editing -> Build Structure -> SMILES string (Paste the SMILES string that we have copied from pubChem) -> Apply -> Close.
5. Now we have our ligand molecule built.
6. Again Tools -> Structure Editing -> Minimize Structure (here set steepest descent steps: 1000 and Conjugate gradient steps:1000) -> Minimize
7. Now Add hydrogens will pop-up click OK, then Assign Charges to minimize select Gasteiger and enter OK. This will show the net charge of the molecule. Click OK.
8. Save ligand to the working directory: save as .mol2

- **For 3D Structures**

1. Open UCSF Chimera
2. Open PubChem in the browser and type inhibitor name.
3. Download the 3D structure as .SDF and open it in UCSF Chimera.
4. Again Tools -> Structure Editing -> Minimize Structure (here set steepest descent steps: 1000 and Conjugate gradient steps:1000) -> Minimize

5. Now Add hydrogens will pop-up click OK, then Assign Charges to minimize select Gasteiger and enter OK. This will show the net charge of the molecule. Click OK.
6. Save ligand to the working directory: save as .mol2

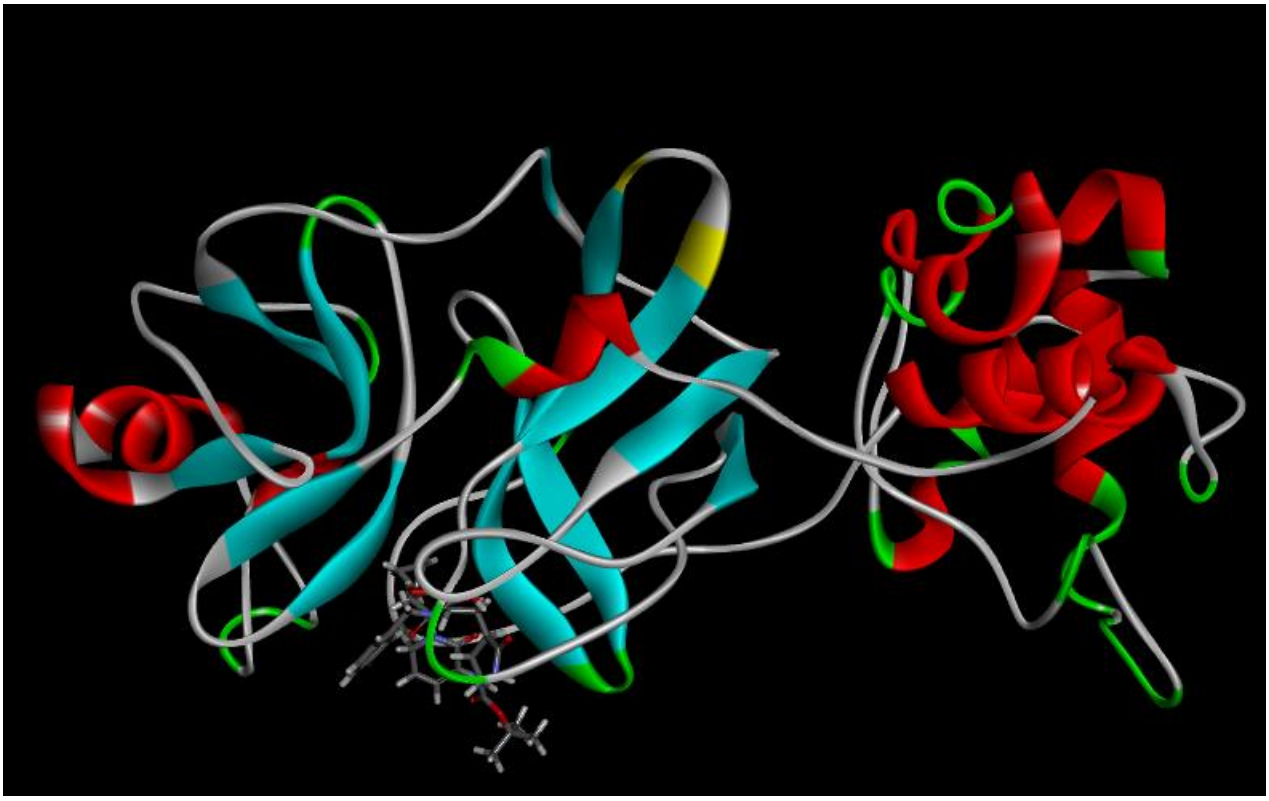


STEP-3 : PROTEIN PREPARATION

- **Protein Preparation**

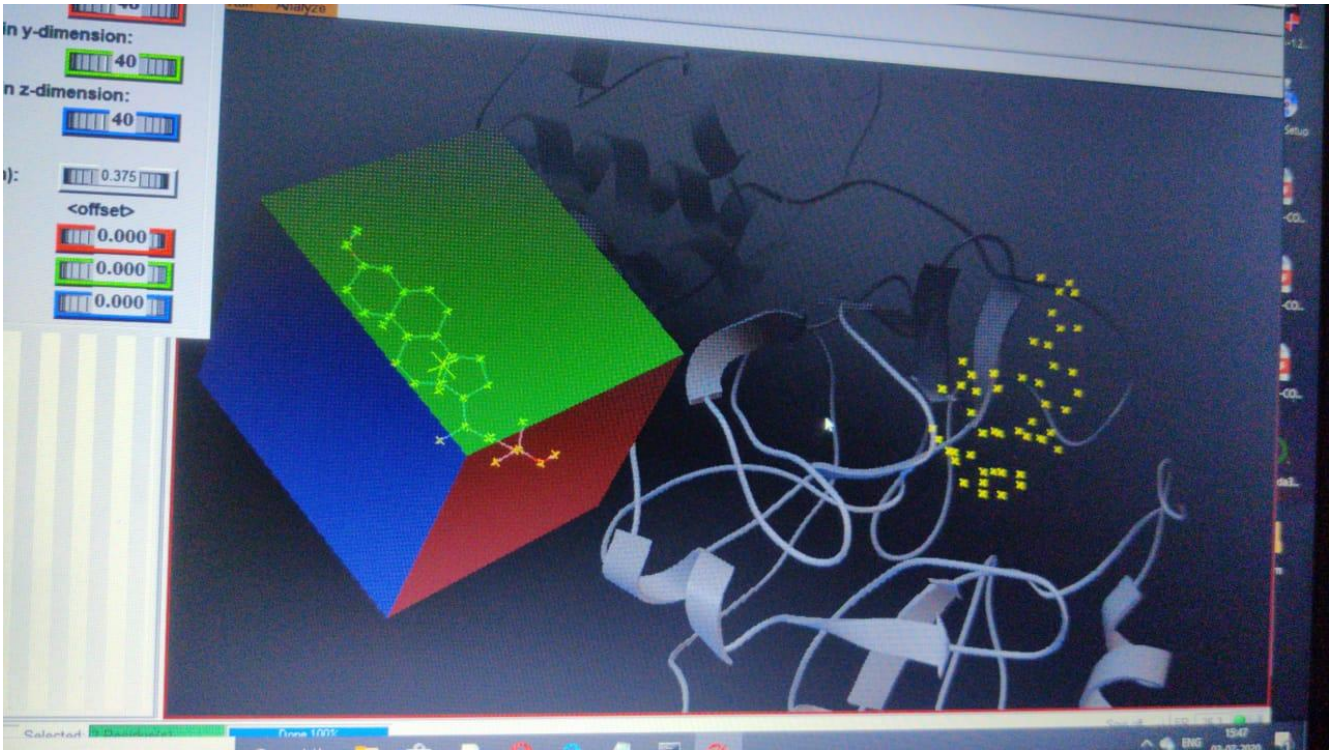
PDB ID: 6Y2G

1.Open Discovery studio.
2.Open RSCB PDB from web browser and search for PDB ID.
3.Download the structure as PDB.
4.Open the pdb structure in Discovery studio.
5.The pdb structure 6Y2G has 2 chains – A and B.
6.Delete chain B .
7.Only keep Ligand A(O6K402) as reference and delete all other ligands.
8.Go to macromolecule -> prepare protein -> clean protein -> show clean report.
9.Now go to minimize protein -> select protein -> select algorithm -> Yes.



Grid Generation

1.File -> Read Molecule -> 6Y2G.pdb
2.Edit -> Delete Water
3.Edit -> Hydrogens -> Add H -> All polar -> Ok
4.Edit -> Charges -> Add Kollman charges
5.Edit -> Charges -> Compute Gastegier charges
6.Atoms -> Assign AD4 type
7.File -> Save -> Write PDBQT
8.Select -> Select from string -> Residue sets -> Ligands -> Dismiss
9.Ligand -> Input -> Open -> .mol2 files -> Ok
10. Ligand -> Output -> Write PDBQT
11. Select ->Select from string -> Residue sets -> Ligands -> Add-> Dismiss
12. Grid -> Macromolecule -> Choose -> 6Y2G -> Save as .pdbqt
13. Grid -> Set map types -> Choose ligand
14. Grid -> Grid Box -> Centre -> Centre on ligand
15. File -> Close saving current
16. Grids -> Output -> gpf -> save as grid.gpf



Docking

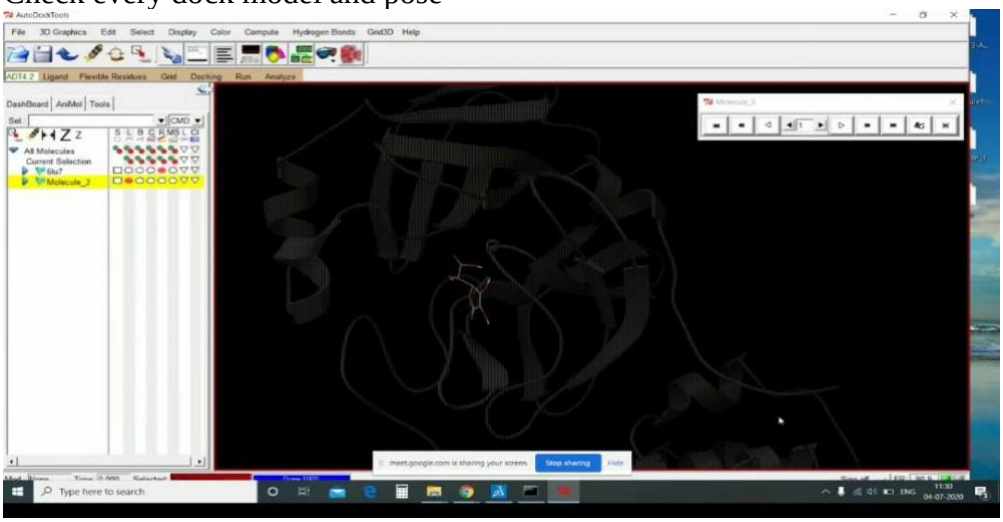
- **Auto Grid**
  1. Run -> Auto-Grid -> Program Pathname -> Browse -> C Drive -> (XProgram Files) -> The Scripps Research Institute -> Autodock -> 4.2.6 -> autogrid.
  2. For parameter filename -> Browse ->grid.gpf.
  3. Automatically a log filename file grid.glg will be created -> Launch
- **Auto Dock**
  1. Docking -> Macromolecule -> RigidFilename -> 6Y2G.pdb
  2. Docking -> Ligand -> Choose -> .mol2 file -> Accept
  3. Docking -> Output -> Lamarkian -> Save as dock.dpf

4. Run -> Auto-Dock -> Program Pathname -> Browse -> C Drive -> (XProgram Files) -> The Scripps Research Institute -> Autodock -> 4.2.6 -> autodock.
5. For parameter filename -> Browse ->dock.dpf.
6. Automatically a log filename file dock.dlg will be created -> Launch

Analyzing 2D and 3D Poses

- **Through Auto dock**
  - Analyze -> Docking -> Open -> File Location -> dock.dlg.
  - Analyze -> Conformations -> Play Rank by Energy(Best pose appears)

- **Through Discovery Studio**
  - File -> Open -> Protein
  - Convert ->dock.dlg to dock.pdb
  - Delete everything except coordinates
  - Remove lower remaining part
  - Drag pdb file from notepad
  - Check every dock model and pose



Software's used

We used UCFS Chimera a molecular visualization tool, was used to visualize the results obtained from the server. Discovery Studio Visualizer was further employed in order to prepare the docked poses and 2 D interaction plots. Autodock 4.2.6 ; a suite of automated docking tools was practiced to predict how small molecules bind to receptor of known 3D structures. While browsing the web we exploited PubChem , Drugbank and NCBI.

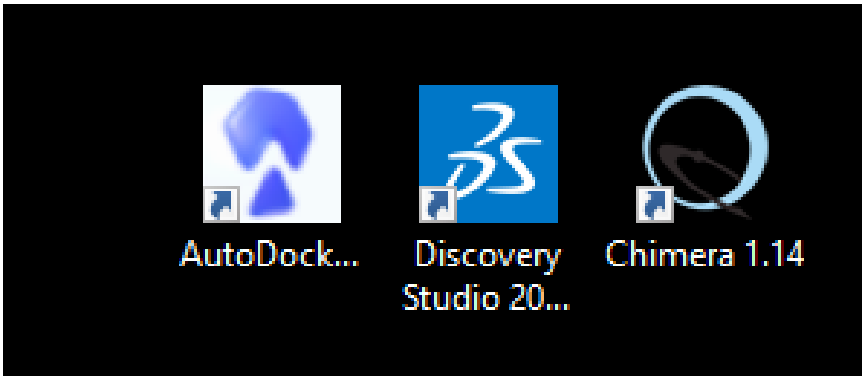


Fig7: Tools used

LITERATURE REVIEW

Review of Literature

The coronavirus disease 2019 (COVID-19) pandemic caused by severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) is a global health emergency. The virus has been named severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) because the RNA genome is about 82% identical to that of the SARS coronavirus (SARS-CoV), both viruses belong to clade b of the genus Betacoronavirus. The best-characterized drug targets among coronaviruses is the main protease (Mpro, also called 3CLpro). Along with the papain-like protease(s), this enzyme is essential for processing the polyproteins that are translated from the viral RNA. The Mpro operates at no fewer than 11 cleavage sites on the large polyprotein 1ab (replicase 1ab, ~790 kDa). The recognition sequence at most sites is Leu-Gln↓(Ser, Ala, Gly) (↓ marks the cleavage site). Inhibiting the activity of this enzyme would block viral replication. Because no human proteases with a similar cleavage specificity are known, such inhibitors are unlikely to be toxic. The three-dimensional structure is highly similar to that of the SARSCoV Mpro, as expected from the 96% sequence identity.

The chymotrypsin-like and picornavirus 3C protease–like domains I and II (residues 10 to 99 and 100 to 182, respectively) are six-stranded antiparallel b barrels that harbor the substrate-binding site between them. Domain III (residues 198 to 303), a globular cluster of five helices, is involved in regulating the

dimerization of the Mpro, mainly through a salt-bridge interaction between Glu290 of one protomer and Arg4 of the other.They used this crystal structure to dock the a-ketoamide 13a which suggested that the pyridine ring might have some steric clash with the side chain of Gln189. However, in their previous work, they had found Gln189 to be quite flexible, and therefore we went ahead with 13a as a lead. However, relative to 11r (IC50 = 0.18 ± 0.02 mM), the structural modification led to some loss of inhibitory activity against the main protease of SARS-CoV-2 (IC50 = 2.39 ± 0.63 mM) cyclopropyl in 13b.

Through the nucleophilic attack of the catalytic Cys145 onto the a-keto group of the inhibitor, a thiohemiketal is formed in a reversible reaction. The oxyanion (or hydroxyl) group of this thiohemiketal is stabilized by a hydrogen bond from His41, whereas the amide oxygen of 13b accepts a hydrogen bond from the main-chain amides of Gly143, Cys145, and partly Ser144, which form the canonical "oxyanion hole" of the cysteine protease. It is an advantage of the a-ketoamides that their warhead can interact with the catalytic center of the target proteases through two hydrogen-bonding interactions rather than only one, as with other warheads such as aldehydes or Michael acceptors . To assess the absorption-distribution-metabolism-excretion (ADME) properties of the pyridine containing a-ketoamides, they investigated compound 13a and 13b .The ADME parameters of 13b were similar to those of 13a. In addition, binding to human plasma proteins was found to be 90%. The Cmax of 13b is around 37% of the Cmax detected for 13a, although the 13b dosage was lower by a factor of ~7.

In addition, 13b showed a less rapid clearance relative to 13a. During the pharmacokinetic study with 13b, we monitored its lung tissue levels. After 4 hours, 13b was still found at ~13 ng g−1 in lung tissue. This lung tropism of 13a and 13b is beneficial given that COVID-19 affects the lungs. In addition 13b was nebulized using an inhalation device at 3mg kg−1. After 24 hours, 13b was found at 33 ng g−1 in lung tissue. Thus, this study provides a useful framework for development of pyridone-containing inhibitors toward anticoronaviral drugs. To date no specific medications have been developed, and therefore considering the risk factors associated with this disease, there is an urgent need for a treatment method to treat this disease in order to limit the transmission. This study is focused on the repurposing/identification of compounds with a sole aim to expedite the identification of specific drugs for the treatment of COVID-19. Among all the treatment strategies, the uses of already known viral medications have great advantages as the pharmacokinetics, pharmacodynamics, and safety profiles of these drugs have already been established. This drug repurposing strategy has gained significance as they are expected to be faster with less investment .

Recently, anti-malarial drug chloroquine and hydroxychloroquine along with some antiviral drugs have been reported to have certain curative effect on COVID-19. Due to diverse bioactivity and less toxicity, naturally occurring bioactive flavonoid molmolecules have also been screened for their potential therapeutic effects. The MPro is one of the most explored drug target among the corona viruses that plays a major role in the translation and replication of new generation viruses from the viral genomic RNA The 3D structure of SARS-CoV-2 Mpro (PDB ID. 6Y84), is made up of three domains, where domain I, II and III spans across 8-101, 102-184 and 201-306 amino acid residues, repectively. Domain I and II mainly consists of b-barrels while domain III mainly consists of a-helices .The substrate/active site of binding is located at the cleft of domain I and II, which consists of two catalytic residues, namely, HIS41 and CYS145 .Here in this report, a total of 33 compounds belonging to different classes (i) control drugs, (ii) natural products, (iii) anti-virals, (iv) anti-fungals, (v) anti-nematodes and antiprotozoalwere identified to investigate their inhibitory effects towards MPro by molecular docking analysis.

Ritonavir, hydroxychloroquine, penciclovir and lopinavir are known drugs that have been screened for the treatment of COVID-19. The reason for them being used as control drugs in the study is that, lopinavir/ritonavir combination,and anti-malarial drug hydroxychloroquine has recently been found to be a potential inhibitor of the virus, Considering the diverse pharmaceutical properties of the natural products including anti-viral properties, a total of 17 compounds: curcumin, demethoxycurcumin, (-)-Epigallocatechin gallate (EGCG), (-)-epigallocatechin, (EGC), hesperidin, myricitrin, puerarin, scutellarin, rutin, quercitrin, capsaicin, ursolic acid, glabridin, apiin, rhoifolin, glycyrrhizin, and vitexin were screened for their inhibitory potential against SARS-CoV-2 Mpro. Azidothymidine, indinavir, tipranavir, and saquinavir are the well-known anti-viral drugs while diethylcarbamazine, primaquine, mepacrine, artemisinin and niclosamide are the anti-nematodes and emetine, an anti-protozoal drug ,which have also been screened for their inhibitory potentials. Further, two anti-fungals, namely, fluconazole and itraconazole were also docked to the main protease of COVID-19.

The 3 D coordinates of the ligands wereobtained from ChemSpider as a .mol file and further geometry optimization was carried out in ArgusLab using PM3 methods .The drug likeliness of a molecule is indicated by the Lipinski's rule of five parameters (molecular weight <500 Da,no more than 5 hydrogen bond donors, no. of hydrogen bond acceptors should be less than 10 and logP should not be greater than 5. The Lipinski's rule of five parameters were obtained from the SWISSADME server. The crystal structure of MPro (PDB ID: 6Y84) was obtained from Protein Data Bank (PDB) . The obtained structure was a dimer of two homologous amino acid chains (A and B). The chain A was used for molecular docking. Water molecules were removed from the PBD using PyMOL .

The final PDB file of the protease and geometry optimized ligand structures were selected for molecular docking analyses in the SwissDock server. According to the SwissDock server, the binding modes of the ligands are ranked according to their fullfitness score, therefore the conformers having the minimum fullfitness score were analyzed for further evaluations. The fullfitness score and the free binding energy associated with each corresponding docked pose were calculated and results were seen. Within the control drugs , the best pose was found to be of penciclovir with a fullfitness score of -1314.77 kcal/mol followed by ritonavir. Looking to naturally occurring compounds curcumin had best fulfitness score(-1236.50 kcal/mol). Coming forward to anti-fungal drugs Flucanazole (-1168.54 kcal/mol). The anti-viral drug with Azidothymidine (-1324.25 kcal/mol) and anti-nematodal and anti-protozoal drugs with Diethylcarbamazine(-1272.14 kcal/mol).

Among all the molecules, the inhibition activity of rutin was found to be the highest as its DG value (_9.55 kcal/mol) is the minimum, followed by ritonavir (_9.52 kcal/mol), emetine (_9.07 kcal/mol), hesperidin (_9.02 kcal/mol), and indinavir(_8.84 kcal/mol).

Summary of Literature Review

We used a-ketoamide13b inhibitor as our reference compound for our project based on the results of above mentioned article, whereas some reference inhibitors were also used including penciclovir, hydroxychloroquine according to fullfitness score and free energy from the results drawn.

CONCLUSION

Cutting edge chemical science technology and computer-aided drug design (CADD) is bringing together leading minds from across the world to help tackle the COVID-19 crisis.

The recent outbreak of novel coronavirus disease-19 (COVID-19) calls for and welcomes possible treatment strategies using drugs on the market. It is very efficient to apply computer-aided drug design techniques to quickly identify promising drug repurposing candidates, especially after the detailed 3D structures of key viral proteins are resolved. The virus causing COVID-19 is SARS-CoV-2. Successful entry of a virus into a cell depends on the activation of envelope glycoproteins by host cell proteases. Protease enzymes are therefore excellent targets for antiviral intervention and this is why inhibitors such as lopinavir, ritonavir, and darunavir have been used for many years in the treatment of HIV infections. The COVID-19 is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).Taking advantage of a recently released crystal structure of SARS-CoV-2 main protease in complex with a covalently bonded inhibitor, we have successfully proposed a study focused on the

repurposing/identification of compounds with a sole aim to expedite the identification of specific drugs for the treatment of COVID-19.A great application of drug repurposing is to identify drugs that were developed for treating other diseases to treat a new disease. Drug repurposing can be achieved by conducting systematic drug–drug target interaction (DTI) analyses by using various tools like UCSF Chimera(ligand preparation), Discovery studio(protein preparation) and autodock4 (molecular docking) followed by binding free energy calculations.

FUTURE SCOPE

Discovery and development of a new drug is generally known as a very complex process which takes a lot of time and resources. So now a day's computer aided drug design approaches are used very widely to increase the efficiency of the drug discovery and development course. Various approaches of CADD are evaluated as promising techniques according to their need, in between all these structure-based drug design and ligand-based drug design approaches are known as very efficient and powerful techniques in drug discovery and development. These both methods can be applied with molecular docking to virtual screening for lead identification and optimization. In the recent times computational tools are widely used in pharmaceutical industries and research areas to improve effectiveness and efficacy of drug discovery and development Pipeline, through it we can find the most promising drug candidate in a very cost-effective way. It always provides a hope for betterment in drug discovery area. In the past years through Computer aided drug design many impressive researches are achieved so it will play a very much important role in the near future. With the current achievement's, there is a promising future of computer aided drug design to aid drug discovery of many more curatives in covid-19 for future.

REFRENCES

1. Sourav Das, Sharat Sarmah, Sona Lyndem & Atanu Singha Roy (2020) An investigation into the identification of potential inhibitors of SARS-CoV-2 main protease using molecular docking study, Journal of Biomolecular Structure and Dynamics, DOI: 10.1080/07391102.2020.1763201

2. Aanouz, I., Belhassan, A., El Khatabi, K., Lakhlifi, T., El Idrissi, M., & Bouachrine, M. (2020). Moroccan medicinal plants as inhibitors of COVID-19: Computational investigations. Journal of Biomolecular Structure & Dynamics.

3. S. Voss, C. NitscheInhibitors of the Zika virus protease NS2B-NS3 Bioorg. Med. Chem. Lett., 30 (2020), p. 126965, 10.1016/j.bmcl.2020.126965

4. D. Musso, A.I. Ko, D. BaudZika virus infection – after the pandemic N Engl J Med, 381 (2019), pp. 1444-1457, 10.1056/NEJMra1808246

5. https://www.rcsb.org/
6. https://pubchem.ncbi.nlm.nih.gov/
7. https://www.drugbank.ca/
8. https://www.who.int/

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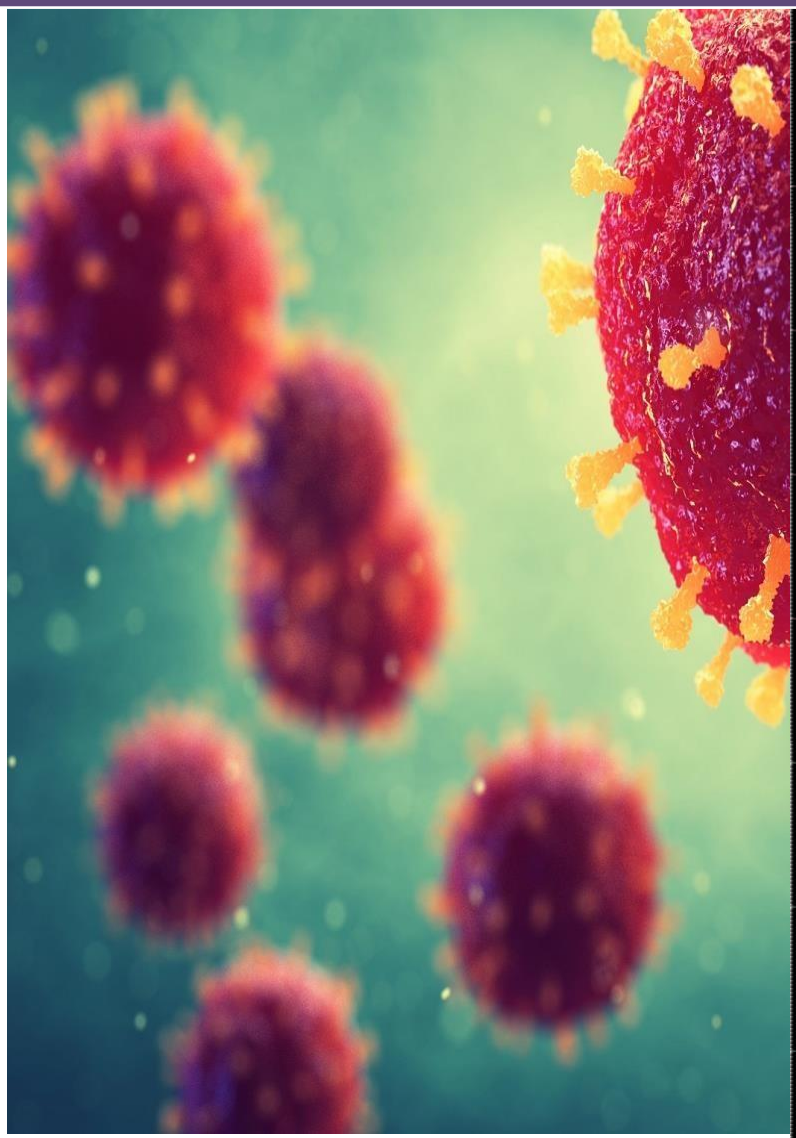
SIGNATURE OF TEACHER; DR. RAJKUMAR





2020

TARGETING SARS-CoV-2 MAIN PROTEASE FOR COVID-19



TARGERTING SARS-CoV-2 MAIN PROTEASE FOR COVID-19

A Report

Submitted in fulfillment of the requirements for the internship in the degree of

BACHELOR OF TECHNOLOGY
IN
BIOINFORMATICS

Under the supervision of

Dr. Raj Kumar
Assistant professor

By

Mehak Kapoor
(171519)

to



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY

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TABLE OF CONTENT

CONTENT	PAGE NO.
Abstract	**6**
Chapter 1: Introduction	**7-9**
• **1.1 General**	
• **1.2 Drug –Repurposing**	
• **1.3 Protease Inhibitors**	
• **1.4 Why is it called $3CL^{pro}$ or M^{pro}**	
• **1.5 Structure**	
• **1.5.1 Domains of SARS-CoV $3CL^{pro}$ or M^{pro}**	
• **1.5.2 SARS-CoV-2 M^{pro} is a dimer**	
Chapter 2: Methodology	**11-23**
• **2.1 Finding existing inhibitors**	
• **2.1.1 About HIV**	
• **2.1.1.1 Structure of HIV**	
• **2.2 Table of Protease Inhibitors**	
• **2.3 Ligand Preparation**	
• **2.3.1 For 2D Structures**	
• **2.3.2 For 3D Structures**	
• **2.4 Protein Preparation**	
• **2.5 Grid Generation**	
• **2.6 Docking**	
• **2.6.1 Auto Grid**	
• **2.6.2 Auto Dock**	

- **2.7 Analyzing 2D 3D Poses**
- **2.7.1 Through Auto Dock**
- **2.7.2 Through Discovery Studio**
- **2.7.3 Binding Energy**
- **2.8 Software's used**

Chapter 3: Literature Review **24-28**

- **3.1 Review of Literature**
- **3.2 Summary**

Chapter 4: Conclusions **29**

Chapter 5: Future scope **30**

References **31**

ABSTRACT

A newly come to light severe acute respiratory syndrome corona virus 2 reported 7 months ago in Wuhan, China better known as COVID-19 has become the current health concern to the entire world ,and declared a pandemic by the World Health Organization (WHO). Precautionary measures remain the sole obliging tactic to cease the human to human transmissions till any effective method of treatment or vaccine is developed. Amidst the pandemic, research and development of new molecule is labor-intensive and tedious process. In this report we have used Drug repurposing method, it is a concept of identifying therapeutically potent molecule from the library of pre-existing molecules. The main protease of SARS-CoV-2 (M^{pro}) is a critical target for designing potent antiviral agents against COVID-19. It aims at analyzing binding properties of existing inhibitors using molecular docking of other viral proteases. In this report **HIV virus** is used against SARS-CoV-2.

INTRODUCTION

1.1 General

The recent outbreak of a novel corona virus disease (COVID-19), occurring from a severe acute respiratory syndrome (SARS), which is now considered as a global pandemic. WHO, on 30 January 2020, declared this outbreak as Public Health Emergency of International Concern and later on 11 February 2020 named it as COVID-19. According to the data of WHO currently (as on July 4, 2020), more than 11,206,722 COVID-19 cases have been confirmed globally, and the number of death toll rose to 5, 29,403 which are increasing exponentially. To date no specific medications have been developed, and therefore considering the risk factors associated with this disease, there is an urgent need for a treatment method to treat this disease in order to limit the transmission.

1.2 Drug-Repurposing

It is also known as drug repositioning, is a drug development strategy predicated on the reuse of existing licensed drugs for new medical indications. Among all the treatment strategies, the uses of already known viral medications have great advantages as the pharmacokinetics, pharmacodynamics, and safety profiles of these drugs have already been established. This drug repurposing strategy has gained significance as they are expected to be faster with less investment.

1.3 Protease Inhibitors

Preliminary studies revealed Lopinavir/ritonavir combined therapy as a potential inhibitor of the virus. Along with these two drugs, many other antiviral drugs have also been screened. Recently, anti-malarial drug chloroquine (and hydroxychloroquine have

been reported to have certain curative effect on COVID-19. Numerous reports to identify the potential inhibitors of novel corona virus (COVID-19) have recently been published using computational methods .The transcription of the genomic RNA inside the cell generates a polypeptide which is proteolytically cleaved by the main protease (MPro which is also known as 3CLPro or chymotrypsin-like protease) at 11 different sites to produce proteins necessary for the replication of the virus. Inhibition of the activity of the main protease is expected to block the viral replication as no human proteases are known having similar cleavage specificity. Therefore MPro is one of the most explored drug targets among the corona viruses that plays a major role in the translation and replication of new generation viruses from the viral genomic.

1.4 Why it is called $3CL^{pro}$ or M^{pro}

The functional polypeptides are released from the polyproteins by extensive proteolytic processing. This is primarily achieved by 33.1-kD HCoV 229E main proteinase (M^{pro}), which is frequently also called 3C-like proteinase ($3CL^{pro}$) to indicate a similarity of its cleavage-site specificity to that observed for picoronavirus 3C proteinases.

1.5 Structure

SARS-CoV-2 was found to be a positive-sense, single-stranded RNA virus belonging to the genus Betacoronavirus. Phylogenetic analysis revealed that SARS-CoV-2 is closely related (88–89% similarity) to two bat-derived SARS-like corona viruses, namely bat-SL-CoVZC45 (GenBank accession no. **MG772933.1**) and bat-SL-CoVZXC21 (GenBank accession no. **MG772934.1**), but it is more distant from SARS-CoV (~79% similarity) and Middle East respiratory syndrome corona virus (MERS-CoV) (~50% similarity). RNA-based metagenomic next-generation sequencing approach was applied to identify a human coronavirus from two pneumonia cases during the Wuhan outbreak in 2019. Its entire genome was 29 881 bp in length. Phylogenetic analysis indicates that SARS-CoV-2 is similar to the corona virus circulating in *Rhinolophus* (horseshoe bats), with 98.7% nucleotide similarity to the partial RNA-dependent RNA polymerase (*RdRp*) gene of the bat corona virus strain BtCoV/4991 (GenBank **KP876546**, 370 bp sequence of *RdRp*) and

87.9% nucleotide similarity to bat corona virus strain bat-SL-CoVZC45 and bat-SL-CoVZXC21. Evolutionary analysis based on ORF1a/1b, S and N genes suggests that SARS-CoV-2 is more likely a novel corona virus that was independently introduced from animals to humans. Based on the findings of genomic investigations and the presence of some bats and live animals in the seafood market in Wuhan, SARS-CoV-2 may have originated from bats or bat droppings associated with contaminated materials in the market or surrounding region. At this time, there are no specific vaccines or treatments for COVID-19. However, there are many ongoing clinical trials evaluating potential treatments.

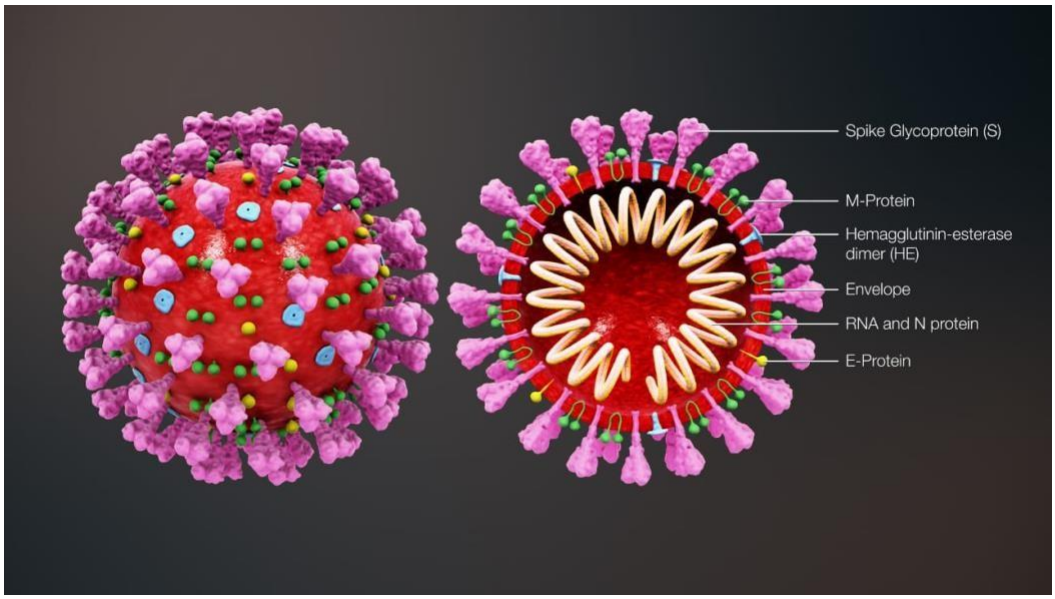


Fig1: Structure of COVID-19

1.5.1 Domains of SARS-CoV 3CL^{pro} or M^{pro}

The 3DstructureofSARS-CoV-2Mpro (PDB ID. 6Y2G), is made up of three domains, where domain I, II and III spans across 8-101, 102-184 and 201-306 amino acid residues, respectively. Domain I and II mainly consists of b-barrels while domain III mainly consists of a-helices. The substrate/active site of binding is located at the cleft of domain I and II, which consists of two catalytic residues, namely, HIS41 and CYS145.

It has following features:

- ✓ SARS-CoV M^{pro} and SARS-CoV-2 M^{pro} share more than 96% similarity

- ✓ Therefore, their 3D structures are highly similar
- ✓ Substrate/inhibitors bind to the same binding site
- ✓ Substrate/inhibitor binding site lies between domain-I and domain-II

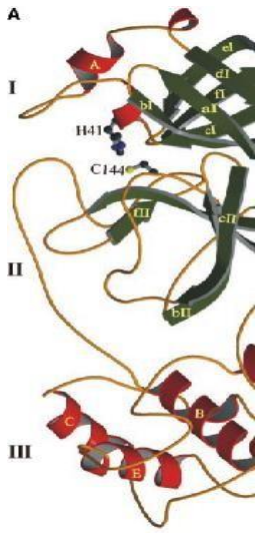


Fig2: Domain

1.5.2 SARS-CoV-2 M^{pro} is a dimer

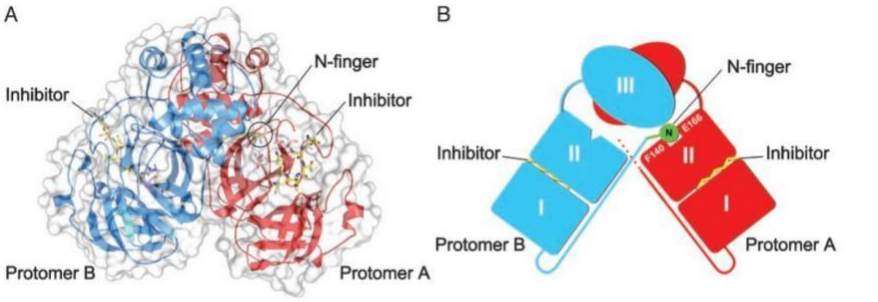


Fig. 1. The SARS-CoV M^{pro} dimer structure complexed with a substrate-analogue hexapeptidyl CMK inhibitor. (*A*) The SARS-CoV M^{pro} dimer structure is presented as ribbons, and inhibitor molecules are shown as ball-and-stick models. Protomer A (the catalytically competent enzyme) is red, protomer B (the inactive enzyme) is blue, and the inhibitor molecules are yellow. The N-finger residues of protomer B are green. The molecular surface of the dimer is superimposed. (*B*) A cartoon diagram illustrating the important role of the N-finger in both dimerization and maintenance of the active form of the enzyme.

Fig3: Dimer

METHODOLOGY

2.1 Finding existing inhibitors

Found 13 existing inhibitors for HIV (clinically tested). We will use these inhibitors to check their binding with SARS-CoV-2 M^{pro} using molecular docking.

2.1.1 About HIV (Human immune-deficiency virus)

Drugs that attack HIV-1 protease are one of the triumphs of modern medicine. The AIDS epidemic started a few short decades ago--before that, HIV was unknown. These drugs demonstrate the powerful tools that medical science has to combat a new disease. HIV belongs to the class of viruses called retroviruses, which carry genetic information in the form of RNA. HIV infects T cells that carry the CD4 antigen on their surface. The infection of the virus requires fusion of the viral and cellular membranes, a process that is mediated by the viral envelope glycoprotein (gp120, gp41) and receptors (CD4 and coreceptors, such as CCR5 or CXCR4) on the target cell. As a member of the aspartic protease family, the protease contains a catalytic triad (Asp25-Thr26-Gly27) in both the chains keeping functional aspartate residues at the dimer interface. The Asp residues are essential both catalytically and structurally while the Thr and Gly residues functions are still unknown at this time and are buried in the active site. HIV-1 protease performs an essential step in the life cycle of HIV. Like many viruses, HIV makes many of its proteins in one long piece, with several proteins strung together. HIV-1 protease has the job of cutting this long "polyprotein" into the proper protein-sized pieces. The timing of this step is critical. The intact polyprotein is necessary early in the life cycle, when it assembles the immature form of the virus. Then, the polyprotein must be cut into the proper pieces to form the mature virus, which can then infect a new cell. The cleavage reactions must be timed perfectly, allowing the immature virus to assemble properly before the polyprotein is broken. Because of its sensitive and essential function, HIV-1 protease is an

excellent target for drug therapy. Drugs bind tightly to the protease, blocking its action, and the virus perishes because it is unable to mature into its infectious form.

2.1.1.1 Structure of HIV

The first structures were reported in 1989. A decade later, over one hundred structures are available in the PDB, including several genetic strains of the enzyme, complexes of the enzyme with many different drugs and inhibitors, and dozens of mutant enzymes. Hundreds more are stored in the proprietary databases of pharmaceutical companies, where they are used to test and refine new drug candidates. Overall, HIV-1 protease is now one of the best-studied enzymes known to medicine. It is an enigmatic enzyme, however, that still hides many of its secrets. HIV-1 protease is a small enzyme, composed of two identical protein chains, each only 99 amino acids long. The active site is at the center of the tunnel, where a water molecule is used to break the protein chain.

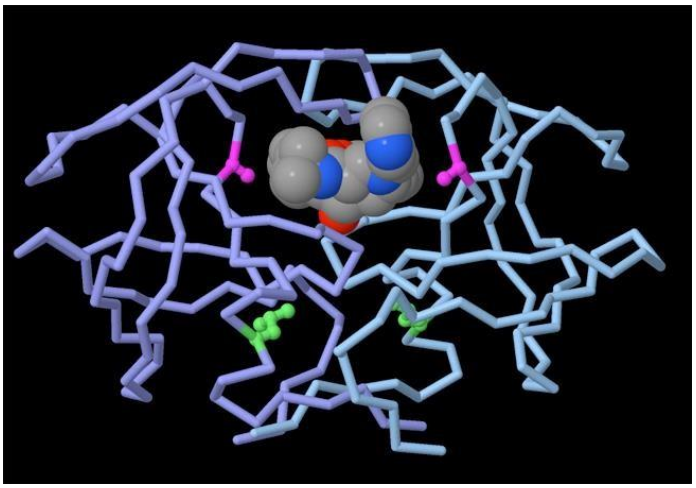
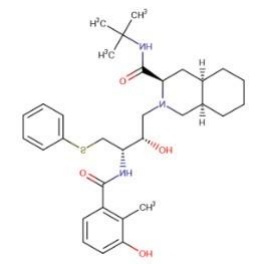
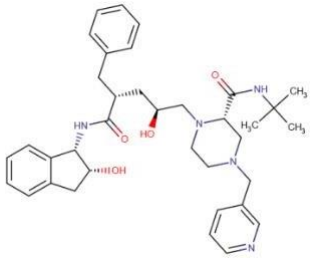
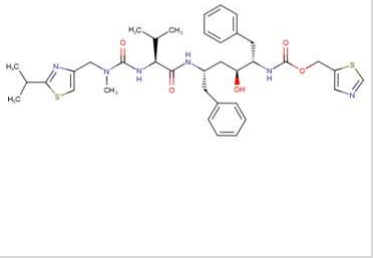
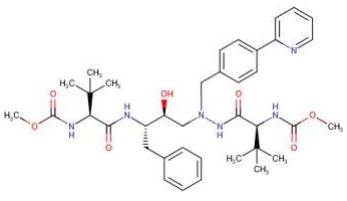
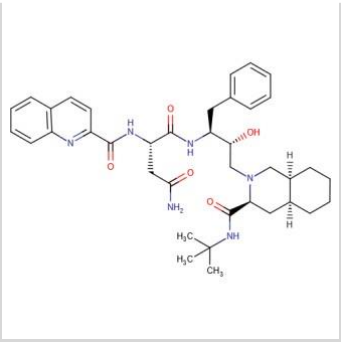
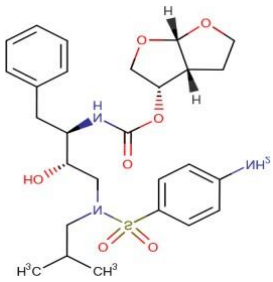
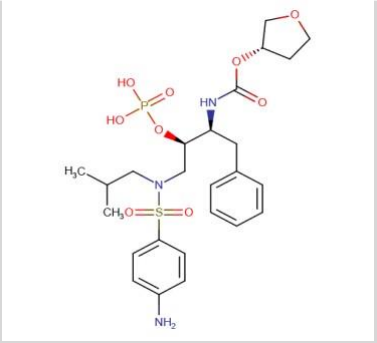
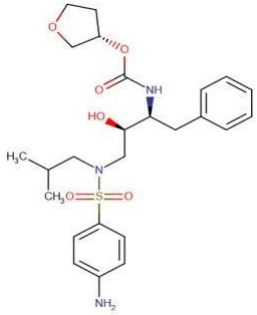


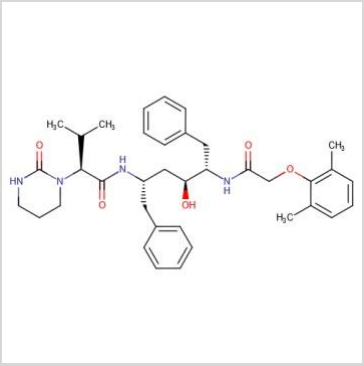
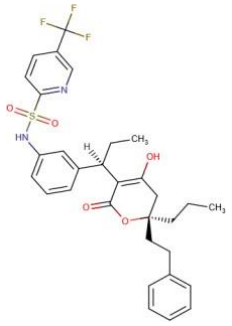
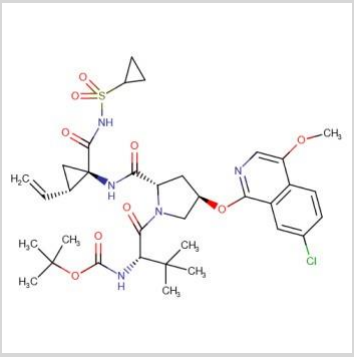
Fig4: HIV

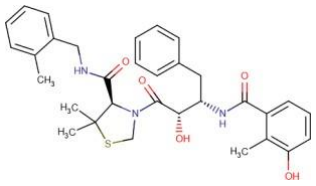
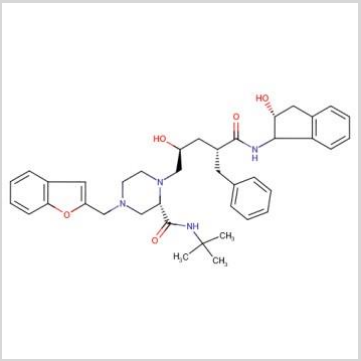
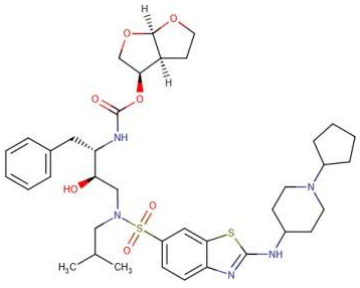
2.2Table of Protease Inhibitors

TABLE

SNO	NAME /AGENT	DETAILS OF CLINICAL TRIALS	CITATION	Brand Name	STRUCTURE
1	Nelfinavir	Phase III , approved 1997	https://www.drugbank.ca/drugs/DB00220	Viracept	
2	Indinavir	Phase II , approved 1996	https://www.drugbank.ca/drugs/DB00224/clinical_trials?conditions=DBCOND0035016&phase=2&purpose=treatment&status=completed	Crixivan	
3	Ritonavir	Phase III , approved 1996	https://www.drugbank.ca/drugs/DB00503/clinical_trials?conditions=DBCOND0035352%2CDBCOND0035016&phase=3&purpose=treatment&status=completed	Norvir	
4	Saquinavir	Phase 4 , approved 2003	https://www.drugbank.ca/drugs/DB01072/clinical_trials?conditions=DBCOND0035016&phase=4&purpose=treatment&status=completed	Reyataz	

5	Saquinavir	Phase II/III , approved 1995	https://www.drugbank.ca/drugs/DB01232/clinical_trials?conditions=DBCOND0035016&phase=2%2C3&purpose=treatment&status=completed	Invirase	
6	Darunavir	Phase 4 , approved 2006	https://www.drugbank.ca/drugs/DB01264/clinical_trials?conditions=DBCOND0035016%2CDBCOND0018907&phase=4&status=completed	Prezista	
7	Fosamprenavir	Phase I , approved 2003	https://www.drugbank.ca/drugs/DB01319/clinical_trials?conditions=DBCOND0035016&phase=1&purpose=treatment&status=completed	Lexiva	
8	Amprenavir	Phase II , approved 1999	https://www.drugbank.ca/drugs/DB00701/clinical_trials?conditions=DBCOND0035016&phase=2&purpose=treatment&status=completed	Agenerase	

9	Lopinavir	Phase 4 , approved 2000	https://www.drugbank.ca/drugs/DB01601/clinical_trials?conditions=DBCOND0035016&phase=4&purpose=treatment&status=completed	Kaletra	
10	Tipranavir	Phase III , approved 2005	https://www.drugbank.ca/drugs/DB00932/clinical_trials?conditions=DBCOND0035016&phase=3&purpose=treatment&status=completed	Aptivus	
11	Asunaprevir	Phase II	https://clinicaltrials.gov/ct2/show/NCT02124044	Sunvepra	
12	JE-2147	Phase I	https://books.google.co.in/books?id=-NpGAQAAMAAJ&pg=PA113&lpg=PA113&dq=which+phase+is+JE2147+in&source=bl&ot	-	

			s =QHa5 AtYf&sig=ACfU3U1OiMc8WCS3P3TltN AgitXFIPxf5A&hl=en&sa=X&ved=2ahUKEwj9jY7BgfjpAhVI8HMBHa9fAmgQ6AEwBXoECAkQAQ#v=onepage&q=which%20phase%20is%20JE-2147%20in&f=false		
13	L-756423	Phase II , approved 1999	https://www.drugbank.ca/drugs/DB02009/clinical_trials conditions= DBCOND0035016&phase=2& purpose=treatment&status=completed	-	
14	TMC-310911	Phase III approved 2005	https://clinicaltrials.gov/ct2/show/NCT00258557	ASC-09	

2.3 Ligand Preparation

2.3.1 For 2D Structures

1. Open UCSF Chimera
2. Open PubChem in the browser and type inhibitor name.
3. Get the SMILES string

4. Go to UCSF Chimera Tools -> Structure Editing -> Build Structure -> SMILES string (Paste the SMILES string that we have copied from pubChem) -> Apply -> Close.
5. Now we have our ligand molecule built.
6. Again Tools -> Structure Editing -> Minimize Structure (here set steepest descent steps: 1000 and Conjugate gradient steps:1000) -> Minimize
7. Now Add hydrogens will pop-up click OK, then Assign Charges to minimize select Gasteiger and enter OK. This will show the net charge of the molecule. Click OK.
8. Save ligand to the working directory: save as .mol2

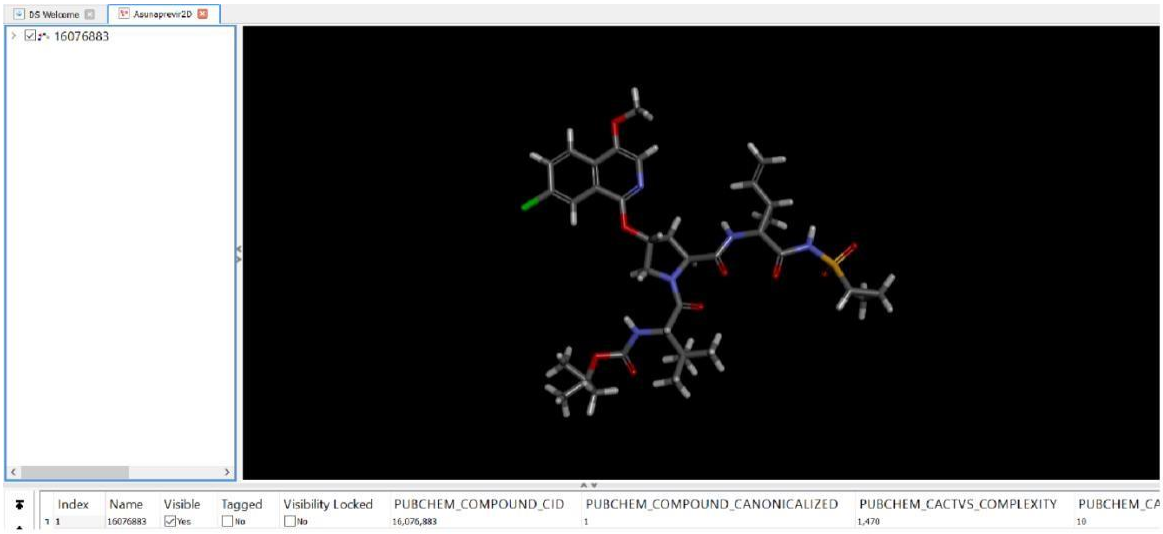


Fig5: Asunaprevir

2.3.2 For 3D Structures

1. Open UCSF Chimera
2. Open PubChem in the browser and type inhibitor name.
3. Download the 3D structure as .SDF and open it in UCSF Chimera.
4. Again Tools -> Structure Editing -> Minimize Structure (here set steepest descent steps: 1000 and Conjugate gradient steps:1000) -> Minimize

5. Now Add hydrogens will pop-up click OK, then Assign Charges to minimize select Gasteiger and enter OK. This will show the net charge of the molecule. Click OK.
6. Save ligand to the working directory: save as .mol2

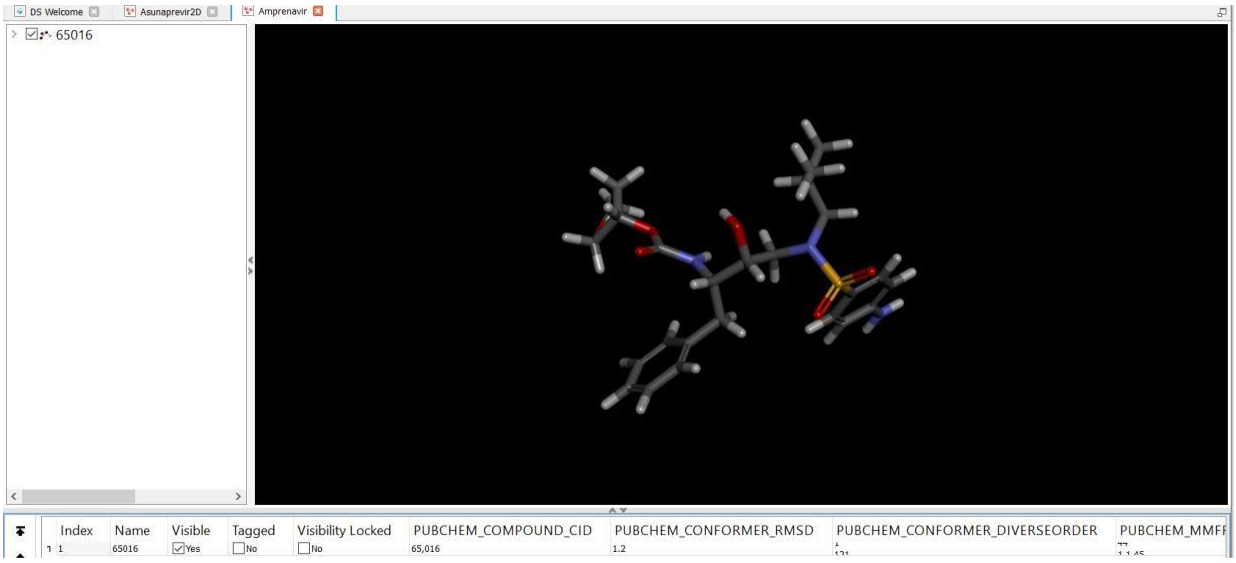


Fig 6: Amprenavir

2.4 Protein Preparation

PDB ID: 6Y2G

1. Open Discovery studio.
2. Open RSCB PDB from web browser and search for PDB ID.
3. Download the structure as PDB.
4. Open the pdb structure in Discovery studio.
5. The pdb structure 6Y2G has 2 chains – A and B.
6. Delete chain B .
7. Only keep Ligand A(O6K402) as reference and delete all other ligands.
8. Go to macromolecule -> prepare protein -> clean protein -> show clean report.
9. Now go to minimize protein -> select protein -> select algorithm -> Yes.

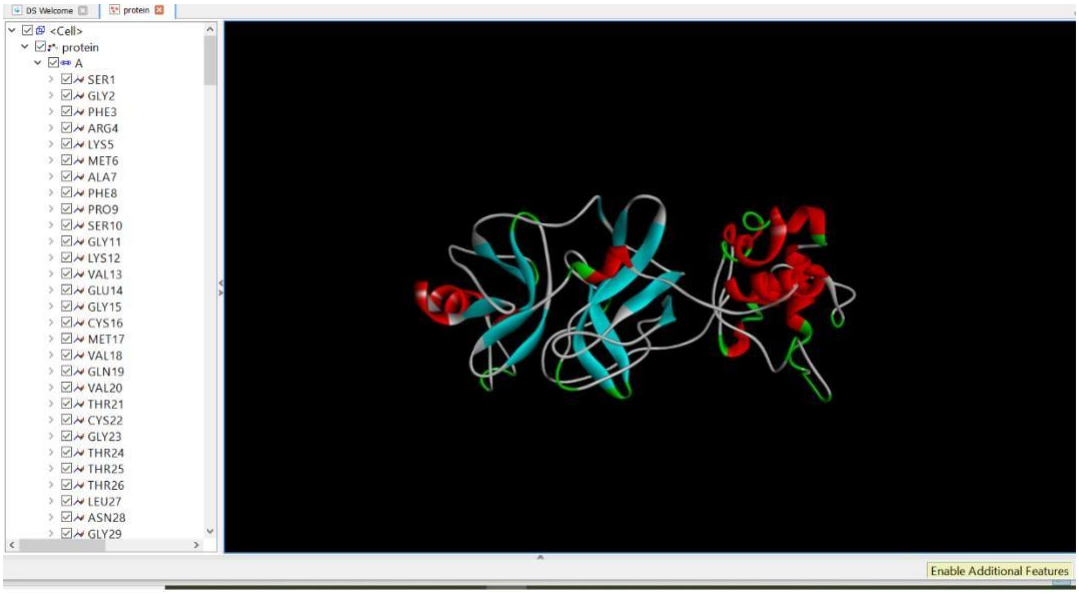


Fig7 Minimized protein

2.5 Grid Generation

1. File -> Read Molecule -> 6Y2G.pdb
2. Edit -> Delete Water
3. Edit -> Hydrogens -> Add H -> All polar -> Ok
4. Edit -> Charges -> Add Kollman charges
5. Edit -> Charges -> Compute Gastegier charges
6. Atoms -> Assign AD4 type
7. File -> Save -> Write PDBQT
8. Select -> Select from string -> Residue sets -> Ligands -> Dismiss
9. Ligand -> Input -> Open -> .mol2 files -> Ok
10. Ligand -> Output -> Write PDBQT
11. Select ->Select from string -> Residue sets -> Ligands -> Add-> Dismiss
12. Grid -> Macromolecule -> Choose -> 6Y2G -> Save as .pdbqt
13. Grid -> Set map types -> Choose ligand
14. Grid -> Grid Box -> Centre -> Centre on ligand
15. File -> Close saving current
16. Grids -> Output -> gpf -> save as grid.gpf

2.6 Docking

2.6.1 Auto Grid

1. Run -> Auto-Grid -> Program Pathname -> Browse -> C Drive -> (XProgram Files) -> The Scripps Research Institute -> Autodock -> 4.2.6 -> autogrid.
2. For parameter filename -> Browse ->grid.gpf.
3. Automatically a log filename file grid.glg will be created -> Launch

2.6.2 Auto Dock

1. Docking -> Macromolecule -> RigidFilename -> 6Y2G.pdb
2. Docking -> Ligand -> Choose -> .mol2 file -> Accept
3. Docking -> Output -> Lamarkian -> Save as dock.dpf
4. Run -> Auto-Dock -> Program Pathname -> Browse -> C Drive -> (XProgram Files) -> The Scripps Research Institute -> Autodock -> 4.2.6 -> autodock.
5. For parameter filename -> Browse ->dock.dpf.
6. Automatically a log filename file dock.dlg will be created -> Launch

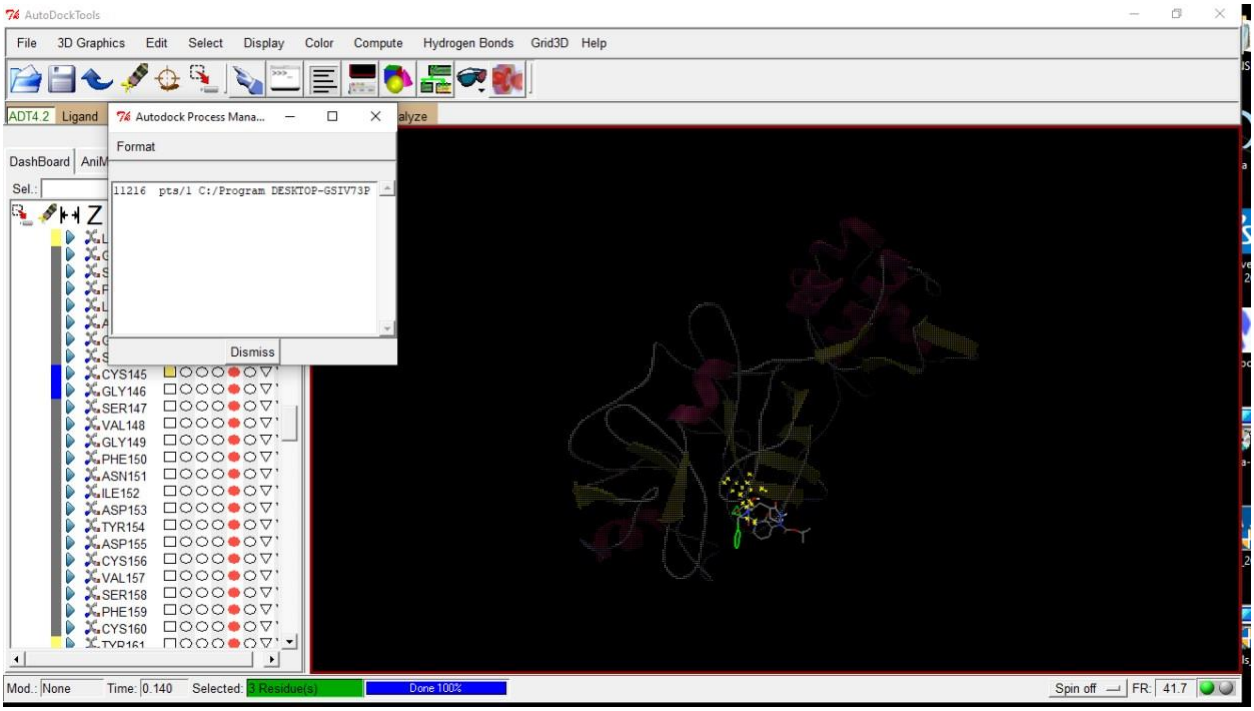


Fig 8 Autodock

2.7 Analyzing 2D and 3D Poses

2.7.1 Through Auto dock

- Analyze -> Docking -> Open -> File Location -> dock.dlg.
- Analyze -> Conformations -> Play Rank by Energy(Best pose appears)

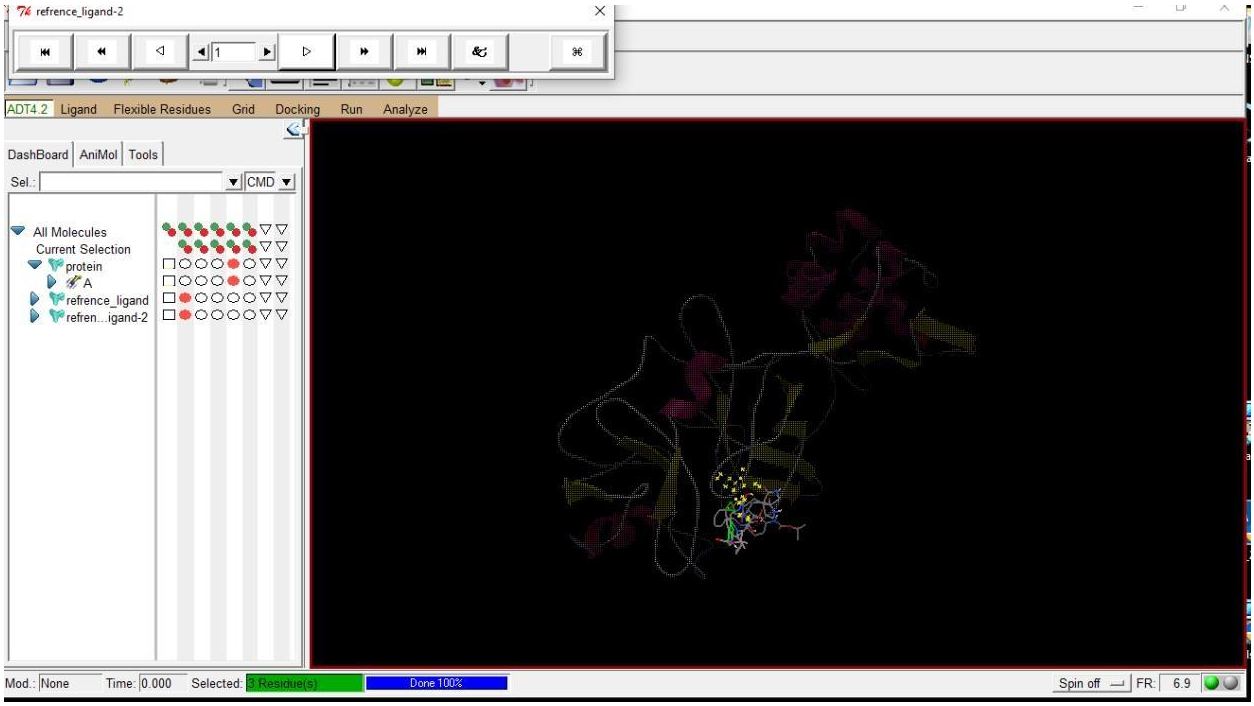


Fig 9 Best Pose from 10 different poses

2.7.2 Through Discovery Studio

- File -> Open -> Protein
- Convert ->dock.dlg to dock.pdb
- Delete everything except coordinates
- Remove lower remaining part
- Drag pdb file from notepad
- Check every dock model and pose

2.7.3 Binding Energy

Minimum binding energy of only on cluster is obtained and a best pose is created.

Cluster Rank	Lowest Binding Energy	Run	Mean Binding Energy	Num in Clus	Histogram 5 10 15 20 25 30 35
1	-5.93	9	-5.84	2	##
2	-5.58	4	-4.82	2	##
3	-5.41	1	-4.76	2	##
4	-5.38	5	-5.38	1	#
5	-4.71	8	-4.71	1	#
6	-4.31	10	-4.31	1	#
7	-3.75	6	-3.75	1	#

Number of multi-member conformational clusters found = 3, out of 10 runs.

RMSD TABLE

Rank	Sub-Rank	Run	Binding Energy	Cluster RMSD	Reference RMSD	Grep Pattern
1	1	9	-5.93	0.00	29.89	RANKING
1	2	3	-5.76	1.27	29.81	RANKING
2	1	4	-5.58	0.00	30.59	RANKING
2	2	7	-4.07	1.96	31.48	RANKING
3	1	1	-5.41	0.00	30.35	RANKING
3	2	2	-4.11	1.92	30.82	RANKING
4	1	5	-5.38	0.00	29.03	RANKING
5	1	8	-4.71	0.00	30.84	RANKING
6	1	10	-4.31	0.00	30.33	RANKING
7	1	6	-3.75	0.00	31.15	RANKING

Fig 10 Binding Energy

2.8 Software's used

We used UCFS Chimera a molecular visualization tool, was used to visualize the results obtained from the server. Discovery Studio Visualizer was further employed in

order to prepare the docked poses and 2 D interaction plots. Autodock 4.2.6 ; a suite of automated docking tools was practiced to predict how small molecules bind to receptor of known 3D structures. While browsing the web we exploited PubChem , Drugbank and NCBI.

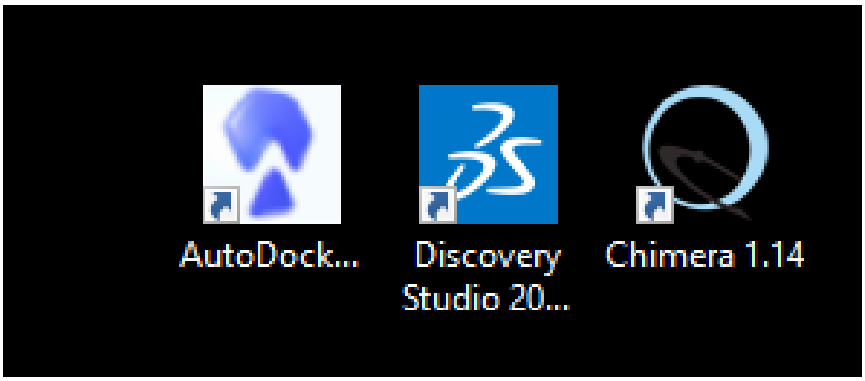


Fig11: Tools used

LITERATURE REVIEW

3.1 Review of Literature

The coronavirus disease 2019 (COVID-19) pandemic caused by severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) is a global health emergency. The virus has been named severe acute respiratory syndrome–coronavirus 2 (SARS-CoV-2) because the RNA genome is about 82% identical to that of the SARS coronavirus (SARS-CoV), both viruses belong to clade b of the genus Betacoronavirus. The best-characterized drug targets among coronaviruses is the main protease (Mpro, also called 3CLpro). Along with the papain-like protease(s), this enzyme is essential for processing the polyproteins that are translated from the viral RNA. The Mpro operates at no fewer than 11 cleavage sites on the large polyprotein 1ab (replicase 1ab, ~790 kDa). The recognition sequence at most sites is Leu-Gln↓(Ser, Ala, Gly) (↓ marks the cleavage site). Inhibiting the activity of this enzyme would block viral replication. Because no human proteases with a similar cleavage specificity are known, such inhibitors are unlikely to be toxic. The three-dimensional structure is highly similar to that of the SARSCoV Mpro, as expected from the 96% sequence identity.

The chymotrypsin-like and picornavirus 3C protease–like domains I and II (residues 10 to 99 and 100 to 182, respectively) are six-stranded antiparallel b barrels that harbor the substrate-binding site between them. Domain III (residues 198 to 303), a globular cluster of five helices, is involved in regulating the dimerization of the Mpro, mainly through a salt-bridge interaction between Glu290 of one protomer and Arg4 of the other.They used this crystal structure to dock the a-ketoamide 13a which suggested that the pyridine ring might have some steric clash with the side chain of Gln189. However, in their previous work, they had found Gln189 to be quite flexible, and therefore we went ahead with 13a as a lead. However, relative to 11r (IC50 = 0.18 ± 0.02 mM), the structural modification led to some loss of inhibitory activity against the main protease of SARS-CoV-2 (IC50 =

2.39 ± 0.63 mM) cyclopropyl in 13b. Through the nucleophilic attack of the catalytic Cys145 onto the a-keto group of the inhibitor, a thiohemiketal is formed in a reversible reaction. The oxyanion (or hydroxyl) group of this thiohemiketal is stabilized by a hydrogen bond from His41, whereas the amide oxygen of 13b accepts a hydrogen bond from the main-chain amides of Gly143, Cys145, and partly Ser144, which form the canonical "oxyanion hole" of the cysteine protease. It is an advantage of the a-ketoamides that their warhead can interact with the catalytic center of the target proteases through two hydrogen-bonding interactions rather than only one, as with other warheads such as aldehydes or Michael acceptors . To assess the absorption-distribution-metabolism-excretion (ADME) properties of the pyridine containing a-ketoamides, they investigated compound 13a and 13b .The ADME parameters of 13b were similar to those of 13a. In addition, binding to human plasma proteins was found to be 90%. The Cmax of 13b is around 37% of the Cmax detected for 13a, although the 13b dosage was lower by a factor of ~7. In addition, 13b showed a less rapid clearance relative to 13a. During the pharmacokinetic study with 13b, we monitored its lung tissue levels. After 4 hours, 13b was still found at ~13 ng g−1 in lung tissue. This lung tropism of 13a and 13b is beneficial given that COVID-19 affects the lungs. In addition 13b was nebulized using an inhalation device at 3mg kg−1. After 24 hours, 13b was found at 33 ng g−1 in lung tissue. Thus, this study provides a useful framework for development of pyridone-containing inhibitors toward anticoronaviral drugs. To date no specific medications have been developed, and therefore considering the risk factors associated with this disease, there is an urgent need for a treatment method to treat this disease in order to limit the transmission. This study is focused on the repurposing/identification of compounds with a sole aim to expedite the identification of specific drugs for the treatment of COVID-19. Among all the treatment strategies, the uses of already known viral medications have great advantages as the pharmacokinetics, pharmacodynamics, and safety profiles of these drugs have already been established. This drug repurposing strategy has gained significance as they are expected to be faster with less investment .

Recently, anti-malarial drug chloroquine and hydroxychloroquine along with some antiviral drugs have been reported to have certain curative effect on COVID-19. Due to diverse bioactivity and less toxicity, naturally occurring bioactive flavonoid molmolecules have also been screened for their potential therapeutic effects. The MPro is one of the most explored drug target among the corona viruses that plays a major role in the translation and replication of new generation viruses from the viral genomic RNA The 3D structure of SARS-CoV-2 Mpro (PDB ID. 6Y84), is made up of three domains, where domain I, II and III spans across 8-101, 102-184 and 201-306 amino acid residues, repectively. Domain I and II mainly consists of b-barrels while domain III mainly consists of a-helices .The substrate/active site of binding is located at the cleft of domain I and II, which consists of two catalytic residues, namely, HIS41 and CYS145 .Here in this report, a total of 33 compounds belonging to different classes (i) control drugs, (ii) natural products, (iii) anti-virals, (iv) anti-fungals, (v) anti-nematodes and antiprotozoal

were identified to investigate their inhibitory effects towards MPro by molecular docking analysis. Ritonavir, hydroxychloroquine, penciclovir and lopinavir are known drugs that have been screened for the treatment of COVID-19. The reason for them being used as control drugs in the study is that, lopinavir/ritonavir combination, and anti-malarial drug hydroxychloroquine has recently been found to be a potential inhibitor of the virus, Considering the diverse pharmaceutical properties of the natural products including anti-viral properties, a total of 17 compounds: curcumin, demethoxycurcumin, (-)-Epigallocatechin gallate (EGCG), (-)-epigallocatechin, (EGC), hesperidin, myricitrin, puerarin, scutellarin, rutin, quercitrin, capsaicin, ursolic acid, glabridin, apiin, rhoifolin, glycyrrhizin, and vitexin were screened for their inhibitory potential against SARS-CoV-2 Mpro. Azidothymidine, indinavir, tipranavir, and saquinavir are the well-known anti-viral drugs while diethylcarbamazine, primaquine, mepacrine, artemisinin and niclosamide are the anti-nematodes and emetine, an anti-protozoal drug , which have also been screened for their inhibitory potentials. Further, two anti-fungals, namely, fluconazole and itraconazole were also docked to the main protease of COVID-19. The 3 D coordinates of the ligands were obtained from ChemSpider as a .mol file and further geometry

optimization was carried out in ArgusLab using PM3 methods .The drug likeliness of a molecule is indicated by the Lipinski's rule of five parameters (molecular weight <500 Da, no more than 5 hydrogen bond donors, no. of hydrogen bond acceptors should be less than 10 and logP should not be greater than 5. The Lipinski's rule of five parameters were obtained from the SWISSADME server. The crystal structure of MPro (PDB ID: 6Y84) was obtained from Protein Data Bank (PDB) . The obtained structure was a dimer of two homologous amino acid chains (A and B). The chain A was used for molecular docking. Water molecules were removed from the PBD using PyMOL .

The final PDB file of the protease and geometry optimized ligand structures were selected for molecular docking analyses in the SwissDock server. According to the SwissDock server, the binding modes of the ligands are ranked according to their fullfitness score, therefore the conformers having the minimum fullfitness score were analyzed for further evaluations. The fullfitness score and the free binding energy associated with each corresponding docked pose were calculated and results were seen. Within the control drugs , the best pose was found to be of penciclovir with a fullfitnessscore of -1314.77 kcal/mol followed by ritonavir. Looking to naturally occurring compounds curcumin had best fulfitness score(-1236.50 kcal/mol). Coming forward to anti-fungal drugs Flucanazole (-1168.54 kcal/mol). The anti-viral drug with Azidothymidine (-1324.25 kcal/mol) and anti-nematodal and anti-protozoal drugs with Diethylcarbamazine(-1272.14 kcal/mol).

Among all the molecules, the inhibition activity of rutin was found to be the highest as its DG value (_9.55 kcal/mol) is the minimum, followed by ritonavir (_9.52 kcal/mol), emetine (_9.07 kcal/mol), hesperidin (_9.02 kcal/mol), and indinavir(_8.84 kcal/mol).

3.2 Summary of Literature Review

We used a-ketoamide13b inhibitor as our reference compound for our project based on the results of above mentioned article, whereas some reference inhibitors were also used

including penciclovir, hydroxychloroquine according to fullfitness score and free energy from the results drawn.

CONCLUSION

Cutting edge chemical science technology and computer-aided drug design (CADD) is bringing together leading minds from across the world to help tackle the COVID-19 crisis. The recent outbreak of novel coronavirus disease-19 (COVID-19) calls for and welcomes possible treatment strategies using drugs on the market. It is very efficient to apply computer-aided drug design techniques to quickly identify promising drug repurposing candidates, especially after the detailed 3D structures of key viral proteins are resolved. The virus causing COVID-19 is SARS-CoV-2. Taking advantage of a recently released crystal structure of SARS-CoV-2 main protease in complex with a covalently bonded inhibitor, we have successfully proposed a study focused on the repurposing/identification of compounds with a sole aim to expedite the identification of specific drugs for the treatment of COVID-19.A great application of drug repurposing is to identify drugs that were developed for treating other diseases to treat a new disease. Drug repurposing can be achieved by conducting systematic drug–drug target interaction (DTI) analyses by using various tools like UCSF Chimera(ligand preparation), Discovery studio(protein preparation) and autodock4 (molecular docking) followed by binding free energy calculations.

FUTURE SCOPE

Discovery and development of a new drug is generally known as a very complex process which takes a lot of time and resources. So now a day's computer aided drug design approaches are used very widely to increase the efficiency of the drug discovery and development course. Various approaches of CADD are evaluated as promising techniques according to their need, in between all these structure-based drug design and ligand-based drug design approaches are known as very efficient and powerful techniques in drug discovery and development. These both methods can be applied with molecular docking to virtual screening for lead identification and optimization. In the recent times computational tools are widely used in pharmaceutical industries and research areas to improve effectiveness and efficacy of drug discovery and development Pipeline, through it we can find the most promising drug candidate in a very cost-effective way. It always provides a hope for betterment in drug discovery area. In the past years through Computer aided drug design many impressive researches are achieved so it will play a very much important role in the near future. With the current achievement's, there is a promising future of computer aided drug design to aid drug discovery of many more curatives in covid-19 for future.

REFERENCES

[1] Cheung, G., & Sundram, F. (2017). Understanding the progression from physical illness to suicidal behavior: A case study based on a newly developed conceptual model. Clinical gerontologist, 40(2), 124-129.

[2] Aanouz, I., Belhassan, A., El-Khatabi, K., Lakhlifi, T., El-Ldrissi, M., & Bouachrine, M. (2020). Moroccan Medicinal plants as inhibitors against SARS-CoV-2 main protease: Computational investigations. Journal of Biomolecular Structure and Dynamics, 1-9.

[3] https://www.rcsb.org/

[4]https://pubchem.ncbi.nlm.nih.gov/

[5] https://www.drugbank.ca/categories/DBCAT000552

[6]https://www.who.int/

[7] Lv, Z., Chu, Y., & Wang, Y. (2015). HIV protease inhibitors: a review of molecular selectivity and toxicity. HIV/AIDS (Auckland, N.Z.), 7, 95–104.

[8] Henrich, T. J., & Kuritzkes, D. R. (2013). HIV-1 entry inhibitors: recent development and clinical use. Current opinion in virology, 3(1), 51–57.

PHYSICO-CHEMICAL EVALUATION OF BIOSURFACTANTS FOR THEIR POTENTIAL APPLICATIONS IN BIOTECHNOLOGY

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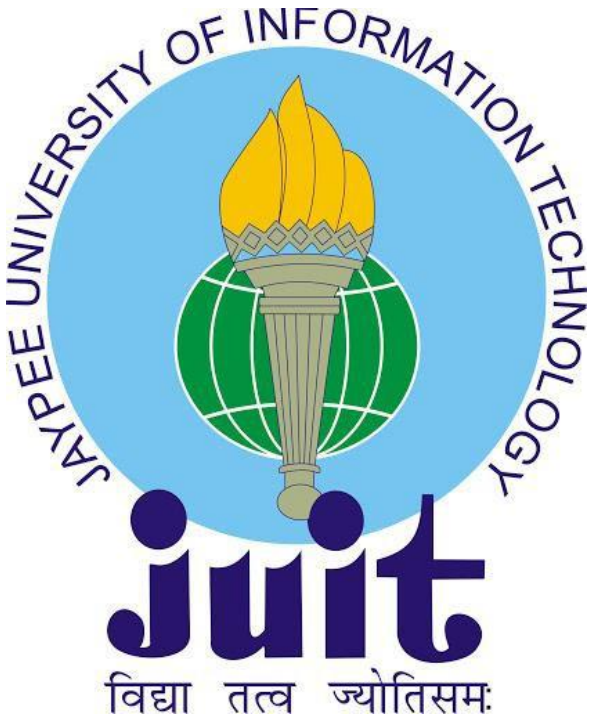

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Student Signature

Supervisor Signature

ACKNOWLEDGEMENT

In quest for this scholastic undertaking I feel that I have been particularly lucky as motivation, direction, course, co-activity, love and care all came in my way in plenitude and it appears to be very nearly an inconceivable assignment for me to recognize the equivalent in sufficient terms.

I express my true gratitude to my chief, Dr. Poonam Sharma, Professor, Division of Biotechnology and Bioinformatics, JUIT Waknaghat, for her regarded oversight, ceaseless help, motivation and productive analysis all through my exploration work.

Further, I stretch out my genuine gratitude to the entire Division of Biotechnology and Bioinformatics for giving the caring authorization and giving me the important authoritative offices during the exploration work.

ABSTRACT

Surfactants are amphiphilic compounds having both hydrophobic as well as hydrophilic moieties, thereby expressing the characteristics of both the groups. They tend to possess surface active characteristics, thereby decreasing the surface tension between the interfaces of either two liquids, liquid-air, oil-water interfaces etc. A common surfactant consists of a lipophilic group, usually a long-chain hydrocarbon moiety, and a hydrophilic group, which is both a charged or an uncharged polar group. Therefore, a surfactant consists of each a water-insoluble thing and a water-soluble component. Surfactants diffuse in water and adsorb at interfaces.

They resemble the chemical surfactants, containing each hydrophilic and hydrophobic moieties in the equal molecule. The hydrophobic tails structure the core of the aggregates, whilst the hydrophilic head is in contact with the liquid floor surrounding it. The form of aggregates relies upon on the chemical shape of the surfactants, due to the stability of measurement between the hydrophobic tail and hydrophilic head, which is measured by way of hydrophilic lipophilic stability i.e. HLB.

Diverse classes of surfactants can be characterized by the charge of their head gatherings, specifically cationic (positive charge); anionic (negative charge); non-ionic (non-charged and exceptionally hydrophilic); and zwitterionic (nearness of both negative and positive charge places, and a net charge equivalent to zero). The surface rheology of surfactant layers, including the versatility and thickness of the layer, assume a significant job in the solidness of froths and emulsions.

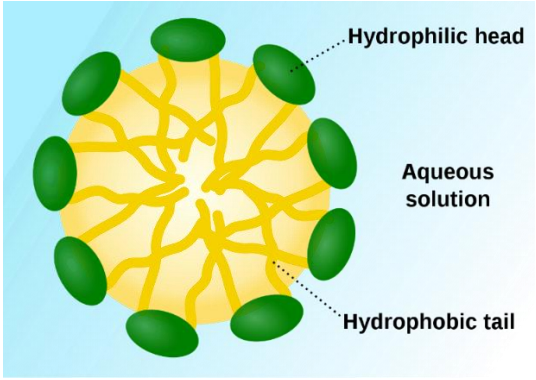

Fig 1: Structure of a typical surfactin molecule.

The biological entities themselves produce a wide array of surfactants, which are referred to as biosurfactants. The human body creates a wide cluster of surfactants like the Pneumonic Surfactant, being delivered in lungs, encourage breathing by expanding the complete Lung capacity. Microbial Surfactants are a wide assortment of basically differing mixes from microbial birthplace showing surface movement at the interfaces and possess ground-breaking attributes including high biodegradability, low poisonousness and unique organic exercises, emulsification activities, biocompatibility, thus making them suitable alternatives compared to their chemical/synthetic counterparts. Microbial surfactants are handily corrupted and are commonly considered as low or non-poisonous mixes. Microbial surfactants are known to segment at interfaces of liquid stages with particular polarities and hydrogen holding, in this way influencing the attachment of microorganisms.

TABLE OF CONTENTS

1. INTRODUCTION……. 5
2. OBJECTIVE…….. 6
3. BIOSURFACTANTS…… 6
4. PRODUCTION……. 7
5. PROPERTIES……10
6. CHARACTERIZATION……. 11
7. APPLICATION……. 14
8. CONCLUSION…….. 29
9. FUTURE PERSPECTIVE AND CHALLENGES……. 30
10. REFERENCES…….. 31

1. INTRODUCTION:

The phrase surfactant is a combination of surface-active agent. Surfactants alter the properties of the surface and interfacial tension of a liquid allowing the formation of microemulsions, which lead to solubilization of oil in water and water in oil. It is due to this phenomenon that they are widely used in many industries. Surface tension is a phenomenon which measures the force of attraction between the liquid molecules. It is a critical parameter for evaluating the effectiveness of a surfactant, leading to decrease in the surface tension when their concentration in the solution increases, which leads to formation of micelles. Micelles are formed due to the inability of lipophilic region of the surfactant to form hydrogen bond in aqueous phase and thereby lead to increase in free energy of the system. Dealing with this increased free energy is required to aid in isolation of hydrocarbon tail from water by its absorption onto organic or aqueous surfaces enabling the hydrophobic region oriented towards the centre while hydrophilic region facing water. Surfactants lower the interfacial tension between immiscible fluids making them miscible, due to formation of new additional surfaces. Micelles are defined as aggregated molecules containing both hydrophobic and hydrophilic groups, with hydrophilic groups oriented towards water, while hydrophobic group oriented towards oil. The formation of micelles leads to distribution of hydrophobic compounds into the pseudo core residing in the centre thereby enhancing solubility. This leads to better dispersion od compounds and lead to increased mobility of adsorbed hydrophobic soil contaminants by decreasing the capillary forces. The minimum concentration of surfactant required to produce a maximum decrease in surface tension of a liquid is regarded as Critical Micelle Concentration (CMC).

Biosurfactants are surface active bio-compounds produced by microorganisms and are considered as alternatives to petroleum derived chemical surfactants. These green compounds have lower critical micellar concentration compared to that of synthetic ones and they lead to higher decrease in surface tension of oil-water or air-water interfaces to a very low value. This property makes microbial surfactants great froth stabilizers and emulsifiers. Microbial surfactants present various focal points over the compound ones, in particular with respect to their biodegradability, mild creation conditions, ecological compatibility, lower toxicity, high selectivity, and explicit action at extraordinary temperatures, pH, and salinities.

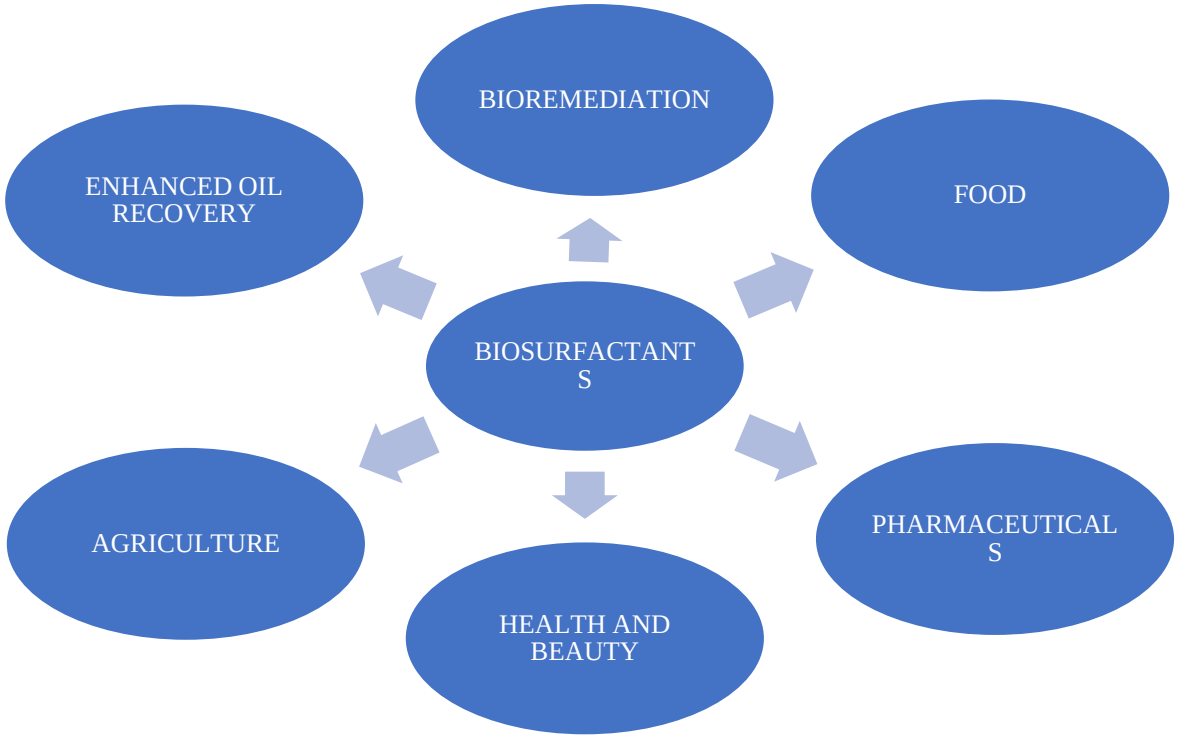

Fig 2: Applications of biosurfactants in various industries.

2. OBJECTIVE:

The target of this examination audit was to get comfortable with the properties, creation, and uses of biosurfactants in present day times. With the assistance of this audit, I hope to have a superior knowledge for biosurfactant creation and discover more applications which can be helpful for humankind.

3. BIOSURFACTANTS:

Surfactants are typically natural compounds that are amphiphilic, that means they incorporate each hydrophobic groups and hydrophilic groups. Biosurfactants are amphiphilic compounds having both hydrophilic and hydrophobic groups in it.[1] The hydrophilic region might be carbohydrate, amino acid, cyclic peptides, phosphate, carboxyl acid or alcoholic groups, while hydrophobic region comprises of a long chain fatty acid, hydroxyl fatty acids, α-alkyl-β-

hydroxy fatty acids etc. Other than bringing down the fluids surface pressure, these moieties can likewise incredibly affect the interfacial conduct and mass exchange, as they likewise bring down the interfacial strain between diverse fluid stages on the interfacial limit existing between immiscible stages.[11] Microbial surfactants possess an intense ability to lower the interfacial tension and show diverse properties as emulsification, lubrication ability, phase dispersion, detergency etc.[17] They are majorly used in food, petroleum, cosmetics industries, environmental, bioremediation, environmental and even pharmaceutical industries. Surfactant molecules are amphipathic in nature that get partitioned between two phases, having varying degree of polarity. Microbial surfactants are best and productive at their CMC which can be 10-40 times lower than that of substance surfactants, in this way less surfactant is important to get a most extreme lessening in surface pressure. Microbial surfactants are handily corrupted and are commonly considered as low or non-poisonous mixes. Microbial surfactants are known to segment at interfaces of liquid stages with particular polarities and hydrogen holding, in this way influencing the attachment of microorganisms. The presence of biosurfactant in a media can be detected by various techniques using colorimetric analysis, emulsification index determination, drop collapsing test and thin layer chromatography.

4. PRODUCTION:

Biosurfactants are obtained from non-exhaustible renewable sources thus having high surface activities, along with high specificity and the ability to function under extremes of conditions. Generally produced by aerobically growing microorganisms utilizing feedstocks as source of carbohydrates, fats etc. Biosurfactants are actively secreted into the culture medium and are supposed to aid in growth of microbes, by facilitating transport of solutes that are insoluble, across the cell membrane. They are usually non-ionic or anionic moieties and have both the lipophilic as well as hydrophobic groups.

Both high and low molecular weight biosurfactants are derived from microorganisms. Low molecular weight biosurfactants includes glycolipids like trehalose, fructose lipids, sophorolipids while peptidyl lipids include surfactin, polymyxin, etc. Surfactin is a biosurfactant produced by *Bacillus subtilis*, which possesses amphiphilic structure and serve as a potent inhibitor of bacterial and tumour growth, and are associated in lowering the surface

tension of the fluids. High molecular weight biosurfactants on the other hand are amphiphilic polysaccharides which are concerned in providing a stable emulsion and do not lower the interfacial tension.[21] Due to their ability of producing of stable emulsions they facilitate in strong adhesion of bacteria to hydrophobic surfaces. Most of the biosurfactants are obtained from *Arthrobacter*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Acinetobacter calcoaceticus*, *Candida lipolytica*, *Corynebacterium*, *Nocardia*, *Bacillus subtilis*, *Bacillus licheniformis*, *Candida spp.*, etc. Majority of biosurfactants are produced from substrates which are insoluble in water.

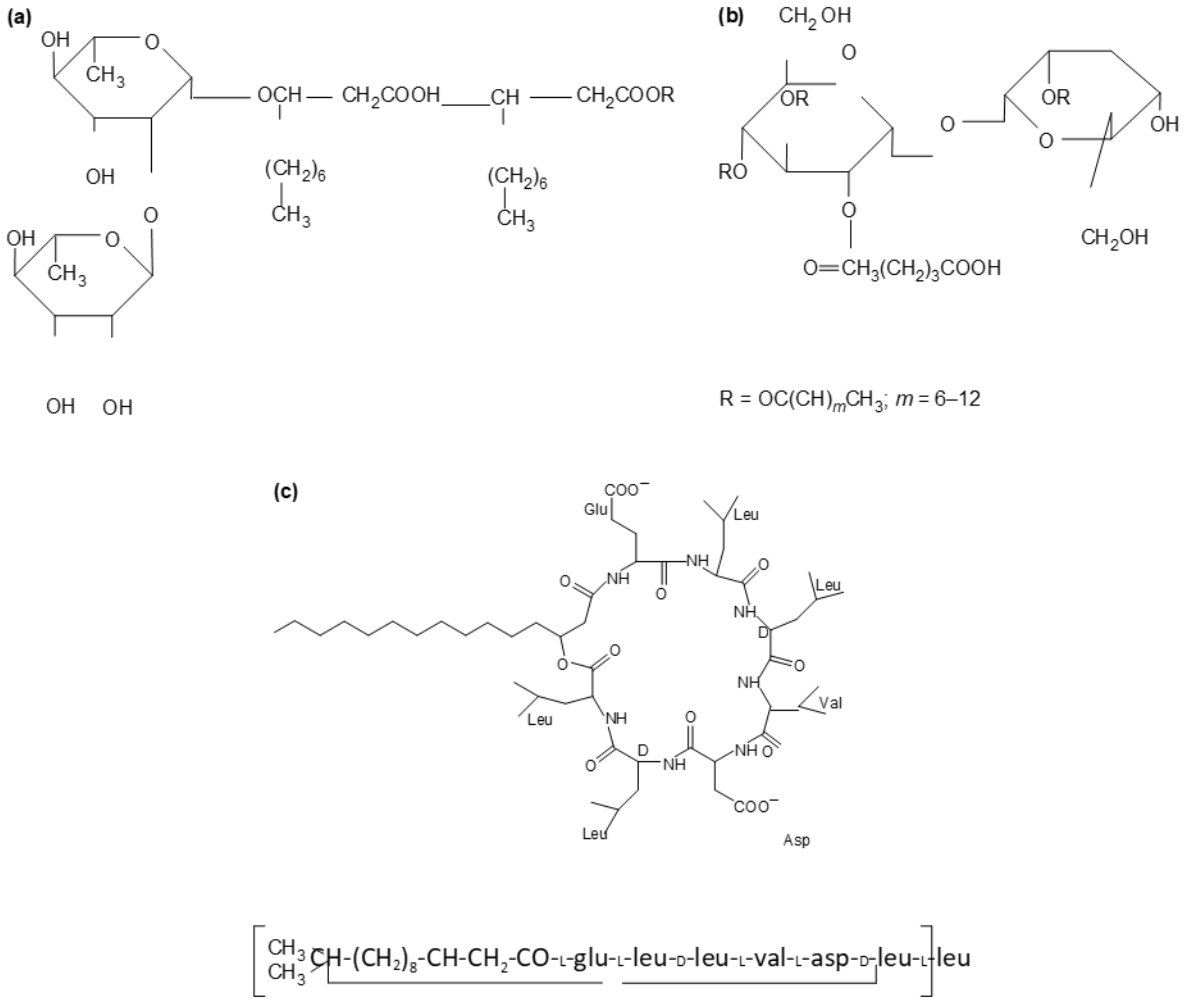

Fig 3: (a) Structure of dirhamnolipid. (b) Structure of trehalose lipid. (c) Surfactin structure

Researchers have obtained biosurfactants by growing a culture of *Candida lipolytica* on groundnut oil. Similarly, *Candida glabrata* was grown on vegetable oil to produce biosurfactants. Similarly, rhamnolipids were also produced from low cost carbon sources using

Pseudomonas aeruginosa like soybean, cottonseed, corn oil etc. Also, rhamnolipids were obtained using restaurant waste oil in bioreactor configuration using the strain *Pseudomonas aeruginosa.* Another low-cost medium was reported having Cassava waste water and waste cooking oil to obtain rhamnolipids.[30] Endophytic fungi are also been used to obtain biosurfactants, they are found in tropical areas on trees like *Piper hispidum*, which act as a potent source for ultimate production of biosurfactants.[8] The biosurfactant derived from *Candida utilis*, has low cytotoxicity, high antioxidant activity along with thermal stability, which makes it a suitable choice to be utilized in food industries. The best portrayed microbial surfactants incorporate Glycolipids and lipopeptides. *Pseudomonas aeruginosa* produce rhamnolipids (example of glycolipids),[19] trehalolipids created by *Rhodococcus erythopolis*, sophorolipids delivered by *Candida bombicola* and mannosylerythritol lipids (MEL) created by *Pseudozyma* yeasts.

To optimize the conditions for enhanced production of biosurfactants, metabolic pathway of the producing organism should be well known, also the chemical structure of biosurfactants should be well known too. Poultry farming waste and butter milk are found to be potential sources of nitrogen and carbon.[7] Hence this mixture was found efficient for production of SPB1 lipopeptide.

Petroleum derived synthetic surfactants happen to be the most widely used across different industries, primarily due to high cost of production of biosurfactants, also the fact that widescale production of these has not been defined yet to meet the industrial demands. This domain is being worked upon to find the ways to reduce cost of production, mainly focusing on use of alternate substates, microbial culture, culture conditions. Also use of low-cost medium can also aid in decreasing the cost of production.

A huge amount of organic waste is being produced via food, forest, municipalities and agriculture industries. Although biosurfactants are quite advantageous over synthetic surfactants they still are a bit costly to prepare. The only way to reduce their cost of production is modification in fermentation technologies and using renewable substrates and different microbial strains for production of biosurfactants. Further optimising operating parameters like temperature, pH, agitation speed and duration and efficient recovery of products, make them more efficient, but still a bit costly compared to synthetic ones. Use of low cost agro-industrial waste may overcome the issue of cost. It is necessary to develop techniques which allow easy

production and downstream processing of the product so as to be able to be used at a large scale. It depends upon the structure, composition and concentration of surfactant to choose a viable recovery method.it can be solved by using industrial by products like vegetal waste oil, like glycerol in appropriate concentrations does not inhibit growth and serves an excellent source of carbon.[22] Since huge amounts of waste generated by industries can be refined and used as excellent alternative substrates, thus producing low cost alternatives for production of surfactants as compared to that of petroleum derived surfactants.[11]

5. PROPERTIES:

Biosurfactants house certain unique properties like:

- Surface activity
- Biodegradation
- Detergency abilities
- Emulsification and de-emulsification activities
- Lubrication
- Wetting ability
- Foaming
- Solubilization
- Dispersion of phase etc.

Surface properties: Expansion of a surfactant to a given arrangement will bring down its surface strain because of the surfactant adsorption at the interface.[27] For a weakened arrangement, the more atoms adsorb at the interface, the lower the surface strain of the arrangement will be.

Hydrophilic-lipophilic balance: This boundary influences the soundness of the emulsion, speaking to the general commitment of hydrophobic tails and hydrophilic leader of the surfactant.[28] A low HLB favours water-oil microemulsions, and high worth favours oil-water microemulsions.

Critical packing parameter: To lessen the contact edge of the water with hydrocarbon chains, surfactant atoms will in general structure totals in arrangement with the chains situated to the inside and encased in the total.

Spontaneous curvature: Conglomeration can be legitimized dependent on the spontaneous bend. The favoured arch will likewise rely upon the general extent of polar and non-polar volumes.

Winsor R ratio: The proportion of the complete interaction energies (per unit zone of the interface) of the surfactant for the Oil and Water stages is known as the Winsor-R proportion. R< 1, demonstrates the water-surfactant connection is stronger than the oil-surfactant collaboration; R>1, proposing that the quality of oil surfactant cooperation is more grounded than the water-surfactant association; and R=1, the circumstance in which the communications are balanced.[3]

Self-assembly: Self-assembly comprises in the capacity of surfactant particles to self-associate in a given solvent, framing various kinds of totals and structures of colloidal measurements. These structures can be of restricted size or huge with network in one, a few measurements.

6. CHARACTERIZATION:

The characterization of structures was carried out using various spectroscopic techniques by obtaining Infrared spectra, Nuclear Magnetic Resonance was also carried out to characterize structures. Fatty acids were characterized using a characteristic reaction with diazomethane followed by final analysis using Gas chromatography and Mass spectroscopy. The results of FABMS were obtained by dissolving glycolipidic samples in glycerol to be used as probe matrix. Following it the alkaline lysis of glycolipids were carried out using reflux with 0.5 N NaOH solution for 12 hrs at 40°C. Fatty acids upon extraction with chloroform and methylation with diazomethane yielded a lipid sample for GC-MS analysis. Acid hydrolysis was carried out using refluxing of the sample with 2 N HCl for 2 and a half hours. Thin layer chromatography was carried out using different solvent systems to analyse sugar moiety. The interfacial and surface tensions of organic extract was measured using Lauda Automatic

Tensiometer TE-1 using De Nuoy ring method. Aqueous solutions here were acidified with pH 3 and 1 N HCl, then made basic with pH 9 and 1 N NaOH, the pH was recorded using Radiometer pH meter 28.

Added NaOH to the extracted biosurfactant leading to production of carboxylic acid salt of sodium, followed by washing with acetone and filtration using sintered glass. The precipitate so obtained was diluted with distilled water and was acidified using HCl for acid recovery and ethyl acetate was used for extraction. The gas filtration was performed using esterification of biosurfactant to get methyl esters of fatty acids.

The thermal analysis was performed in a thermal analyser, following successive steps of heating and cooling in an atmosphere of nitrogen.

Antioxidant activity was tested out by using an aliquot of 0.1 ml at varying concentrations of the biosurfactant having 1 ml of sulphuric acid, sodium phosphate, ammonium molybdate and subjected to water bath at a temperature of 90°C for 1 and a half hour. Optical density was recorded at 695 nm and expressed relative to a control of ascorbic acid having 100% antioxidant capacity. It was also tested using DPPH assay, which stands for 2,2-diphenyl-1-picrylhydrazyl. It was added to different tubes having different concentrations of biosurfactants and was incubated in the dark for 30 mins. Absorbance was measured at 517 nm and the percentage of inhibition activity was calculated using the formulae:

$$\%I = \frac{(Absi - Absf)x\ 100}{Absi}$$

where Absi is absorbance of control while Absf is that of biosurfactant.[6]

For Superoxide Sequestering test to check the antioxidant activity, the isolated biosurfactant was diluted using phosphate buffer, methionine solution, EDTA, riboflavin solution and nitro tetrazolium blue chloride and placed in a tube, the control had all of these except the biosurfactant. They were subjected for 15 mins to fluorescent lights, and reading was recorded at 560 nm.[6]

The cytotoxic activity of the biosurfactant was evaluated using MTT assay. (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) i.e. MTT protocol was designed using

fibroblast cells of mice and macrophage cells of mouse, kept in a culture flask having 5% CO2 and 37°C. Trypsin was used to detach the adhered cells and were then added to a 96 well plate having Dulbecco modified eagle medium, incubating this setup at 37°C with 5% CO2 for a day. Following this biosurfactant was added to this mixture under the prevailing same atmospheric conditions for 72 hours. DMEM medium alone acted as negative control, while positive control comprised of phosphate buffer. After the incubation MTT stain was added to the mixture and allowed incubation of 3 hrs. Following it, dimethyl sulfoxide was added and OD was recorded at 560 nm. Inhibition percentage was calculated by means of computer software.

Various classes of surfactants can be characterized by the charge of their head gatherings, specifically cationic (positive charge); anionic (negative charge); non-ionic (non-charged and exceptionally hydrophilic); and zwitterionic (nearness of both negative and positive charge places, and a net charge equivalent to zero).[1] The elements of assimilation rely upon the diffusion coefficient of the surfactant. As the interface is made, the adsorption is restricted by the dispersion of the surfactant to the interface. At times, there can exist a vivacious hindrance to adsorption or desorption of the surfactant. Such vitality hindrances can be expected to steric or electrostatic shocks. The surface rheology of surfactant layers, including the versatility and thickness of the layer, assume a significant job in the solidness of froths and emulsions.[29]

Microbial surfactants can be sorted by their method of activity, sub-atomic weight and general physicochemical properties. microbial surfactants are commonly sorted by their synthetic strategy and sub-atomic weight, as low (for example glycolipids and lipopeptides) and high atomic weight (for example polysaccharides, proteins and lipoproteins) surfactants. In heterogeneous frameworks, microbial surfactants structure an atomic interfacial film that influences the wettability and surface vitality of the first surface. Other than bringing down the fluids surface pressure, these movies can likewise incredibly affect the interfacial conduct and mass exchange, as they likewise bring down the interfacial strain between diverse fluid stages on the interfacial limit existing between immiscible stages.

7. APPLICATIONS:

Commercially available biosurfactants are obtained using chemical methods from petrochemical industries. To reduce the use of chemicals, microbes and other sources have been explored for the production of surfactants. Plants synthesize saponins, humans synthesize biliary salts and glycolipids secreted by microorganisms are some examples of organic surfactants.

Since the term is being used in a broad sense, it also includes some of the by-products produced by yeasts, bacteria and some filamentous bacteria, like emulsifiers and dispersing agents, which are generally used in petrochemical industries, food and pharmaceutical industries. Surfactants are generally used in cleaning industries which produce detergents and soaps. Surfactants are also being used for bioremediation of hydrocarbon pollution and enhanced oil recovery. Biosurfactants are being used as emulsifiers in food industries. Some major applications are:

Gene transfection:

Transfecting genes into a cell is the premise of clinical quality treatment. Lipofection utilizing cationic liposomes is viewed as a promising strategy for bringing outside qualities into the focus on cells because of their high transfection productivity, low toxicity, and immunogenicity, simplicity of arrangement, and focused on application. Physicochemical properties of cationic liposomes namely, lipid pressing density, zeta potential, and shape influence the proficiency of quality transfection. The biosurfactant actuates the layer combination between the objective cells and the cationic liposomes, quickening the proficiency of quality transfection fundamentally.

It was discovered monolayers made out of L-α-dipalmitoyl phosphatidylcholine (DPPC) containing MEL-A had more prominent film ease than those containing just DPPC. MELs are structurally classified into four types Mel a, Mel b, Mel c and Mel d. these variations are derived by the organism are the carbon source used. Mel has a property of self assembly that can be

used in chain delivery and drug encapsulation processes.[12] It was observed a higher unsaturated fat proportion liposome had the option to combine the plasma film yet didn't convey DNA into the core, while a lower unsaturated fat proportion liposome neither intertwined with the plasma layer nor conveyed DNA into the core.

As drug delivery agents:

They show properties like emulsification, frothing, detergency and scattering, help discover their application as medication conveyance vectors.[16] Rhamnolipids and sophorolipids can be blended in with lecithin to get ready biocompatible microemulsions in which the stage conduct is practically harsh toward changes in temperature and salt fixation, in this manner making them alluring for corrective and medication conveyance applications.[1] Microemulsions acquired utilizing microbial surfactants are thermodynamically steady and their isotropic frameworks that structure immediately, notwithstanding their drawn-out soundness, simple arrangement and high solubilization limit are viewed as exceptionally encouraging fluid vehicles for future medication conveyance frameworks.[13] The consolidation of an emulsion into a gel expands its strength and proficiency when contrasted with other topical medication conveyance frameworks.

Micro-emulsion systems:

The basic components to create a microemulsion-based colloidal DDS contain a watery stage, an oil stage, a surfactant and typically a co-surfactant or co-dissolvable.[23] These structures can exemplify or potentially solubilize hydrophobic or hydrophilic medications within the sight of a scattered stage inside its basic centre, in this manner dividing the scattered stage from the constant stage. These frameworks are thermodynamically steady and display high solubilization limit and ultralow interfacial strains of oil and water, accordingly making them attractive for medicate conveyance applications.[18]

Silver nanoparticles have been orchestrated utilizing a quick microbial surfactant interceded amalgamation, by blending the surfactant and AgNO3 arrangements, trailed by NaBH4 and incredible mixing. Fluid arrangements of AgNO3, sanitized biosurfactant, n-butanol, and n-heptane were overwhelmingly mixed until homogeneous converse micelles were framed. At that point, NaBH4 was utilized to frame other opposite micelles. The two converse micelle arrangements were blended and a short time later ethanol was added to break switch micelles. The silver nanoparticles were hastened from the arrangement and disengaged by centrifugation. Rhamnolipids have been effectively used to integrate circular nickel oxide nanoparticles. Unsaturated fats have been proposed to assume a twofold job in the blend of nanoparticles, by settling O/W emulsions in this way adjusting the decreasing gatherings on the external side; and additionally, by diminishing metal salts into nanometals.

In production of nano-particles:

Nanoparticles are portrayed by their novel size and stable shape. The accessible procedures are capital serious, produce perilous squanders and flimsy nanoparticles with diminished focused on action. To follow greener bio-handling microbial surfactants are being used as another option. Gold nanoparticles are by and large progressively utilized in the field of medication and quality conveyance, directed treatment and imaging advances. Its helpful applications incorporate enemy of HIV action, hostile to angiogenesis, antimalarial movement, against ligament action and biohydrogen creation. Microbial surfactants can be utilized for elite nanomaterial creation, since they effectively structure an assortment of fluid precious stones in watery arrangements. Analysts balanced out the gold and silver nanoparticles delivered by surfactin. At pH 7 the nanoparticles were uniform in size, while they were anisotropic at pH 5 and 9. Organic combination of gold and silver nanoparticles were additionally completed utilizing the microorganisms *Bacillus subtilis*[1]. Gold nanoparticles were blended both intra- and extracellularly, while silver nanoparticles were solely shaped extracellularly. The nanoparticles were balanced out by surface-dynamic particles, to be specific surfactin or different biomolecules discharged by B. subtilis. Surfactin created by *Bacillus amyloliquefaciens* KSU-109 was likewise utilized for the combination of cadmium sulphide nanoparticles which stayed stable as long as a half year. Purged rhamnolipids from *P. aeruginosa* strain BS-161R were utilized to blend silver nanoparticles showing great anti-

infection movement against both gram +ve and - ve microorganisms. A glycolipid microbial surfactant delivered by *Brevibacterium casei* MSA19 was utilized as a stabilizer for the combination of steady and uniform silver nanoparticles. The production of nanoparticles is either intra or extra cellular.

Biofilm disruption:

Bacteria's possess the ability to adapt to their environment and express themselves accordingly. Some gram +ve and gram +ve bacteria show a unique phenomenon known as Quorum sensing by which they can communicate with each other and sense their own cell density. This ability of bacteria has been involved in formation of biofilms, although it further depends upon the nutritional environment available to bacteria to carry out QS activity. During the biofilm formation and maturation event the cells attached to the surface start to aggregate into microcolonies, which are surrounded by few cells referred to as water channels. Biofilms in food industries act as a prominent source of contamination and disease. Therefore, use of biosurfactants to disrupt the adherence of microbial cells on the surface prevent formation of biofilm on food surface and thus their spoilage is prevented. The use of surfactin and rhamnolipids in particular decreased the adhesion of microbial cells on the polypropylene surfaces.[26] Biosurfactants may also be used in health and hygiene products to prevent biofilm formation in the oral cavity.

Microbial surfactants or biosurfactants possess the ability of anti-adhesion and biofilm degradation. Biofilms produced by many fungi and bacteria are degraded by synthetically derived enzymatic surfactants like lauryl-glucose. *Pseudomonas aeruginosa* derived rhamnolipids, are a class of surfactants which are efficiently used in biofilm disruption. The overproduction of rhamnolipids inhibits biofilm production by blocking cellular aggregation and secondary colonization onto the preformed biofilms. They also disperse cells from biofilms.

The biofilms produced by *Pseudomonas aeruginosa* were allowed to form on the flow cells which acted as a growth chamber for the biofilm. The chamber was supplied with oxygen and nutrients from a medium flask containing 50% TSB using a peristaltic pump. The spent

medium was collected in a waste container. The air bubbles could have disrupted the process of biofilm formation, so they were confined from the tubing using a bubble trapper, and incubated this at 30°C for 48hr. For the analysis of biofilm production in flow conditions, a Bio Flux system having the ability to acquire image from the specialized cells housed within it, was used. To facilitate the growth of biofilms the microfluid channels were primed with 50% TSB, following which they were loaded with 10^7 CFU from an overnight incubated microbial culture of *Pseudomonas aeruginosa*[2]. The cells were allowed to adhere to the plate by allowing an incubation of 48hrs at 30°C. After the formation of biofilm following the incubation period, the planktonic cells were removed and PBS along with different treatments (containing rhamnolipids 0.4 g/L, caprylic acid 0.1 g/L, a combination of rhamnolipid and caprylic acid, SDS 0.8 g/L, a combination of SDS and caprylic acid) were added to the plate for 30 mins. The cells were stained using LIVE/DEAD cells to check the growth of biofilm.

The effects of different treatments were determined on the biofilm produced upon cover slips by observing under a microscope and used fluorescence microscopy to determine the cells attached to the coverslips, which were stained using the bacterial viability kit, which helped the visualisation of microcolonies and individual cells. It was observed that biofilm produced by the bacteria was inhibited in the presence of rhamnolipids as depicted by reduction in the active cell number and appearance of reddish-brown fluorescent cells. Addition of adjuvant like caprylic acid alone had no effect ton biofilm dispersion. Addition of caprylic acid with rhamnolipid had an enhanced effect on biofilm degradation, also this combination is quite effective even at low concentrations.

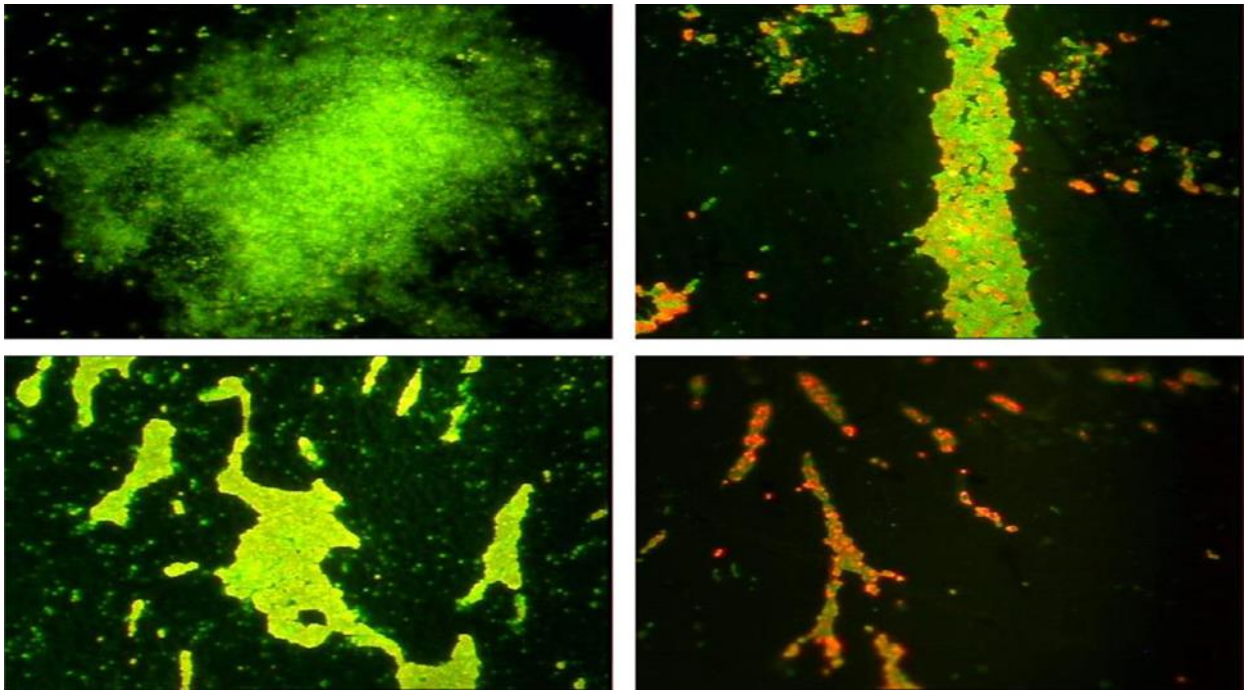

Fig 4: (a) Biofilm formation under Control

(b) Biofilm formation under the presence of rhamnolipid at a concentration of 0.4 g/L

(c) Biofilm formation under the presence of caprylic acid at a concentration of 0.1 g/L

(d) Biofilm formation under the presence of a combination of rhamnolipid (0.4 g/L) and caprylic acid (0.1 g/L).

To determine the effects of different treatments on biofilm disruption upon flow cells, rhamnolipids and caprylic acid were used. The cells were stained using the LIVE/DEAD bacterial viability kit and observed under confocal microscope. The biofilm was allowed to grow for about 2 days in the continuous flow mode. After about 30 minutes of treatment with rhamnolipid along with caprylic acid, the biofilm showed remarkable disintegration at its most important position. It was assumed to be due to the synergistic effect of rhamnolipid and caprylic acid.

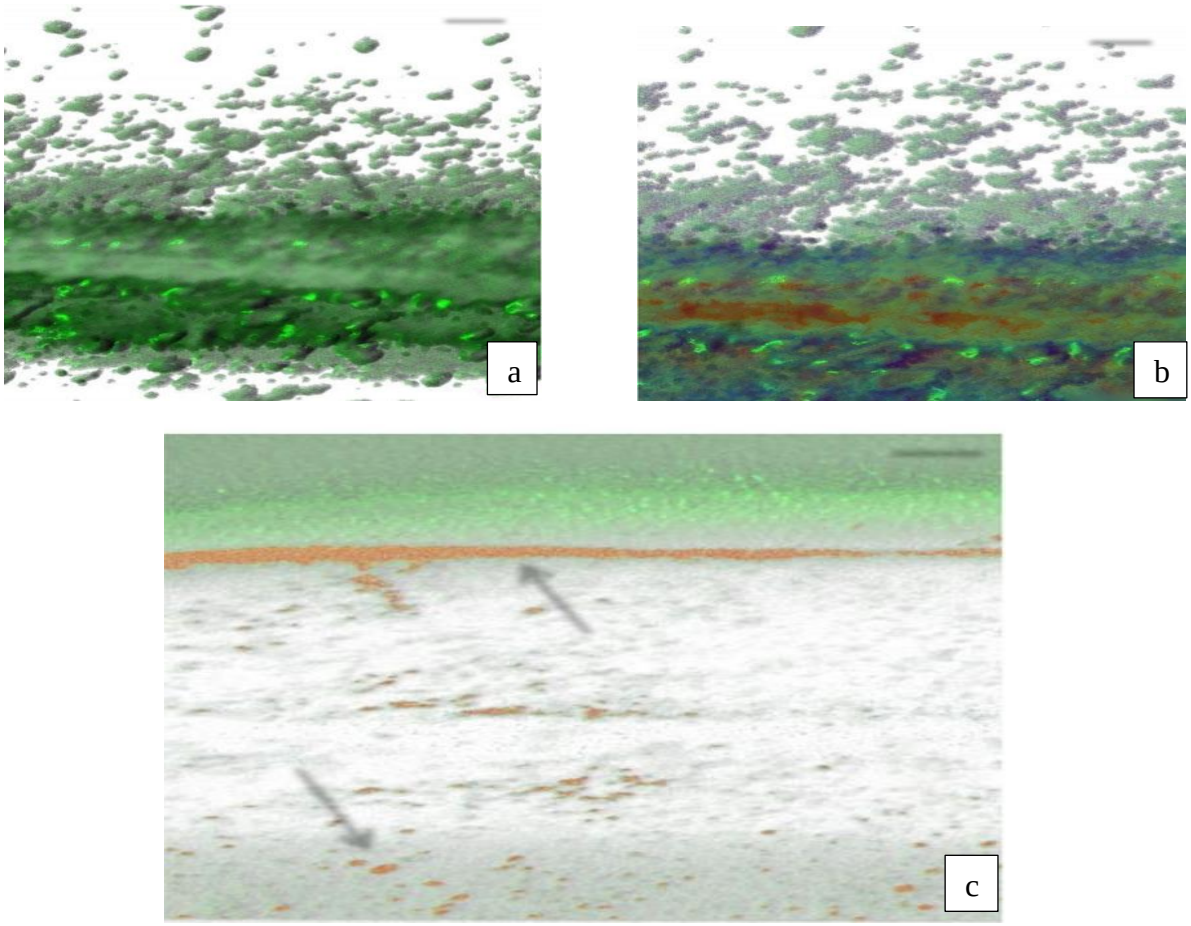

Fig 5: (a) Depicts the effect of rhamnolipid on cell viability.
(b) Depicts a significant effect due to rhamnolipid and caprylic acid treatment
(c) Depicts the compromised portion of biofilm where the cells are disrupted.

Biofilms are heterogenous structures displaying a high degree of resistance to antibiotics and biocidal compounds. Rhamnolipids have been associated to enhance the transport of bacteria through columns due to steric hinderance due to the contact between the surface and the bacteria. Rhamnolipids had been tested with various strains, media, etc. but they always tend to disrupt cell to cell adherence and biofilm disruption. The increased efficiency of biofilm disruption when rhamnolipid is used in combination with caprylic acid maybe due to synergistic effect. The rhamnolipids seem to removes the extracellular polymeric substances and microcolonies thus altering the biofilm environment and making cells more sensitive to intervention of caprylic acid which traverse through the cell membrane and causing cell death. The dispersal of biofilm may also occur due to the mechanical breakage of biofilms due to shear forces. SDS the anionic surfactant exhibits bactericidal activity against majority of oral

bacteria by penetrating the cell membrane and lysing the cell. Since SDS at a concentration greater than CMC causes protein unfolding, suggesting that SDS mediated disruption of the biofilm is due to denaturation of proteinaceous adhesions of the matrix. SDS when combined with caprylic acid had no effect. This was due to the shielding effect of caprylic acid thus protecting the cell membrane from the action of SDS, and therefore SDS is unable to disrupt the biofilm. Therefore, Rhamnolipids were proven to be the efficient antimicrobial agents in the presence of caprylic acid at a pH 5, as they induce cell death and lead to disruption of biofilms, even at low concentrations as compared to that of conventional methods.[24]

As anti-oxidants:

Mannosylerythritol lipids are versatile biosurfactants having interfacial and biochemical properties. MEL-C possesses free radical ion scavenging activity and have the highest antioxidant activity thus serves the highest protection, and are actively used in skin care cosmetics manufacturing. Similar activity is shown by RW1 a biosurfactant derived from *Bacillus subtilis,* proving a natural alternative to antioxidants.

As anti-adhesives:

Numerous biosurfactants display antimicrobial properties, as well as antiadhesive properties. Rhamnolipids and surfactin were shown to possess antiadhesive properties against *Listeria monocytogenes*, *Staphylococcus aureus* on polystyrene surfaces. Similar antiadhesive activity was shown by Lunasan produced by *Candida sphaerica* against many strains of *Streptococcus*, *Staphylococcus*, and *Candida* on plastic tissues.[25] These properties of biosurfactants serve their use as coating agents or in cooking utensils to reduce fouling, also in dairy industries. They are also being utilized as probiotics like *Lactobacillus acidophilus* strain.[20]

In food industries:

In a quest to find natural sources for obtaining biosurfactants rather than those obtained from genetically modified plants, many natural resources are being explored, mostly microbial sources as they are inexhaustible. An emulsion is a heterogenous system which has at-least one immiscible liquid dispersed in another one in the form of droplets. Their stability can be enhanced by using surfactants. Emulsification imparts, texture, consistency and dispersion patterns to food products. An emulsifier stabilized the emulsion by managing the clustering of globules.[14]

Additives are compounds having no nutritional value, but are added to modify, physical, chemical and biological properties during manufacturing, packaging and transport. Additives provide properties like thickening gelling, stabilizing and emulsifying. Glyceryl monostearate, a synthetic additive is widely used in food industries.[3]

Emulsifiers are generally surface-active agents which aid in emulsion formation due to their ability to reduce interfacial tension and stabilize the emulsion. Low molecular weight amphiphiles are used here to provide stability to various food products as beverages, dressings, sauces etc. Emulsifiers such and lecithin and gum Arabic derived from plants are being used as emulsifiers but they suffer some issues as functional limitations like use of microwaves. Lecithin is employed for production of cocoa powders which are a common ingredient for many desserts. Many of the modern-day food products like mayonnaise, butter, cream, salad dressings are produced using emulsions. Therefore, natural resources are being explored to produce bio-emulsifiers, e.g. one from *candida utilis.* Manno-proteins produced via *Saccharomyces cerevisiae* stabilizes water oil emulsion and is used to produce mayonnaise, butters etc. Most of the biosurfactants produced from yeasts and bacteria are operational at wide range of pH and temperature and are therefore used instead of conventional emulsifiers. Microbial surfactants are also used to provide texture, improve shelf life, and modify rheological properties of dough. In ice cream formulations they enhance texture, delay staling and stabilize fats.

Microbial biosurfactants are also utilized for making cookie formulations. The dough for the cookie was prepared in 3 different ways. Standard had all the normal formulations, while one of the formulations had biosurfactant replacing 50% of the pasteurized egg yolk of the standard formulation, while other formulation saw 100% replacement of pasteurized egg yolk with the biosurfactant, and they were ultimately baked.[10] Physical characteristics of the cookie was characterized after baking. Shape, texture, diameter, thickness, and spread ability were measured. Texture analyser was used to record the texture profile of the cookie dough before baking, while only firmness could be recorded after baking them. The protein content in both the alternative formulations was lower compared to that of standard formulation, since biosurfactant used here was a carboxylic acid derivative from *Candia utilis* and lacked proteins. Since the formulation which replaced egg yolk by 100% had high lipid contents, which happens to be the reason due to which energy formulation of this formulation was high.

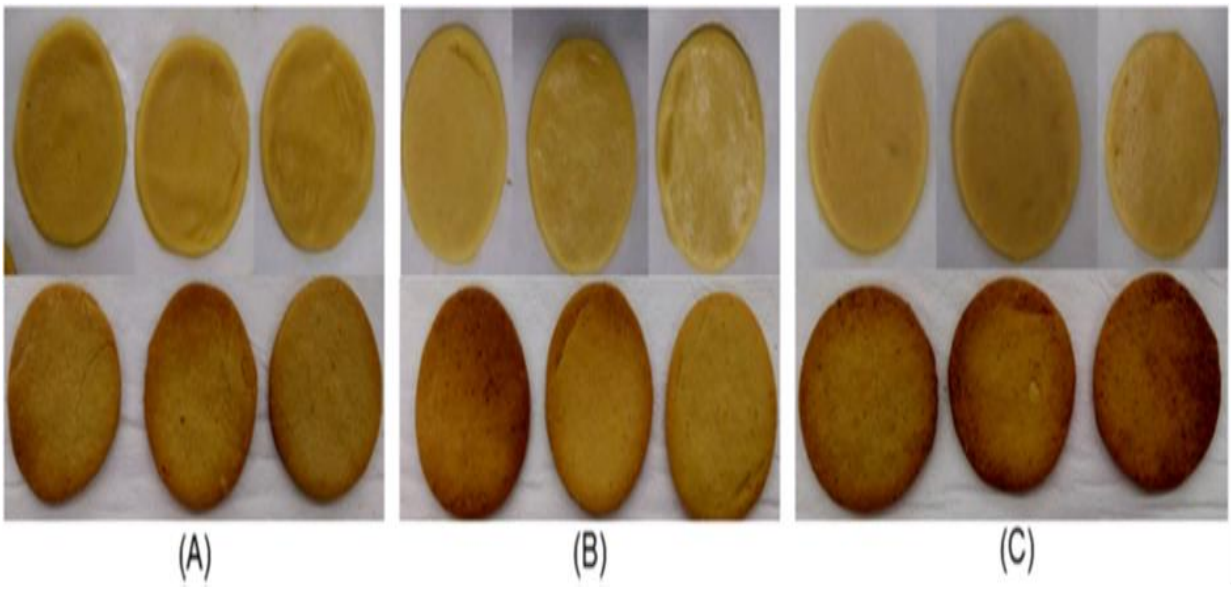

Fig 6: Cookies before and after being baked.

(a) Standard Formulation
(b) Formulation having 50% replaced egg yolk with biosurfactant
(c) Formulation having 100% replaced egg yolk with biosurfactant

Biodegradation:

Surfactants increase the access of the microorganism to low solubility compounds also compounds having recalcitrance, during the biodegradation process. Compounds being less soluble i.e. with high hydrophobicity get bonded strongly to organic matrix and are not desorbed easily to be available for degradation. During the hydrocarbon degradation, low molecular weight hydrocarbons are degraded first leaving recalcitrant compounds. Since surfactants increase the solubility in water and leads to better mass transfer, they are used to enhance biodegradation of hydrocarbons. To facilitate diesel hydrocarbon biodegradation, a suitable biosurfactant is assessed by assessing its physico-chemical properties, its biodegradability and its effect on the rate of biodegradation.[5] For selection purposes, environmental fate and toxicity was assessed by using K_{OC} and EC_{50} using a QSAR model. K_{OC} is defined as the soil organic carbon-water partition coefficient which is the ratio of chemical mass adsorbed on the soil per unit mass of the organic carbon of the soil divided by the equilibrium concentration of chemical in aqueous solution. EC_{50} is the half maximal effective concentration which is that concentration of a toxic compound which induce a response halfway between the maximum and baseline value, and is used to determine toxicity. QSAR is Quantitative structure activity relationship, a process using which the chemical structure of a molecule is correlated with a defined property like biological activity etc. Respirometric analysis was used to assess the biodegradability of the surfactants, using Biochemical oxygen demand apparatus. It was used to calculate the ratio of actual BOD to theoretical BOD. Solid phase respirometric tests were carried out to obtain, biodegradation of surfactants in soil samples.

The mobilities and the residence time of surfactant within the soil is affected by biodegradability, and sorption characteristics. For being efficient in biodegradation the surfactant must be less toxic and persistent, and must not have affinity towards soil, to allow proper distribution into the soil. Non-ionic surfactants are more biodegradable and less toxic as compared to other.

Bioremediation:

The level of relationship between natural and inorganic toxins is represented by the complex physical-concoction communications at interfaces. This relationship includes the sorption of toxins on the soil surface followed by their sequestering into the matrix of the soil, forming a Non-Aqueous Phase liquid (NAPL). NAPL are natural compounds which are insoluble in water thereby acting as a long-term pollutant, they are used in a continuous manner in water phase to replace dissipated concentrations, thereby decreasing the availability of contaminating particles to get biodegraded.[4] Bioremediation is a technique to enhance the degradation of biological compounds to lower the effect of toxins. Bioaugmentation is the practice of adding cultured microbes to facilitate degradation of pollutants, supplemented by using surfactants to facilitate desorption of pollutants lead to enhanced degradation of hydrocarbons. Surfactants are used to recover secondary oil during oil washing, and also in cleaning of oil pipes. Many synthetic and biosurfactants are employed for desorption purposes. Biosurfactants are not majorly used for bioremediation due to their high cost of production, but it may be overcome by using cheaper substrates for the microorganisms producing them like, industrial oil waste and agro-industrial wastes. Some of the major sources of biosurfactant production are *Pseudomonas aeruginosa, Corynebacterium, Nocardia, Bacillus subtilis, Bacillus licheniformis, Candida spp*., etc. The quality and quantity of nitrogen and carbon present in the substrate and the soil greatly determines the kind of biosurfactant produced. Limited nitrogen leads to increased production of biosurfactants aiding in bioremediation, therefore many bioremediation systems are not supplied with nitrogen to increase the microbial activity and lead to increased production of biosurfactants. Biosurfactants may be produced in the presence of oils and hydrocarbons.

Addition of hydrophobic organic substances in the culture media favours the isolation of hydrocarbon degrading bacteria from sites contaminated by oil, and are able to produce biosurfactants.[15] Aliphatic and aromatic hydrocarbons are used as a source of carbon for this purpose. The presence of organic compounds and metallic pollutants in the soil are the major cause of soil pollution. Organic hydrocarbons include Polycyclic aromatic hydrocarbons (PHA), Polychlorinated biphenyls (PCB), out of which PHA are more common due to it being involved in crude oil processing. Transport of pollutants in the soil is a function of non-linear rate limited biodegradation and sorption. Majority of hydrophobic contaminants bind to organic fractions in the soil due to sorption. Compounds like humic (like humic acid, humic)

and nonhumics (like proteins and waxes) are involved in the process of sorption.

The process of degrading pollutants in the soil depends upon physico-chemical and biological interaction of the pollutants and other biological factors. Degradation by means of microbial activity is in turn controlled by many factors like availability of contaminants to the microbes, pH, water, aeration, nutrients, temperature etc. Biodegradation can be enhanced by having a detailed insight of the metabolic activities of the microorganism. Microorganism form a stable oil in water emulsion which leads to increased oil degradation, thereby enhancing the availability of nutrients to the microorganisms. This phenomenon is achieved in natural systems by utilisation of autochthonous surfactant bio-population which lead to production of stable emulsions. Biosurfactants are able to solubilize the natural organic materials sorbed into the soil. Monorhabdolipid acid are utilized to remove NAPL which stays as a residue, while some *Rhodococcus* strains were used to degrade oil from sand etc. Endosulfan present in the soil was degraded by means of biosurfactant produced by *Bacillus subtilis*. Bio emulsifier alasan is used to increase the solubility of PAH, therefore leading to many folds increased in degradation and solubilities.

Soil is cleaned up using various techniques using soil exaction and disposal to landfill, phytoremediation, also plants immobilize the metals preventing their vertical or horizontal movement, thereby reducing the groundwater pollution. Microbes also have the ability to bind and form complex with association with the pollutants, thereby require more efforts and difficulties in degrading pollutants. Therefore, microorganisms can be used to remove heavy metals, by means of alkylation, or sulphur reducing bacteria is also used to remove heavy metals. Synthetic surfactants are toxic to degrading microorganisms therefore microbial surfactants are used for degradation of oil spills. Composting systems are used to increase the oxygen transfer and thereby reduce the pollutants in soil in a time of some months. An efficient way to enhance crude oil degradation in oil polluted environments is the introduction of hydrocarbon-oxidizing bacteria with high oxygenase activity, like Acinetobacter. Many complexes isolated from biosurfactant produced by bacteria, are isolated using methyl tertiary-butyl ether following sonication.

The main reason why the organic and metallic pollutants remain is soil for so long without being degraded is dependent on many factors like, they are not able to degrade them due to it being not available to them, also microorganism might not be able to carry out the essential

catabolic reactions, or inadequate interaction of the pollutants with the environment and the microorganism. Therefore, fungi and bacteria involved in the production of biosurfactants are important as they tend to solubilize the hydrophobic contaminants, facilitating their easy degradation. It was observed by keeping the contaminated sites devoid of Nitrogen, to enhance the activity of microbes degrading the soil pollutants.

Agriculture:

The health and productivity of plant crops are monitored on a regular basis to be sure about the quality of the food being obtained, and its availability to be able to meet the increasing demands of the growing population. Metabolic compounds referred to as green surfactants are produced by actinomycetes, yeast, fungi etc. Epiphytic and endophytic microbes are involved in biosurfactant production and they aid seed germination, inhibit the action of phytopathogens and as biocontrol agents for bioremediation. Since, we are trying to avoid the use of pesticides on plants to obtain chemically free plant products, rhizospheric bacteria are being explored that secrete metabolites which increase the yield of plant product. *Bacillus* and *Pseudomonas* are the majority of bacteria in Rhizobacteria group, which secrete metabolites having versatile applications as plant growth promoters, fungicidal agents like siderophores, phenazines, pyrrol nitrin, cyclic peptides, compounds such as biosurfactants and enzymes like chitinase and glucanase which possess hydrolysing activities.[9] These green compounds have lower critical micellar concentration compared to that of synthetic ones and they lead to higher decrease in surface tension of oil-water or air-water interfaces to a very low value. Rhamnolipids and lipopeptides are the majorly studied biosurfactants, which have found tremendous application in agricultural fields, along with other industries like pharmaceuticals, cosmetics, petrochemicals, food etc. Since they house amphipathic structures, due to which they promote seed germination, reduce the growth of phytopathogens and tend to induce systemic resistance in the plants.

The Rhizosphere portion of many cereals were used like rice, sorghum, millets, legumes like chickpea, groundnut, oil crops like sunflower", castor, grass etc were obtained from different districts were used for isolating the bacteria. They secrete metabolites which tend to promote plant growth and also act as antifungal. This ability was screened testing for Ammonia

production, by incubating bacterial isolates with 10 mL of peptone water for 48 hrs and 28-30°C. After incubation, 1 ml of culture broth was transferred to other tube and mixed with 1 ml of Nessler's reagent. Phosphate solubility was assessed by using Pikovskaya's agar medium having tricalcium phosphate. Phytase activity was assessed using phytic acid medium, following incubation for 2-4 days at 28-30°C temperature. After incubation zone of hydrolysis around the colonies was observed as a sign of confirmation. Isolates of the bacteria were tested for their antifungal activity. A culture of *F. oxysporum f. sp. ricini* was cultured on potato dextrose agar.

$$I\% = \frac{(C - T) \text{ x } 100}{C}$$

Where I= % inhibition of microbial growth

C= Radial growth of fungus recorded in the control plate

T= Radial growth of fungus recorded in the plate having bacteria.

All the bacteria were tested for ammonia production, antifungal activity, ability to solubilize phosphates and the capability to produce Indole Acetic Acid, via various experimental setups described above. The antifungal ability of bacteria against *F. oxysporum f. sp. ricini* was in between 72-80%. 67% of *Pseudomonas sp.* while 58% of *Bacillus sp.* possessed PGP traits.[9]

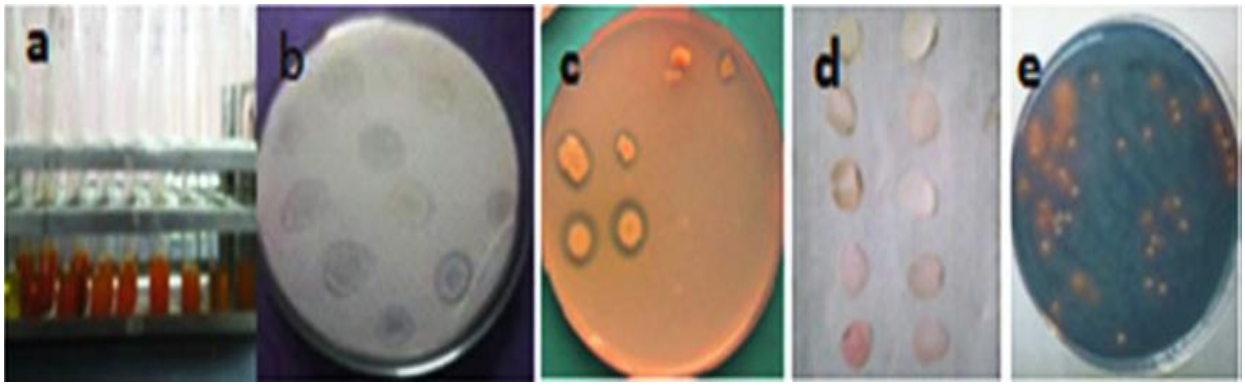

Fig 7: Different PGP traits tested.
(a) Ammonia production
(b) Solubilization of phosphate
(c) Phytase activity
(d) Indole acetic acid production
(e) Production of siderophore

It was observed that crude biosurfactant containing rhamnolipid and iturin, showed fungicidal activity against *F.oxysporum f.sp. ricini.*

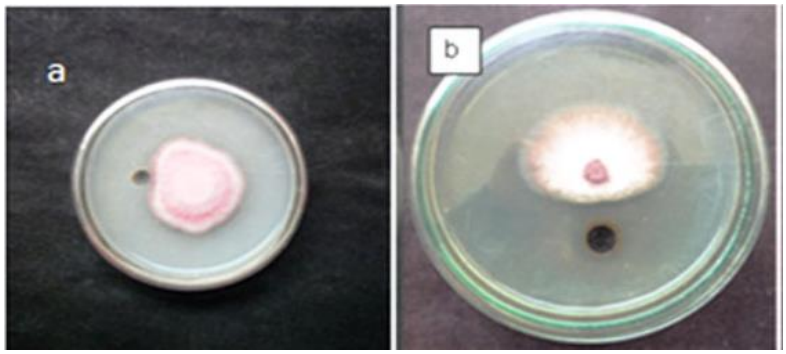

Fig 8: Antifungal activity of the biosurfactant against the chosen fungi.
(a) F.oxysporum f. sp. ricini inhibited by means of lipopeptide
(b) F.oxysporum f. sp. ricini inhibited by means of rhamnolipids

Rhizobacteria have been known to have plant growth promoting activity, alongside which they also depict strong antifungal or fungicidal activities making them a preferable choice as bioinoculants and in agriculture. Crop yield and sustainable agricultural conditions still prevail due to the regular application of chemicals which also pollute the environment. To overcome this shortcoming, bacterial metabolites which are non-toxic, tend to inhibit the growth of fungal pathogens and enhance seed germination are suitable alternatives for chemical compounds.

8. CONCLUSION:

Biosurfactants have certain unique properties like, surface activity, biodegradation, detergency abilities, emulsification and de-emulsification activities, lubrication, wetting ability, foaming, solubilization, dispersion of phase etc. Due to this diversity in properties they are used in a wide array of industries like petrochemical, petroleum, coal, metallurgical and mining industries, dairy, cosmetics, pharmaceuticals, food, agricultural and fertilizer, cosmetics, food and beverages etc. These compounds have been majorly obtained from bacteria and this is well documented, while obtaining these compounds from fungi is also possible, though there is less data on this subject. Many tropical species of plants both in India and Brazil have been used to isolate numerous endophytic microorganisms which produce biosurfactants. They are not used

at industrial scale, since their effect needs to be first determined by an experimental setup in greenhouse conditions and actual field studies, following which it can be stated if they can act as potential alternatives against the chemical agents.

9. FUTURE PERSPECTIVE AND CHALLENGES:

Microbial surfactants are non-ionic at low pH esteems, and anionic at high pH esteems because of the nearness of carboxylic gatherings. The total of surfactants in lamellar courses of action can happen on the off chance that one of the following conditions are watched. High surfactant focuses lead to a lamellar fluid crystalline stage, while twofold followed amphiphiles regularly structure bilayer sheets. After shutting, these sheets structure vesicles. Microbial surfactants can possibly be utilized in the targeted drug delivery. Additionally, pH-delicate liposomes containing rhamnolipids and di-oleoyl-phosphatidyl-ethanolamide have been depicted as effective frameworks for cytoplasmic conveyance of particles into cells. There is a critical need to investigate microbial frameworks to acquire surfactants and use them as effective drug delivery systems. Industries are seeking to find natural alternatives for biosurfactant production, to be utilized at industrial scale. Since currently biosurfactants are economically bit costly to prepare, we need to find ways to decrease the cost of production. Through the application of specialized cost-effective testing and discussion we might find a breakthrough to allow the use of biosurfactant at a large scale.

Since they are costly to produce therefore research found that the bacterial culture (producer of biosurfactant) could be grown using poultry waste flour and buttermilk, waste cassava fry oil, agro-industrial waste etc, thus serving as low cost alternative for producing the biosurfactants. Also, *Piper hispidum* was also identified as a potential alternative source for the isolation of microorganism producing biosurfactants, which can be utilized in various industries. Biosurfactants due to their higher biodegradability, biocompatibility and low toxicity, can be optimized by tweaking fermentation conditions, to obtain biosurfactants at an affordable cost and we might be able to produce them at a large scale.

10. REFERENCES:

1) Rodrigues, Ligia R. "Microbial surfactants: fundamentals and applicability in the formulation of nano-sized drug delivery vectors." *Journal of colloid and interface science* 449 (2015): 304-316.

2) Díaz De Rienzo, M. A., P. S. Stevenson, Roger Marchant, and Ibrahim M. Banat. "Pseudomonas aeruginosa biofilm disruption using microbial surfactants." *Journal of applied microbiology* 120, no. 4 (2016): 868-876.

3) Campos, Jenyffer Medeiros, Tania Lucia Montenegro Stamford, Leonie Asfora Sarubbo, Juliana Moura de Luna, Raquel Diniz Rufino, and Ibrahim M. Banat. "Microbial biosurfactants as additives for food industries." Biotechnology progress 29, no. 5 (2013): 1097-1108.

4) Christofi, N., and I. B. Ivshina. "Microbial surfactants and their use in field studies of soil remediation." *Journal of Applied Microbiology* 93, no. 6 (2002): 915-929.

5) Franzetti, A., P. Di Gennaro, G. Bestetti, M. Lasagni, D. Pitea, and E. Collina. "Selection of surfactants for enhancing diesel hydrocarbons-contaminated media bioremediation." *Journal of hazardous materials* 152, no. 3 (2008): 1309-1316.

6) Parra, J. L., J. Guinea, M. A. Manresa, M. Robert, M. E. Mercade, F. Comelles, and M. P. Bosch. "Chemical characterization and physicochemical behavior of biosurfactants." *Journal of the American Oil Chemists Society* 66, no. 1 (1989): 141-145.

7) Zouari, Raida, Semia Ellouze-Chaabouni, and Dhouha Ghribi. "USE OF BUTTER MILK AND POULTRY-TRANSFORMING WASTES FOR ENHANCED PRODUCTION OF Bacillus subtilis SPB1 BIOSURFACTANT IN SUBMERGED FERMENTATION." *Journal of Microbiology, Biotechnology and Food Sciences* 2019 (2019): 462-466.

8) Silva, M. E. T., Sergio Duvoisin Jr, R. L. Oliveira, E. F. Banhos, A. Q. L. Souza, and Patrícia Melchionna Albuquerque. "Biosurfactant production of Piper hispidum endophytic fungi." *Journal of Applied Microbiology* (2019).

9) Bee, Hameeda, Mohamed Yahya Khan, and R. Z. Sayyed. "Microbial Surfactants and Their Significance in Agriculture." In *Plant growth promoting rhizobacteria (PGPR): prospects for sustainable agriculture*, pp. 205-215. Springer, Singapore, 2019.

10) Ribeiro, Beatriz Galdino, Bruno Oliveira de Veras, Jaciana dos Santos Aguiar, Jenyffer Medeiros Campos Guerra, and Leonie Asfora Sarubbo. "Biosurfactant produced by Candida utilis UFPEDA1009 with potential application in cookie formulation." *Electronic Journal of Biotechnology* (2020).

11) Jahan et. al. 'Biosurfactants, natural alternatives to synthetic surfactants: Physicochemical properties and applications.' Advances in Colloid and Interface Science, Volume 275, January 2020, 102061.

12) Madihalli, Chandraprasad, Harshal Sudhakar, and Mukesh Doble. "Production and investigation of the physico-chemical properties of MEL-A from glycerol and coconut water." World Journal of Microbiology and Biotechnology 36 (2020): 1-11.

13) Sadeghi et. al. 'Design and physicochemical characterization of lysozyme loaded Niosomal formulations as a new drug delivery system.' Pharmaceutical Chemistry Journal, Vol. 53, No. 10, January, 2020 (Russian Original Vol. 53, No. 10, October, 2019).

14) Choudhury, Samrat Roy, Amrita Mandal, Dipankar Chakravorty, Madhuban Gopal, and Arunava Goswami. "Evaluation of physicochemical properties, and antimicrobial efficacy of monoclinic sulfur-nanocolloid." Journal of nanoparticle research 15, no. 4 (2013): 1491.

15) Jain et. al. 'Physicochemical characterization of biosurfactant and its potential to remove oil from soil and cotton cloth.' Discipline of Marine Biotechnology and Ecology, CSIR – Central Salt and Marine Chemicals Research Institute (CSIR – CSMCRI).

16) Baferani, A. Hasani, R. Keshavarz, M. Asadi, and A. R. Ohadi. "Effects of Silicone Surfactant on the Properties of Open-Cell Flexible Polyurethane Foams." Advances in Polymer Technology 37, no. 1 (2018): 71-83.

17) Chen, Yu-Fen, Chao-Hsun Yang, Ming-Shiang Chang, Yong-Ping Ciou, and Yu-Chun Huang. "Foam properties and detergent abilities of the saponins from Camellia oleifera." International Journal of Molecular Sciences 11, no. 11 (2010): 4417-4425.

18) Ohadi, Mandana, Arash Shahravan, Negar Dehghannoudeh, Touba Eslaminejad, Ibrahim M. Banat, and Gholamreza Dehghannoudeh. "Potential use of microbial surfactant in microemulsion drug delivery system: a systematic review." Drug Design, Development and Therapy 14 (2020): 541.

19) Benincasa, M., A. Abalos, I. Oliveira, and A. Manresa. "Chemical structure, surface properties and biological activities of the biosurfactant produced by Pseudomonas aeruginosa LBI from soapstock." Antonie Van Leeuwenhoek 85, no. 1 (2004): 1-8.

20) Rodrigues, Lígia, Ibrahim M. Banat, José Teixeira, and Rosario Oliveira. "Biosurfactants: potential applications in medicine." Journal of Antimicrobial Chemotherapy 57, no. 4 (2006): 609-618.

21) Parra, J. L., J. Guinea, M. A. Manresa, M. Robert, M. E. Mercade, F. Comelles, and M. P. Bosch. "Chemical characterization and physicochemical behavior of biosurfactants." Journal of the American Oil Chemists Society 66, no. 1 (1989).

22) Fu, Xiaowei, Fengqin Feng, and Bin Huang. "Physicochemical characterization and evaluation of a microemulsion system for antimicrobial activity of glycerol monolaurate." International journal of pharmaceutics 321.

23) Feng, Chao-Hui, Juan Francisco García Martín, Cheng Li, Bao-Lin Liu, Xiao-Yan Song, Qing-Li Dong, Wei Wang, and Yong Yang. "Evaluation of physicochemical properties and microbial attributes of cooked sausages stuffed in casing modified by surfactants and lactic acid after immersion vacuum cooling and long-term storage." International Journal of Food Science & Technology 51, no. 10 (2016).

24) Lorite, Gabriela S., João M. Rocha, Noora Miilumäki, Paula Saavalainen, Tuula Selkälä, Gabriel Morales-Cid, M. P. Gonçalves, Eva Pongrácz, Cristina MR Rocha, and Geza Toth. "Evaluation of physicochemical/microbial properties and licycle assessment (LCA) of PLA-based nanocomposite active packaging."

25) Pornsunthorntawee, Orathai, Panya Wongpanit, Sumaeth Chavadej, Masahiko Abe, and Ratana Rujiravanit. "Structural and physicochemical characterization of crude biosurfactant produced by Pseudomonas aeruginosa SP4 isolated from petroleum-contaminated soil." Bioresource technology 99.

26) Huang, Hui, Qisheng Yu, Hongqiang Ren, Jinju Geng, Ke Xu, Yan Zhang, and Lili Ding. "Towards physicochemical and biological effects on detachment and activity recovery of aging biofilm by enzyme and surfactant treatments." Bioresource technology 247 (2018): 319-326.

27) Raza, Zulfiqar A., Muhammad S. Khan, and Zafar M. Khalid. "Physicochemical and surface-active properties of biosurfactant produced using molasses by a Pseudomonas aeruginosa mutant." Journal of Environmental Science and Health Part A 42.

28) Rodrigues, Lígia R., José A. Teixeira, Henny C. van der Mei, and Rosário Oliveira. "Physicochemical and functional characterization of a biosurfactant produced by Lactococcus lactis 53." Colloids and Surfaces B: Biointerfaces 49, no. 1 (2006).

29) Saini, Harvinder S., Blanca E. Barragán-Huerta, Ariel Lebrón-Paler, Jeanne E. Pemberton, Refugio R. Vázquez, Anna M. Burns, Marilyn T. Marron, Chistopher J. Seliga, AA Leslie Gunatilaka, and Raina M. Maier. "Efficient purification of the biosurfactant viscosin from Pseudomonas libanensis strain M9-3 and its physicochemical and biological properties." Journal of natural products 71, no. 6 (2008).

30) Yuan, X. Z., Y. T. Meng, G. M. Zeng, Y. Y. Fang, and J. G. Shi. "Evaluation of tea-derived biosurfactant on removing heavy metal ions from dilute wastewater by ion flotation." Colloids and Surfaces A: Physicochemical and Engineering Aspects 317, no. 1-3 (2008).

SUMMER TRAINING REPORT

ON

FERMENTATION TECHNOLOGY

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OBJECTIVE 1- To acknowledge the working and components of a bioreactor.

Theory: Bioreactor- It is a flask type structure which has the advantage of controlling environmental conditions and it also provide cell and microbial plant cultivation under sterile conditions. It consist of following parts;

- **Agitator-** It is used to carry out mixing of the contents present in the reactor in order to keep cells in perfect homogenous condition for better transport of nutrients and oxygen.
- **Baffle-** It is mainly used to prevent the vortex formation in the reactor as it can change the centre of gravity of the system and consumes additional power.
- **Sparger-** It supplies oxygen to the growing cells and it also helps in mixing the contents which results in less usage of power.
- **Jacket-** It helps in keeping the temperature of bioreactor down by providing water and removing extra heat from its surface.

- **Basic protocol for the operation of bioreactor:**
  - **Temperature Measurement and Control-** Temperature measurement is carried out by either using thermocouple or Pt-100 sensor which send signal to the temperature controller. Measured value is compared with set point which is entered in the controller, depending on it heating or cooling of the bioreactor is activated slowly to decrease the error.
  - **pH measurement and control-** pH measurement is carried out using autoclavable pH probe. Before using pH probe it needs to be calibrated with the two buffers used in the bioreactor cultivation experiment. Measured pH is compared with the set point which then activated the acid or alkali to bring the measured value close to the set point.
- **Identification of pH controller settings for Bio-Engineering AG:**

i. **Bioreactor-** A suitable control action setting is required for the addition of certain concentration of acid/alkali which can give quick action to measured value around the set point. It is also noted that activation of alkali/acid is done in a phased manner, this ensures adequate mixing of acid/alkali in the broth before next instalment is added. On/off time of the controller has to be adjusted by separate experiments and will depend on the buffering capacity of the broth. It is essential to maintain these settings before the start of the experiment in order to have efficient control.

ii. **Dissolved oxygen controller-** It is measured by a dissolved oxygen probe. In this probe is to be calibrated for its zero and 100% values.

iii. **Foam control-** It controls the foam which arises due to the organic compound and the broth is vigorously agitated to keep the cells in suspension and ensure efficient nutrient transfer from the dissolved nutrients and oxygen.

Procedure:

- **To understand the significance of each part of the bioreactor;**

i. Press Start.

ii. **Speed control system-** Mainly used to provide mixing of reactor contents. Set the upper limit and actual speed then press RUN.

iii. **Gas Supply System-** It supplies air which serves as the source of the oxygen to the growing cells. Enter value and run.

iv. **Temperature Control System-** It is used to maintain the cultivation temperature in the bioreactor. Measure the value and compare it with the set point.

v. **pH measurement and control system-** Enter pH value and set point . Press run. Measure the pH and compare it with the set point.

vi. **Dissolved Oxygen Measurement and Control-** Enter value of dissolved oxygen levels and press run. Using the magenta sensor, compare the value with the set point and depending on the error the controller action is activated.

vii. **Foam Control System-** It is used to remove the foam from the system as it can lead to heavy losses to the system. It is detected by red sensor and anti foam is triggered It is added slowly so that only minimum amount is added. Over addition of antifoam may create serious problem.

OBJETIVE 2: Determination of characteristics of pH controller of Bio- Engineering AG fermenter

Theory: The pH control method is dependent on various parameters of factors such as density, viscosity and strength of acid and bases etc. Faulty settings of these parameters will lead to delayed control response. It is possible to design the controller according to the above parameters.

- **Description of the pH controller;**
  i. **pH/mV potentiometer-** It enables the adjustment of the slope of pH electrode by calibration.
  ii. **Asymmetry potentiometer-** It adjust the zero mV point of the pH signal.
  iii. **Temperature potentiometer-** It manually control temperature coefficient of pH electrode.
  iv. **Set point potentiometer-** Set pH or mV.
  v. **P-band potentiometer-** Adjust the width of the P-band potentiometer. Low P band translates to strong amplification.
  vi. **TON/TOFF potentiometer-** Adjust the opening and closing of the valve by keeping both the potentiometer at the same value which will lead to the linear transfer function.

Procedure:

i. Switch 1 connected to pH.
ii. Switch 5 and switch 8 to hand.
iii. Adjust 4 to the temperature of the solution.
iv. Dip the electrode in standard buffer of pH 7 & adjust until pH comes at 7.
v. Clear the electrode and dip it in buffer (pH 4).
vi. Adjust 3 till the meter reads at 4 pH.

OBJECTIVE 3: 15 L Bioreactor Manual

- **Preparation for sterilization**
  - Media was prepared and added to the reactor.
  - The functioning of probes was verified and electrolytes in pH and DO probes refilled.
  - Probes were inserted into the reactor.
  - Air outlet filter was used to maintain pressure equilibrium in and outside the reactor.
- **For Autoclaving**
  - The reactor was now placed inside the horizontal Autoclave,
  - Pressure was maintained in the jacket at 15psi by keeping valve in fast mode.
  - Closed the autoclave lid; adjusted valve in sterile mode.
  - Waited for maintaining equilibrium at 15 psi in reactor and jacket.
- **For login to controller**
  - Switched on the controller and a screen appeared
  - After that a home screen will appeared. Pressed view button on home page and entered into System engineer.
  - A login screen appeared. Pressed login and specified password. Pressed enter button.
- **For priming tubes**
  - Attached the autoclaved reactor and pipes to controller. Went to home page and pressed main menu.
  - Tubing prime control button was selected on the main menu.
  - Primed all the tubes for alkali, acids and antifoam.
  - Went to main menu and entered into manual controller. All the pumps and valves were controlled manually.
- **Setting parameters set points**

  <u>Temperature</u>
  - Pressed main menu and entered the temperature.
  - Specified temperature set point and pressed enter button.

  <u>Stirrer setting</u>
  - Went to the main menu and entered into stirrer settings.
  - On stirrer setting screen, pressed cascade speed limit button.
  - On cascade limit screen, the upper and lower speed limit cascade will appeared.
  - Set the upper stirrer speed limits and pressed enter.
  - Set the lower speed limit cascade and pressed enter.
  - Entered into stirrer settings and pressed stirrer set point button.
  - Wrote stirrer set point and pressed enter button.

  <u>pH setting</u>
  - On main menu, pressed pH settings and entered into pH set point.
  - Set pH point and pressed enter.

  <u>DO settings</u>
  - On home page, entered into DO settings. Then press DO set point button.

- Set DO point and pressed enter button.

❖ **Switched on controllers and ran fermentation**

1. On the home page, pressed menu button. Inside the menu, pressed start/stop all the controllers.
2. Then pressed start all controllers.
3. Then ran fermentation.
4. All the profiles of parameters i.e. pH, DO and temp were monitored by entering into respective controller sections on home page.
5. On completion, harvested the entire fermentation broth from the reactor.

OBJECTIVE 4: Biopolymer Production by Microbes

❖ **Basic Requirements**

Microorganism: *R. eutropha NRRL B14690*. The culture was maintained on nutrient agar slants at about 5ºC.It requires being sub cultured every month.

Media preparation [shake flash cultivation:

- For mineral salt medium: 2.0 g/L (NH4)2SO4, 2.0 g/L KH2PO4, 0.6 g/L Na2HPO4, 0.2 g/L MgSO4.7H2O, 20 mg/L CaCl2, 10 mL/L trace metal solution, 0.1 g/L yeast extract is to be used.
- For trace metal solution: 1.3 mg/L ZnSO4.7H2O, 0.2 mg/L FeSO4.7H2O, 0.6 mg/L (NH4)6Mo7O24.4H2O and 0.6 mg/L H3BO3.
- Fructose is used as a carbon source in concentration of 40 and 10 g/L for production media and inoculum development, respectively. Fructose, yeast extract and salt solutions are to be sterilized separately at 121ºC and then aseptically reconstituted at room temperature prior to inoculation.
- The pH of the resulting broth needs to be adjusted to 7.0 with 2N NaOH/2N HCl.

Bioreactor cultivation:

- Seed culture was prepared in a 1 L Erlenmeyer flask containing 200 mL media. Batch cultivation was then carried out at 30ºC in a 7 L LF-1523 Bioengineering (Bioengineering AG, Switzerland) bioreactor containing 4 L of media.
- The reactor was sterilized in-situ at 121ºC for 20 min, cooled and then inoculated with 5% inoculum (v/v).
- Culture pH needs was maintained at 7.0 by automatic addition of acid or base by pH–mV controller M 7832 N.
- Dissolved oxygen concentration was maintained at 30% saturation value by manually adjusting the speed of the agitator and/or airflow rate.
- Samples were withdrawn at regular intervals and analysed for biomass, PHB and residual nutrients.

❖ **Protocol for operation of simulator**

- Bioreactor:

  The Bioreactor portion shows different components which described the purging of the sterile from the sparger and rotation of the impeller. The

impeller is bottom driven. This arrangement is possible with Bioengineering AG Switzerland Bioreactor. This kind of agitation gives more space on the lid because of which there is no overcrowding of different inlet ports & sensors and it is particularly useful when flame is used to connect acid /alkali pipes and when transfer of inoculum is done to the reactor. The constant temperature water flows in the jacket of the reactor (marked green) to maintain the temperature of the reactor.

- Run Simulation:
  After entering the necessary details, RUN Simulation button was pressed and the graph and table for X, S, P vs time was printer on the screen.
- Out put Graph :
  The graph described the kinetic profile of different fermentations.
- Save Results:
  Pressed on the save button.
  Results were saved in the form of an Excel Sheet where all the values of kinetic profile were tabulated.

OBJECTIVE 5: Acetone-Butanol-Ethanol Production

❖ **Basic Requirements -**

- Culture - *Clostridium acetobutylicurn* strain ATCC 824 was used for production of Acetone-Butanol-Ethanol.
- Medium requirements - A standard culture media with respect to ammonium sulfate and yeast extract for the specific glucose concentrations has to be used in this study while maintaining the same concentrations of minor nutrients. It typically consists of the following components in g/L: glucose, 50; ammonium sulfate, 9.0; yeast extract, 11.0**;** K2HP04, 0.8; KH2P04 0.8; MgS04, **0.3;** MnS04 .H20, 0.02; NaCI, 0.02; FeS04 . 7H20, 0.02; and L-cysteine, 0.5. Temperature 37ºC, pH 4.5 or 6.0 .
- Flask and Bioreactor development - Heat shocks the spores kept up in RCM by putting the test tube in a bubbling water shower (100ºC for one minutes). This is to be trailed by cooling to 4ºC for 3 minutes. The temperature of the cylinder is standardized to room temperature for 60 minutes. The 3% inoculum is to be moved into 15 mL hungate top test tubes containing 10 mL of the RCM. The test tube containing the spore arrangement was saved for spore actuation at 37ºC in an anaerobic container for 20-24 hours. Satisfactory development for ensuing exchange of the inoculums was portrayed by the beginning of gas creation. 3 % inoculums were moved into a fluid glucose medium (50 g/L) in a shake flagon. Following 10 hours of development, tests were pulled back from the way of life jar each hour. The pH of the inoculum was not permitted to fall underneath 4.6 by manual expansion of 0.1 N NaOH. The suitable planning for vaccination (14-15 hours) was distinguished by the way of life corrosive break point through the examination of extracellular items by gas chromatography. A 3 % inoculum is moved to the fermenter containing cleaned 50 g/L glucose medium at pH 4.6 Before immunization the fermenter was sparged in the head space by Nitrogen.

The nitrogen sparging proceeded until the gases were being created by the way of life. The way of life was permitted to develop in a clump mode.

❖ **Analytical protocols -**

- Dry wieght - 20 ml sample of the fresh fermentation stock is centrifuged at 10,000 g and 4ºC for 15 minutes. The supernatant is solidified in a profound cooler for extracellular metabolite and glucose examination. The biomass is washed multiple times with equivalent measure of refined water. The pellet is re-suspended in 10-15 mL of refined water, moved to a preweighed aluminum dish and dried in a stove at 100ºC for 24 hours. In the wake of cooling the aluminum dish to room temperature in a desiccator the dry load of the cells is estimated.
- Glucose - Glucose concentration was determined by DNS method.
- Solvent and Acid concentration- This was done by Gas-liquid Chromatography.

❖ **Protocol for operation -**

- Bioreactor - The Bioreactor portion represents the various parts it likewise depicts the cleansing of the sterile air (if it's not too much trouble see the air channel noticeable all around delta) from the sparger and pivot of the impeller. The impeller is base driven. This sort of plan is conceivable with BioEngineering AG Switzerland Bioreactor. This sort of unsettling gives more space on the top so that there is no congestion of various bay ports and sensors and it is especially helpful when fire is utilized to interface corrosive/salt funnels and when move of inoculum is done to the reactor. The consistent temperature water streams in the coat of the reactor (stamped green) to keep up the temperature of the reactor.

The Simulation was run to understand the basic working and result formation.

OBJECTIVE 6: Propanoic Acid Production

❖ **Basic Requirements -**

- Culture - *Propionibacterium acidipropionici* ATCC 4875.
- Medium Requirements - Engineered medium is to be utilized for the arrangement of inoculum. 100 mL (20 g/L lactose) medium with the accompanying organization is to be utilized: 1 g yeast separate, 0.5 g trypticase, 0.025 g K2PHO4, 0.005 g MnSO4, 2 g lactose. pH is to be acclimated to 6.5 with 3 N NaOH/HCl. For sanitization, lactose and rest of the medium parts (basal medium) are to be autoclaved independently at 121º C and 15 psig for 20 min. Blend the two arrangements aseptically under laminar flow hood.
- Inoculum Preparation - 20 mL of the engineered medium is to be taken in a 100 mL serum bottle, Cap it by an elastic plug and seal by aluminum top by crimper. Prior to immunization, N2 is to be sparged through the serum bottle for around 15 min. A leave valve with sterile channel must be given at the cup outlet to forestall development of extreme weight inside it. Vaccination is to be finished utilizing a two days old inclination development rejected in 1 mL sterile refined water. A uniform suspension is to be made in the water before aseptically

moving the inoculum to the serum bottle with the assistance of a sterile syringe. Development is to be done at 30º C in a shaker (Adolf Kuhner AG, Basel, Switzerland) kept up at 150 rpm. Utilize sterile syringes to pull back samples. Move the inoculum at around 40 h utilizing 6% (v/v) inoculum.

- Bioreactor Cultivation - Start fermentation in a bioreactor at an underlying grouping of lactose (utilizing) 50 g/L (7-l (Bioengineering, Switzerland) glass reactor) working volume 5 liter. Autoclave the fermentor with refined water in it, in situ. In the wake of autoclaving, when the temperature drops down to 60º C, the water is to be evacuated through the examining port by applying N2 pressure. Keep flushing the headspace of the reactor with nitrogen gas to keep up anaerobiosis all through the fermentation. The instigator is to be kept at 150 rpm. Control the temperature at 30±1 ºC and keep up the pH at 6.5±0.1 via programmed expansion of clean 6 N NaOH. A pH estimation of 6.5 has been accounted for to be appropriate for propionic corrosive amassing (Hsu and Yang 1991). Develop the inoculum in a specially designed 500-ml serum flagons (headspace flushed with nitrogen gas). Aseptically immunize the bioreactor containing 5 l of medium with 250 ml of 1-day-old log-stage culture. Gather 10 mL fluid samples at standard stretches Measure the optical thickness and rotator the rest of the volume of the sample at 10,000 g for 20 min. Store the supernatant at – 20 ºC for HPLC examination to build up the item focuses.

❖ **Analytical Protocol -**

- Biomass Estimation - Biomass estimation is done by the measurement of optical density.
- Substrate/Product Estimation - For estimation of product formed HPLC technique is used.

The Simulation was run to understand the basic working and result formation.

OBJECTIVE 7: 1, 3 Propanediol Fermentation

❖ **Basic Requirements -**

- Culture - *Clostridium diolis* DSM 15410 (previously known as *Clostridium butyricum* DSM 5431)is used for 1,3-PD production.
- Modification for maintaining Ideal condition - Customary Erlenmeyer flasks (500 ml) must be changed for completing anaerobic development outside the anaerobic tent. The mouth size (30 mm) is decreased to 10 mm and flasks are furnished with an edge to encourage fixing with elastic and aluminum tops by methods for a crimper. Sparge nitrogen gas in the carafes to cleanse out the dissolved oxygen of stock and keep up anaerobic conditions.
- Medium Requirements - Build up the inoculum in 120 ml serum bottles which contain 50 ml clean medium having arrangement (per liter): unadulterated glycerol 20 g; K2HPO4 3.4 g; KH2PO4 1.3 g; (NH4)2SO4 2 g; MgSO4.7H2O 0.2 g; CaCl2.2H2O 0.02 g; FeSO4.7H2O 5 mg; Yeast extricate 2 g; Trace component arrangement (TES) 2 ml. The follow component arrangement (per liter) comprised of: 70 mg ZnCl2; 0.1 g MnCl2.4H2O; 60 mg H3BO3; 0.2 g CoCl2.2H2O; 20 mg

CuCl2.2H2O; 25 mg NiCl2.6H2O; 0.9 ml HCl (37%). Sparge the jugs with nitrogen and hatch immunized jugs at 330C and 150 rpm in an orbital incubator shaker. Move aseptically exponentially developing culture from the serum bottle (24 h) to sterile nitrogen gassed medium in an uncommonly altered 500 ml Erlenmeyer carafe containing 100 ml medium. Brood the vaccinated flasks in an orbital shaker at 330C and foment at 150 rpm for 12 h after which utilize the effectively developing culture from the carafe as inoculum for the bioreactor.

- **Fermentation Bioreactor Setup -** Batch development of C. diolis is completed in a 3.7 L bioreactor (Bioengineering AG, Switzerland) (working volume 1.5 L) utilizing measurably improved nutrient medium formula. The medium comprises (per liter): unadulterated glycerol 54.45 g; K2HPO4 3.21 g; KH2PO4 2.75 g; (NH4)2SO4 2 g; MgSO4.7H2O 0.2 g; CaCl2.2H2O 0.02 g; FeSO4.7H2O 5 mg; Yeast extricate 2 g; Trace component solution (TES) 2 ml. The follow component solution (per liter) comprised of: 70 mg ZnCl2; 0.1 g MnCl2.4H2O; 60 mg H3BO3; 0.2 g CoCl2.2H2O; 20 mg CuCl2.2H2O; 25 mg NiCl2.6H2O; 0.9 ml HCl (37%). Disinfect bioreactor and tubing via autoclaving at 1210C and 15 psi for 40 minutes. Utilize 10% (v/v) effectively developing culture from the shake flagon as inoculum for the bioreactor. Control medium pH in bioreactor at 7.0 via programmed expansion of 2N NaOH/HCl through corrosive/base peristaltic siphons. Upset the medium in the bioreactor utilizing a level sharp edge turbine impeller turning at 150 rpm and keep up temperature at 330C by coursing chilled water utilizing FP 50 chiller (Julabo, Germany). Sparge nitrogen gas at 0.5 vvm in the bioreactor to give anaerobic conditions during the fermentation. Pull back samples at ordinary time frames h from the bioreactor and break down for biomass, lingering glycerol and 1,3-PD.

❖ **1,3-PD MODEL EQUATIONS:**

The model consists of a system of differential material balance equations which describe the batch dynamics of growth & 1,3-PD production. These equations are summarized below:

$$\mu = \mu max\ (S/S + KS)\ [1- (S / Sm)a]\ [1- (P/Pm)b] \quad (1)$$

$$qs = - \{(1/Ymax)\ \mu + m\} \quad (2)$$

$$qp = K1\mu + K2 \quad (3)$$

where μ- specific growth rate, qs - specific substrate consumption rate, qp- specific product formation rate, Sm- critical substrate concentration, m- maintenance energy constant, Pm- critical product concentration.

PCR TECHNIQUES

Report Submitted in fulfillment of Summer Training of

BACHELORS OF TECHNOLOGY

IN

BIOTECHNOLOGY

BY

HARMEET SINGH (171804)

UNDER THE SUPERVISION OF

Dr. JATA SHANKAR

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY WAKNAGHAT,

SOLAN

DECLARATION

We hereby declare that the summer training work entitled "**PCR TECHNIQUES**" has been solely submitted to the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat have carried out under guidance of our supervisor **DR. JATA SHANKAR .**

Name: **HARMEET SINGH (171804)**

Department of Biotechnology and Bioinformatics

Jaypee University of Information Technology, Solan

Waknaghat.

Date: 4 july 2020

SUPERVISOR'S CERTIFICATE

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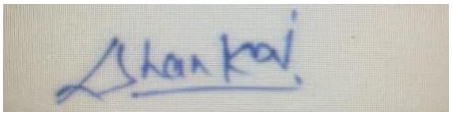
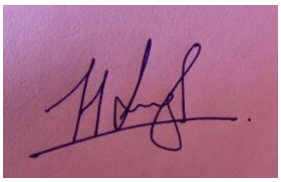
Signature of supervisor-



Signature of student -



Name of Supervisor **- Dr. jata Shankar**

Designation **- Associate Professor**

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Special thanks to my parents for their infinite patience and understanding and most importantly God, who in his mysterious ways, always made things work out in the end.

In gratitude,

HARMEET (171804)

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Standard fixings in the blend are:

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New strands of DNA are made utilizing the first strands as layouts. A DNA polymerase catalyst consolidates free DNA nucleotides. This chemical is frequently Taq polymerase, a protein initially separated from a thermophilic microscopic organisms called Thermus aquaticus. The request where the free nucleotides are included is controlled by the arrangement of nucleotides in the first (format) DNA strand.

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There are many Types of PCR (Polymerase Chain Reaction)

One of the most well-known strategies utilized in present day research facilities is the polymerase chain response (PCR). PCR empowers us to repeat explicit strands of DNA a huge number of times over through quick temperature controlled responses, which is incredible when we have to work with huge amounts of indistinguishable DNA. The strategy itself is the thing that permits us to perform complex DNA sequencing, electrophoresis or in any event, making custom DNA chains by straightforwardly cloning the DNA strands into plasmids. Throughout the years, numerous varieties of the fundamental PCR method have been grown, some which follow the first strategy intently, and others which follow on from, or look like another procedure altogether.

Nested PCR

Nested PCR is procedure, which plans to decrease what number of blunders are made during the enhancement of the DNA. In reality, the RNA-preliminaries utilized in ordinary PCR are inclined to official to vague destinations of the DNA, which weakens the measure of usable DNA inside your example. To address this, settled PCR utilizes two arrangements of groundworks. The main pair expects to enhance a more drawn out section of DNA than is required and as such are pointed outside of the objective DNA area. The subsequent pair are then pointed, or settled inside the objective DNA district, and just translate the region of enthusiasm from the first PCR item. The utilization of twofold matches immensely decreases the likelihood that any undesirable item will sneak past, fundamentally filling in as a sort of "twofold check" for the procedure.

Multiplex PCR

A subsequent variety is known as multiplex PCR, which is ideal for when you need to intensify a few diverse DNA groupings inside a similar example, which would be very tedious and testing to finish with various standard PCR's thus. Basically, this is accomplished by utilizing different groundworks simultaneously. In any case, care must be taken to guarantee that there is insignificant cover between preliminary particularity, as cross-layout restricting can spell catastrophe for the procedure. It is helpful to utilize short preliminaries, regularly just ~18-22 bases in size, with the end goal that the possibility of any cross-hybridisation is limited. Besides, it is profoundly significant that the various preliminaries all react and strengthen at comparable temperatures during the warm cycling process. On the off chance that these conditions are met, at that point it is conceivable to copy tremendous measures of various DNA in a solitary PCR process, boundlessly decreasing both the time and cash required to finish the procedure.

. **Reverse transcription PCR**

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Assembly PCR

A typical strategy utilized inside counterfeit quality amalgamation is known as get together PCR. This method takes many short segments of DNA, and uses DNA polymerase to successfully join them together, shaping huge strands of associated DNA. As you would envision, the sewing together of numerous little parts requires cautious enhancement of the gathering, in any case the whole procedure can come up short. The initial phase in the process includes building the long succession. For this, the many covering oligonucleotides of DNA are gradually bound together during every temperature cycle. When the whole objective arrangement is developed, ordinary PCR can be used to intensify the huge chain, free of the entirety of the littler parts

Quantitative PCR

Quantitative PCR (qPCR), which is additionally frequently called constant PCR, is an extraordinary case of an expansion to the first procedure. The point of qPCR is to gauge precisely the amount of the DNA is being created and communicated after some time, this empowers specialists to measure the specific measure of DNA inside an example. It works in nearly precisely the same route as normal PCR, anyway to follow the measure of DNA being delivered we should add a test to the blend before the response happens. These tests, called oligonucleotides, are named with a fluorescent journalist head which is discharged from the test once the DNA strand has been completely duplicated. As you would envision, as a huge number of DNA strands finish interpretation, these fluorescent heads start to produce a solid fluorescent reaction, which can be legitimately caught by an optical camera in the qPCR machine. The abundancy of this reaction would then be able to be plotted out, with a more brilliant fluorescence relating to a more noteworthy grouping of interpreted DNA.

Another option, less complex strategy for estimating the measure of twofold abandoned DNA in an example includes the utilization of fluorescent color. Which ties to the twofold abandoned DNA and transmits fluorescence which would then be able to be identified by an appropriate magnifying instrument. The issue with this strategy is that the color is vague and will tie to any DNA inside the example, regularly prompting off base evaluation. Relatively, the oligonucleotide tests are profoundly explicit and will just tie to coordinating arrangements of DNA, prompting a significantly more exact estimation in general. Which technique you use will probably come down to the costs in question and how exact you need the outcomes to be.

How is the COVID-19 Virus Detected using Real Time RT-PCR?

As the coronavirus that causes the COVID-19 infection spreads over the world, the IAEA, in association with the Food and Agriculture Organization of the United Nations (FAO), is offering its help and skill to assist nations with utilizing ongoing opposite interpretation polymerase chain response (continuous RT–PCR), one of the most precise research facility strategies for recognizing, following and contemplating the COVID-19 coronavirus

An example is gathered from the pieces of the body where the COVID-19 infection accumulates, for example, an individual's nose or throat. The example is treated with a few synthetic arrangements that evacuate substances, for example, proteins and fats and that remove just the RNA present in the example. This removed RNA is a blend of the individual's own hereditary material and, if present, the infection's RNA.

The RNA is converse deciphered to DNA utilizing a particular protein. Researchers at that point include extra short pieces of DNA that are reciprocal to explicit pieces of the translated viral DNA. On the off chance that the infection is available in an example, these pieces join themselves to target areas of the viral DNA. A portion of the additional hereditary parts are utilized for building DNA strands during enhancement, while the others are utilized for building the DNA and adding marker names to the strands, which are then used to distinguish the infection.

The blend is then positioned in a RT–PCR machine. The machine spins through temperatures that warmth and cool the blend to trigger explicit synthetic responses that make new, indistinguishable duplicates of the objective areas of viral DNA. The cycle is rehashed again and again to keep duplicating the objective segments of viral DNA. Each cycle duplicates the past number: two duplicates become four, four duplicates become eight, etc. A standard constant RT–PCR set-up for the most part experiences 35 cycles, which implies that, before the finish of the procedure, around 35 billion new duplicates of the segments of viral DNA are made from each strand of the infection present in the example.

As new duplicates of the viral DNA areas are assembled, the marker names join to the DNA strands and afterward discharge a fluorescent color, which is estimated by the machine's PC

and introduced progressively on the screen. The PC tracks the measure of fluorescence in the test after each cycle. At the point when a specific degree of fluorescence is outperformed, this affirms the infection is available. Researchers likewise screen what number of cycles it takes to arrive at this level so as to assess the seriousness of the contamination: the less the cycles, the more extreme the viral disease is.

Why use real time RT–PCR?

The ongoing RT–PCR procedure is profoundly touchy and explicit and can convey a dependable finding in as meager as three hours, however labs take on normal somewhere in the range of six and eight hours. Contrasted with other accessible infection detachment techniques, ongoing RT–PCR is essentially quicker and has a lower potential for defilement or blunders, as the whole procedure can be done inside a shut cylinder. It keeps on being the most precise strategy accessible for the recognition of the COVID-19 infection.

In any case, ongoing RT–PCR can't be utilized to recognize past diseases, which is significant for understanding the turn of events and spread of the infection, as infections are just present in the body for a particular window of time. Different techniques are important to recognize, track and study past diseases, especially those which may have created and spread without side effects.

What is PCR and how is it different from real time RT–PCR?

RT–PCR is a variety of PCR, or polymerase chain response. The two methods utilize a similar procedure with the exception of that RT–PCR has an additional progression of converse interpretation of RNA to DNA, or RT, to take into consideration enhancement. This implies PCR is utilized for pathogens, for example, infections and microbes, that as of now contain DNA for intensification, while RT–PCR is utilized for those containing RNA that should be deciphered to DNA for enhancement. The two methods can be acted 'continuously', which means results are obvious very quickly, while when utilized 'ordinarily', results are just noticeable toward the finish of the response.

PCR is one of the most broadly utilized indicative tests for recognizing pathogens, including infections, that cause ailments, for example, Ebola, African pig fever and foot-and-mouth malady. Since the COVID-19 infection just contains RNA, constant or ordinary RT–PCR is utilized to recognize it.

For more than 20 years, the IAEA, in association with the FAO, has prepared and prepared specialists from everywhere throughout the world to utilize the continuous RT–PCR strategy, especially through its VETLAB Network of veterinary demonstrative research centers. As of late, this strategy has likewise been utilized to analyze different sicknesses, for example, Ebola, Zika, MERS and SARS, just as other significant creature ailments. It has additionally been utilized to identify major zoonotic ailments, which are creature illnesses that can likewise contaminate people.

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BY

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UNDER THE SUPERVISION OF

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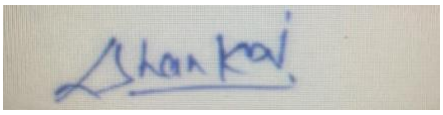
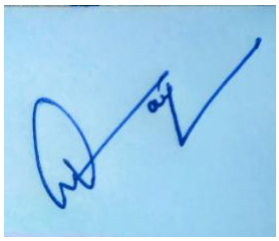


Signature of student -



Name of Supervisor **- Dr. jata Shankar**

Designation **- Associate Professor**

Department of Biotechnology and Bioinformatics

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One of the most well-known strategies utilized in present day research facilities is the polymerase chain response (PCR). PCR empowers us to repeat explicit strands of DNA a huge number of times over through quick temperature controlled responses, which is incredible when we have to work with huge amounts of indistinguishable DNA. The strategy itself is the thing that permits us to perform complex DNA sequencing, electrophoresis or in any event, making custom DNA chains by straightforwardly cloning the DNA strands into plasmids. Throughout the years, numerous varieties of the fundamental PCR method have been grown, some which follow the first strategy intently, and others which follow on from, or look like another procedure altogether.

Nested PCR

Nested PCR is procedure, which plans to decrease what number of blunders are made during the enhancement of the DNA. In reality, the RNA-preliminaries utilized in ordinary PCR are inclined to official to vague destinations of the DNA, which weakens the measure of usable DNA inside your example. To address this, settled PCR utilizes two arrangements of groundworks. The main pair expects to enhance a more drawn out section of DNA than is required and as such are pointed outside of the objective DNA area. The subsequent pair are then pointed, or settled inside the objective DNA district, and just translate the region of enthusiasm from the first PCR item. The utilization of twofold matches immensely decreases the likelihood that any undesirable item will sneak past, fundamentally filling in as a sort of "twofold check" for the procedure.

Multiplex PCR

A subsequent variety is known as multiplex PCR, which is ideal for when you need to intensify a few diverse DNA groupings inside a similar example, which would be very tedious and testing to finish with various standard PCR's thus. Basically, this is accomplished by utilizing different groundworks simultaneously. In any case, care must be taken to guarantee that there is insignificant cover between preliminary particularity, as cross-layout restricting can spell catastrophe for the procedure. It is helpful to utilize short preliminaries, regularly just ~18-22 bases in size, with the end goal that the possibility of any cross-hybridisation is limited. Besides, it is profoundly significant that the various preliminaries all react and strengthen at comparable temperatures during the warm cycling process. On the off chance that these conditions are met, at that point it is conceivable to copy tremendous measures of various DNA in a solitary PCR process, boundlessly decreasing both the time and cash required to finish the procedure.

. **Reverse transcription PCR**

A subsequent variety is known as multiplex PCR, which is ideal for when you need to intensify a few diverse DNA groupings inside a similar example, which would be very tedious and testing to finish with various standard PCR's thus. Basically, this is accomplished by utilizing different groundworks simultaneously. In any case, care must be taken to guarantee that there is insignificant cover between preliminary particularity, as cross-layout restricting can spell catastrophe for the procedure. It is helpful to utilize short preliminaries, regularly just ~18-22 bases in size, with the end goal that the possibility of any cross-hybridisation is limited. Besides, it is profoundly significant that the various preliminaries all react and strengthen at comparable temperatures during the warm cycling process. On the off chance that these conditions are met, at that point it is conceivable to copy tremendous measures of various DNA in a solitary PCR process, boundlessly decreasing both the time and cash required to finish the procedure.

Assembly PCR

A typical strategy utilized inside counterfeit quality amalgamation is known as get together PCR. This method takes many short segments of DNA, and uses DNA polymerase to successfully join them together, shaping huge strands of associated DNA. As you would envision, the sewing together of numerous little parts requires cautious enhancement of the gathering, in any case the whole procedure can come up short. The initial phase in the process includes building the long succession. For this, the many covering oligonucleotides of DNA are gradually bound together during every temperature cycle. When the whole objective arrangement is developed, ordinary PCR can be used to intensify the huge chain, free of the entirety of the littler parts

Quantitative PCR

Quantitative PCR (qPCR), which is additionally frequently called constant PCR, is an extraordinary case of an expansion to the first procedure. The point of qPCR is to gauge precisely the amount of the DNA is being created and communicated after some time, this empowers specialists to measure the specific measure of DNA inside an example. It works in nearly precisely the same route as normal PCR, anyway to follow the measure of DNA being delivered we should add a test to the blend before the response happens. These tests, called oligonucleotides, are named with a fluorescent journalist head which is discharged from the test once the DNA strand has been completely duplicated. As you would envision, as a huge number of DNA strands finish interpretation, these fluorescent heads start to produce a solid fluorescent reaction, which can be legitimately caught by an optical camera in the qPCR machine. The abundancy of this reaction would then be able to be plotted out, with a more brilliant fluorescence relating to a more noteworthy grouping of interpreted DNA.

Another option, less complex strategy for estimating the measure of twofold abandoned DNA in an example includes the utilization of fluorescent color. Which ties to the twofold abandoned DNA and transmits fluorescence which would then be able to be identified by an appropriate magnifying instrument. The issue with this strategy is that the color is vague and will tie to any DNA inside the example, regularly prompting off base evaluation. Relatively, the oligonucleotide tests are profoundly explicit and will just tie to coordinating arrangements of DNA, prompting a significantly more exact estimation in general. Which technique you use will probably come down to the costs in question and how exact you need the outcomes to be.

How is the COVID-19 Virus Detected using Real Time RT-PCR?

As the coronavirus that causes the COVID-19 infection spreads over the world, the IAEA, in association with the Food and Agriculture Organization of the United Nations (FAO), is offering its help and skill to assist nations with utilizing ongoing opposite interpretation polymerase chain response (continuous RT–PCR), one of the most precise research facility strategies for recognizing, following and contemplating the COVID-19 coronavirus

An example is gathered from the pieces of the body where the COVID-19 infection accumulates, for example, an individual's nose or throat. The example is treated with a few synthetic arrangements that evacuate substances, for example, proteins and fats and that remove just the RNA present in the example. This removed RNA is a blend of the individual's own hereditary material and, if present, the infection's RNA.

The RNA is converse deciphered to DNA utilizing a particular protein. Researchers at that point include extra short pieces of DNA that are reciprocal to explicit pieces of the translated viral DNA. On the off chance that the infection is available in an example, these pieces join themselves to target areas of the viral DNA. A portion of the additional hereditary parts are utilized for building DNA strands during enhancement, while the others are utilized for building the DNA and adding marker names to the strands, which are then used to distinguish the infection.

The blend is then positioned in a RT–PCR machine. The machine spins through temperatures that warmth and cool the blend to trigger explicit synthetic responses that make new, indistinguishable duplicates of the objective areas of viral DNA. The cycle is rehashed again and again to keep duplicating the objective segments of viral DNA. Each cycle duplicates the past number: two duplicates become four, four duplicates become eight, etc. A standard constant RT–PCR set-up for the most part experiences 35 cycles, which implies that, before the finish of the procedure, around 35 billion new duplicates of the segments of viral DNA are made from each strand of the infection present in the example.

As new duplicates of the viral DNA areas are assembled, the marker names join to the DNA strands and afterward discharge a fluorescent color, which is estimated by the machine's PC

and introduced progressively on the screen. The PC tracks the measure of fluorescence in the test after each cycle. At the point when a specific degree of fluorescence is outperformed, this affirms the infection is available. Researchers likewise screen what number of cycles it takes to arrive at this level so as to assess the seriousness of the contamination: the less the cycles, the more extreme the viral disease is.

Why use real time RT–PCR?

The ongoing RT–PCR procedure is profoundly touchy and explicit and can convey a dependable finding in as meager as three hours, however labs take on normal somewhere in the range of six and eight hours. Contrasted with other accessible infection detachment techniques, ongoing RT–PCR is essentially quicker and has a lower potential for defilement or blunders, as the whole procedure can be done inside a shut cylinder. It keeps on being the most precise strategy accessible for the recognition of the COVID-19 infection.

In any case, ongoing RT–PCR can't be utilized to recognize past diseases, which is significant for understanding the turn of events and spread of the infection, as infections are just present in the body for a particular window of time. Different techniques are important to recognize, track and study past diseases, especially those which may have created and spread without side effects.

What is PCR and how is it different from real time RT–PCR?

RT–PCR is a variety of PCR, or polymerase chain response. The two methods utilize a similar procedure with the exception of that RT–PCR has an additional progression of converse interpretation of RNA to DNA, or RT, to take into consideration enhancement. This implies PCR is utilized for pathogens, for example, infections and microbes, that as of now contain DNA for intensification, while RT–PCR is utilized for those containing RNA that should be deciphered to DNA for enhancement. The two methods can be acted 'continuously', which means results are obvious very quickly, while when utilized 'ordinarily', results are just noticeable toward the finish of the response.

PCR is one of the most broadly utilized indicative tests for recognizing pathogens, including infections, that cause ailments, for example, Ebola, African pig fever and foot-and-mouth malady. Since the COVID-19 infection just contains RNA, constant or ordinary RT–PCR is utilized to recognize it.

For more than 20 years, the IAEA, in association with the FAO, has prepared and prepared specialists from everywhere throughout the world to utilize the continuous RT–PCR strategy, especially through its VETLAB Network of veterinary demonstrative research centers. As of late, this strategy has likewise been utilized to analyze different sicknesses, for example, Ebola, Zika, MERS and SARS, just as other significant creature ailments. It has additionally been utilized to identify major zoonotic ailments, which are creature illnesses that can likewise contaminate people.

Embryo Culture For In-vitro Micropropagation of New Varities of Cicer arietinum (Chickpea)

Report submitted in fulfillment of Summer Training of

BACHELORS OF TECHNOLOGY

IN

BIOTECHNOLOGY

By

DEVASHISH (171806)

UNDER THE SUPERVISION OF

DR. HEMANT SOOD



May-June (2020)

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY WAKNAGHAT,

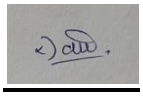
SOLAN

DECLARATION OF CANDIDATE

We hereby declare that the summer training work entitled "**Embryo Culture For In-vitro Micropropagation of New Varities of Cicer arietinum (Chickpea)**" has been solely submitted to the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat have carried out under guidance of our supervisor **DR. HEMANT SOOD.**

Name: **Devashish (171806)**

Signature of Candidate:



Department of Biotechnology and Bioinformatics

Jaypee University of Information Technology, Solan

Waknaghat.

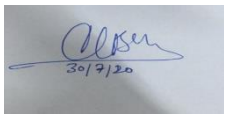
Date: 03-07-20

SUPERVISOR'S CERTIFICATE

This is to certify that the minor project work titled "**Embryo Culture For In-vitro Micropropagation of New Varities of Cicer arietinum (Chickpea)**" by **Devashish** during his 6Th semester in May-June 2020 in fulfillment for the summer training in Plant tissue culture in Biotechnology of Jaypee University of Information Technology, Solan has been carried out under my supervision. This work has not been submitted partially to any other University or Institute for the award of any degree or appreciation.

Name of Supervisor **- Dr. Hemant Sood**

Signature of Supervisor :



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I take this opportunity to express my first and foremost gratitude to my "DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS" for the confidence bestowed upon us and entrusting our project titled "**Embryo Culture For In-vitro Micropropagation of New Varities of Cicer arietinum (Chickpea)**".

At this juncture, with proud privilege and profound sense of gratitude, I feel honored in expressing my deepest appreciation to **Dr. Hemant Sood,** for being a lot more than just a supervisor and going beyond the call of duty in my guidance, support, advice, and motivation throughout. She has been the source of inspiration of come what may; these issues cannot bring you down. Sincere thanks for her insightful advice, motivating suggestions, invaluable guidance, help and support in successful completion of this summer training and also for her constant encouragement and advice throughout my summer training.

Special thanks to my parents for their infinite patience and understanding and most importantly God, who in his mysterious ways, always made things work out in the end.

In gratitude,

Devashish (171806)

INTRODUCTION

The chickpea (*Cicer arietinum*) is an annual legume of the family Fabaceae, subfamily Faboideae. It is variously called as gram and it's seeds contain high protein content. This plant is widely grown in many countries around world and it is also one of the important staple crop in some countries. Global chickpea production is about 8.0 million metric tonnes, secondly to dry beans among edible pulses in year 2004. Chickpea are produced in over 45 different countries all over the world and India typically produced 2/3 of the world Chickpea output alone.

Many breds and genetically modified varities has been successfully produced of this crop and to get more production rapidly we are going to use one of the in vitro micropropagation technique to grow chickpea (Cicer arietinum) plant which is one of the most efficient and effective plant tissue culture technique.

Currently use of the In vitro plant tissue culture technology for improvement of chick pea is rapid, sustainable and option. However,this crop is also very difficult to manipulate in In vitro due to its high sensitive response during culturing practices (Iqbal et al., 1991). Therefore very extensive and broader approach is needed and applied in this study in selection of explants, media and other physiochemical methods and parameters.

In the late 1950s Frederick Campion Steward, a botanist discovered and pioneered micropropagation. Micropropation is a practice that is used to rapidly multiply or grow the stock explant to produce many progeny plants.

Micropropagation can be done in 4 stages –

- Selection of mother plant -
- Multiplication
- Rooting and acclimatization
- Transfer new plant to soil

This method is used to grow plants that has been genetically modified and it is also a practice which provides sufficient number of plantlets from a plant which does not even produce seeds or doesn't respond well to vegitative propagation which can be done using various techniques such as meristem culture, callus culture, suspension culture, embryo culture , etc. and we are specifically look into embryo culturing as it is one of the advance tissue culture method as well high in demand.

Embryo culture is a method of in vitro fertilisation where in resultant embryos are allowed to grow for some time in an artificial medium. After fertilization zygote formation occurs followed by embryo formation then Embryo is taken out by removing seed coat aseptically which is grown on MS media to generate somatic embryos as explants which further grow into plant. Embryo culture is also an important method to study the relationship between embryo and endosperm and is an important tool to analyse various embryonic growth phases which can be very helpful on research purpose. It is one of the rapid and successful methods.

Embryo rescue is one of the techniques of in vitro culturing and it is used to assist in the development of plant embryos that might not survive to become viable plants i.e. whose purpose is to promote development of a weak or immature embryo into a successful viable plant. It has been widely used for producing hybrid plants in which failure of endosperm to properly develop an embryo causes embryo abortion.

REVIEW OF LITERATURE

Somatic embryogenesis is the primary mode of plant regeneration from immature embryos, mature embryos and cotyledons of different legumes e.g. Glycene max (Korbes & Droste, 2005), Pisum sativum (Kysely & Jacobson, 1990) and Arachis hypogaea (Roja et al., 2005). Little progress has been made towards developing an In vitro regeneration system of chick pea which is an important food legume crop. Chickpeas are very much valued for their nutritive seeds that have protein content ranging from 25-29%.In addition to that the nutritional attributes of chickpeas include 67% total carbohydrates, 47% starch, 8% crude fibres, 5% fats and over 3% ash (Popelka et al., 2006). Chickpea seeds are being eaten fresh as green vegetable, roasted, fried, in snacks, boiled foods, etc. and their flour can be used as dhal, soup and to make a very popular snack like Pakoras (McNew & Bixlez, 2001). Keeping in mind the growing demand, supply and demand gap and huge import bill this is extremely important to address this crop seriously and the related problems.

Somatic embryogenesis was induced in both direct and indirect pathways from immature cotyledons and young leaf explants respectively of chickpea (Cicer arietinum).The two varieties that were taken are ICCV10 and annigeri that were developed using Agrobacterium mediated transformation out of which ICCV10 is more successful and have shown better results compared to annigeri.The two varieties were cultured on MS medium with various concentrations of hormones i.e. auxins and cytokinins. 2,4-D and NAA were used in the range of 1.0-16.0 mg/l. NAA (10-14 mg/l) induced direct embryo formation on the cut edges of immature cotyledons on adaxial surface side. These pro-embryonic structures enlarged and formed the distinct globular pro-embryoids within 3-4 weeks of incubation. Further growth of these pro-embryoids was limited and very few of these exhibited either root or shoot polarity. Auxins:cytokinins (plant

hormones) combinations promoted induction of indirect embryogenesis as well.The best response that was noticed in the medium 0.1 mg/l BAP + 3 mg/l 2,4-D. After 10-15 days leaf explants induced nodular callus consisted of pro-embryoids and after 5-6 weeks, the pro-embryoids has been transformed into embryo development phase ranging from globular, heart to torpedo stages. The sustainability and further growth of somatic embryos was investigated by shifting both direct and indirect embryoids on basal media. The frequency of embryogenesis and subsequent plantlet regeneration was found higher in indirect embryogenesis as compared to direct embryo formation.

The survival %age of indirect embryoids was higher as compared to direct embryoids. After 4 weeks the %age survival was reduced to 75%, which remained constant even up to 12th week of incubation in case of direct embryoids.

However, all attempts were failed to stimulate the further growth of these embryoids. Another major obstacle in further embryoids growth and plantlet differentiation was the lack of complete bipolar embryo formation. Most of the embryoids produced either root or shoot but no simultaneous root and shoot formation was observed in any case whereas in case of indirect embryogenesis differentiation response was fairly good compared to that of direct embryogenesis. Vigorous embryo germination, elongation, axillary shoot formation and development of leaf primordia and their different phases were clearly evident. Further growth of induced shoots with formation of roots was accomplished successfully on same media.

The survival %'ages of induced embryo and developed organs swiftly increased with increasing incubation period. At 8th weeks, the survival %age had reached to 89.14% after which hardening off of the platlets were done and then successfully grown on soil.

The major obstacle in this study was to overcome the notoriously recalcitrant behaviour of chickpea in In vitro culturing. However, with extremely large range manipulation practices resulted a significance success in obtaining embryo formation; regeneration and plantlet formation were pulled out.

MATERIALS AND METHODS

Plant materials:

The seeds of Cicer arietinum L. were surface sterilized using mercuric chloride for 4-5 minutes and then rinsed with distilled water for 10 minutes and were grown aseptically on MS basal medium devoid of any vitamin and growth hormones. These In vitro grown two week old seedlings were then used for the preparation of leaf explant. Immature pods containing seeds were harvested after 15-20 days of anthesis and were surface sterilized using mercuric chloride. Green pods were agitated in soapy water i.e. surf excel liquid for 5 minutes followed by three

rinses in distilled water in different intervals. Under aseptic conditions, the washed pods were immersed in 20% Sodium hypochlorite solution for 15 minutes with frequent agitation. After this the pods were rinsed twice in sterile distilled water. The disinfected pods were cut open and the seeds were removed and taken out carefully avoiding damage to the seed coat. Seeds were again soaked in 20% Sodium hypochlorite for 6-8 minutes and were immediately rinsed in sterile distilled water. Immature embryos were dissected from pods and their axis was removed to yield two cotyledonary explants.

Effect of plant growth regulators on induction of somatic embryogenesis:

Immature cotyledons were cultured on MS medium (Murashige & Skoog, 1962) facing abaxial side and supplemented with NAA and 2,4-D alone or in combination with cytokinins BAP or kinetin in different concentrations. The medium was supplemented with 3% sucrose. The medium was adjusted to pH 5.5 before autoclaving and gelled with 0.8% agar for solidification and then autoclaved for 20 minutes at 120psi. The freshly prepared cultures were grown under carefully regulated temperature and light conditions providing suitable environment. The temperature of culture room was 22 ± 2°C and the light intensity varied from 2,000 to 3,000 lux with 14-16 hours photoperiod. Data about type of callus produced and frequency of embryogenesis of different explants was recorded after 4 weeks.

Multiplication of callus and regeneration of plantlets:

After 4 weeks, the calli and directly induced embryoids were sub-cultured on to basal medium containing different concentrations of auxins and Auxins: cytokinins combinations for further growth. The medium had a pH value of 5.5. The cultures were maintained at 22 ± 2ºC.

Hardening off before planting into soil:

The plantlets regenerated were then transferred to half strength MS basal medium for acclimatization in culture room for 4-6 weeks approximately. After this stage the hardened plants were shifted in autoclaved sand and then in different mixtures of compost for further growth and then they were grown on pots containing soil and sand in 3:1 ratio

A

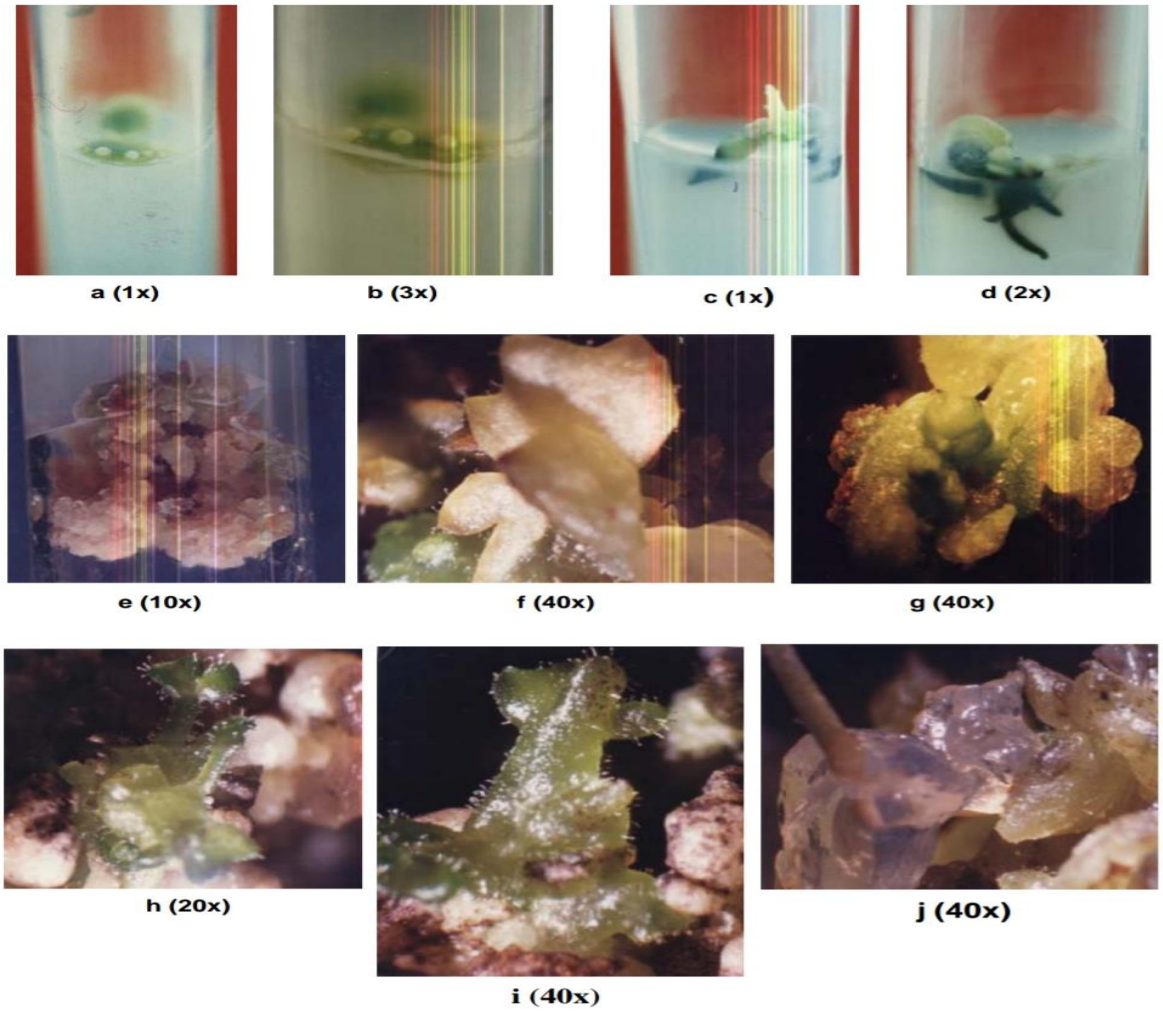


Fig. 1. a-d: Direct somatic embryogenesis. a –b:Induction of direct embryoids on the surface of cotyledons on MS+NAA 10 mg/l after 1-2 week of incubation. c,d: Shoot and root initiation on same media after 6 weeks of incubation. e-I: Indirect somatic embryogenesis: Embryogenic callus derived from immature leaf on MS+2,4-D2.0 mg/l after 3 weeks of incubation. e,g: Different stages of embryo development i.e. globular and heart shaped after 4 weeks of incubation. g-h: Elongation of shoots from embryo.Glandular trichomes are also visible on the surface of leaf primordia. i.j: Root initiation from basal part of embryogenic callus.

As we can see the different stages of somatic embryogenesis in figure shown above taken from Department of Botany, Lahore College for Women University, Lahore, Pakistan 2Department of Biological Sciences, University of Sargodha, Pakistan 3AgriBiotech (Pvt. Ltd.) 14-km, Maltan Road, Lahore, Pakistan as refrence.

CONCLUSION

- The success rate of germination is more than 40% in ICCV10 and was around 30% in annigeri varities of Chickpea.
- The survival %age of direct embryoids was lower as compared to indirect embryoid
- The survival %ages of induced embryo and developed organs in plant swiftly increased with increasing incubation period.
- At 8th weeks, the survival %age had reached to 89.14%.

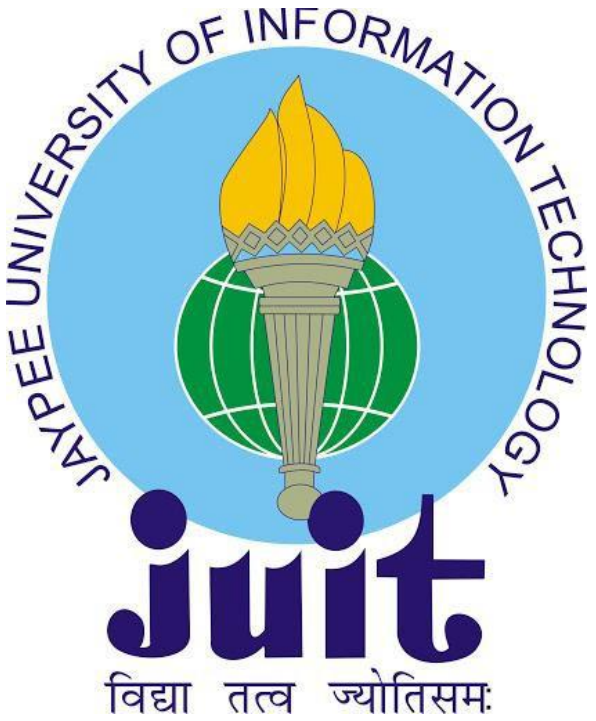
REFERENCES

1. Adkins Godwin, I.D. and S.W. Adkins. 1995. An efficient in vitro regeneration system for Australian-grown chickpea (Cicer arietinum). Aust. J. of Bot., 43: 491-497.
2. Baker, C.M. and Wetzstein. 2004 Leaflet development, induction time, and medium influence somatic embryogenesis in peanut (Arachis hypogaea L.) Plant Cell Rorept., 12:925-929.
3. Barna, K.S. and A.K. Wakhlu. 1993. Somatic embryogenesis and plant regeneration from callus culture of chickpea (Cicer arietinum). Plant Cell Reports, 12: 521-524.
4. Iqbal, J., S. Naz, F. Aftab and M.S. Ahmad. 1991. Total phenolics, phenylalanine ammonia –lyase and polyphenol oxidase in in vitro calli of chickpea. Pak. J. Bot., 23: 227-235.
5. Islam, R. 1994. Somatic embryogenesis from immature cotyledons of chickpea. Ph.D. Thesis University of the Punjab, Lahore. pp. 42-59.
6. Ramnaua, R.V., C. Venu, T. Jayasree and A. Sadanadam. 1996. Direct somatic embryogenesis and transformation in Cicer arietinum. Ind. J. Exp. Biol., 34: 716-718.
7. Haware, M.P., J. Marayan Rao & R.P.S. Pundir, 1992. Evaluation of wild *Cicer* species for resistance to four chickpea diseases. Int Chickpea Newslett 27: 16-18.
8. Badami, P.S., Nalini Mallikarjuna & J.P. Moss, 1997. Interspecific hybridization between *Cicer arietinum* and *Cicer pinnatifidum*. Plant Breeding 116: 393-395.

PHYSICO-CHEMICAL EVALUATION OF BIOSURFACTANTS FOR THEIR POTENTIAL APPLICATIONS IN BIOTECHNOLOGY

Submitted By:
Aakanksha Pandey (171807)

Supervisor: Dr. Poonam Sharma



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Student Signature



Supervisor Signature

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In quest for this scholastic undertaking I feel that I have been particularly lucky as motivation, direction, course, co-activity, love and care all came in my way in plenitude and it appears to be very nearly an inconceivable assignment for me to recognize the equivalent in sufficient terms.

I express my true gratitude to my chief, Dr. Poonam Sharma, Professor, Division of Biotechnology and Bioinformatics, JUIT Waknaghat, for her regarded oversight, ceaseless help, motivation and productive analysis all through my exploration work.

Further, I stretch out my genuine gratitude to the entire Division of Biotechnology and Bioinformatics for giving the caring authorization and giving me the important authoritative offices during the exploration work.

ABSTRACT

Surfactants are amphiphilic compounds having both hydrophobic as well as hydrophilic moieties, thereby expressing the characteristics of both the groups. They tend to possess surface active characteristics, thereby decreasing the surface tension between the interfaces of either two liquids, liquid-air, oil-water interfaces etc. A common surfactant consists of a lipophilic group, usually a long-chain hydrocarbon moiety, and a hydrophilic group, which is both a charged or an uncharged polar group. Therefore, a surfactant consists of each a water-insoluble thing and a water-soluble component. Surfactants diffuse in water and adsorb at interfaces.

They resemble the chemical surfactants, containing each hydrophilic and hydrophobic moieties in the equal molecule. The hydrophobic tails structure the core of the aggregates, whilst the hydrophilic head is in contact with the liquid floor surrounding it. The form of aggregates relies upon on the chemical shape of the surfactants, due to the stability of measurement between the hydrophobic tail and hydrophilic head, which is measured by way of hydrophilic lipophilic stability i.e. HLB.

Diverse classes of surfactants can be characterized by the charge of their head gatherings, specifically cationic (positive charge); anionic (negative charge); non-ionic (non-charged and exceptionally hydrophilic); and zwitterionic (nearness of both negative and positive charge places, and a net charge equivalent to zero). The surface rheology of surfactant layers, including the versatility and thickness of the layer, assume a significant job in the solidness of froths and emulsions.

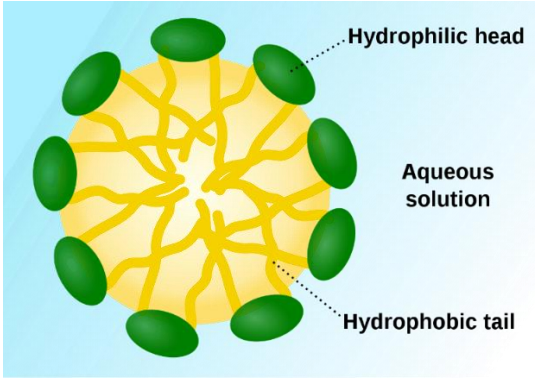

Fig 1: Structure of a typical surfactin molecule.

The biological entities themselves produce a wide array of surfactants, which are referred to as biosurfactants. The human body creates a wide cluster of surfactants like the Pneumonic Surfactant, being delivered in lungs, encourage breathing by expanding the complete Lung capacity. Microbial Surfactants are a wide assortment of basically differing mixes from microbial birthplace showing surface movement at the interfaces and possess ground-breaking attributes including high biodegradability, low poisonousness and unique organic exercises, emulsification activities, biocompatibility, thus making them suitable alternatives compared to their chemical/synthetic counterparts. Microbial surfactants are handily corrupted and are commonly considered as low or non-poisonous mixes. Microbial surfactants are known to segment at interfaces of liquid stages with particular polarities and hydrogen holding, in this way influencing the attachment of microorganisms.

TABLE OF CONTENTS

1. INTRODUCTION……. 5
2. OBJECTIVE…….. 6
3. BIOSURFACTANTS…… 6
4. PRODUCTION……. 7
5. PROPERTIES……10
6. CHARACTERIZATION……. 11
7. APPLICATION……. 14
8. CONCLUSION…….. 29
9. FUTURE PERSPECTIVE AND CHALLENGES……. 30
10. REFERENCES…….. 31

1. INTRODUCTION:

The phrase surfactant is a combination of surface-active agent. Surfactants alter the properties of the surface and interfacial tension of a liquid allowing the formation of microemulsions, which lead to solubilization of oil in water and water in oil. It is due to this phenomenon that they are widely used in many industries. Surface tension is a phenomenon which measures the force of attraction between the liquid molecules. It is a critical parameter for evaluating the effectiveness of a surfactant, leading to decrease in the surface tension when their concentration in the solution increases, which leads to formation of micelles. Micelles are formed due to the inability of lipophilic region of the surfactant to form hydrogen bond in aqueous phase and thereby lead to increase in free energy of the system. Dealing with this increased free energy is required to aid in isolation of hydrocarbon tail from water by its absorption onto organic or aqueous surfaces enabling the hydrophobic region oriented towards the centre while hydrophilic region facing water. Surfactants lower the interfacial tension between immiscible fluids making them miscible, due to formation of new additional surfaces. Micelles are defined as aggregated molecules containing both hydrophobic and hydrophilic groups, with hydrophilic groups oriented towards water, while hydrophobic group oriented towards oil. The formation of micelles leads to distribution of hydrophobic compounds into the pseudo core residing in the centre thereby enhancing solubility. This leads to better dispersion od compounds and lead to increased mobility of adsorbed hydrophobic soil contaminants by decreasing the capillary forces. The minimum concentration of surfactant required to produce a maximum decrease in surface tension of a liquid is regarded as Critical Micelle Concentration (CMC).

Biosurfactants are surface active bio-compounds produced by microorganisms and are considered as alternatives to petroleum derived chemical surfactants. These green compounds have lower critical micellar concentration compared to that of synthetic ones and they lead to higher decrease in surface tension of oil-water or air-water interfaces to a very low value. This property makes microbial surfactants great froth stabilizers and emulsifiers. Microbial surfactants present various focal points over the compound ones, in particular with respect to their biodegradability, mild creation conditions, ecological compatibility, lower toxicity, high selectivity, and explicit action at extraordinary temperatures, pH, and salinities.

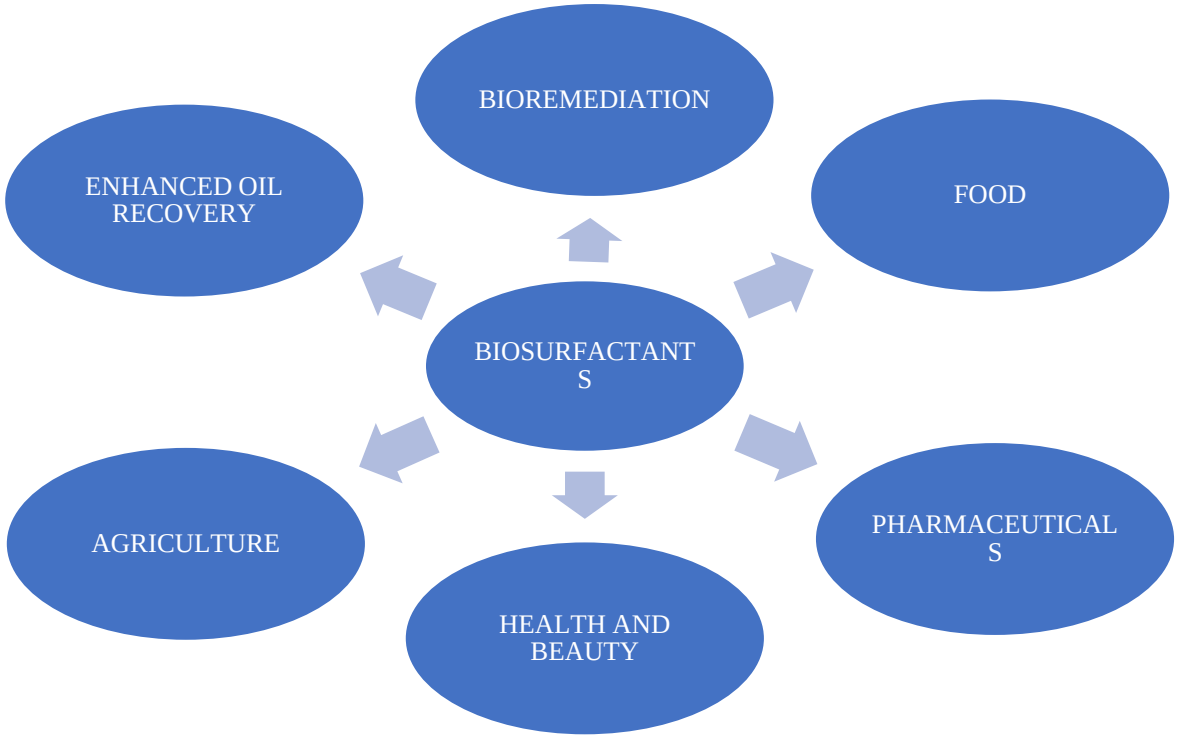

Fig 2: Applications of biosurfactants in various industries.

2. OBJECTIVE:

The target of this examination audit was to get comfortable with the properties, creation, and uses of biosurfactants in present day times. With the assistance of this audit, I hope to have a superior knowledge for biosurfactant creation and discover more applications which can be helpful for humankind.

3. BIOSURFACTANTS:

Surfactants are typically natural compounds that are amphiphilic, that means they incorporate each hydrophobic groups and hydrophilic groups. Biosurfactants are amphiphilic compounds having both hydrophilic and hydrophobic groups in it.[1] The hydrophilic region might be carbohydrate, amino acid, cyclic peptides, phosphate, carboxyl acid or alcoholic groups, while hydrophobic region comprises of a long chain fatty acid, hydroxyl fatty acids, α-alkyl-β-

hydroxy fatty acids etc. Other than bringing down the fluids surface pressure, these moieties can likewise incredibly affect the interfacial conduct and mass exchange, as they likewise bring down the interfacial strain between diverse fluid stages on the interfacial limit existing between immiscible stages.[11] Microbial surfactants possess an intense ability to lower the interfacial tension and show diverse properties as emulsification, lubrication ability, phase dispersion, detergency etc.[17] They are majorly used in food, petroleum, cosmetics industries, environmental, bioremediation, environmental and even pharmaceutical industries. Surfactant molecules are amphipathic in nature that get partitioned between two phases, having varying degree of polarity. Microbial surfactants are best and productive at their CMC which can be 10-40 times lower than that of substance surfactants, in this way less surfactant is important to get a most extreme lessening in surface pressure. Microbial surfactants are handily corrupted and are commonly considered as low or non-poisonous mixes. Microbial surfactants are known to segment at interfaces of liquid stages with particular polarities and hydrogen holding, in this way influencing the attachment of microorganisms. The presence of biosurfactant in a media can be detected by various techniques using colorimetric analysis, emulsification index determination, drop collapsing test and thin layer chromatography.

4. PRODUCTION:

Biosurfactants are obtained from non-exhaustible renewable sources thus having high surface activities, along with high specificity and the ability to function under extremes of conditions. Generally produced by aerobically growing microorganisms utilizing feedstocks as source of carbohydrates, fats etc. Biosurfactants are actively secreted into the culture medium and are supposed to aid in growth of microbes, by facilitating transport of solutes that are insoluble, across the cell membrane. They are usually non-ionic or anionic moieties and have both the lipophilic as well as hydrophobic groups.

Both high and low molecular weight biosurfactants are derived from microorganisms. Low molecular weight biosurfactants includes glycolipids like trehalose, fructose lipids, sophorolipids while peptidyl lipids include surfactin, polymyxin, etc. Surfactin is a biosurfactant produced by *Bacillus subtilis*, which possesses amphiphilic structure and serve as a potent inhibitor of bacterial and tumour growth, and are associated in lowering the surface

tension of the fluids. High molecular weight biosurfactants on the other hand are amphiphilic polysaccharides which are concerned in providing a stable emulsion and do not lower the interfacial tension.[21] Due to their ability of producing of stable emulsions they facilitate in strong adhesion of bacteria to hydrophobic surfaces. Most of the biosurfactants are obtained from *Arthrobacter*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Acinetobacter calcoaceticus*, *Candida lipolytica*, *Corynebacterium*, *Nocardia*, *Bacillus subtilis*, *Bacillus licheniformis*, *Candida spp.*, etc. Majority of biosurfactants are produced from substrates which are insoluble in water.

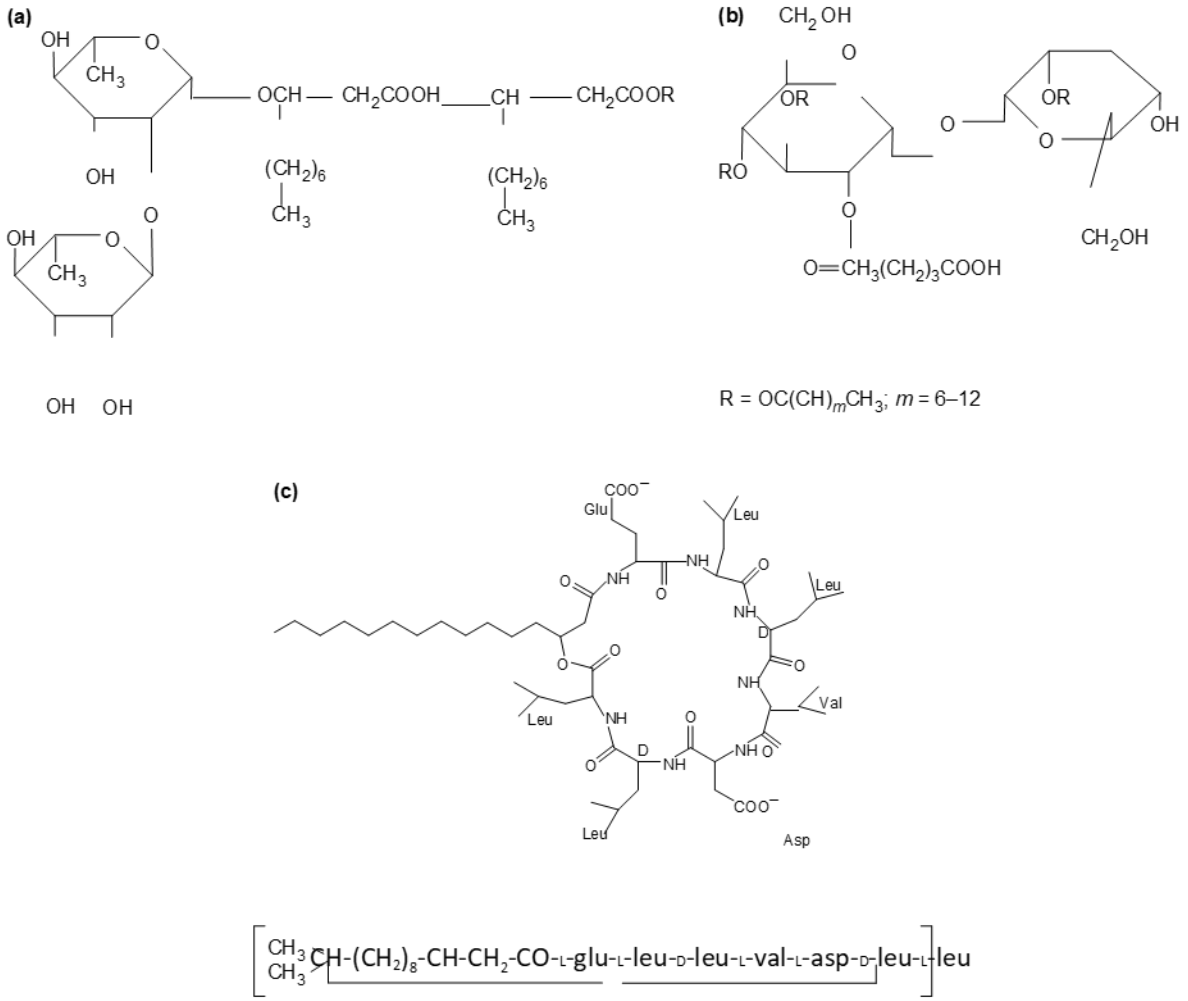

Fig 3: (a) Structure of dirhamnolipid. (b) Structure of trehalose lipid. (c) Surfactin structure

Researchers have obtained biosurfactants by growing a culture of *Candida lipolytica* on groundnut oil. Similarly, *Candida glabrata* was grown on vegetable oil to produce biosurfactants. Similarly, rhamnolipids were also produced from low cost carbon sources using

Pseudomonas aeruginosa like soybean, cottonseed, corn oil etc. Also, rhamnolipids were obtained using restaurant waste oil in bioreactor configuration using the strain *Pseudomonas aeruginosa.* Another low-cost medium was reported having Cassava waste water and waste cooking oil to obtain rhamnolipids.[30] Endophytic fungi are also been used to obtain biosurfactants, they are found in tropical areas on trees like *Piper hispidum*, which act as a potent source for ultimate production of biosurfactants.[8] The biosurfactant derived from *Candida utilis*, has low cytotoxicity, high antioxidant activity along with thermal stability, which makes it a suitable choice to be utilized in food industries. The best portrayed microbial surfactants incorporate Glycolipids and lipopeptides. *Pseudomonas aeruginosa* produce rhamnolipids (example of glycolipids),[19] trehalolipids created by *Rhodococcus erythopolis*, sophorolipids delivered by *Candida bombicola* and mannosylerythritol lipids (MEL) created by *Pseudozyma* yeasts.

To optimize the conditions for enhanced production of biosurfactants, metabolic pathway of the producing organism should be well known, also the chemical structure of biosurfactants should be well known too. Poultry farming waste and butter milk are found to be potential sources of nitrogen and carbon.[7] Hence this mixture was found efficient for production of SPB1 lipopeptide.

Petroleum derived synthetic surfactants happen to be the most widely used across different industries, primarily due to high cost of production of biosurfactants, also the fact that widescale production of these has not been defined yet to meet the industrial demands. This domain is being worked upon to find the ways to reduce cost of production, mainly focusing on use of alternate substates, microbial culture, culture conditions. Also use of low-cost medium can also aid in decreasing the cost of production.

A huge amount of organic waste is being produced via food, forest, municipalities and agriculture industries. Although biosurfactants are quite advantageous over synthetic surfactants they still are a bit costly to prepare. The only way to reduce their cost of production is modification in fermentation technologies and using renewable substrates and different microbial strains for production of biosurfactants. Further optimising operating parameters like temperature, pH, agitation speed and duration and efficient recovery of products, make them more efficient, but still a bit costly compared to synthetic ones. Use of low cost agro-industrial waste may overcome the issue of cost. It is necessary to develop techniques which allow easy

production and downstream processing of the product so as to be able to be used at a large scale. It depends upon the structure, composition and concentration of surfactant to choose a viable recovery method.it can be solved by using industrial by products like vegetal waste oil, like glycerol in appropriate concentrations does not inhibit growth and serves an excellent source of carbon.[22] Since huge amounts of waste generated by industries can be refined and used as excellent alternative substrates, thus producing low cost alternatives for production of surfactants as compared to that of petroleum derived surfactants.[11]

5. PROPERTIES:

Biosurfactants house certain unique properties like:

- Surface activity
- Biodegradation
- Detergency abilities
- Emulsification and de-emulsification activities
- Lubrication
- Wetting ability
- Foaming
- Solubilization
- Dispersion of phase etc.

Surface properties: Expansion of a surfactant to a given arrangement will bring down its surface strain because of the surfactant adsorption at the interface.[27] For a weakened arrangement, the more atoms adsorb at the interface, the lower the surface strain of the arrangement will be.

Hydrophilic-lipophilic balance: This boundary influences the soundness of the emulsion, speaking to the general commitment of hydrophobic tails and hydrophilic leader of the surfactant.[28] A low HLB favours water-oil microemulsions, and high worth favours oil-water microemulsions.

Critical packing parameter: To lessen the contact edge of the water with hydrocarbon chains, surfactant atoms will in general structure totals in arrangement with the chains situated to the inside and encased in the total.

Spontaneous curvature: Conglomeration can be legitimized dependent on the spontaneous bend. The favoured arch will likewise rely upon the general extent of polar and non-polar volumes.

Winsor R ratio: The proportion of the complete interaction energies (per unit zone of the interface) of the surfactant for the Oil and Water stages is known as the Winsor-R proportion. R< 1, demonstrates the water-surfactant connection is stronger than the oil-surfactant collaboration; R>1, proposing that the quality of oil surfactant cooperation is more grounded than the water-surfactant association; and R=1, the circumstance in which the communications are balanced.[3]

Self-assembly: Self-assembly comprises in the capacity of surfactant particles to self-associate in a given solvent, framing various kinds of totals and structures of colloidal measurements. These structures can be of restricted size or huge with network in one, a few measurements.

6. CHARACTERIZATION:

The characterization of structures was carried out using various spectroscopic techniques by obtaining Infrared spectra, Nuclear Magnetic Resonance was also carried out to characterize structures. Fatty acids were characterized using a characteristic reaction with diazomethane followed by final analysis using Gas chromatography and Mass spectroscopy. The results of FABMS were obtained by dissolving glycolipidic samples in glycerol to be used as probe matrix. Following it the alkaline lysis of glycolipids were carried out using reflux with 0.5 N NaOH solution for 12 hrs at 40°C. Fatty acids upon extraction with chloroform and methylation with diazomethane yielded a lipid sample for GC-MS analysis. Acid hydrolysis was carried out using refluxing of the sample with 2 N HCl for 2 and a half hours. Thin layer chromatography was carried out using different solvent systems to analyse sugar moiety. The interfacial and surface tensions of organic extract was measured using Lauda Automatic

Tensiometer TE-1 using De Nuoy ring method. Aqueous solutions here were acidified with pH 3 and 1 N HCl, then made basic with pH 9 and 1 N NaOH, the pH was recorded using Radiometer pH meter 28.

Added NaOH to the extracted biosurfactant leading to production of carboxylic acid salt of sodium, followed by washing with acetone and filtration using sintered glass. The precipitate so obtained was diluted with distilled water and was acidified using HCl for acid recovery and ethyl acetate was used for extraction. The gas filtration was performed using esterification of biosurfactant to get methyl esters of fatty acids.

The thermal analysis was performed in a thermal analyser, following successive steps of heating and cooling in an atmosphere of nitrogen.

Antioxidant activity was tested out by using an aliquot of 0.1 ml at varying concentrations of the biosurfactant having 1 ml of sulphuric acid, sodium phosphate, ammonium molybdate and subjected to water bath at a temperature of 90°C for 1 and a half hour. Optical density was recorded at 695 nm and expressed relative to a control of ascorbic acid having 100% antioxidant capacity. It was also tested using DPPH assay, which stands for 2,2-diphenyl-1-picrylhydrazyl. It was added to different tubes having different concentrations of biosurfactants and was incubated in the dark for 30 mins. Absorbance was measured at 517 nm and the percentage of inhibition activity was calculated using the formulae:

$$\%I = \frac{(Absi - Absf)x\ 100}{Absi}$$

where Absi is absorbance of control while Absf is that of biosurfactant.[6]

For Superoxide Sequestering test to check the antioxidant activity, the isolated biosurfactant was diluted using phosphate buffer, methionine solution, EDTA, riboflavin solution and nitro tetrazolium blue chloride and placed in a tube, the control had all of these except the biosurfactant. They were subjected for 15 mins to fluorescent lights, and reading was recorded at 560 nm.[6]

The cytotoxic activity of the biosurfactant was evaluated using MTT assay. (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) i.e. MTT protocol was designed using

fibroblast cells of mice and macrophage cells of mouse, kept in a culture flask having 5% CO2 and 37°C. Trypsin was used to detach the adhered cells and were then added to a 96 well plate having Dulbecco modified eagle medium, incubating this setup at 37°C with 5% CO2 for a day. Following this biosurfactant was added to this mixture under the prevailing same atmospheric conditions for 72 hours. DMEM medium alone acted as negative control, while positive control comprised of phosphate buffer. After the incubation MTT stain was added to the mixture and allowed incubation of 3 hrs. Following it, dimethyl sulfoxide was added and OD was recorded at 560 nm. Inhibition percentage was calculated by means of computer software.

Various classes of surfactants can be characterized by the charge of their head gatherings, specifically cationic (positive charge); anionic (negative charge); non-ionic (non-charged and exceptionally hydrophilic); and zwitterionic (nearness of both negative and positive charge places, and a net charge equivalent to zero).[1] The elements of assimilation rely upon the diffusion coefficient of the surfactant. As the interface is made, the adsorption is restricted by the dispersion of the surfactant to the interface. At times, there can exist a vivacious hindrance to adsorption or desorption of the surfactant. Such vitality hindrances can be expected to steric or electrostatic shocks. The surface rheology of surfactant layers, including the versatility and thickness of the layer, assume a significant job in the solidness of froths and emulsions.[29]

Microbial surfactants can be sorted by their method of activity, sub-atomic weight and general physicochemical properties. microbial surfactants are commonly sorted by their synthetic strategy and sub-atomic weight, as low (for example glycolipids and lipopeptides) and high atomic weight (for example polysaccharides, proteins and lipoproteins) surfactants. In heterogeneous frameworks, microbial surfactants structure an atomic interfacial film that influences the wettability and surface vitality of the first surface. Other than bringing down the fluids surface pressure, these movies can likewise incredibly affect the interfacial conduct and mass exchange, as they likewise bring down the interfacial strain between diverse fluid stages on the interfacial limit existing between immiscible stages.

7. APPLICATIONS:

Commercially available biosurfactants are obtained using chemical methods from petrochemical industries. To reduce the use of chemicals, microbes and other sources have been explored for the production of surfactants. Plants synthesize saponins, humans synthesize biliary salts and glycolipids secreted by microorganisms are some examples of organic surfactants.

Since the term is being used in a broad sense, it also includes some of the by-products produced by yeasts, bacteria and some filamentous bacteria, like emulsifiers and dispersing agents, which are generally used in petrochemical industries, food and pharmaceutical industries. Surfactants are generally used in cleaning industries which produce detergents and soaps. Surfactants are also being used for bioremediation of hydrocarbon pollution and enhanced oil recovery. Biosurfactants are being used as emulsifiers in food industries. Some major applications are:

Gene transfection:

Transfecting genes into a cell is the premise of clinical quality treatment. Lipofection utilizing cationic liposomes is viewed as a promising strategy for bringing outside qualities into the focus on cells because of their high transfection productivity, low toxicity, and immunogenicity, simplicity of arrangement, and focused on application. Physicochemical properties of cationic liposomes namely, lipid pressing density, zeta potential, and shape influence the proficiency of quality transfection. The biosurfactant actuates the layer combination between the objective cells and the cationic liposomes, quickening the proficiency of quality transfection fundamentally.

It was discovered monolayers made out of L-α-dipalmitoyl phosphatidylcholine (DPPC) containing MEL-A had more prominent film ease than those containing just DPPC. MELs are structurally classified into four types Mel a, Mel b, Mel c and Mel d. these variations are derived by the organism are the carbon source used. Mel has a property of self assembly that can be

used in chain delivery and drug encapsulation processes.[12] It was observed a higher unsaturated fat proportion liposome had the option to combine the plasma film yet didn't convey DNA into the core, while a lower unsaturated fat proportion liposome neither intertwined with the plasma layer nor conveyed DNA into the core.

As drug delivery agents:

They show properties like emulsification, frothing, detergency and scattering, help discover their application as medication conveyance vectors.[16] Rhamnolipids and sophorolipids can be blended in with lecithin to get ready biocompatible microemulsions in which the stage conduct is practically harsh toward changes in temperature and salt fixation, in this manner making them alluring for corrective and medication conveyance applications.[1] Microemulsions acquired utilizing microbial surfactants are thermodynamically steady and their isotropic frameworks that structure immediately, notwithstanding their drawn-out soundness, simple arrangement and high solubilization limit are viewed as exceptionally encouraging fluid vehicles for future medication conveyance frameworks.[13] The consolidation of an emulsion into a gel expands its strength and proficiency when contrasted with other topical medication conveyance frameworks.

Micro-emulsion systems:

The basic components to create a microemulsion-based colloidal DDS contain a watery stage, an oil stage, a surfactant and typically a co-surfactant or co-dissolvable.[23] These structures can exemplify or potentially solubilize hydrophobic or hydrophilic medications within the sight of a scattered stage inside its basic centre, in this manner dividing the scattered stage from the constant stage. These frameworks are thermodynamically steady and display high solubilization limit and ultralow interfacial strains of oil and water, accordingly making them attractive for medicate conveyance applications.[18]

Silver nanoparticles have been orchestrated utilizing a quick microbial surfactant interceded amalgamation, by blending the surfactant and AgNO3 arrangements, trailed by NaBH4 and incredible mixing. Fluid arrangements of AgNO3, sanitized biosurfactant, n-butanol, and n-heptane were overwhelmingly mixed until homogeneous converse micelles were framed. At that point, NaBH4 was utilized to frame other opposite micelles. The two converse micelle arrangements were blended and a short time later ethanol was added to break switch micelles. The silver nanoparticles were hastened from the arrangement and disengaged by centrifugation. Rhamnolipids have been effectively used to integrate circular nickel oxide nanoparticles. Unsaturated fats have been proposed to assume a twofold job in the blend of nanoparticles, by settling O/W emulsions in this way adjusting the decreasing gatherings on the external side; and additionally, by diminishing metal salts into nanometals.

In production of nano-particles:

Nanoparticles are portrayed by their novel size and stable shape. The accessible procedures are capital serious, produce perilous squanders and flimsy nanoparticles with diminished focused on action. To follow greener bio-handling microbial surfactants are being used as another option. Gold nanoparticles are by and large progressively utilized in the field of medication and quality conveyance, directed treatment and imaging advances. Its helpful applications incorporate enemy of HIV action, hostile to angiogenesis, antimalarial movement, against ligament action and biohydrogen creation. Microbial surfactants can be utilized for elite nanomaterial creation, since they effectively structure an assortment of fluid precious stones in watery arrangements. Analysts balanced out the gold and silver nanoparticles delivered by surfactin. At pH 7 the nanoparticles were uniform in size, while they were anisotropic at pH 5 and 9. Organic combination of gold and silver nanoparticles were additionally completed utilizing the microorganisms *Bacillus subtilis*[1]. Gold nanoparticles were blended both intra- and extracellularly, while silver nanoparticles were solely shaped extracellularly. The nanoparticles were balanced out by surface-dynamic particles, to be specific surfactin or different biomolecules discharged by B. subtilis. Surfactin created by *Bacillus amyloliquefaciens* KSU-109 was likewise utilized for the combination of cadmium sulphide nanoparticles which stayed stable as long as a half year. Purged rhamnolipids from *P. aeruginosa* strain BS-161R were utilized to blend silver nanoparticles showing great anti-

infection movement against both gram +ve and - ve microorganisms. A glycolipid microbial surfactant delivered by *Brevibacterium casei* MSA19 was utilized as a stabilizer for the combination of steady and uniform silver nanoparticles. The production of nanoparticles is either intra or extra cellular.

Biofilm disruption:

Bacteria's possess the ability to adapt to their environment and express themselves accordingly. Some gram +ve and gram +ve bacteria show a unique phenomenon known as Quorum sensing by which they can communicate with each other and sense their own cell density. This ability of bacteria has been involved in formation of biofilms, although it further depends upon the nutritional environment available to bacteria to carry out QS activity. During the biofilm formation and maturation event the cells attached to the surface start to aggregate into microcolonies, which are surrounded by few cells referred to as water channels. Biofilms in food industries act as a prominent source of contamination and disease. Therefore, use of biosurfactants to disrupt the adherence of microbial cells on the surface prevent formation of biofilm on food surface and thus their spoilage is prevented. The use of surfactin and rhamnolipids in particular decreased the adhesion of microbial cells on the polypropylene surfaces.[26] Biosurfactants may also be used in health and hygiene products to prevent biofilm formation in the oral cavity.

Microbial surfactants or biosurfactants possess the ability of anti-adhesion and biofilm degradation. Biofilms produced by many fungi and bacteria are degraded by synthetically derived enzymatic surfactants like lauryl-glucose. *Pseudomonas aeruginosa* derived rhamnolipids, are a class of surfactants which are efficiently used in biofilm disruption. The overproduction of rhamnolipids inhibits biofilm production by blocking cellular aggregation and secondary colonization onto the preformed biofilms. They also disperse cells from biofilms.

The biofilms produced by *Pseudomonas aeruginosa* were allowed to form on the flow cells which acted as a growth chamber for the biofilm. The chamber was supplied with oxygen and nutrients from a medium flask containing 50% TSB using a peristaltic pump. The spent

medium was collected in a waste container. The air bubbles could have disrupted the process of biofilm formation, so they were confined from the tubing using a bubble trapper, and incubated this at 30°C for 48hr. For the analysis of biofilm production in flow conditions, a Bio Flux system having the ability to acquire image from the specialized cells housed within it, was used. To facilitate the growth of biofilms the microfluid channels were primed with 50% TSB, following which they were loaded with 10^7 CFU from an overnight incubated microbial culture of *Pseudomonas aeruginosa*[2]. The cells were allowed to adhere to the plate by allowing an incubation of 48hrs at 30°C. After the formation of biofilm following the incubation period, the planktonic cells were removed and PBS along with different treatments (containing rhamnolipids 0.4 g/L, caprylic acid 0.1 g/L, a combination of rhamnolipid and caprylic acid, SDS 0.8 g/L, a combination of SDS and caprylic acid) were added to the plate for 30 mins. The cells were stained using LIVE/DEAD cells to check the growth of biofilm.

The effects of different treatments were determined on the biofilm produced upon cover slips by observing under a microscope and used fluorescence microscopy to determine the cells attached to the coverslips, which were stained using the bacterial viability kit, which helped the visualisation of microcolonies and individual cells. It was observed that biofilm produced by the bacteria was inhibited in the presence of rhamnolipids as depicted by reduction in the active cell number and appearance of reddish-brown fluorescent cells. Addition of adjuvant like caprylic acid alone had no effect ton biofilm dispersion. Addition of caprylic acid with rhamnolipid had an enhanced effect on biofilm degradation, also this combination is quite effective even at low concentrations.

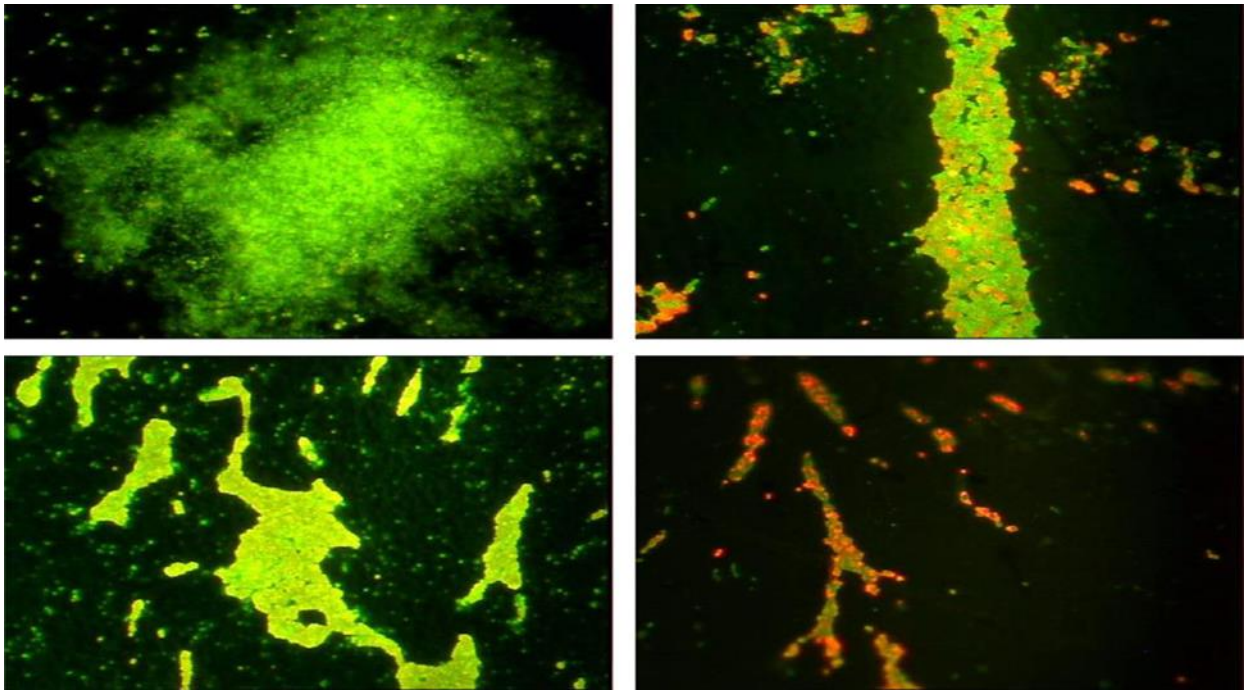

Fig 4: (a) Biofilm formation under Control

(b) Biofilm formation under the presence of rhamnolipid at a concentration of 0.4 g/L

(c) Biofilm formation under the presence of caprylic acid at a concentration of 0.1 g/L

(d) Biofilm formation under the presence of a combination of rhamnolipid (0.4 g/L) and caprylic acid (0.1 g/L).

To determine the effects of different treatments on biofilm disruption upon flow cells, rhamnolipids and caprylic acid were used. The cells were stained using the LIVE/DEAD bacterial viability kit and observed under confocal microscope. The biofilm was allowed to grow for about 2 days in the continuous flow mode. After about 30 minutes of treatment with rhamnolipid along with caprylic acid, the biofilm showed remarkable disintegration at its most important position. It was assumed to be due to the synergistic effect of rhamnolipid and caprylic acid.

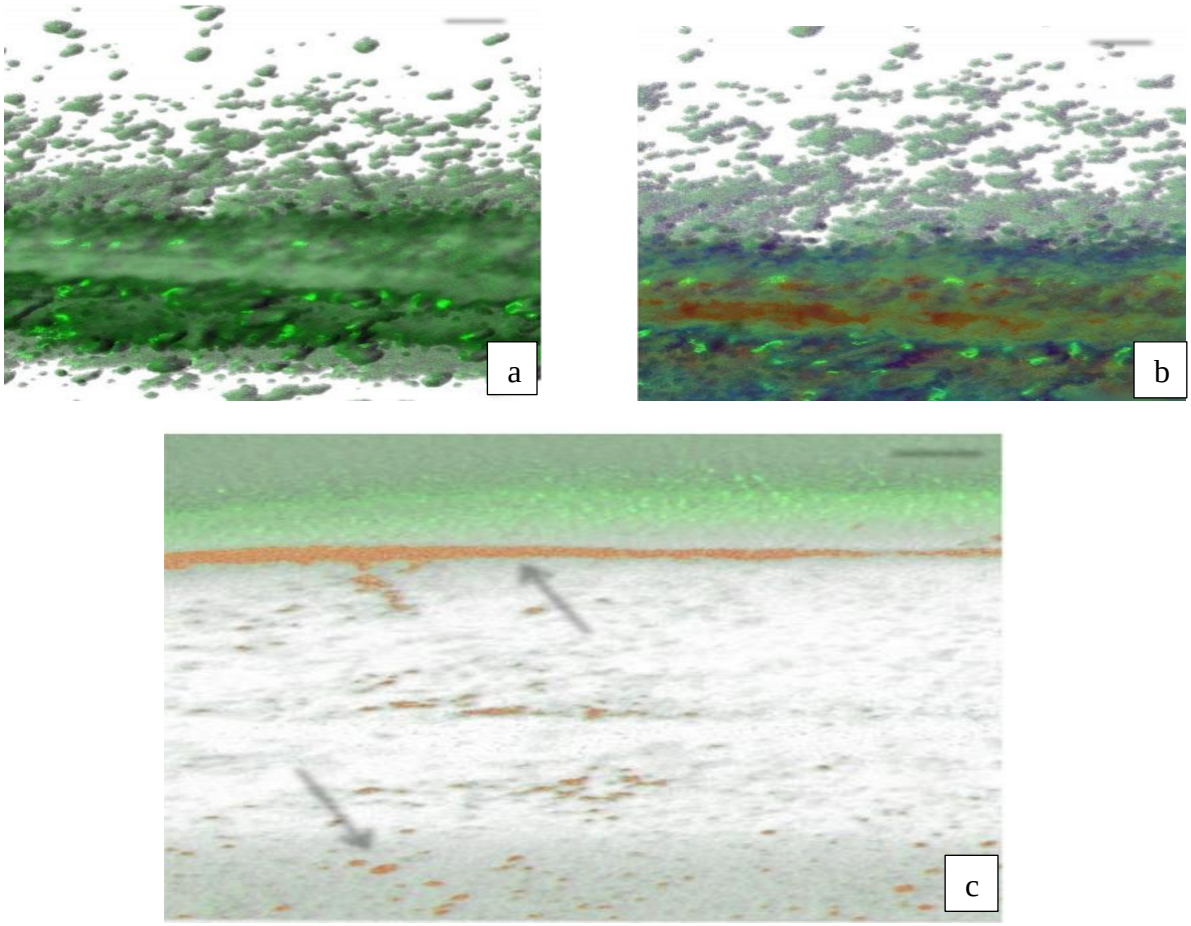

Fig 5: (a) Depicts the effect of rhamnolipid on cell viability.
(b) Depicts a significant effect due to rhamnolipid and caprylic acid treatment
(c) Depicts the compromised portion of biofilm where the cells are disrupted.

Biofilms are heterogenous structures displaying a high degree of resistance to antibiotics and biocidal compounds. Rhamnolipids have been associated to enhance the transport of bacteria through columns due to steric hinderance due to the contact between the surface and the bacteria. Rhamnolipids had been tested with various strains, media, etc. but they always tend to disrupt cell to cell adherence and biofilm disruption. The increased efficiency of biofilm disruption when rhamnolipid is used in combination with caprylic acid maybe due to synergistic effect. The rhamnolipids seem to removes the extracellular polymeric substances and microcolonies thus altering the biofilm environment and making cells more sensitive to intervention of caprylic acid which traverse through the cell membrane and causing cell death. The dispersal of biofilm may also occur due to the mechanical breakage of biofilms due to shear forces. SDS the anionic surfactant exhibits bactericidal activity against majority of oral

bacteria by penetrating the cell membrane and lysing the cell. Since SDS at a concentration greater than CMC causes protein unfolding, suggesting that SDS mediated disruption of the biofilm is due to denaturation of proteinaceous adhesions of the matrix. SDS when combined with caprylic acid had no effect. This was due to the shielding effect of caprylic acid thus protecting the cell membrane from the action of SDS, and therefore SDS is unable to disrupt the biofilm. Therefore, Rhamnolipids were proven to be the efficient antimicrobial agents in the presence of caprylic acid at a pH 5, as they induce cell death and lead to disruption of biofilms, even at low concentrations as compared to that of conventional methods.[24]

As anti-oxidants:

Mannosylerythritol lipids are versatile biosurfactants having interfacial and biochemical properties. MEL-C possesses free radical ion scavenging activity and have the highest antioxidant activity thus serves the highest protection, and are actively used in skin care cosmetics manufacturing. Similar activity is shown by RW1 a biosurfactant derived from *Bacillus subtilis,* proving a natural alternative to antioxidants.

As anti-adhesives:

Numerous biosurfactants display antimicrobial properties, as well as antiadhesive properties. Rhamnolipids and surfactin were shown to possess antiadhesive properties against *Listeria monocytogenes*, *Staphylococcus aureus* on polystyrene surfaces. Similar antiadhesive activity was shown by Lunasan produced by *Candida sphaerica* against many strains of *Streptococcus*, *Staphylococcus*, and *Candida* on plastic tissues.[25] These properties of biosurfactants serve their use as coating agents or in cooking utensils to reduce fouling, also in dairy industries. They are also being utilized as probiotics like *Lactobacillus acidophilus* strain.[20]

In food industries:

In a quest to find natural sources for obtaining biosurfactants rather than those obtained from genetically modified plants, many natural resources are being explored, mostly microbial sources as they are inexhaustible. An emulsion is a heterogenous system which has at-least one immiscible liquid dispersed in another one in the form of droplets. Their stability can be enhanced by using surfactants. Emulsification imparts, texture, consistency and dispersion patterns to food products. An emulsifier stabilized the emulsion by managing the clustering of globules.[14]

Additives are compounds having no nutritional value, but are added to modify, physical, chemical and biological properties during manufacturing, packaging and transport. Additives provide properties like thickening gelling, stabilizing and emulsifying. Glyceryl monostearate, a synthetic additive is widely used in food industries.[3]

Emulsifiers are generally surface-active agents which aid in emulsion formation due to their ability to reduce interfacial tension and stabilize the emulsion. Low molecular weight amphiphiles are used here to provide stability to various food products as beverages, dressings, sauces etc. Emulsifiers such and lecithin and gum Arabic derived from plants are being used as emulsifiers but they suffer some issues as functional limitations like use of microwaves. Lecithin is employed for production of cocoa powders which are a common ingredient for many desserts. Many of the modern-day food products like mayonnaise, butter, cream, salad dressings are produced using emulsions. Therefore, natural resources are being explored to produce bio-emulsifiers, e.g. one from *candida utilis.* Manno-proteins produced via *Saccharomyces cerevisiae* stabilizes water oil emulsion and is used to produce mayonnaise, butters etc. Most of the biosurfactants produced from yeasts and bacteria are operational at wide range of pH and temperature and are therefore used instead of conventional emulsifiers. Microbial surfactants are also used to provide texture, improve shelf life, and modify rheological properties of dough. In ice cream formulations they enhance texture, delay staling and stabilize fats.

Microbial biosurfactants are also utilized for making cookie formulations. The dough for the cookie was prepared in 3 different ways. Standard had all the normal formulations, while one of the formulations had biosurfactant replacing 50% of the pasteurized egg yolk of the standard formulation, while other formulation saw 100% replacement of pasteurized egg yolk with the biosurfactant, and they were ultimately baked.[10] Physical characteristics of the cookie was characterized after baking. Shape, texture, diameter, thickness, and spread ability were measured. Texture analyser was used to record the texture profile of the cookie dough before baking, while only firmness could be recorded after baking them. The protein content in both the alternative formulations was lower compared to that of standard formulation, since biosurfactant used here was a carboxylic acid derivative from *Candia utilis* and lacked proteins. Since the formulation which replaced egg yolk by 100% had high lipid contents, which happens to be the reason due to which energy formulation of this formulation was high.

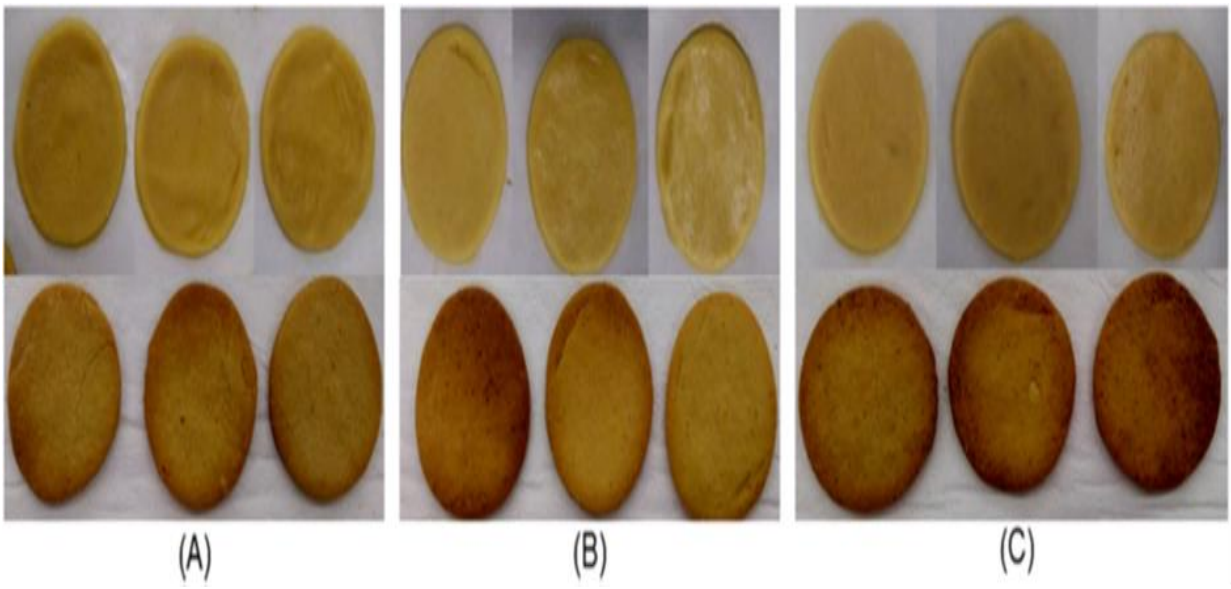

Fig 6: Cookies before and after being baked.

(a) Standard Formulation
(b) Formulation having 50% replaced egg yolk with biosurfactant
(c) Formulation having 100% replaced egg yolk with biosurfactant

Biodegradation:

Surfactants increase the access of the microorganism to low solubility compounds also compounds having recalcitrance, during the biodegradation process. Compounds being less soluble i.e. with high hydrophobicity get bonded strongly to organic matrix and are not desorbed easily to be available for degradation. During the hydrocarbon degradation, low molecular weight hydrocarbons are degraded first leaving recalcitrant compounds. Since surfactants increase the solubility in water and leads to better mass transfer, they are used to enhance biodegradation of hydrocarbons. To facilitate diesel hydrocarbon biodegradation, a suitable biosurfactant is assessed by assessing its physico-chemical properties, its biodegradability and its effect on the rate of biodegradation.[5] For selection purposes, environmental fate and toxicity was assessed by using K_{OC} and EC_{50} using a QSAR model. K_{OC} is defined as the soil organic carbon-water partition coefficient which is the ratio of chemical mass adsorbed on the soil per unit mass of the organic carbon of the soil divided by the equilibrium concentration of chemical in aqueous solution. EC_{50} is the half maximal effective concentration which is that concentration of a toxic compound which induce a response halfway between the maximum and baseline value, and is used to determine toxicity. QSAR is Quantitative structure activity relationship, a process using which the chemical structure of a molecule is correlated with a defined property like biological activity etc. Respirometric analysis was used to assess the biodegradability of the surfactants, using Biochemical oxygen demand apparatus. It was used to calculate the ratio of actual BOD to theoretical BOD. Solid phase respirometric tests were carried out to obtain, biodegradation of surfactants in soil samples.

The mobilities and the residence time of surfactant within the soil is affected by biodegradability, and sorption characteristics. For being efficient in biodegradation the surfactant must be less toxic and persistent, and must not have affinity towards soil, to allow proper distribution into the soil. Non-ionic surfactants are more biodegradable and less toxic as compared to other.

Bioremediation:

The level of relationship between natural and inorganic toxins is represented by the complex physical-concoction communications at interfaces. This relationship includes the sorption of toxins on the soil surface followed by their sequestering into the matrix of the soil, forming a Non-Aqueous Phase liquid (NAPL). NAPL are natural compounds which are insoluble in water thereby acting as a long-term pollutant, they are used in a continuous manner in water phase to replace dissipated concentrations, thereby decreasing the availability of contaminating particles to get biodegraded.[4] Bioremediation is a technique to enhance the degradation of biological compounds to lower the effect of toxins. Bioaugmentation is the practice of adding cultured microbes to facilitate degradation of pollutants, supplemented by using surfactants to facilitate desorption of pollutants lead to enhanced degradation of hydrocarbons. Surfactants are used to recover secondary oil during oil washing, and also in cleaning of oil pipes. Many synthetic and biosurfactants are employed for desorption purposes. Biosurfactants are not majorly used for bioremediation due to their high cost of production, but it may be overcome by using cheaper substrates for the microorganisms producing them like, industrial oil waste and agro-industrial wastes. Some of the major sources of biosurfactant production are *Pseudomonas aeruginosa, Corynebacterium, Nocardia, Bacillus subtilis, Bacillus licheniformis, Candida spp*., etc. The quality and quantity of nitrogen and carbon present in the substrate and the soil greatly determines the kind of biosurfactant produced. Limited nitrogen leads to increased production of biosurfactants aiding in bioremediation, therefore many bioremediation systems are not supplied with nitrogen to increase the microbial activity and lead to increased production of biosurfactants. Biosurfactants may be produced in the presence of oils and hydrocarbons.

Addition of hydrophobic organic substances in the culture media favours the isolation of hydrocarbon degrading bacteria from sites contaminated by oil, and are able to produce biosurfactants.[15] Aliphatic and aromatic hydrocarbons are used as a source of carbon for this purpose. The presence of organic compounds and metallic pollutants in the soil are the major cause of soil pollution. Organic hydrocarbons include Polycyclic aromatic hydrocarbons (PHA), Polychlorinated biphenyls (PCB), out of which PHA are more common due to it being involved in crude oil processing. Transport of pollutants in the soil is a function of non-linear rate limited biodegradation and sorption. Majority of hydrophobic contaminants bind to organic fractions in the soil due to sorption. Compounds like humic (like humic acid, humic)

and nonhumics (like proteins and waxes) are involved in the process of sorption.

The process of degrading pollutants in the soil depends upon physico-chemical and biological interaction of the pollutants and other biological factors. Degradation by means of microbial activity is in turn controlled by many factors like availability of contaminants to the microbes, pH, water, aeration, nutrients, temperature etc. Biodegradation can be enhanced by having a detailed insight of the metabolic activities of the microorganism. Microorganism form a stable oil in water emulsion which leads to increased oil degradation, thereby enhancing the availability of nutrients to the microorganisms. This phenomenon is achieved in natural systems by utilisation of autochthonous surfactant bio-population which lead to production of stable emulsions. Biosurfactants are able to solubilize the natural organic materials sorbed into the soil. Monorhabdolipid acid are utilized to remove NAPL which stays as a residue, while some *Rhodococcus* strains were used to degrade oil from sand etc. Endosulfan present in the soil was degraded by means of biosurfactant produced by *Bacillus subtilis*. Bio emulsifier alasan is used to increase the solubility of PAH, therefore leading to many folds increased in degradation and solubilities.

Soil is cleaned up using various techniques using soil exaction and disposal to landfill, phytoremediation, also plants immobilize the metals preventing their vertical or horizontal movement, thereby reducing the groundwater pollution. Microbes also have the ability to bind and form complex with association with the pollutants, thereby require more efforts and difficulties in degrading pollutants. Therefore, microorganisms can be used to remove heavy metals, by means of alkylation, or sulphur reducing bacteria is also used to remove heavy metals. Synthetic surfactants are toxic to degrading microorganisms therefore microbial surfactants are used for degradation of oil spills. Composting systems are used to increase the oxygen transfer and thereby reduce the pollutants in soil in a time of some months. An efficient way to enhance crude oil degradation in oil polluted environments is the introduction of hydrocarbon-oxidizing bacteria with high oxygenase activity, like Acinetobacter. Many complexes isolated from biosurfactant produced by bacteria, are isolated using methyl tertiary-butyl ether following sonication.

The main reason why the organic and metallic pollutants remain is soil for so long without being degraded is dependent on many factors like, they are not able to degrade them due to it being not available to them, also microorganism might not be able to carry out the essential

catabolic reactions, or inadequate interaction of the pollutants with the environment and the microorganism. Therefore, fungi and bacteria involved in the production of biosurfactants are important as they tend to solubilize the hydrophobic contaminants, facilitating their easy degradation. It was observed by keeping the contaminated sites devoid of Nitrogen, to enhance the activity of microbes degrading the soil pollutants.

Agriculture:

The health and productivity of plant crops are monitored on a regular basis to be sure about the quality of the food being obtained, and its availability to be able to meet the increasing demands of the growing population. Metabolic compounds referred to as green surfactants are produced by actinomycetes, yeast, fungi etc. Epiphytic and endophytic microbes are involved in biosurfactant production and they aid seed germination, inhibit the action of phytopathogens and as biocontrol agents for bioremediation. Since, we are trying to avoid the use of pesticides on plants to obtain chemically free plant products, rhizospheric bacteria are being explored that secrete metabolites which increase the yield of plant product. *Bacillus* and *Pseudomonas* are the majority of bacteria in Rhizobacteria group, which secrete metabolites having versatile applications as plant growth promoters, fungicidal agents like siderophores, phenazines, pyrrol nitrin, cyclic peptides, compounds such as biosurfactants and enzymes like chitinase and glucanase which possess hydrolysing activities.[9] These green compounds have lower critical micellar concentration compared to that of synthetic ones and they lead to higher decrease in surface tension of oil-water or air-water interfaces to a very low value. Rhamnolipids and lipopeptides are the majorly studied biosurfactants, which have found tremendous application in agricultural fields, along with other industries like pharmaceuticals, cosmetics, petrochemicals, food etc. Since they house amphipathic structures, due to which they promote seed germination, reduce the growth of phytopathogens and tend to induce systemic resistance in the plants.

The Rhizosphere portion of many cereals were used like rice, sorghum, millets, legumes like chickpea, groundnut, oil crops like sunflower", castor, grass etc were obtained from different districts were used for isolating the bacteria. They secrete metabolites which tend to promote plant growth and also act as antifungal. This ability was screened testing for Ammonia

production, by incubating bacterial isolates with 10 mL of peptone water for 48 hrs and 28-30°C. After incubation, 1 ml of culture broth was transferred to other tube and mixed with 1 ml of Nessler's reagent. Phosphate solubility was assessed by using Pikovskaya's agar medium having tricalcium phosphate. Phytase activity was assessed using phytic acid medium, following incubation for 2-4 days at 28-30°C temperature. After incubation zone of hydrolysis around the colonies was observed as a sign of confirmation. Isolates of the bacteria were tested for their antifungal activity. A culture of *F. oxysporum f. sp. ricini* was cultured on potato dextrose agar.

$$I\% = \frac{(C - T) \text{ x } 100}{C}$$

Where I= % inhibition of microbial growth

C= Radial growth of fungus recorded in the control plate

T= Radial growth of fungus recorded in the plate having bacteria.

All the bacteria were tested for ammonia production, antifungal activity, ability to solubilize phosphates and the capability to produce Indole Acetic Acid, via various experimental setups described above. The antifungal ability of bacteria against *F. oxysporum f. sp. ricini* was in between 72-80%. 67% of *Pseudomonas sp.* while 58% of *Bacillus sp.* possessed PGP traits.[9]

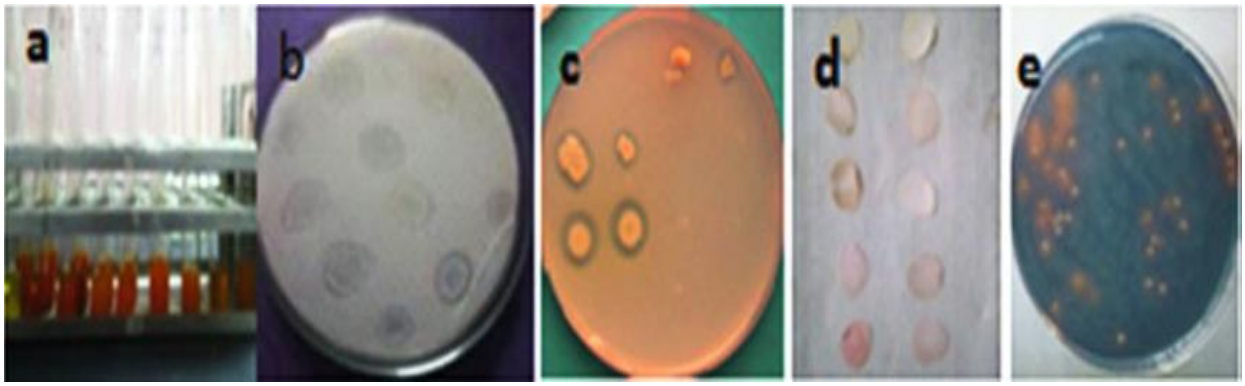

Fig 7: Different PGP traits tested.
(a) Ammonia production
(b) Solubilization of phosphate
(c) Phytase activity
(d) Indole acetic acid production
(e) Production of siderophore

It was observed that crude biosurfactant containing rhamnolipid and iturin, showed fungicidal activity against *F.oxysporum f.sp. ricini.*

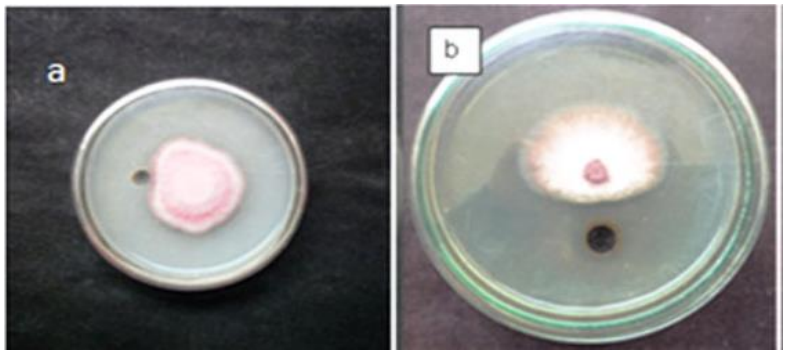

Fig 8: Antifungal activity of the biosurfactant against the chosen fungi.
(a) F.oxysporum f. sp. ricini inhibited by means of lipopeptide
(b) F.oxysporum f. sp. ricini inhibited by means of rhamnolipids

Rhizobacteria have been known to have plant growth promoting activity, alongside which they also depict strong antifungal or fungicidal activities making them a preferable choice as bioinoculants and in agriculture. Crop yield and sustainable agricultural conditions still prevail due to the regular application of chemicals which also pollute the environment. To overcome this shortcoming, bacterial metabolites which are non-toxic, tend to inhibit the growth of fungal pathogens and enhance seed germination are suitable alternatives for chemical compounds.

8. CONCLUSION:

Biosurfactants have certain unique properties like, surface activity, biodegradation, detergency abilities, emulsification and de-emulsification activities, lubrication, wetting ability, foaming, solubilization, dispersion of phase etc. Due to this diversity in properties they are used in a wide array of industries like petrochemical, petroleum, coal, metallurgical and mining industries, dairy, cosmetics, pharmaceuticals, food, agricultural and fertilizer, cosmetics, food and beverages etc. These compounds have been majorly obtained from bacteria and this is well documented, while obtaining these compounds from fungi is also possible, though there is less data on this subject. Many tropical species of plants both in India and Brazil have been used to isolate numerous endophytic microorganisms which produce biosurfactants. They are not used

at industrial scale, since their effect needs to be first determined by an experimental setup in greenhouse conditions and actual field studies, following which it can be stated if they can act as potential alternatives against the chemical agents.

9. FUTURE PERSPECTIVE AND CHALLENGES:

Microbial surfactants are non-ionic at low pH esteems, and anionic at high pH esteems because of the nearness of carboxylic gatherings. The total of surfactants in lamellar courses of action can happen on the off chance that one of the following conditions are watched. High surfactant focuses lead to a lamellar fluid crystalline stage, while twofold followed amphiphiles regularly structure bilayer sheets. After shutting, these sheets structure vesicles. Microbial surfactants can possibly be utilized in the targeted drug delivery. Additionally, pH-delicate liposomes containing rhamnolipids and di-oleoyl-phosphatidyl-ethanolamide have been depicted as effective frameworks for cytoplasmic conveyance of particles into cells. There is a critical need to investigate microbial frameworks to acquire surfactants and use them as effective drug delivery systems. Industries are seeking to find natural alternatives for biosurfactant production, to be utilized at industrial scale. Since currently biosurfactants are economically bit costly to prepare, we need to find ways to decrease the cost of production. Through the application of specialized cost-effective testing and discussion we might find a breakthrough to allow the use of biosurfactant at a large scale.

Since they are costly to produce therefore research found that the bacterial culture (producer of biosurfactant) could be grown using poultry waste flour and buttermilk, waste cassava fry oil, agro-industrial waste etc, thus serving as low cost alternative for producing the biosurfactants. Also, *Piper hispidum* was also identified as a potential alternative source for the isolation of microorganism producing biosurfactants, which can be utilized in various industries. Biosurfactants due to their higher biodegradability, biocompatibility and low toxicity, can be optimized by tweaking fermentation conditions, to obtain biosurfactants at an affordable cost and we might be able to produce them at a large scale.

10. REFERENCES:

1) Rodrigues, Ligia R. "Microbial surfactants: fundamentals and applicability in the formulation of nano-sized drug delivery vectors." *Journal of colloid and interface science* 449 (2015): 304-316.

2) Díaz De Rienzo, M. A., P. S. Stevenson, Roger Marchant, and Ibrahim M. Banat. "Pseudomonas aeruginosa biofilm disruption using microbial surfactants." *Journal of applied microbiology* 120, no. 4 (2016): 868-876.

3) Campos, Jenyffer Medeiros, Tania Lucia Montenegro Stamford, Leonie Asfora Sarubbo, Juliana Moura de Luna, Raquel Diniz Rufino, and Ibrahim M. Banat. "Microbial biosurfactants as additives for food industries." Biotechnology progress 29, no. 5 (2013): 1097-1108.

4) Christofi, N., and I. B. Ivshina. "Microbial surfactants and their use in field studies of soil remediation." *Journal of Applied Microbiology* 93, no. 6 (2002): 915-929.

5) Franzetti, A., P. Di Gennaro, G. Bestetti, M. Lasagni, D. Pitea, and E. Collina. "Selection of surfactants for enhancing diesel hydrocarbons-contaminated media bioremediation." *Journal of hazardous materials* 152, no. 3 (2008): 1309-1316.

6) Parra, J. L., J. Guinea, M. A. Manresa, M. Robert, M. E. Mercade, F. Comelles, and M. P. Bosch. "Chemical characterization and physicochemical behavior of biosurfactants." *Journal of the American Oil Chemists Society* 66, no. 1 (1989): 141-145.

7) Zouari, Raida, Semia Ellouze-Chaabouni, and Dhouha Ghribi. "USE OF BUTTER MILK AND POULTRY-TRANSFORMING WASTES FOR ENHANCED PRODUCTION OF Bacillus subtilis SPB1 BIOSURFACTANT IN SUBMERGED FERMENTATION." *Journal of Microbiology, Biotechnology and Food Sciences* 2019 (2019): 462-466.

8) Silva, M. E. T., Sergio Duvoisin Jr, R. L. Oliveira, E. F. Banhos, A. Q. L. Souza, and Patrícia Melchionna Albuquerque. "Biosurfactant production of Piper hispidum endophytic fungi." *Journal of Applied Microbiology* (2019).

9) Bee, Hameeda, Mohamed Yahya Khan, and R. Z. Sayyed. "Microbial Surfactants and Their Significance in Agriculture." In *Plant growth promoting rhizobacteria (PGPR): prospects for sustainable agriculture*, pp. 205-215. Springer, Singapore, 2019.

10) Ribeiro, Beatriz Galdino, Bruno Oliveira de Veras, Jaciana dos Santos Aguiar, Jenyffer Medeiros Campos Guerra, and Leonie Asfora Sarubbo. "Biosurfactant produced by Candida utilis UFPEDA1009 with potential application in cookie formulation." *Electronic Journal of Biotechnology* (2020).

11) Jahan et. al. 'Biosurfactants, natural alternatives to synthetic surfactants: Physicochemical properties and applications.' Advances in Colloid and Interface Science, Volume 275, January 2020, 102061.

12) Madihalli, Chandraprasad, Harshal Sudhakar, and Mukesh Doble. "Production and investigation of the physico-chemical properties of MEL-A from glycerol and coconut water." World Journal of Microbiology and Biotechnology 36 (2020): 1-11.

13) Sadeghi et. al. 'Design and physicochemical characterization of lysozyme loaded Niosomal formulations as a new drug delivery system.' Pharmaceutical Chemistry Journal, Vol. 53, No. 10, January, 2020 (Russian Original Vol. 53, No. 10, October, 2019).

14) Choudhury, Samrat Roy, Amrita Mandal, Dipankar Chakravorty, Madhuban Gopal, and Arunava Goswami. "Evaluation of physicochemical properties, and antimicrobial efficacy of monoclinic sulfur-nanocolloid." Journal of nanoparticle research 15, no. 4 (2013): 1491.

15) Jain et. al. 'Physicochemical characterization of biosurfactant and its potential to remove oil from soil and cotton cloth.' Discipline of Marine Biotechnology and Ecology, CSIR – Central Salt and Marine Chemicals Research Institute (CSIR – CSMCRI).

16) Baferani, A. Hasani, R. Keshavarz, M. Asadi, and A. R. Ohadi. "Effects of Silicone Surfactant on the Properties of Open-Cell Flexible Polyurethane Foams." Advances in Polymer Technology 37, no. 1 (2018): 71-83.

17) Chen, Yu-Fen, Chao-Hsun Yang, Ming-Shiang Chang, Yong-Ping Ciou, and Yu-Chun Huang. "Foam properties and detergent abilities of the saponins from Camellia oleifera." International Journal of Molecular Sciences 11, no. 11 (2010): 4417-4425.

18) Ohadi, Mandana, Arash Shahravan, Negar Dehghannoudeh, Touba Eslaminejad, Ibrahim M. Banat, and Gholamreza Dehghannoudeh. "Potential use of microbial surfactant in microemulsion drug delivery system: a systematic review." Drug Design, Development and Therapy 14 (2020): 541.

19) Benincasa, M., A. Abalos, I. Oliveira, and A. Manresa. "Chemical structure, surface properties and biological activities of the biosurfactant produced by Pseudomonas aeruginosa LBI from soapstock." Antonie Van Leeuwenhoek 85, no. 1 (2004): 1-8.

20) Rodrigues, Lígia, Ibrahim M. Banat, José Teixeira, and Rosario Oliveira. "Biosurfactants: potential applications in medicine." Journal of Antimicrobial Chemotherapy 57, no. 4 (2006): 609-618.

21) Parra, J. L., J. Guinea, M. A. Manresa, M. Robert, M. E. Mercade, F. Comelles, and M. P. Bosch. "Chemical characterization and physicochemical behavior of biosurfactants." Journal of the American Oil Chemists Society 66, no. 1 (1989).

22) Fu, Xiaowei, Fengqin Feng, and Bin Huang. "Physicochemical characterization and evaluation of a microemulsion system for antimicrobial activity of glycerol monolaurate." International journal of pharmaceutics 321.

23) Feng, Chao-Hui, Juan Francisco García Martín, Cheng Li, Bao-Lin Liu, Xiao-Yan Song, Qing-Li Dong, Wei Wang, and Yong Yang. "Evaluation of physicochemical properties and microbial attributes of cooked sausages stuffed in casing modified by surfactants and lactic acid after immersion vacuum cooling and long-term storage." International Journal of Food Science & Technology 51, no. 10 (2016).

24) Lorite, Gabriela S., João M. Rocha, Noora Miilumäki, Paula Saavalainen, Tuula Selkälä, Gabriel Morales-Cid, M. P. Gonçalves, Eva Pongrácz, Cristina MR Rocha, and Geza Toth. "Evaluation of physicochemical/microbial properties and licycle assessment (LCA) of PLA-based nanocomposite active packaging."

25) Pornsunthorntawee, Orathai, Panya Wongpanit, Sumaeth Chavadej, Masahiko Abe, and Ratana Rujiravanit. "Structural and physicochemical characterization of crude biosurfactant produced by Pseudomonas aeruginosa SP4 isolated from petroleum-contaminated soil." Bioresource technology 99.

26) Huang, Hui, Qisheng Yu, Hongqiang Ren, Jinju Geng, Ke Xu, Yan Zhang, and Lili Ding. "Towards physicochemical and biological effects on detachment and activity recovery of aging biofilm by enzyme and surfactant treatments." Bioresource technology 247 (2018): 319-326.

27) Raza, Zulfiqar A., Muhammad S. Khan, and Zafar M. Khalid. "Physicochemical and surface-active properties of biosurfactant produced using molasses by a Pseudomonas aeruginosa mutant." Journal of Environmental Science and Health Part A 42.

28) Rodrigues, Lígia R., José A. Teixeira, Henny C. van der Mei, and Rosário Oliveira. "Physicochemical and functional characterization of a biosurfactant produced by Lactococcus lactis 53." Colloids and Surfaces B: Biointerfaces 49, no. 1 (2006).

29) Saini, Harvinder S., Blanca E. Barragán-Huerta, Ariel Lebrón-Paler, Jeanne E. Pemberton, Refugio R. Vázquez, Anna M. Burns, Marilyn T. Marron, Chistopher J. Seliga, AA Leslie Gunatilaka, and Raina M. Maier. "Efficient purification of the biosurfactant viscosin from Pseudomonas libanensis strain M9-3 and its physicochemical and biological properties." Journal of natural products 71, no. 6 (2008).

30) Yuan, X. Z., Y. T. Meng, G. M. Zeng, Y. Y. Fang, and J. G. Shi. "Evaluation of tea-derived biosurfactant on removing heavy metal ions from dilute wastewater by ion flotation." Colloids and Surfaces A: Physicochemical and Engineering Aspects 317, no. 1-3 (2008).

IMMOBLISATION OF ENZYMES ONTO THE NANOPARTICLES AND THEIR CHARACTERIZATION TECHNIQUES

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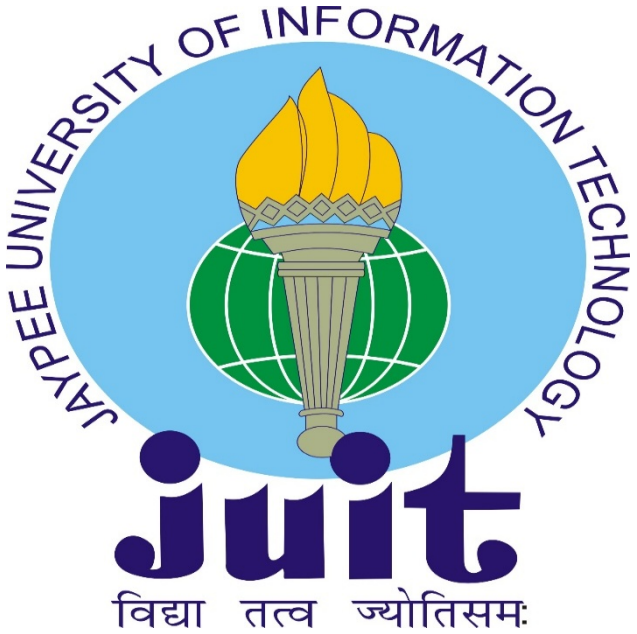

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INTRODUCTION

Immobilization is a technique by which we can fix an enzyme, cell or microbe to a surface and use it for various applications. This increases enzyme activity and stability, it gives better separation from the product and easy and continuous operation of the reaction. For an enzyme to be immobilized, it is attached to an insoluble and inert material like calcium alginate. An immobilized enzyme is resistant to environmental changes like pH and temperature. This enzyme is immobile and thus can be easily separated from the products and can be used again.

It can be done by various techniques like adsorption, adhesion, covalent binding, cross-linking, encapsulation and inclusion. Every technique has it's own advantages and disadvantages and are thus used for different operations.

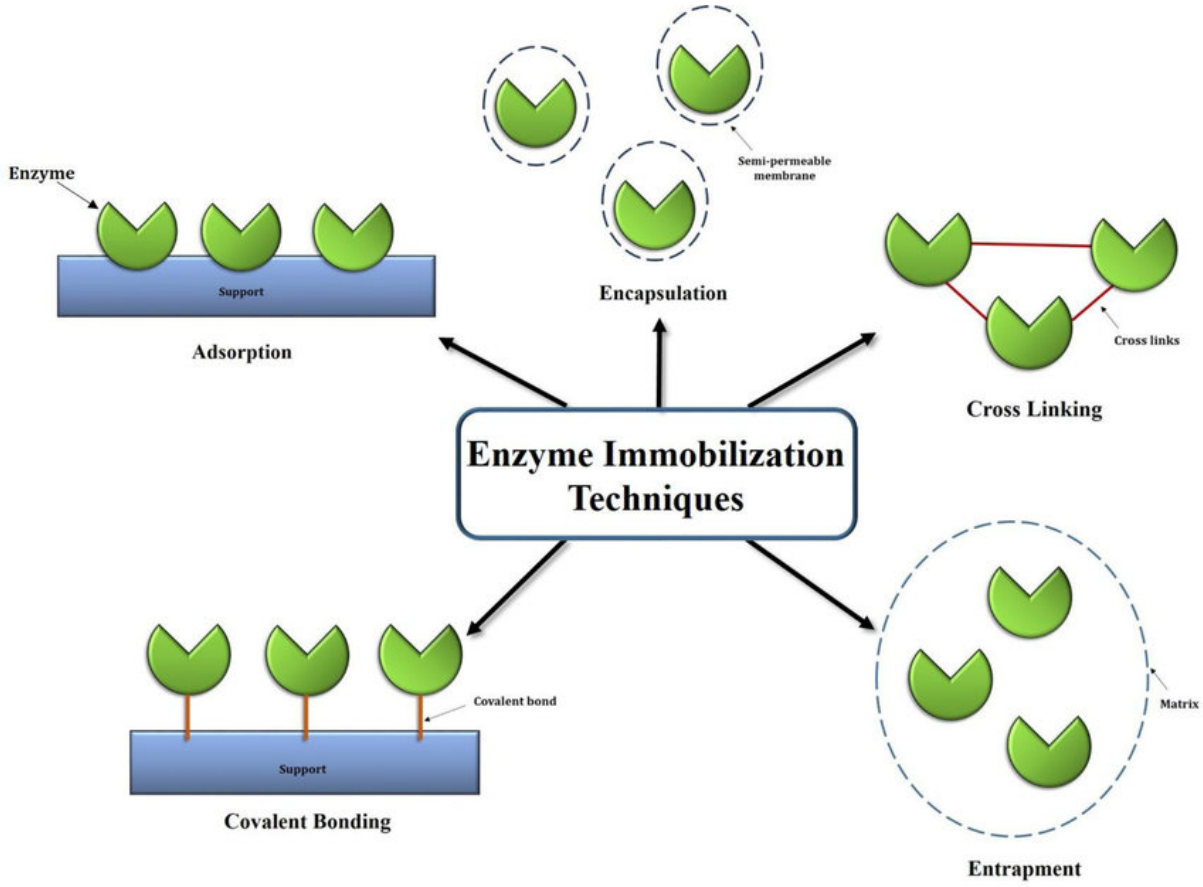


Figure : This figure represents enzyme immobilisation techniques.

Methods of immobilization

- **Physical adsorption mode-** Binding of the enzyme to the matrix is mainly by hydrogen bonding, Van der Waal's forces and multiple salt linkages. It is simple and cheap as it is merely a surface binding phenomena and causes little or no change in the conformation of the enzyme. It also has disadvantages because of its weak binding force between the enzyme and matrix or the enzyme and carrier and it may thus cause leakage of the enzyme. The binding is non-specific and the separation of enzyme from product is difficult which can result in desorption. For example: production of vinegar by adsorption of *Acetobacter sp.* on wood chips. Beer manufacturing is done by adsorption of *Saccharomyces cerevisiae* on polystyrene carrier coated with DEAE-cellulose.
- **Ionic bonding-** It is the electrostatic interaction between the opposite charges of enzyme and matrix or water-insoluble carriers. For example: synthetic polymers and polysaccharides are usually used as carriers.
- **Covalent bonding-** Binding between the enzyme and water-insoluble carriers by sharing of electron pairs between atoms. Amino group, carboxyl group, hydroxyl group, imidazole group, phenolic group, thiol group, indole group etc. are used as functional groups taking part in this interaction. This type of interaction is strong due to the presence of solution or substrate of high ionic strength and thus, do not cause leakage of enzyme. The high ionic strength causes change in conformational structure and active site of the enzyme which causes a major loss of activity.
- **Cross-linking-** Immobilization is done by inter-molecular cross-linking between protein molecules or between protein molecules and functional groups on a water-insoluble matrix. Glutaraldehyde is the most common reagent used in cross-linking.
- **Entrapping enzymes-** We use different polymerizing agents like polyvinyl alcohol or polystyrene to create a water-insoluble lattice. Lattice-type entrapment involves entrapping enzymes within the interstitial spaces, the enzyme does not bind to the gel-matrix or membrane itself.

Microcapsule entrapping involves enclosing the enzymes within semi-permeable polymer membranes using polymerizing agents like starch.

Usage of heterogeneous biocatalysts:

- The biocatalysts can really increase the speed of a biochemical reaction. Biocatalysts are used in the production of chemicals at a industrial scale.
- Heterogeneous biocatalysts basically involves enzyme dissolved in solid for or water insoluble form
- We generally prefer the heterogeneous biocatalysis in industries because the recycling of the enzymes will become less difficult if it is insoluble and it also supports continuous processing activity.
- So, the idea is to immobilize the initial soluble enzyme onto the support surface.
- Selection of the support material is also critical, as the support provides resistance against the conditions like pH and temperature. The support surface also proves a large internal surface area which is chemically suitable to the enzyme.
- The specific activity of the heterogeneous biocatalysts should be very high for its economical and practical use.

Parameters to consider while immobilising enzymes:

- The support material provides high internal surface area and maximizes the specific activity of the enzymes.
- Interactions between the support surface and the enzymes is also critical.

Immobilization efficiency: Immobilization efficiency is the protein binding capacity of a particular matrix/support that you are using. The percent of the total protein bound onto the matrix indicate its immobilization efficiency.

Immobilization yield: Immobilization yield represents the total enzyme we use for immobilization vs the enzyme we finally receive in the carrier.

BET analysis : BET analysis tries to explain the physical adsorption of gas molecules on a solid surface and it can used to calculate the specific surface area of materials. It explains about multilayer adsorption and utilizes gases which do not react chemically with the surface material, Nitrogen is commonly employed gaseous adsorbate.

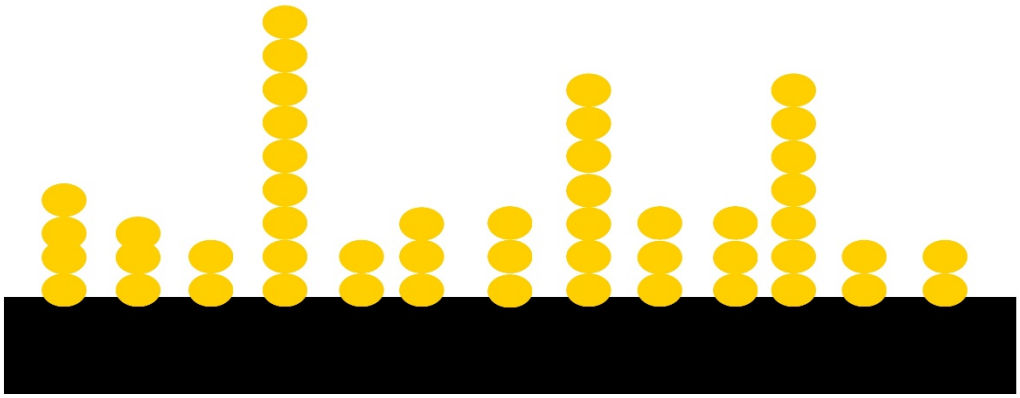


Figure: This figure represents BET analysis technique

- The gaseous molecules start to get adsorbed in the surface infinitely
- The molecules of gas interacts only with adjacent layers
- The enthalpy of the adsorption for the first layer is constant and will always be greater than the second layer

Working of BET:

The samples are degased in a vacuum at high temperatures, the samples are placed in the glass cells and then are analysed by the BET machine then, the cells are placed into heating mantles and lastly connected to the output port. After that the liquid nitrogen is employed which is used to cool the cells or the samples and by doing that , a low temperature is maintained . This ensures adsorption to occur. The nitrogen gas is injected into the sample,on the other hand Helium gad used to run as a blank as helium does not adsorb onto the particles

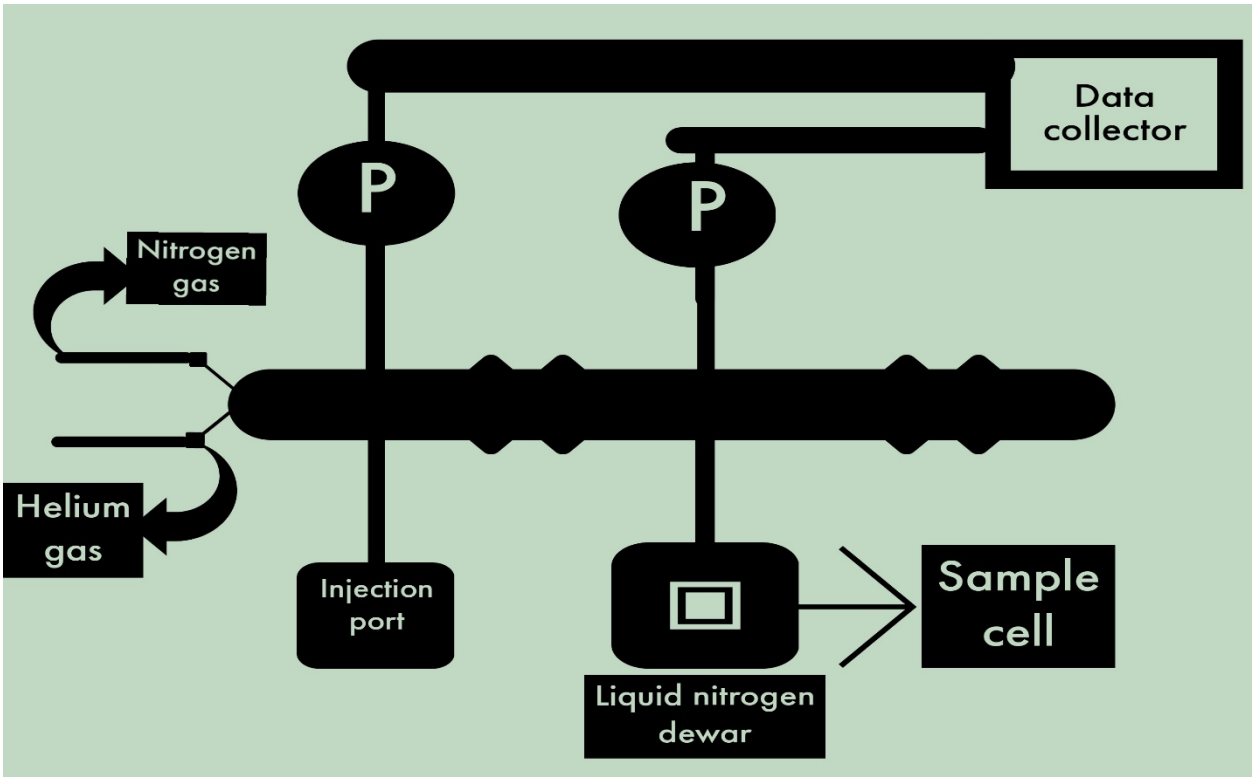


Figure : This figure represents the instrumentation model of BET

Multi-point Bet : At relative pressures higher than 0.5, there is the onset of capillary condensation, and at relative pressures that are too low, only monolayer formation is occurring. When the BET equation is plotted, the graph should be of linear with a positive slope. If such a graph is not obtained, then the BET method was insufficient in obtaining the surface area.

The BET procedure has a few drawbacks when contrasted with NMR, which can likewise be utilized to quantify the surface region of nanoparticles. Wager estimations must be utilized to decide the surface territory of dry powders. This method requires a ton of time for the adsorption of gas particles to happen. A great deal of manual readiness is required.

Protein loading or nanoparticles used as a drug delivery carriers:

Basically, nanoparticles are solid colloidal particles which lie in a size range of 10nm to 1000nm. Nanoparticles can be designed as delivery systems to control surface properties and

extraction of pharmaceutical active compounds. This mechanism is advantageous as the particle size, shape, surface charge can be controlled and these drug delivery systems can deliver drugs of therapeutic and diagnostic agents.

Nanoparticles can be derived from the following:

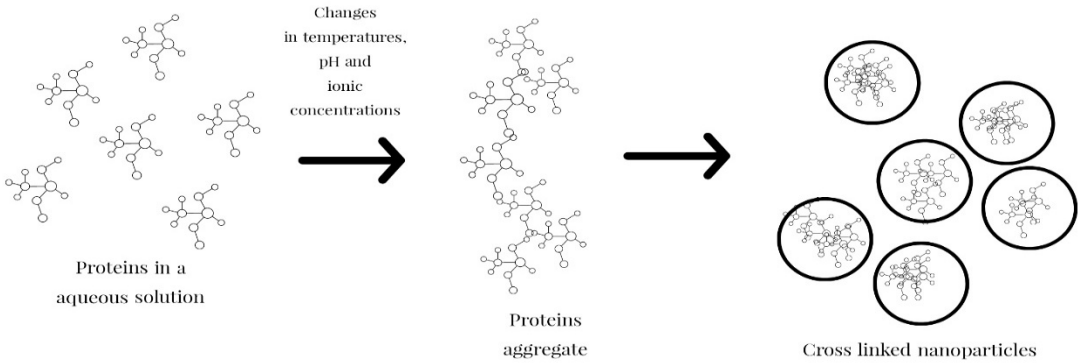
1. Albumin : Albumin is derived from many sources such as Bovin serum albumin (BSA) and Human serum albumin (HSA). It is used in the body to maintain osmotic pressure. Albumin can serve as a transporter protein and also Albumin has a high solubility. It is also very stable and intact at ph 4-9. Albumin nanoparticles are widely used as they are easy to make and also are biodegradable.
2. Gelatin : Also used for the production of nanoparticles. This is obtained from the hydrolysis of collagen. Two different types of gelatin A and Bcan be prepared by acid or base hydrolysis. Gelatin A has a PI of 7-9 while Gelatin B has a PI of 4-5. Just like albumin, gelatin is also biodegradable. It is also non toxic and can be modified chemically. It has advantages like being inexpensive and having very low antigenicity which makes it suitable for the effective drug delivery mechanisms.
3. Milk proteins : Two milk proteins Beta lactoglobulin (BLG) and casein have been identified to have an effective role in drug delivery systems. BLG has a ability to preserve its native confirmation at acidic pH which makes it suitable for drug delivery. On the other hand casein has hydrophilic and hydrophobic regions which favour its confirmational changes in solutions. Surfaces coated with k – casein can bear any heat or mechanical treatments. And many other substances like whey proteins, soy Proteins, Zein etc.

PREPARATION OF PROTEIN NANOPARTICLES:

Readiness of protein nanoparticles depends on adjusting the appealing and terrible powers in the protein. It is by and large acknowledged that expanding protein unfurling and diminishing intramolecular hydrophobic interactions are critical to the development of protein nanoparticles. During such molecule development, the protein experiences conformational changes contingent upon its structure, focus, crosslinking, what's more, arrangement conditions, for example, pH, ionic quality, and sort of dissolvable. For the most part, surfactants are required to balance out the nanoparticles of water-insoluble proteins, for

example, gliadin. Unfurling of proteins during the readiness procedure uncovered intelligent gatherings, for example, disulfides and thiols. Ensuing warm or concoction crosslinking prompts the development of cross-connected nanoparticles with ensnared medicate particles. Coacervation/desolvation and emulsion-based techniques are most usually utilized for the planning of protein nanoparticles.

Figure : This figure represents preparation of nanoparticles



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suitable carrier for targeted drugs . paclitaxel drug is mixed with Human serum albumin or HSA and then that mixture is passed through very high pressure homogenizer to form drug based albumin nanoparticles. Further to promote this drug targeting ability the nanoparticles are chemically modified so that they recognise specific cells and tissues.

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The utilization of a compound related to an amperometric cathode gives an adaptable technique for the advancement of a wide scope of biosensors. The methodology joins the particularity of the protein for its normal substrate with the focal points of electrochemical identification. Various cathodes of this sort are accessible. These can work in one of three different ways: the terminal can basically distinguish an item (or reactant) in the common enzymatic response, a homogeneous go between might be utilized , or the protein may respond at the terminal itself . For various applications especially for in vivo investigations, it is beneficial to have the option to make little terminals. A promising way to deal with this issue is to utilize an electrochemical strategy for the immobilization of the compound. This has the potential preferences that the measure of compound immobilized is promptly controlled, that its spatial conveyance is very much characterized, that multilayer structures can be created, and that the technique is anything but difficult to complete. Lowe et al., had portrayed work on the immobilization of glucose oxidase in electrochem-ically developed films of polypyrrole.

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diameters less than 10 nm we see a general decrease in protein loading as the enzymes find physical restrictions in accessing the high surface offered in this pore diameter range. At pore sizes greater than 100 nm, protein loading generally decreases due to a concomitant reduction in available surface area. In the pore range of 10–100 nm there it is expected to see a decrease in protein loading level with increasing pore diameter. In fact protein loading in this range remains largely constant, suggesting some degree of protein–protein interaction blocking pores and restricting access to the increasing surface area available at decreasing pore diameters.

References

1. Sirisha, V. L., Ankita Jain, and Amita Jain. "Enzyme immobilization: an overview on methods, support material, and applications of immobilized enzymes." In *Advances in food and nutrition research*, vol. 79, pp. 179-211. Academic Press, 2016.
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3. Hwang, Nina, and Andrew R. Barron. "BET surface area analysis of nanoparticles." *The Connexions project* (2011): 1-11.
4. Lohcharoenkal, Warangkana, Liying Wang, Yi Charlie Chen, and Yon Rojanasakul. "Protein nanoparticles as drug delivery carriers for cancer therapy." *BioMed research international* 2014 (2014).
5. Sharifi, Majid, Mohammad Javad Sohrabi, Sara Haji Hosseinali, Anwarul Hasan, Pegah Hashemi Kani, Amir Jouya Talaei, Abdulkarim Yasin Karim et al. "Enzyme immobilization onto the nanomaterials: application in enzyme stability and prodrug-activated cancer therapy." *International Journal of Biological Macromolecules* 143 (2020): 665-676
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7. Li, Chunfang, Shuhui Jiang, Xinying Zhao, and Hao Liang. "Co-immobilization of enzymes and magnetic nanoparticles by metal-nucleotide hydrogelnanofibers for improving stability and recycling." *Molecules* 22, no. 1 (2017): 179.
8. Sheldon, R. A. "Cross-linked enzyme aggregates (CLEA® s): stable and recyclable biocatalysts." *Biochemical Society Transactions* 35, no. 6 (2007): 1583-1587.
9. Kumar, Ashok, In-Won Kim, Sanjay KS Patel, and Jung-Kul Lee. "Synthesis of protein-inorganic nanohybrids with improved catalytic properties using Co 3 (PO 4) 2." *Indian journal of microbiology* 58, no. 1 (2018): 100-104.
10. Freag, May S., and Ahmed O. Elzoghby. "Protein-inorganic nanohybrids: a potential symbiosis in tissue engineering." *Current Drug Targets* 19, no. 16 (2018): 1897-1904.
11. Bartlett PN, Whitaker RG. Electrochemical immobilisation of enzymes: Part I. Theory. Journal of electroanalytical chemistry and interfacial electrochemistry. 1987 Jun 10;224(1-2):27-35.
12. NC. Foulds and C.R. Lowe, J. Chem. Sot., Faraday Trans. 1, 82 (1986) 1259.
13. https://pubs.rsc.org/en/content/articlelanding/2013/cs/c3cs60270b
14. https://www.youtube.com/watch?v=oVJ2LJxO6tU&t=1027s
15. https://www.youtube.com/watch?v=-dh8goOimPk
16. https://www.youtube.com/watch?v=CSDnJvTufDI
17. https://www.youtube.com/watch?v=h1Q-_sL_2kA
18. https://www.youtube.com/watch?v=oiTVJ91-YxQ
19. https://www.youtube.com/watch?v=M8o5ymKyu2U
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IMMOBLISATION OF ENZYMES ONTO THE NANOPARTICLES AND THEIR CHARACTERIZATION TECHNIQUES

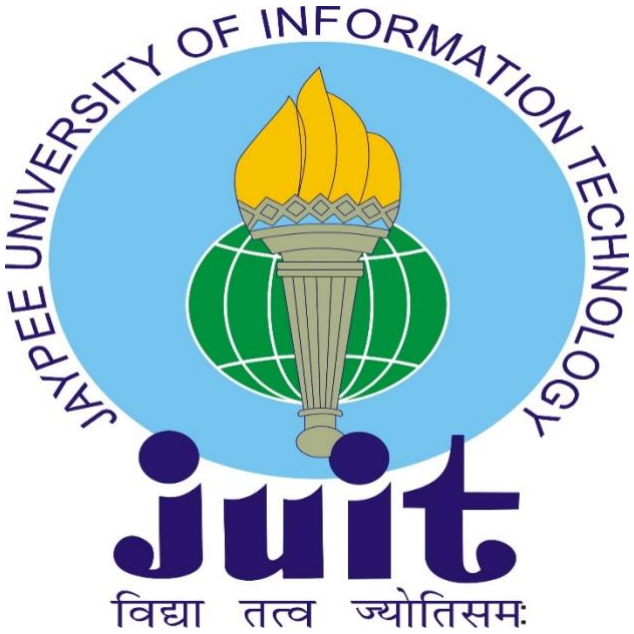
Report submitted by :

Reva Bhardwaj (171809)

Divyansh Rana (171810)

Under the supervision of :

Dr. Ashok Kumar Nadda



JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY DEPARTMENT OF BIOTECHNOLOGY & BIOINFORMATICS WAKNAGHAT, H.P.-173234

INTRODUCTION

Immobilization is a technique by which we can fix an enzyme, cell or microbe to a surface and use it for various applications. This increases enzyme activity and stability, it gives better separation from the product and easy and continuous operation of the reaction. For an enzyme to be immobilized, it is attached to an insoluble and inert material like calcium alginate. An immobilized enzyme is resistant to environmental changes like pH and temperature. This enzyme is immobile and thus can be easily separated from the products and can be used again.

It can be done by various techniques like adsorption, adhesion, covalent binding, cross-linking, encapsulation and inclusion. Every technique has it's own advantages and disadvantages and are thus used for different operations.

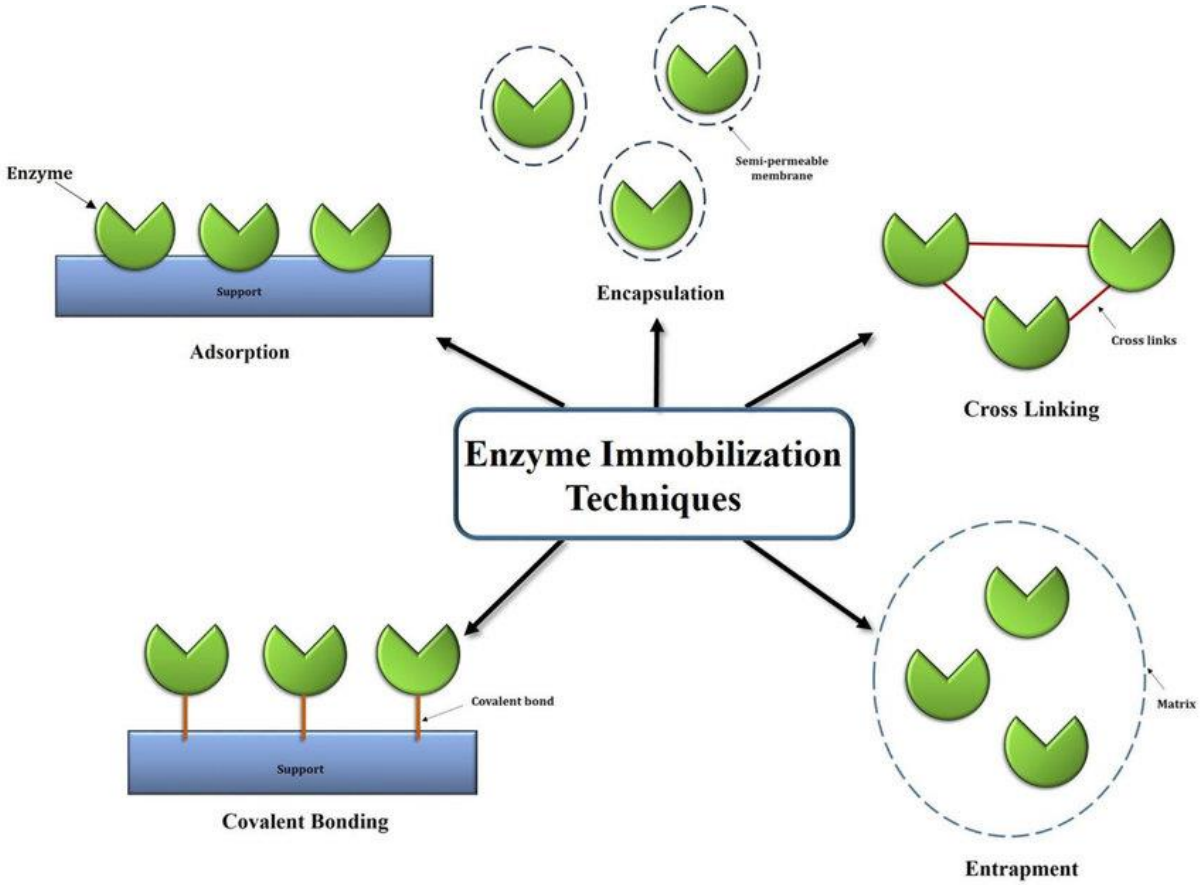


Figure : This figure represents enzyme immobilisation techniques.

Methods of immobilization

- **Physical adsorption mode-** Binding of the enzyme to the matrix is mainly by hydrogen bonding, Van der Waal's forces and multiple salt linkages. It is simple and cheap as it is merely a surface binding phenomena and causes little or no change in the conformation of the enzyme. It also has disadvantages because of its weak binding force between the enzyme and matrix or the enzyme and carrier and it may thus cause leakage of the enzyme. The binding is non-specific and the separation of enzyme from product is difficult which can result in desorption. For example: production of vinegar by adsorption of *Acetobacter sp.* on wood chips. Beer manufacturing is done by adsorption of *Saccharomyces cerevisiae* on polystyrene carrier coated with DEAE-cellulose.
- **Ionic bonding-** It is the electrostatic interaction between the opposite charges of enzyme and matrix or water-insoluble carriers. For example: synthetic polymers and polysaccharides are usually used as carriers.
- **Covalent bonding-** Binding between the enzyme and water-insoluble carriers by sharing of electron pairs between atoms. Amino group, carboxyl group, hydroxyl group, imidazole group, phenolic group, thiol group, indole group etc. are used as functional groups taking part in this interaction. This type of interaction is strong due to the presence of solution or substrate of high ionic strength and thus, do not cause leakage of enzyme. The high ionic strength causes change in conformational structure and active site of the enzyme which causes a major loss of activity.
- **Cross-linking-** Immobilization is done by inter-molecular cross-linking between protein molecules or between protein molecules and functional groups on a water-insoluble matrix. Glutaraldehyde is the most common reagent used in cross-linking.
- **Entrapping enzymes-** We use different polymerizing agents like polyvinyl alcohol or polystyrene to create a water-insoluble lattice. Lattice-type entrapment involves

entrapping enzymes within the interstitial spaces, the enzyme does not bind to the gel-matrix or membrane itself.

Microcapsule entrapping involves enclosing the enzymes within semi-permeable polymer membranes using polymerizing agents like starch.

Usage of heterogeneous biocatalysts:

- The biocatalysts can really increase the speed of a biochemical reaction. Biocatalysts are used in the production of chemicals at a industrial scale.
- Heterogeneous biocatalysts basically involves enzyme dissolved in solid for or water insoluble form
- We generally prefer the heterogeneous biocatalysis in industries because the recycling of the enzymes will become less difficult if it is insoluble and it also supports continuous processing activity.
- So, the idea is to immobilize the initial soluble enzyme onto the support surface.
- Selection of the support material is also critical, as the support provides resistance against the conditions like pH and temperature. The support surface also proves a large internal surface area which is chemically suitable to the enzyme.
- The specific activity of the heterogeneous biocatalysts should be very high for its economical and practical use.

Parameters to consider while immobilising enzymes:

- The support material provides high internal surface area and maximizes the specific activity of the enzymes.
- Interactions between the support surface and the enzymes is also critical.

Immobilization efficiency: Immobilization efficiency is the protein binding capacity of a particular matrix/support that you are using. The percent of the total protein bound onto the matrix indicate its immobilization efficiency.

Immobilization yield: Immobilization yield represents the total enzyme we use for immobilization vs the enzyme we finally receive in the carrier.

BET analysis : BET analysis tries to explain the physical adsorption of gas molecules on a solid surface and it can used to calculate the specific surface area of materials. It explains about multilayer adsorption and utilizes gases which do not react chemically with the surface material, Nitrogen is commonly employed gaseous adsorbate.

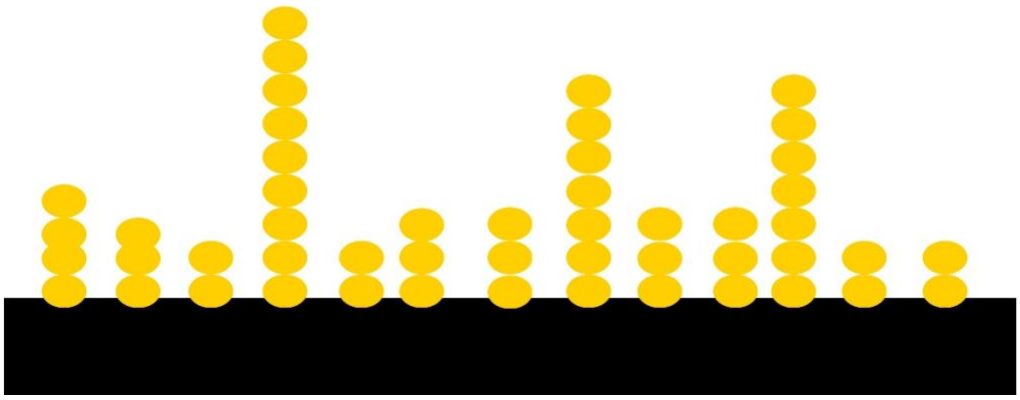


Figure: This figure represents BET analysis technique

- The gaseous molecules start to get adsorbed in the surface infinitely
- The molecules of gas interacts only with adjacent layers
- The enthalpy of the adsorption for the first layer is constant and will always be greater than the second layer

Working of BET:

The samples are degased in a vacuum at high temperatures, the samples are placed in the glass cells and then are analysed by the BET machine then, the cells are placed into heating mantles and lastly connected to the output port. After that the liquid nitrogen is employed which is used to cool the cells or the samples and by doing that , a low temperature is maintained . This ensures adsorption to occur. The nitrogen gas

is injected into the sample,on the other hand Helium gad used to run as a blank as helium does not adsorb onto the particles

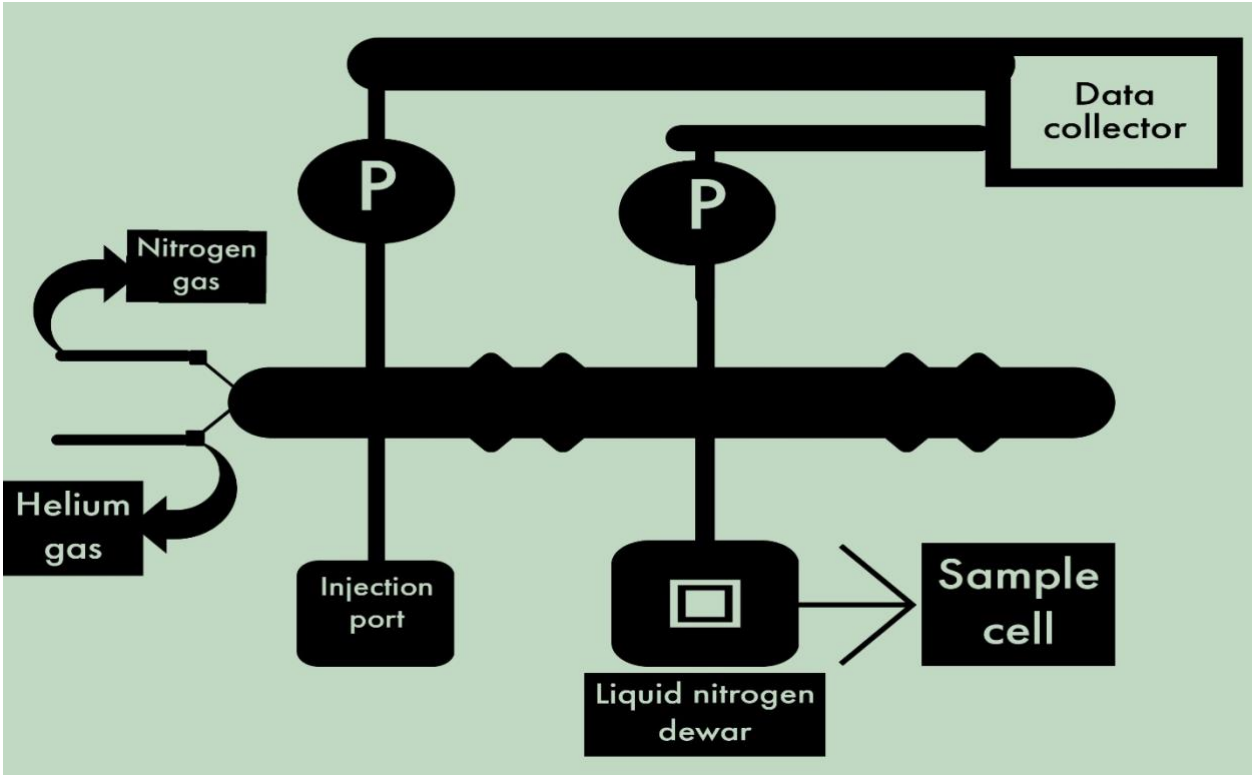


Figure : This figure represents the instrumentation model of BET

Multi-point Bet : At relative pressures higher than 0.5, there is the onset of capillary condensation, and at relative pressures that are too low, only monolayer formation is occurring. When the BET equation is plotted, the graph should be of linear with a positive slope. If such a graph is not obtained, then the BET method was insufficient in obtaining the surface area.

The BET procedure has a few drawbacks when contrasted with NMR, which can likewise be utilized to quantify the surface region of nanoparticles. Wager estimations must be utilized to decide the surface territory of dry powders. This method requires a ton of time for the adsorption of gas particles to happen. A great deal of manual readiness is required.

Protein loading or nanoparticles used as a drug delivery carriers:

Basically, nanoparticles are solid colloidal particles which lie in a size range of 10nm to 1000nm. Nanoparticles can be designed as delivery systems to control surface properties and extraction of pharmaceutical active compounds. This mechanism is advantageous as the particle size, shape, surface charge can be controlled and these drug delivery systems can deliver drugs of therapeutic and diagnostic agents.

Nanoparticles can be derived from the following:

1. Albumin : Albumin is derived from many sources such as Bovin serum albumin (BSA) and Human serum albumin (HSA). It is used in the body to maintain osmotic pressure. Albumin can serve as a transporter protein and also Albumin has a high solubility. It is also very stable and intact at ph 4-9. Albumin nanoparticles are widely used as they are easy to make and also are biodegradable.
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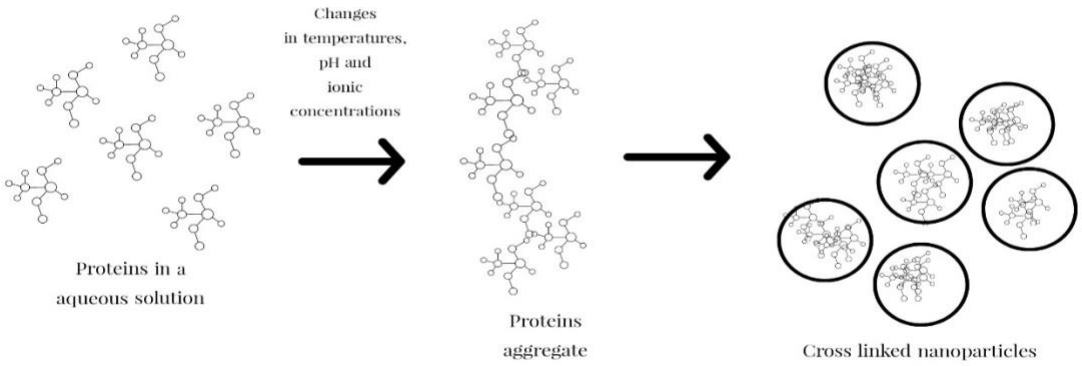

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References

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11. Bartlett PN, Whitaker RG. Electrochemical immobilisation of enzymes: Part I. Theory. Journal of electroanalytical chemistry and interfacial electrochemistry. 1987 Jun 10;224(1-2):27-35.
12. NC. Foulds and C.R. Lowe, J. Chem. Sot., Faraday Trans. 1, 82 (1986) 1259.
13. https://pubs.rsc.org/en/content/articlelanding/2013/cs/c3cs60270b
14. https://www.youtube.com/watch?v=oVJ2LJxO6tU&t=1027s
15. https://www.youtube.com/watch?v=-dh8goOimPk
16. https://www.youtube.com/watch?v=CSDnJvTufDI
17. https://www.youtube.com/watch?v=h1Q-_sL_2kA
18. https://www.youtube.com/watch?v=oiTVJ91-YxQ
19. https://www.youtube.com/watch?v=M8o5ymKyu2U
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Student signature : **Supervisor signature:**





A
Project Report
on

Proteomics: Technologies and Application



Submitted in partial fulfillment for the requirement of the Degree

of

BACHELOR OF TECHNOLOGY

in

BIOTECHNOLOGY

By

Submitted by:

Soumi Biswas (171811)

Under the supervision of:

Dr. Jitendraa Vashistt

Assistant Professor (SG)

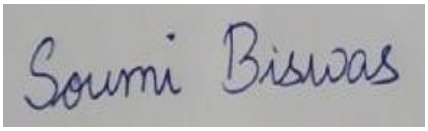
Jaypee University of Information Technology, Waknaghat, Solan, Himachal Pradesh

TABLE OF CONTENTS

Chapter No	Chapter Name	Page No.
	Candidate's Declaration	(i)
	Acknowledgement	(ii)
	Abstract	(iii)
1.	**Introduction**	**1**
1.1	What is proteomics?	1
1.2	Importance of proteomics	1-2
	Types of proteomics study	3
1.3	Proteomics workflow	3
2.	**Modern technologies in proteomics**	**4-8**
3.	**Applications of proteomics**	**9**
4.	**Conclusion**	**10**
5.	**References**	**11**

CANDIDATE'S DECLARATION

I hereby declare that work presented in this report entitled "Proteomics: Technologies and Application" in partial fulfilment of the requirements for the award of degree in Bachelor of Technology in the Department of Biotechnology and Bioinformatics [BT & BI] from Jaypee University of Information Technology Waknaghat, Solan, H.P. is an authentic record of my own work carried out under the supervision of Dr. Jitendraa Vashistt, Assistant Professor in the Department of BT &BI.



Soumi Biswas (171811)

This is to certify that the above statement made is true to best of my knowledge.



Dr. Jitendraa Vashistt

(Professor in the Department of Biotechnology and Bioinformatics)

ACKNOWLEDGEMENT

The satisfaction that accompanies with the successful completion of any task would be incomplete without the mention of people whose ceaseless cooperation made it possible, whose constant guidance and encouragement crown all efforts with success. I'm very much grateful to my project supervisor Dr. Jitendraa Vashistt and my parents for constantly supporting me and encouraging me towards the completion of the project, it wouldn't have been possible without them. I would also like to thank the university's library which has been a constant source for gaining knowledge and keeping one updated about the ongoing researches in the field of biotechnology and its related fields.

Soumi Biswas (171811)

ABSTRACT

I learnt Proteomics: Technologies and Applications with the help of online tools and under the guidance of my mentor Dr. Jitendraa Vashistt. Here, I'm providing with the literature I learned throughout my summer internship time period.

CHAPTER 1: INTRODUCTION

1.1 What is proteomics?

Proteomics is a recent field which was coined in year 1997, in analogy with genomics; the study of genome.

It is the branch of molecular biology studying a set of proteins expressed by the genome of an organism. It is an amalgamation of protein and genome and generally refers to the large-scale experimental analysis of proteins and proteomes, but often is used specifically to refer to protein purification and mass spectrometry. Consecutively, proteomics has both a physical lab component and a computational one; and most of the time these two parts works simultaneously.

1.2 Importance of proteomics:

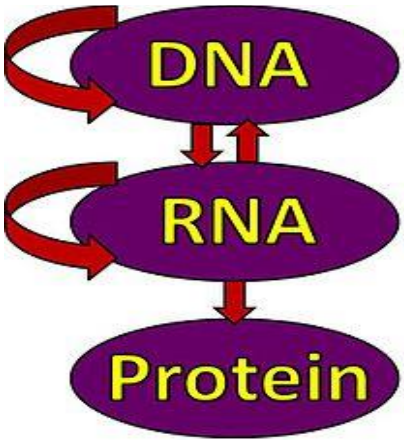
Proteomics is the subspecialty of molecular biology that looks at the function and role of protein in healthy and disease states. Proteins are mainly focused on because they're the products that genes direct to be made through the genetic codes.

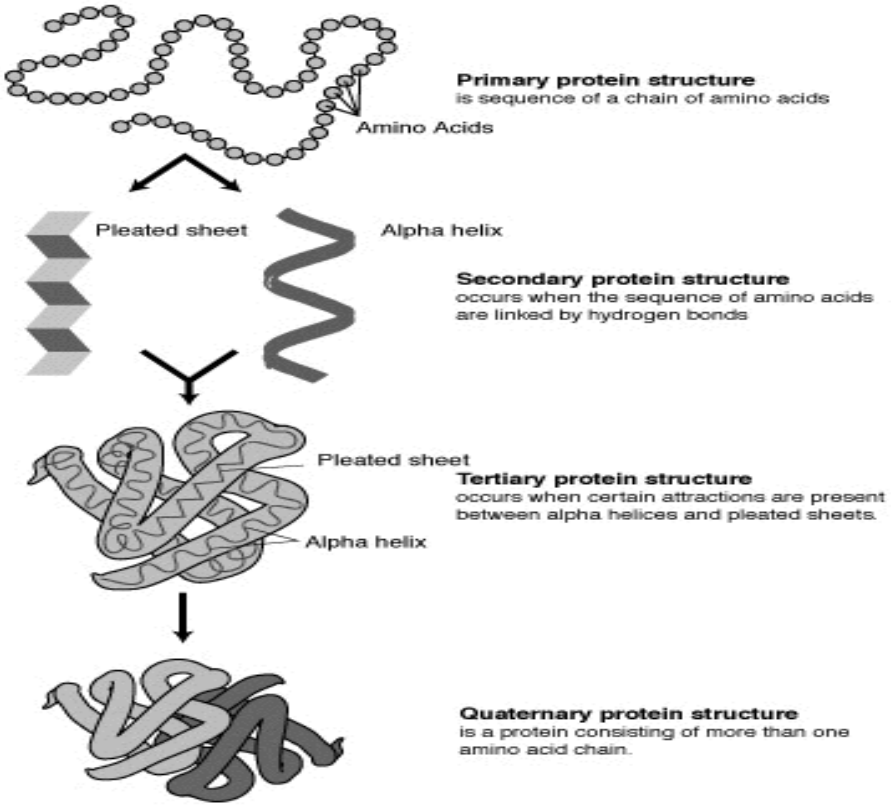
The centre of proteomics is a biological group called proteome. The proteome is defined as the set of proteins expressed in a specific cell, given a particular set of conditions. Within a proteome, the number of proteins can be as large as 2 million.

Proteins play a vital part in many living organism with diverse functions and proteomics helps in the identification of ever increasing number of proteins.

Proteins are macromolecules i.e., long chains of amino acids constructed when the cellular machinery of the ribosome translates RNA transcripts from DNA in the cell's nucleus. The transfer of information within cells follows a path of DNA→RNA→Protein and are organized into four structural levels

1. Primary (1°)→ amino acid sequence containing members of twenty-unit alphabet
2. Secondary (2°)→ having local folding of amino acid sequences into helix and sheets.
3. Tertiary (3°)→ provides 3D conformation of the entire amino acid sequence.
4. Quaternary (4°)→ creating a large unit by interaction between multiple small peptides or protein subunits.





Also, each level of protein structure is very essential for the molecule's function which provides an intricate control of the cellular machinery, generating protein insights on how proteins affect cell processes. Conversely, how protein themselves are affected by cell processes or the external environment is also understood through this proteomic technologies.

Therefore, the goal of proteomics is to analyze varying proteomes of different organism at different times, in order to highlight the differences present between them. It also analyzes the structure and function of biological systems too.

1.3 Types of proteomics study:

The broad field of proteomics can be subdivided into:

1. Structural proteomics: it is the in-depth analysis of a protein's structure.
2. Expression proteomics: it is the analysis of expression and also the differential expression of the proteins.
3. Interaction proteomics: it is the analysis of interactions between the proteins, to characterize complexes and determine its function.

1.4 Proteomics workflow:

1. Sample preparation: It is the first step of proteomics study wherein which we extract the protein from the cells.
2. Apply proteomic methods: we use techniques such as 2D electrophoresis to separate the different proteins.
3. Cutting the proteins into peptides: we do so because, peptides are easier to detect.
4. Mass spectrometry: for the detection of peptides and its fragments.
5. Data analysis: finally, we can determine the sequence of the protein by interpreting the obtained data.



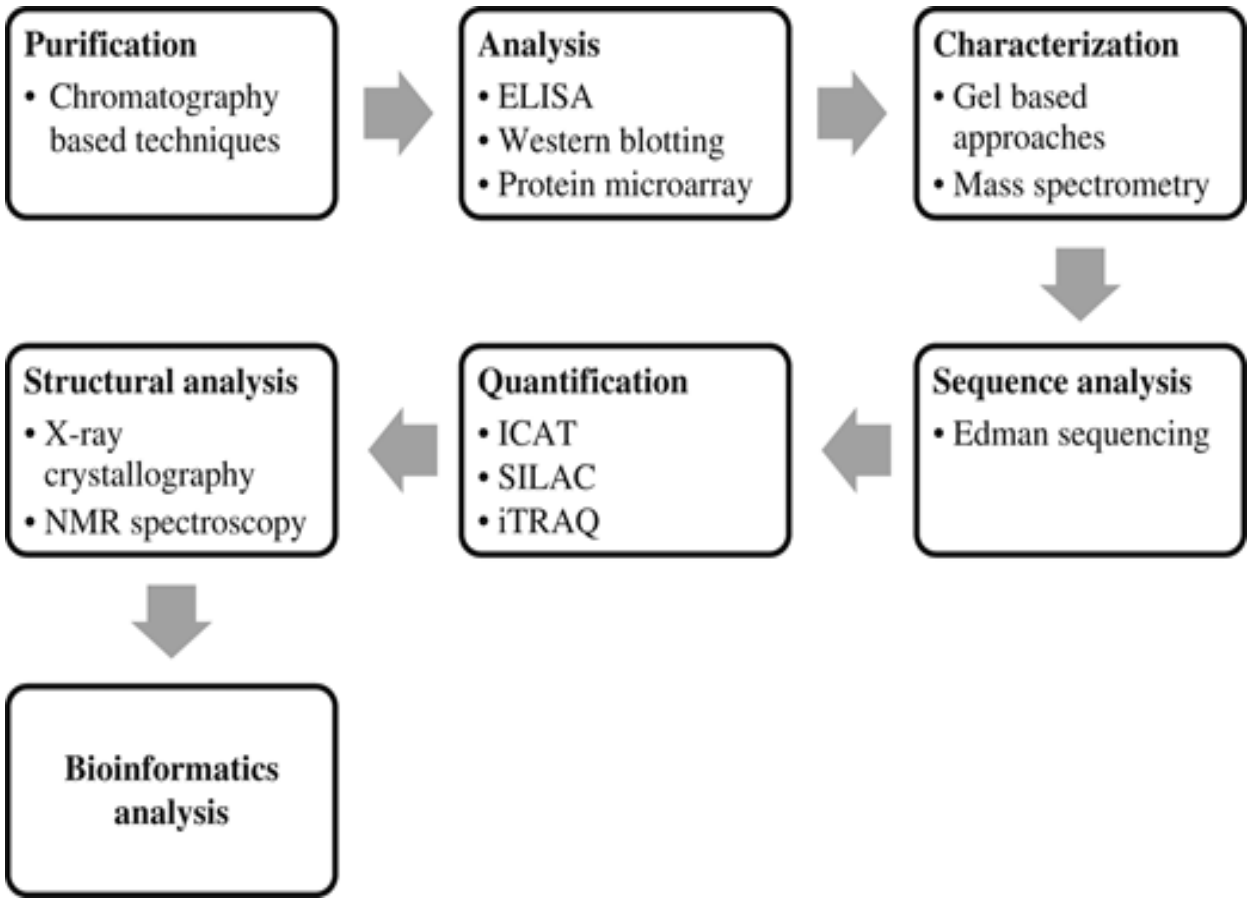
CHAPTER 2: MODERN TECHNOLOGIES IN PROTEOMICS

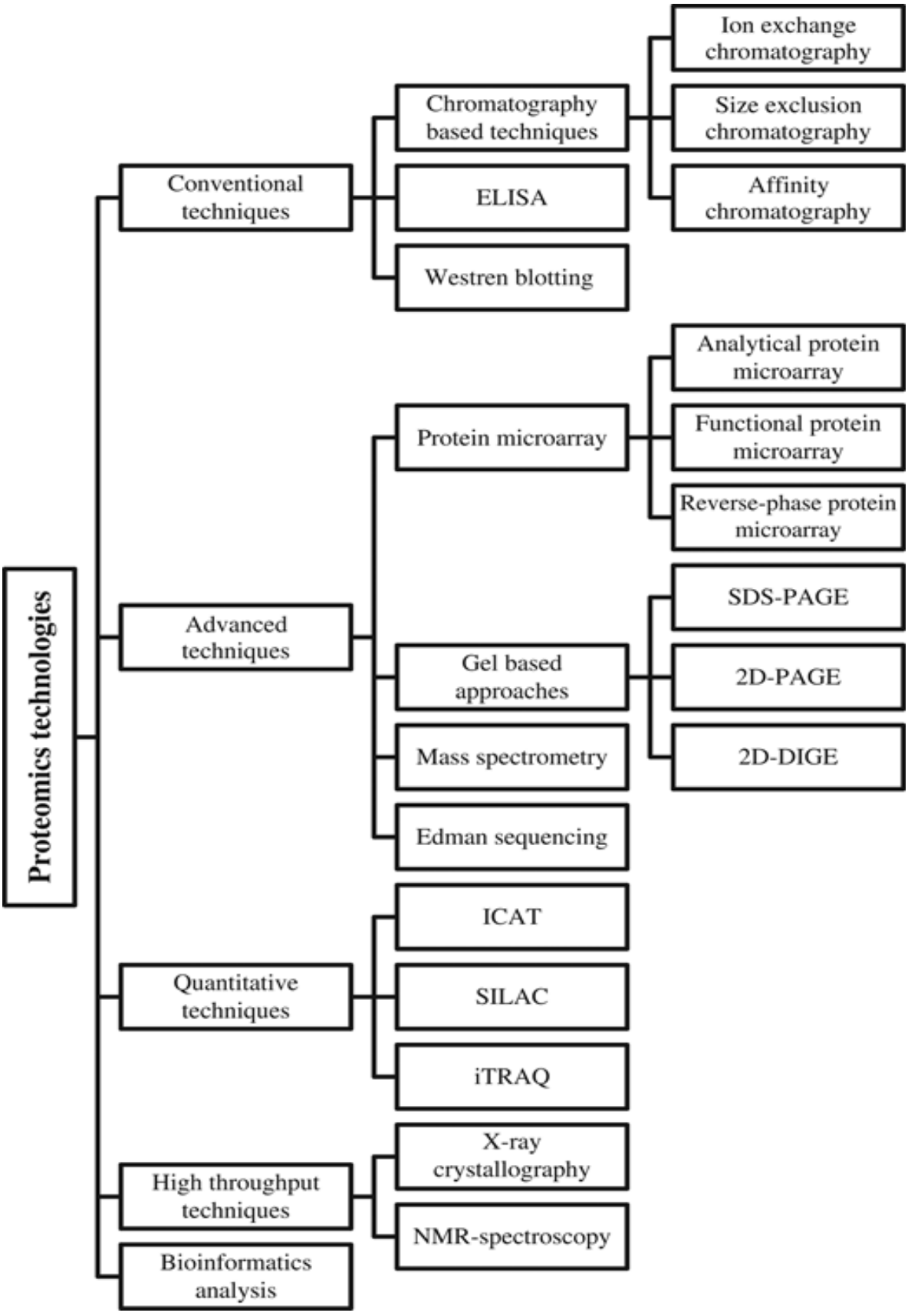
Proteomics is a rapid growing field and there is a shift in the field, from a specialized/focused way of conducting studies to a more global perspective.

Nonetheless, mass spectrometry has feasibly become the core technology in proteomics as the application of techniques is based on mass spectrometry for the qualitative and quantitative analysis of global proteome samples, derived from the complex mixtures that had a pivot role in the understanding of cellular functions. It is an analytical tool useful for measuring the mass-to-charge ratio of one or more molecules present in a certain sample; and these measurements are often used to calculate the exact molecular weight of the components to be found.

Other than that, protein microarray technology has also progressed for identifying, quantifying and functional analysis of proteins mainly in the field of applied proteome research.

Also, techniques like electrospray ionization (ESI) and laser desorption/ionization (MALDI), commonly known as soft-ionization techniques are also utilized. Here, ions are created with the help of low internal energies and therefore, undergo little fragmentation.




Proteomics technologies
Conventional techniques
Chromatography based techniques
Ion exchange chromatography
Size exclusion chromatography
Affinity chromatography
ELISA
Westren blotting
Advanced techniques
Protein microarray
Analytical protein microarray
Functional protein microarray
Reverse-phase protein microarray
Gel based approaches
SDS-PAGE
2D-PAGE
2D-DIGE
Mass spectrometry
Edman sequencing
Quantitative techniques
ICAT
SILAC
iTRAQ
High throughput techniques
X-ray crystallography
NMR-spectroscopy
Bioinformatics analysis

- **Conventional techniques:**

1. Chromatography-based techniques:
   a. Ion exchange chromatography

   IEC is a versatile tool for the purification of proteins on the basis of charged groups on its surface and the proteins vary from each other in their amino-acid sequence, certain amino acid are anionic while others are cationic.

   b. Size exclusion chromatography

   SEC separates the proteins through a porous carrier matrix with distinct pore size on the basis of permeation; therefore the proteins are entirely separated on the basis of molecular size. The SEC is a robust technique capable of handling proteins in diverse physiological conditions in the presence of detergents, ions and co-factors or at various temperatures.

   c. Affinity chromatography

   The affinity chromatography is a reversible interaction between the affinity ligand of chromatographic matrix and the proteins to be purified. Plasma proteins such as factor IX, factor XI, factor VIII, antithrombin III and protein C are mostly purifies using affinity chromatography at industrial scale for therapeutic use.
2. Enzyme-linked immunosorbent assay:

   The ELISA is highly sensitive immunoassay and widely used for diagnostic purposes. The assay utilizes the antigen or antibodies on the solid surface and addition of enzyme-conjugated antibodies and measuring the fluctuations in enzyme activities which are proportional to antibody and antigen concentration in the biological specimen.
3. Western blotting:

   Western blotting is an important and powerful technique for detection of low abundance proteins that involves the separation of proteins using electrophoresis, transfer onto nitrocellulose membranes and the precise detection of target protein by enzyme-conjugated antibodies.
4. Edman sequencing:

   It is used to determine the amino-acid sequence in peptides or proteins and the method comprises of a chemical reactions that eliminates and identify amino acid residues that are present on the N-terminal of the polypeptide chain. Edman sequencing plays a major role in the development of therapeutic proteins and quality assurance of many biopharmaceuticals.

- **Advanced techniques:**

1. Protein microarray: protein microarray also known as protein chips is an emerging class of proteomics technologies, which are capable pf high-throughput detection from small amounts of sample. It is further classified into three categories:
   a. Analytical protein microarray: The most representative class of analytical protein microarray is the antibody microarray. These are typically used to measure the

expression level along with the binding affinities of a protein wherein proteins are detected directly after antibody capture by direct protein labeling.

b. Functional protein microarray: It is constructed by means of purified protein, thus is helpful for the study of various interactions including protein-DNA, protein-RNA and protein-protein, protein-drug, protein-lipid, enzyme-substrate relationship. It was first used to analyze the substrate specificity of protein kinases in yeast.

c. Reverse-phase protein microarray: Reverse-phase protein microarray approach is a quantitative analysis of phosphoproteins and other cancer-related proteins in non-small lung cancer (NSCLC) cell lines monitoring the apoptosis, DNA damage, cell-cycle control and signaling pathways.

- **Gel-based approaches:**

1. Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis:
   SDS-PAGE is a high resolving technique for the separation of proteins according to their size, thus facilitating the approximation of molecular weight.
2. Two-dimensional electrophoresis: 2D-PAGE is an efficient and reliable method for separation of proteins on the basis of their mass and charge. It is capable of resolving ~5000 different proteins depending on their gel size.

- **Quantitative techniques:**

1. ICAT labeling: The ICAT is an isotopic labeling method wherein, chemical labeling reagents are used for quantification of proteins. It can also be used to analyze and permit the accurate quantification and sequence identification of proteins from a complex mixture.
2. Stable Isotopic Labeling with Amino Acids in Cell Culture: SILAC is an MS-based approach for quantitative proteomics that depends on metabolic labeling of whole cellular proteome. It has been developed as an expedient technique to study the regulation of gene expression, cell signaling, post-translational modification whereby proteomes of different cell grown in cell culture are labeled with “light” or “heavy” for of amino acids, differentiated through MS.
3. Isobaric tag for relative and absolute quantitation: iTRAQ is multiple protein labeling technique for protein quantification based on tandem mass spectrometry. This technique relies on labeling the protein with isobaric tags (8-plex and 4-plex) for relative and absolute quantitation.
4. X-ray crystallography: X-ray crystallography is the most preferred technique for 3D structure determination of proteins wherein, the highly purified crystallized samples are exposed to X-rays and the subsequent diffraction patterns are processed to produce information about the size of the repeating units the forms the crystal and crystal packing symmetry. It has extensive application in the study of virus systems, protein-nucleic acid complexes and immune complexes.

- **High-throughput techniques:**

1. Mass spectrometry: MS is used to measure the mass to charge ration (*m/z*), therefore is helpful for determining the molecular weight of proteins. Firstly, the molecules must be transformed to gas-phase ions which pose a challenge for biomolecules in a liquid or solid phase. Secondly, separation of ions on basis of *m/z* values in the presence of electric or magnetic fields in a compartment known as mass analyzer. Finally, the separated ions and the amount of each species with a particular *m/z* are measured.
2. NMR Spectroscopy: The NMR is a leading tool for the investigation of molecular structure, folding and behavior of proteins. It basically involves various phases, each using a discrete set of extremely specific techniques.

- **Bioinformatics analysis:**

Bioinformatics is an interdisciplinary field that takes insights from a range of subjects (statistics, biology, mathematics, computer science, chemistry, etc) to create tools an approaches to understand biological data. It is an essential component in proteomics study, therefore its implications have been progressively increasing with the advent of high-throughput methods that are dependent on powerful data analysis. This newly emergent field presents novel algorithms for management of huge and heterogeneous proteomics data and also led towards the discovery procedure. The use of bioinformatics in proteomics is significantly affluent during the previous few years as the development of new algorithm for the analysis of higher amount of data with increased specificity and accuracy, helps in the identification and quantification of proteins with efficient management of such high quantity of data.

Table 1 Software tools for proteome data exploration available via the Internet

Tool	Description	Source	URL
DARWIN	Data analysis and retrieval with indexed nucleotide and peptide sequences	ETH Zürich, Switzerland	cbrg.in.ethz.ch
EXPASY	Molecular biology server dedicated to the analysis of protein sequences and structures as well as 2-D PAGE	SIB Swiss Institute for Bioinformatics Geneva, Switzerland	www.expasy.ch
LUTEFISK97	Searching sequence databases via de novo peptide sequencing to tandem mass spectrometry	Immunex Corp. Seattle, USA	www.lsbc.com:70/Lutefisk97.html
MASCOT	A search engine which uses mass spectrometry data to identify proteins from primary sequence databases	Matrix Sciences Ltd. London, UK	www.matrixscience.com
MOWSE	Searching the owl protein sequence database with protein fragment information, and return the protein(s) which most likely correspond to your peptide-data	ICRF Imperial Cancer Research Fund London, UK	srs.hgmp.mrc.ac.uk/cgi-bin/mowse
PEPTIDESEARCH	Search the non-redundant protein sequence database by a list of peptide masses or a peptide sequence tag or an amino acid sequence	EMBL European Molecular Biology Laboratory Heidelberg, Germany	www.mann.embl-heidelberg.de/Services/PeptideSearch/PeptideSearchIntro.html
PROSPECTOR	Tools for mining sequence databases in conjunction with mass spectrometry experiments	UCSF University of California, San Francisco, USA	prospector.ucsf.edu
PROWL	Provides an interactive environment for protein analysis. ProFound: a tool for searching a protein sequence database using peptide maps and peptide fragment masses	Rockefeller University New York, USA	prowl1.rockefeller.edu
SEQUEST	Correlates uninterpreted tandem mass spectra of peptides with amino acid sequences from protein and nucleotide databases	University of Washington Seattle, USA	thompson.mbt.washington.edu/sequest/

CHAPTER 3: APPLICATIONS OF PROTEOMICS

Proteomics technology finds a vast application in the field biological sciences wherein which the combination of these technologies has led us in achieving success in purification, analysis, characterization, quantification, sequence and structural analysis and bioinformatics analysis of a large number of proteins in all types of eukaryotic and prokaryotic organisms. Though, the technology is a very rapid, sensitive and provides great proteome coverage, but further work is still required for improving the reproducibility and also performance of the well-known proteomics tools.

Besides, some of the notable applications of proteomics technology include:

1. ***In Biomarker Discovery:*** A biomarker is essentially referred to the disease-related proteins or a biochemical indicator that can be used in the clinic to diagnose the activity of a certain disease, its prognosis, and development of it. Proteomics technology has been extensively used in the molecular medicine for biomarker discovery; by analyzing the global protein profiling in the body fluids, one can easily detect and identify the invaluable disease-specific biomarkers. It is also used in various cancer diseases.
2. ***In Drug Discovery*:** Proteomics studies are also useful for target identification, along with drug action, toxicity, resistance, efficient or not examination. Besides, the various MS-based platforms, including clinical, functional, and chemical proteomics are also involved in the modern drug delivery process.
3. ***In Food Industry***: Quality control is an important factor when it comes to the food and human nutrition along with its safety. Here, proteomics can be a very remarkable tool for the detection of allergens. Checking quality control and safety of raw materials, etc. with the rapidly growing global population, climatic changes and subsequent increasing need of the natural resources, food production with efficient crop yield is yet to achieve. Concurrently, here "Omics" technologies act as a promising tool for such objectives.

CHAPTER 4: CONCLUSION

I, hereby conclude that I fully understand the basic fundaments of the topic taught by my teacher and wish to pursue proteomic research in the near future.

CHAPTER 5: REFERENCES

1. Kim, M. *et al.* A draft map of the human proteome, Nature (575-581), 2014.
2. Willhelm. M. *et al.* Mass spectrometry based draft of the human proteome, Nature (509, 582-587), 2014.
3. Proteomics: Principles and Techniques from http://nptel.iitm.ac.in
4. Roland Kellner, Proteomics: Concepts and perspectives, Springer Verlag (517-524), 1999.
5. http://www.proteome.org.an
6. http://www.proteomeworks.bio-rad.com
7. http://www.genomic-solution.com
8. https://en.wikipedia.org/wiki/Proteomics
9. Hiroyuki Yokota, Applications of proteomics in pharmaceutical research and development, Tsukuba-shi (305-8585), 2018.
10. Mollisa M. Elrick, *et al.*, Proteomics: Recent Applications and New Technologies, Basic & Clinical Pharmocology & Toxicology (98, 432-441), 2006.
11. Linscheid, M. W., Quantitative proteomics, Anal. Bioanal. Chem. (381, 64-66), 2005.
12. Xiao, *et al.*, Proteomics patterns: their potential for disease diagnosis, Mol. Cell. Endorcinol. (230, 95-106), 2005.
13. https://www.biologydiscussion.com/biotechnology/proteomics/proteomics-basic-concepts-technology-and-application/8568
14. Aebersold, *et al*., Quantitative proteome analysis: methods and applications, Ann. N. Y. Acad. Sci. (919, 33-47), 2000.
15. Aebersold R, Mann M, Mass spectrometry-based proteomics, Nature (422, 198-207), 2003.

SUMMER TRAINING REPORT

ON

FERMENTATION TECHNOLOGY

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of

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July, 2020

OBJECTIVE 1- To acknowledge the working and components of a bioreactor.

Theory: Bioreactor- It is a flask type structure which has the advantage of controlling environmental conditions and it also provide cell and microbial plant cultivation under sterile conditions. It consist of following parts;

- **Agitator-** It is used to carry out mixing of the contents present in the reactor in order to keep cells in perfect homogenous condition for better transport of nutrients and oxygen.
- **Baffle-** It is mainly used to prevent the vortex formation in the reactor as it can change the centre of gravity of the system and consumes additional power.
- **Sparger-** It supplies oxygen to the growing cells and it also helps in mixing the contents which results in less usage of power.
- **Jacket-** It helps in keeping the temperature of bioreactor down by providing water and removing extra heat from its surface.

- **Basic protocol for the operation of bioreactor:**
  - **Temperature Measurement and Control-** Temperature measurement is carried out by either using thermocouple or Pt-100 sensor which send signal to the temperature controller. Measured value is compared with set point which is entered in the controller, depending on it heating or cooling of the bioreactor is activated slowly to decrease the error.
  - **pH measurement and control-** pH measurement is carried out using autoclavable pH probe. Before using pH probe it needs to be calibrated with the two buffers used in the bioreactor cultivation experiment. Measured pH is compared with the set point which then activated the acid or alkali to bring the measured value close to the set point.
- **Identification of pH controller settings for Bio-Engineering AG:**

i. **Bioreactor-** A suitable control action setting is required for the addition of certain concentration of acid/alkali which can give quick action to measured value around the set point. It is also noted that activation of alkali/acid is done in a phased manner, this ensures adequate mixing of acid/alkali in the broth before next instalment is added. On/off time of the controller has to be adjusted by separate experiments and will depend on the buffering capacity of the broth. It is essential to maintain these settings before the start of the experiment in order to have efficient control.

ii. **Dissolved oxygen controller-** It is measured by a dissolved oxygen probe. In this probe is to be calibrated for its zero and 100% values.

iii. **Foam control-** It controls the foam which arises due to the organic compound and the broth is vigorously agitated to keep the cells in suspension and ensure efficient nutrient transfer from the dissolved nutrients and oxygen.

Procedure:

- **To understand the significance of each part of the bioreactor;**

i. Press Start.

ii. **Speed control system-** Mainly used to provide mixing of reactor contents. Set the upper limit and actual speed then press RUN.

iii. **Gas Supply System-** It supplies air which serves as the source of the oxygen to the growing cells. Enter value and run.

iv. **Temperature Control System-** It is used to maintain the cultivation temperature in the bioreactor. Measure the value and compare it with the set point.

v. **pH measurement and control system-** Enter pH value and set point . Press run. Measure the pH and compare it with the set point.

vi. **Dissolved Oxygen Measurement and Control-** Enter value of dissolved oxygen levels and press run. Using the magenta sensor, compare the value with the set point and depending on the error the controller action is activated.

vii. **Foam Control System-** It is used to remove the foam from the system as it can lead to heavy losses to the system. It is detected by red sensor and anti foam is triggered It is added slowly so that only minimum amount is added. Over addition of antifoam may create serious problem.

OBJETIVE 2: Determination of characteristics of pH controller of Bio- Engineering AG fermenter

Theory: The pH control method is dependent on various parameters of factors such as density, viscosity and strength of acid and bases etc. Faulty settings of these parameters will lead to delayed control response. It is possible to design the controller according to the above parameters.

- **Description of the pH controller;**
  i. **pH/mV potentiometer-** It enables the adjustment of the slope of pH electrode by calibration.
  ii. **Asymmetry potentiometer-** It adjust the zero mV point of the pH signal.
  iii. **Temperature potentiometer-** It manually control temperature coefficient of pH electrode.
  iv. **Set point potentiometer-** Set pH or mV.
  v. **P-band potentiometer-** Adjust the width of the P-band potentiometer. Low P band translates to strong amplification.
  vi. **TON/TOFF potentiometer-** Adjust the opening and closing of the valve by keeping both the potentiometer at the same value which will lead to the linear transfer function.

Procedure:

i. Switch 1 connected to pH.
ii. Switch 5 and switch 8 to hand.
iii. Adjust 4 to the temperature of the solution.
iv. Dip the electrode in standard buffer of pH 7 & adjust until pH comes at 7.
v. Clear the electrode and dip it in buffer (pH 4).
vi. Adjust 3 till the meter reads at 4 pH.

OBJECTIVE 3: 15 L Bioreactor Manual

- **Preparation for sterilization**
  - Media was prepared and added to the reactor.
  - The functioning of probes was verified and electrolytes in pH and DO probes refilled.
  - Probes were inserted into the reactor.
  - Air outlet filter was used to maintain pressure equilibrium in and outside the reactor.
- **For Autoclaving**
  - The reactor was now placed inside the horizontal Autoclave,
  - Pressure was maintained in the jacket at 15psi by keeping valve in fast mode.
  - Closed the autoclave lid; adjusted valve in sterile mode.
  - Waited for maintaining equilibrium at 15 psi in reactor and jacket.
- **For login to controller**
  - Switched on the controller and a screen appeared
  - After that a home screen will appeared. Pressed view button on home page and entered into System engineer.
  - A login screen appeared. Pressed login and specified password. Pressed enter button.
- **For priming tubes**
  - Attached the autoclaved reactor and pipes to controller. Went to home page and pressed main menu.
  - Tubing prime control button was selected on the main menu.
  - Primed all the tubes for alkali, acids and antifoam.
  - Went to main menu and entered into manual controller. All the pumps and valves were controlled manually.
- **Setting parameters set points**

  <u>Temperature</u>
  - Pressed main menu and entered the temperature.
  - Specified temperature set point and pressed enter button.

  <u>Stirrer setting</u>
  - Went to the main menu and entered into stirrer settings.
  - On stirrer setting screen, pressed cascade speed limit button.
  - On cascade limit screen, the upper and lower speed limit cascade will appeared.
  - Set the upper stirrer speed limits and pressed enter.
  - Set the lower speed limit cascade and pressed enter.
  - Entered into stirrer settings and pressed stirrer set point button.
  - Wrote stirrer set point and pressed enter button.

  <u>pH setting</u>
  - On main menu, pressed pH settings and entered into pH set point.
  - Set pH point and pressed enter.

  <u>DO settings</u>
  - On home page, entered into DO settings. Then press DO set point button.

- Set DO point and pressed enter button.

❖ **Switched on controllers and ran fermentation**

1. On the home page, pressed menu button. Inside the menu, pressed start/stop all the controllers.
2. Then pressed start all controllers.
3. Then ran fermentation.
4. All the profiles of parameters i.e. pH, DO and temp were monitored by entering into respective controller sections on home page.
5. On completion, harvested the entire fermentation broth from the reactor.

OBJECTIVE 4: Biopolymer Production by Microbes

❖ **Basic Requirements**

Microorganism: *R. eutropha NRRL B14690*. The culture was maintained on nutrient agar slants at about 5ºC.It requires being sub cultured every month.

Media preparation [shake flash cultivation:

- For mineral salt medium: 2.0 g/L (NH4)2SO4, 2.0 g/L KH2PO4, 0.6 g/L Na2HPO4, 0.2 g/L MgSO4.7H2O, 20 mg/L CaCl2, 10 mL/L trace metal solution, 0.1 g/L yeast extract is to be used.
- For trace metal solution: 1.3 mg/L ZnSO4.7H2O, 0.2 mg/L FeSO4.7H2O, 0.6 mg/L (NH4)6Mo7O24.4H2O and 0.6 mg/L H3BO3.
- Fructose is used as a carbon source in concentration of 40 and 10 g/L for production media and inoculum development, respectively. Fructose, yeast extract and salt solutions are to be sterilized separately at 121ºC and then aseptically reconstituted at room temperature prior to inoculation.
- The pH of the resulting broth needs to be adjusted to 7.0 with 2N NaOH/2N HCl.

Bioreactor cultivation:

- Seed culture was prepared in a 1 L Erlenmeyer flask containing 200 mL media. Batch cultivation was then carried out at 30ºC in a 7 L LF-1523 Bioengineering (Bioengineering AG, Switzerland) bioreactor containing 4 L of media.
- The reactor was sterilized in-situ at 121ºC for 20 min, cooled and then inoculated with 5% inoculum (v/v).
- Culture pH needs was maintained at 7.0 by automatic addition of acid or base by pH–mV controller M 7832 N.
- Dissolved oxygen concentration was maintained at 30% saturation value by manually adjusting the speed of the agitator and/or airflow rate.
- Samples were withdrawn at regular intervals and analysed for biomass, PHB and residual nutrients.

❖ **Protocol for operation of simulator**

- Bioreactor:

  The Bioreactor portion shows different components which described the purging of the sterile from the sparger and rotation of the impeller. The

impeller is bottom driven. This arrangement is possible with Bioengineering AG Switzerland Bioreactor. This kind of agitation gives more space on the lid because of which there is no overcrowding of different inlet ports & sensors and it is particularly useful when flame is used to connect acid /alkali pipes and when transfer of inoculum is done to the reactor. The constant temperature water flows in the jacket of the reactor (marked green) to maintain the temperature of the reactor.

- Run Simulation:
  After entering the necessary details, RUN Simulation button was pressed and the graph and table for X, S, P vs time was printer on the screen.
- Out put Graph :
  The graph described the kinetic profile of different fermentations.
- Save Results:
  Pressed on the save button.
  Results were saved in the form of an Excel Sheet where all the values of kinetic profile were tabulated.

OBJECTIVE 5: Acetone-Butanol-Ethanol Production

❖ **Basic Requirements -**

- Culture - *Clostridium acetobutylicurn* strain ATCC 824 was used for production of Acetone-Butanol-Ethanol.
- Medium requirements - A standard culture media with respect to ammonium sulfate and yeast extract for the specific glucose concentrations has to be used in this study while maintaining the same concentrations of minor nutrients. It typically consists of the following components in g/L: glucose, 50; ammonium sulfate, 9.0; yeast extract, 11.0**;** K2HP04, 0.8; KH2P04 0.8; MgS04, **0.3;** MnS04 .H20, 0.02; NaCI, 0.02; FeS04 . 7H20, 0.02; and L-cysteine, 0.5. Temperature 37ºC, pH 4.5 or 6.0 .
- Flask and Bioreactor development - Heat shocks the spores kept up in RCM by putting the test tube in a bubbling water shower (100ºC for one minutes). This is to be trailed by cooling to 4ºC for 3 minutes. The temperature of the cylinder is standardized to room temperature for 60 minutes. The 3% inoculum is to be moved into 15 mL hungate top test tubes containing 10 mL of the RCM. The test tube containing the spore arrangement was saved for spore actuation at 37ºC in an anaerobic container for 20-24 hours. Satisfactory development for ensuing exchange of the inoculums was portrayed by the beginning of gas creation. 3 % inoculums were moved into a fluid glucose medium (50 g/L) in a shake flagon. Following 10 hours of development, tests were pulled back from the way of life jar each hour. The pH of the inoculum was not permitted to fall underneath 4.6 by manual expansion of 0.1 N NaOH. The suitable planning for vaccination (14-15 hours) was distinguished by the way of life corrosive break point through the examination of extracellular items by gas chromatography. A 3 % inoculum is moved to the fermenter containing cleaned 50 g/L glucose medium at pH 4.6 Before immunization the fermenter was sparged in the head space by Nitrogen.

The nitrogen sparging proceeded until the gases were being created by the way of life. The way of life was permitted to develop in a clump mode.

❖ **Analytical protocols -**

- Dry wieght - 20 ml sample of the fresh fermentation stock is centrifuged at 10,000 g and 4ºC for 15 minutes. The supernatant is solidified in a profound cooler for extracellular metabolite and glucose examination. The biomass is washed multiple times with equivalent measure of refined water. The pellet is re-suspended in 10-15 mL of refined water, moved to a preweighed aluminum dish and dried in a stove at 100ºC for 24 hours. In the wake of cooling the aluminum dish to room temperature in a desiccator the dry load of the cells is estimated.
- Glucose - Glucose concentration was determined by DNS method.
- Solvent and Acid concentration- This was done by Gas-liquid Chromatography.

❖ **Protocol for operation -**

- Bioreactor - The Bioreactor portion represents the various parts it likewise depicts the cleansing of the sterile air (if it's not too much trouble see the air channel noticeable all around delta) from the sparger and pivot of the impeller. The impeller is base driven. This sort of plan is conceivable with BioEngineering AG Switzerland Bioreactor. This sort of unsettling gives more space on the top so that there is no congestion of various bay ports and sensors and it is especially helpful when fire is utilized to interface corrosive/salt funnels and when move of inoculum is done to the reactor. The consistent temperature water streams in the coat of the reactor (stamped green) to keep up the temperature of the reactor.

The Simulation was run to understand the basic working and result formation.

OBJECTIVE 6: Propanoic Acid Production

❖ **Basic Requirements -**

- Culture - *Propionibacterium acidipropionici* ATCC 4875.
- Medium Requirements - Engineered medium is to be utilized for the arrangement of inoculum. 100 mL (20 g/L lactose) medium with the accompanying organization is to be utilized: 1 g yeast separate, 0.5 g trypticase, 0.025 g K2PHO4, 0.005 g MnSO4, 2 g lactose. pH is to be acclimated to 6.5 with 3 N NaOH/HCl. For sanitization, lactose and rest of the medium parts (basal medium) are to be autoclaved independently at 121º C and 15 psig for 20 min. Blend the two arrangements aseptically under laminar flow hood.
- Inoculum Preparation - 20 mL of the engineered medium is to be taken in a 100 mL serum bottle, Cap it by an elastic plug and seal by aluminum top by crimper. Prior to immunization, N2 is to be sparged through the serum bottle for around 15 min. A leave valve with sterile channel must be given at the cup outlet to forestall development of extreme weight inside it. Vaccination is to be finished utilizing a two days old inclination development rejected in 1 mL sterile refined water. A uniform suspension is to be made in the water before aseptically

moving the inoculum to the serum bottle with the assistance of a sterile syringe. Development is to be done at 30º C in a shaker (Adolf Kuhner AG, Basel, Switzerland) kept up at 150 rpm. Utilize sterile syringes to pull back samples. Move the inoculum at around 40 h utilizing 6% (v/v) inoculum.

- Bioreactor Cultivation - Start fermentation in a bioreactor at an underlying grouping of lactose (utilizing) 50 g/L (7-l (Bioengineering, Switzerland) glass reactor) working volume 5 liter. Autoclave the fermentor with refined water in it, in situ. In the wake of autoclaving, when the temperature drops down to 60º C, the water is to be evacuated through the examining port by applying N2 pressure. Keep flushing the headspace of the reactor with nitrogen gas to keep up anaerobiosis all through the fermentation. The instigator is to be kept at 150 rpm. Control the temperature at 30±1 ºC and keep up the pH at 6.5±0.1 via programmed expansion of clean 6 N NaOH. A pH estimation of 6.5 has been accounted for to be appropriate for propionic corrosive amassing (Hsu and Yang 1991). Develop the inoculum in a specially designed 500-ml serum flagons (headspace flushed with nitrogen gas). Aseptically immunize the bioreactor containing 5 l of medium with 250 ml of 1-day-old log-stage culture. Gather 10 mL fluid samples at standard stretches Measure the optical thickness and rotator the rest of the volume of the sample at 10,000 g for 20 min. Store the supernatant at – 20 ºC for HPLC examination to build up the item focuses.

❖ **Analytical Protocol -**

- Biomass Estimation - Biomass estimation is done by the measurement of optical density.
- Substrate/Product Estimation - For estimation of product formed HPLC technique is used.

The Simulation was run to understand the basic working and result formation.

OBJECTIVE 7: 1, 3 Propanediol Fermentation

❖ **Basic Requirements -**

- Culture - *Clostridium diolis* DSM 15410 (previously known as *Clostridium butyricum* DSM 5431)is used for 1,3-PD production.
- Modification for maintaining Ideal condition - Customary Erlenmeyer flasks (500 ml) must be changed for completing anaerobic development outside the anaerobic tent. The mouth size (30 mm) is decreased to 10 mm and flasks are furnished with an edge to encourage fixing with elastic and aluminum tops by methods for a crimper. Sparge nitrogen gas in the carafes to cleanse out the dissolved oxygen of stock and keep up anaerobic conditions.
- Medium Requirements - Build up the inoculum in 120 ml serum bottles which contain 50 ml clean medium having arrangement (per liter): unadulterated glycerol 20 g; K2HPO4 3.4 g; KH2PO4 1.3 g; (NH4)2SO4 2 g; MgSO4.7H2O 0.2 g; CaCl2.2H2O 0.02 g; FeSO4.7H2O 5 mg; Yeast extricate 2 g; Trace component arrangement (TES) 2 ml. The follow component arrangement (per liter) comprised of: 70 mg ZnCl2; 0.1 g MnCl2.4H2O; 60 mg H3BO3; 0.2 g CoCl2.2H2O; 20 mg

CuCl2.2H2O; 25 mg NiCl2.6H2O; 0.9 ml HCl (37%). Sparge the jugs with nitrogen and hatch immunized jugs at 330C and 150 rpm in an orbital incubator shaker. Move aseptically exponentially developing culture from the serum bottle (24 h) to sterile nitrogen gassed medium in an uncommonly altered 500 ml Erlenmeyer carafe containing 100 ml medium. Brood the vaccinated flasks in an orbital shaker at 330C and foment at 150 rpm for 12 h after which utilize the effectively developing culture from the carafe as inoculum for the bioreactor.

- **Fermentation Bioreactor Setup -** Batch development of C. diolis is completed in a 3.7 L bioreactor (Bioengineering AG, Switzerland) (working volume 1.5 L) utilizing measurably improved nutrient medium formula. The medium comprises (per liter): unadulterated glycerol 54.45 g; K2HPO4 3.21 g; KH2PO4 2.75 g; (NH4)2SO4 2 g; MgSO4.7H2O 0.2 g; CaCl2.2H2O 0.02 g; FeSO4.7H2O 5 mg; Yeast extricate 2 g; Trace component solution (TES) 2 ml. The follow component solution (per liter) comprised of: 70 mg ZnCl2; 0.1 g MnCl2.4H2O; 60 mg H3BO3; 0.2 g CoCl2.2H2O; 20 mg CuCl2.2H2O; 25 mg NiCl2.6H2O; 0.9 ml HCl (37%). Disinfect bioreactor and tubing via autoclaving at 1210C and 15 psi for 40 minutes. Utilize 10% (v/v) effectively developing culture from the shake flagon as inoculum for the bioreactor. Control medium pH in bioreactor at 7.0 via programmed expansion of 2N NaOH/HCl through corrosive/base peristaltic siphons. Upset the medium in the bioreactor utilizing a level sharp edge turbine impeller turning at 150 rpm and keep up temperature at 330C by coursing chilled water utilizing FP 50 chiller (Julabo, Germany). Sparge nitrogen gas at 0.5 vvm in the bioreactor to give anaerobic conditions during the fermentation. Pull back samples at ordinary time frames h from the bioreactor and break down for biomass, lingering glycerol and 1,3-PD.

❖ **1,3-PD MODEL EQUATIONS:**

The model consists of a system of differential material balance equations which describe the batch dynamics of growth & 1,3-PD production. These equations are summarized below:

$$\mu = \mu max\ (S/S + KS)\ [1- (S / Sm)a]\ [1- (P/Pm)b] \quad (1)$$

$$qs = - \{(1/Ymax)\ \mu + m\} \quad (2)$$

$$qp = K1\mu + K2 \quad (3)$$

where μ- specific growth rate, qs - specific substrate consumption rate, qp- specific product formation rate, Sm- critical substrate concentration, m- maintenance energy constant, Pm- critical product concentration.

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Report of Summer Internship – 2020 on the topic

Molecular Circuits Using Synthetic Biology

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Sign of Student

Sign of Supervisor

INTRODUCTION

Synthetic Biology is the branch of Molecular Biology that deals with the use of synthetic or unnatural methods to overcome problems of Biology. The first use of the term was Barbara Hobom who described bacteria that were genetically engineered using rDNA technology. The bacteria is a biological entity that was changed by human intervention and hence synthetic. That is earlier synthetic biology was largely synonymous with bioengineering. [1]

Currently, the term Synthetic Biology is used in 2 broad classes:

- For the use of synthetic molecules to reproduce behaviour similar to natural molecules with the motive of creating artificial life.
- Another use is the process of taking out molecules from one biological system and inserting it into another system for performing unnatural tasks by the system.

Synthetic biologists aim to assemble components that are synthetic to generate systems that support Darwinian evolution and hence are biological. By doing so, scientists hope to understand ‘natural’ biology. [1]

Over the last few decades, sequencing and synthesizing techniques of DNA have made us capable of understanding and engineering biological systems. DNA oligonucleotides and their assembly into synthons, genes, circuits, and even entire genomes by gene synthesis methods have enabled us to design, build, test, and learn biology from a different perspective. [2]

Since the beginning of life on Earth, nature has evolved and created multitudinous gene circuits that enable cells to live and to adapt to environmental changes. These circuits range from simple ON/OFF switches to complex Boolean circuits to oscillatory circuits. Synthetic Biology aims to redesign and/or extract the circuit mechanisms to extract useful information from them and to make new circuits from these that can further help humankind in controlling various biological phenomena. [3]

WHAT COMPRISES OF GENETIC SWITCHES?

Switches play a very important role in any circuit. In any complex electronic circuit, there are a lot of fundamental ON/OFF switches involved to give us the correct output. Similarly in any complex genetic circuit, there are a lot of ON/OFF switches that sum up together to give out the correct output or gene expression. [3]

For engineering advanced genetic control elements or switches, we must first be aware of basic building elements, their characteristics, and their compatibility with each other and within the system. In general, genetic control elements consist of an input domain that senses the presence of a trigger and an output domain that eventually affects the target gene expression. Based on these several types of switches that act as transcriptional or post-transcriptional control elements have been identified and developed over the past few decades. [3]

TRANSCRIPTIONAL REGULATORS

Transcriptional regulators are gene control elements widely used in biotechnology and synthetic biology. The underlying mechanism of these elements is site-specific recruitment or blockage of RNA polymerase at a defined gene. Transcriptional activator domains are widely used in combination with minimal or weak promoters whereas repressors can downregulate strong promoters. [5]

Programmable DNA Binding

Inducers cannot externally control the binding of TALE (transcription activator-like effector) to the DNA yet they have received a lot of attention for the reason being that their DNA recognition motif can be reprogrammed genetically. The structure of these proteins includes central repeat domains that help in a sequence-specific DNA binding. Similarly, zinc finger domains can be reprogrammed for recognition of defined DNA sequence. The drawback of zinc finger domains is that they are much more difficult to reprogram that TALEs. Nevertheless, using these two techniques molecules have been engineered to recognize predefined operator sites on the DNA. Yet programmable target operator sites have been mainly used in genomics research and are yet to find ways into synthetic biology.[6]

Dimerization Dependent Transcriptional Activation

For systems that do not originally respond to an external stimulus, Ligand dependency is engineered into these systems. Systems were developed to exploit ligand inducible protein dimerization by which conditional gene expression relies on the trigger-induced dimerization of two protein domains. The fact that modularity of dimerization dependent transcriptional activators only requires appropriate dimerization domains makes it possible to expand the triggers to EM waves. This can be very useful in case of plants where sunlight that consists of EM waves can act as a trigger. [3]

Bacterial repressor as ligand – dependent repressor

In these systems, in the absence of a ligand, the gene is expressed and when the ligand is present the system turns off gene expression. This works as a NOR gate for biological systems. This system is highly modular and the bacterial repressor is also easily interchangeable. For example, the tetracycline dependent transactivator (tTA) system consists of the tTA protein and our gene of interest under the control of a minimal or weak promoter proximal to tTA binding motif. In the absence of tetracycline the gene expression is turned OFF whereas as soon as tetracycline becomes available, the gene expression is turned ON. [7]

Rewiring internal pathways

Rewiring of cellular pathways is a promising alternative to engineering orthogonal chimeric transcriptional regulators. Downstream signaling chain reactions facilitate the control of the desired gene if its expression is placed under the control of the corresponding transcription factor. An example of this is the heterologous expression of a G-Protein coupled receptor (GPCR) in a mammalian target cell. [8]

POST – TRANSCRIPTIONAL REGULATORS

RNA interference and similar recent techniques have made Post-transcriptional regulators the area of focus recently. Scientists have started harvesting it's potential to engineer novel genetic control elements.

RNA Interference

RNA interference refers to the downregulation of gene expression by sequentially targeting mRNA degradation by RNA induced silencing complex (RISC). Since the machinery for RNAi is pre-existing in mammalian cells, this mechanism can be used to knock down the expression of specific genes by introducing the appropriate dsRNA. To control the efficiency of RNAi, expression of the corresponding dsRNA which is usually by shRNA (short-hairpin RNA) can be placed under the control of ligand-dependent transcriptional effectors. [9]

mRNA stability

In addition to RNAi – mediated post-transcriptional regulation, mRNA stability can be controlled directly. Elements are introduced into the UTRs that removes the 5` cap or the poly-A tail. This reduces the half-life of the mRNA, which ultimately results in inhibition of targeted gene expression. [10]

Splicing Efficiency

The splicing sites can be hindered by proximal RNA aptamers which bind sterically demanding proteins and hence essentially blocking the sites from the reach of the spliceosome. This enables us to decide when splicing would take place and when it would not take place and hence essentially giving us control over the genetic expression. [11]

Protein Stability

Cellular protein levels are defined by the efficiency of gene expression as well as by protein stability. Therefore, if we destabilize the protein, it would get degraded. This would behave as if the protein was never formed which gives us the same results as other gene regulatory elements give. [12]

WHAT ARE GENETIC CIRCUITS?

A complex network of genetic switches represents a genetic circuit. They provide an output response that is based on an input that can be a Ligand or even a process such as transcription.

Gene Expression Cascades

They are the most basic types of circuits that comprise of serial arrangements of control elements discussed earlier that eventually produce feedback loops and expression cascades.

In this, both negative and positive feedback loops are possible. Former ones give a signal to stop the process once the desired or programmed level is achieved. On the other hand, positive feedback loops give a signal to increase production once the required level is reached. [13]

These are multi-step processes which can control the expressional various levels. Thus not only do they provide a higher level of complexity and control but also require the timing of expression to work smoothly. [3]

Logic Gates: Biocomputing

This is a very new and promising subdomain of synthetic biology. Logic Gates are the basis of any electronic device and hence the establishment of efficient logic gates in living cells can be a good way to construct bio computers having great parallel calculation power.

- The Boolean NOT IF gate that exhibits expression output only in the presence of one input alone was engineered by using the pristinamycin I–responsive transsilencer Pip-KRAB and the 2-(1Vhydroxy-6-methylheptyl)-3-(hydroxymethyl) butanolide (SCB1)-responsive transactivator scbRvp16. [14]
- NAND gate, which exhibits repressed reporter output only in the presence of both ligand inputs, was implemented by engineering the two transactivators E-vp16 and Pip-vp16 to control SEAP reporter expression from two distinct constructs. [14]

- NOR gate that gives reporter output only in the absence of either ligand was successfully engineered by using the same transactivators, E-vp16 and Pip-vp16, in a different circuit. In this case, the transactivators were arranged in a regulatory cascade in which an E-vp16-responsive promoter drove Pip-vp16 expression. [14]

These three are considered as the most important gates as these can further create any logic gate we need. Successful implementation of these three is a great achievement towards the creation of biocomputers.

Bandpass Filter

Bandpass filters are devices that originate from optics and electronics. They allow a specific frequency to pass through them and block the frequencies higher or lower than that. Hence, a biological Bandpass filter controls the output of the gene by filtering for a specific inducer concentration and blocking deviant concentration. This allows for a controlled gene expression that is based on the presence of a specific ligand and at a specific concentration of ligand.

These circuits have two major components: One that induces the gene expression upon ligand addition and the other that results in repression. Combination of these components yields peak expression at medium ligand concentration. [15]

They can be of extensive use in biological systems. They can be used to check for correct expression of sensitive genetic products like proto-oncogenes and hence reduce the chances of cancer. Another use can be for the treatment of diseases that occur due to the overexpression of genes. [4]

Toggle Switch

A toggle switch is a circuit that can change output between two domains based on the type of input it gets. In these, the input may or may not have an impact on the maintenance of states but have a role in switching between states. In a biological context, repeated ligand input causes reporter to switch between high and low, whereas removal of the ligand keeps it in the most recent state. The first genetic toggle switch for mammalian cells was engineered based on two transcriptional silencers, E-KRAB and Pip-KRAB, which are macrolide streptogramin responsive respectively. [16]

Oscillator

An oscillator interchanges repeatedly and autonomously between two distinct states. It is of utmost importance in Biology. The natural circadian rhythm of organisms is based on the oscillatory interchanges. Using a complex network the circadian clock controls expression of genes based on the 24-hour circadian rhythm enabling us to perform different functions depending upon the time of the day. These circuits can be very important in P4 medicine. If a gene were inserted into an organism that has a therapeutic effect as a substitute for a medicine, it would be very important for that gene to activate periodically at a given time without any external stimulus. Such a genetic oscillator was reconstructed artificially by following the building principle of the endogenous oscillator. The aim was to achieve self-sustaining oscillation of reporter expression based on transcriptional activators and repressors. Therefore, a destabilized green fluorescent protein (GFP) variant that offered an advanced temporal resolution of gene expression was placed under the control of the tTA transcriptional activator. Because tTA directly controlled GFP transcription, tTA is also required to exhibit an oscillating expression pattern. To this end, tTA transcription was put under auto-regulated control to construct a tTA-dependent feedforward loop that was responsible for the transition from the OFF to the ON state. [17]

Rewiring Internal Pathways with functional RNAs

Rewiring of pathways means changing the series of reactions. Hijacking the internal pathways could make it possible to implement artificial circuits on a limited number of additional constructs that supplement, and therefore rewire existing networks. Smolke and colleagues engineered a transcript that contained three exons and two introns. The first exon encoded a common 5`-UTR, the second a stop codon, and the third the gene of interest. In this splicing setup, the inclusion of the middle exon in the processed mRNA led to no gene expression. However, exclusion resulted in efficient full-length translation of the gene of interest. [18]

Considering the important role that RNAi plays in endogenous gene regulation, rewiring RNA input, in addition to the protein signal cascades, is a promising approach for the engineering of novel gene circuits. The upregulation of specific endogenous miRNAs was shown to trigger cancer formation, which makes such

upregulation a reliable biomarker as well as an interesting target for cancer therapy. [19]

CONCLUSION

Synthetic Biology is a relatively recent scientific discipl9ne that aims to study biological systems synthetically and to use natural elements synthetically to create life. Being such a young discipline whose first appearance in literature is merely 2 decades old in the form that we use it currently, it has achieved some impressive milestones. During this course, many genetic control elements have been discovered and reported by synthetic biologists worldwide. These control elements are at both transcriptional and posttranscriptional level. This has made us able to control the genetic elements using small molecules, Inducers, ligands, metabolites, proteins and even electromagnetic waves. By exploiting these control elements and the high degree of modularity they offer, some very interesting genetic networks have been made. These include positive and negative feedback loops, genetic inverters, oscillators, bandpass filters, toggle switches and even logic gates. This has enabled us to make reprogrammed cells that act as valuable tools for the development of novel and innovative therapeutic approaches.

Looking ahead, the development of chemically traceless and inexpensive gene regulatory systems based on inducers such as EM waves show us a promising future. Along with this, successful implementation of Boolean logic gates has successfully shown us the way for efficient biocomputers having large parallel processing power considering we can create multi-cellular systems deployed with logic gates.

More focus needs to be put on further therapeutic innovations by engineering cells harbouring more complex circuits that enable measurements of several host physiological parameters and that eventually act accordingly.

REFERENCES

1. Benner, Steven A., and A. Michael Sismour. 2005. “Synthetic Biology.” *Nature Reviews Genetics* 6 (7): 533–43. https://doi.org/10.1038/nrg1637.

2. Hughes, Randall A., and Andrew D. Ellington. 2017. “Synthetic DNA Synthesis and Assembly: Putting the Synthetic in Synthetic Biology.” *Cold Spring Harbor Perspectives in Biology* 9 (1). https://doi.org/10.1101/cshperspect.a023812.
3. Wieland, Markus, and Martin Fussenegger. 2012. “Engineering Molecular Circuits Using Synthetic Biology in Mammalian Cells.” *Annual Review of Chemical and Biomolecular Engineering* 3: 209–34. https://doi.org/10.1146/annurev-chembioeng-061010-114145.
4. Prelich, Gregory. 2012. “Gene Overexpression: Uses, Mechanisms, and Interpretation.” *Genetics* 190 (3): 841–54. https://doi.org/10.1534/genetics.111.136911.
5. Slansky, J. E., and P. J. Farnham. 1996. “Introduction to the E2F Family: Protein Structure and Gene Regulation.” In *Transcriptional Control of Cell Growth: The E2F Gene Family*, edited by Peggy J. Farnham, 1–30. Current Topics in Microbiology and Immunology. Berlin, Heidelberg: Springer. https://doi.org/10.1007/978-3-642-79910-5_1.
6. Boch, Jens. 2011. “TALEs of Genome Targeting.” *Nature Biotechnology* 29 (2): 135–36. https://doi.org/10.1038/nbt.1767.
7. Gossen, M., and H. Bujard. 1992. “Tight Control of Gene Expression in Mammalian Cells by Tetracycline-Responsive Promoters.” *Proceedings of the National Academy of Sciences of the United States of America* 89 (12): 5547–51. https://doi.org/10.1073/pnas.89.12.5547.
8. Durocher, Y., S. Perret, E. Thibaudeau, M. H. Gaumond, A. Kamen, R. Stocco, and M. Abramovitz. 2000. “A Reporter Gene Assay for High-Throughput Screening of G-Protein-Coupled Receptors Stably or Transiently Expressed in HEK293 EBNA Cells Grown in Suspension Culture.” *Analytical Biochemistry* 284 (2): 316–26. https://doi.org/10.1006/abio.2000.4698.
9. Jaskiewicz, Lukasz, and Witold Filipowicz. 2008. “Role of Dicer in Posttranscriptional RNA Silencing.” *Current Topics in Microbiology and Immunology* 320: 77–97. https://doi.org/10.1007/978-3-540-75157-1_4.
10. “Exogenous Control of Mammalian Gene Expression Through Modulation of RNA Self-Cleavage - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/15386015/.
11. “Engineering Splicing Factors With Designed Specificities - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/19801992/.

12. Banaszynski, Laura A., Ling-Chun Chen, Lystranne A. Maynard-Smith, A. G. Lisa Ooi, and Thomas J. Wandless. 2006. “A Rapid, Reversible, and Tunable Method to Regulate Protein Function in Living Cells Using Synthetic Small Molecules.” *Cell* 126 (5): 995–1004. https://doi.org/10.1016/j.cell.2006.07.025.
13. Kramer, Beat P., Wilfried Weber, and Martin Fussenegger. 2003. “Artificial Regulatory Networks and Cascades for Discrete Multilevel Transgene Control in Mammalian Cells.” *Biotechnology and Bioengineering* 83 (7): 810–20. https://doi.org/10.1002/bit.10731.
14. “BioLogic Gates Enable Logical Transcription Control in Mammalian Cells - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/15286985/.
15. “An Engineered Mammalian Band-Pass Network - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/20693530/.
16. “An Engineered Epigenetic Transgene Switch in Mammalian Cells - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/15184906/.
17. “System-Level Identification of Transcriptional Circuits Underlying Mammalian Circadian Clocks - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/15665827/.
18. “Reprogramming Cellular Behavior With RNA Controllers Responsive to Endogenous Proteins - PubMed.” n.d. Accessed July 2, 2020. https://pubmed.ncbi.nlm.nih.gov/21109673/.
19. Sayed, Danish, and Maha Abdellatif. 2011. “MicroRNAs in Development and Disease.” *Physiological Reviews* 91 (3): 827–87. https://doi.org/10.1152/physrev.00006.2010.

PHYSICO-CHEMICAL EVALUATION OF BIOSURFACTANTS FOR THEIR POTENTIAL APPLICATIONS IN BIOTECHNOLOGY

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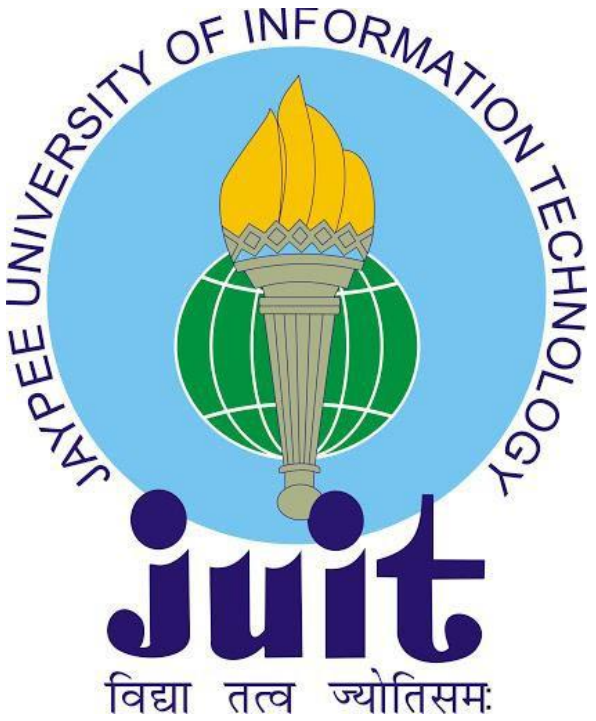

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Student Signature

Supervisor Signature

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In quest for this scholastic undertaking I feel that I have been particularly lucky as motivation, direction, course, co-activity, love and care all came in my way in plenitude and it appears to be very nearly an inconceivable assignment for me to recognize the equivalent in sufficient terms.

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ABSTRACT

Surfactants are amphiphilic compounds having both hydrophobic as well as hydrophilic moieties, thereby expressing the characteristics of both the groups. They tend to possess surface active characteristics, thereby decreasing the surface tension between the interfaces of either two liquids, liquid-air, oil-water interfaces etc. A common surfactant consists of a lipophilic group, usually a long-chain hydrocarbon moiety, and a hydrophilic group, which is both a charged or an uncharged polar group. Therefore, a surfactant consists of each a water-insoluble thing and a water-soluble component. Surfactants diffuse in water and adsorb at interfaces.

They resemble the chemical surfactants, containing each hydrophilic and hydrophobic moieties in the equal molecule. The hydrophobic tails structure the core of the aggregates, whilst the hydrophilic head is in contact with the liquid floor surrounding it. The form of aggregates relies upon on the chemical shape of the surfactants, due to the stability of measurement between the hydrophobic tail and hydrophilic head, which is measured by way of hydrophilic lipophilic stability i.e. HLB.

Diverse classes of surfactants can be characterized by the charge of their head gatherings, specifically cationic (positive charge); anionic (negative charge); non-ionic (non-charged and exceptionally hydrophilic); and zwitterionic (nearness of both negative and positive charge places, and a net charge equivalent to zero). The surface rheology of surfactant layers, including the versatility and thickness of the layer, assume a significant job in the solidness of froths and emulsions.

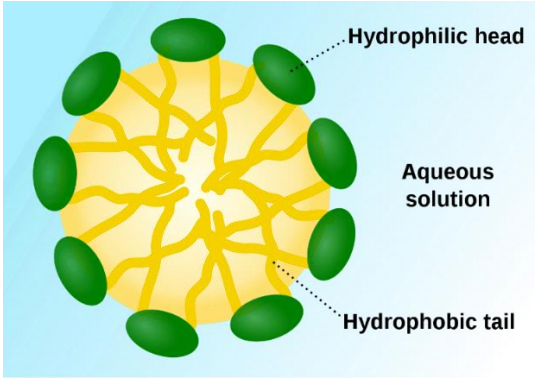


Fig 1: Structure of a typical surfactin molecule.

The biological entities themselves produce a wide array of surfactants, which are referred to as biosurfactants. The human body creates a wide cluster of surfactants like the Pneumonic Surfactant, being delivered in lungs, encourage breathing by expanding the complete Lung capacity. Microbial Surfactants are a wide assortment of basically differing mixes from microbial birthplace showing surface movement at the interfaces and possess ground-breaking attributes including high biodegradability, low poisonousness and unique organic exercises, emulsification activities, biocompatibility, thus making them suitable alternatives compared to their chemical/synthetic counterparts. Microbial surfactants are handily corrupted and are commonly considered as low or non-poisonous mixes. Microbial surfactants are known to segment at interfaces of liquid stages with particular polarities and hydrogen holding, in this way influencing the attachment of microorganisms.

TABLE OF CONTENTS

1. INTRODUCTION……. 5
2. OBJECTIVE…….. 6
3. BIOSURFACTANTS…… 6
4. PRODUCTION……. 7
5. PROPERTIES……10
6. CHARACTERIZATION……. 11
7. APPLICATION……. 14
8. CONCLUSION…….. 29
9. FUTURE PERSPECTIVE AND CHALLENGES……. 30
10. REFERENCES…….. 31

1. INTRODUCTION:

The phrase surfactant is a combination of surface-active agent. Surfactants alter the properties of the surface and interfacial tension of a liquid allowing the formation of microemulsions, which lead to solubilization of oil in water and water in oil. It is due to this phenomenon that they are widely used in many industries. Surface tension is a phenomenon which measures the force of attraction between the liquid molecules. It is a critical parameter for evaluating the effectiveness of a surfactant, leading to decrease in the surface tension when their concentration in the solution increases, which leads to formation of micelles. Micelles are formed due to the inability of lipophilic region of the surfactant to form hydrogen bond in aqueous phase and thereby lead to increase in free energy of the system. Dealing with this increased free energy is required to aid in isolation of hydrocarbon tail from water by its absorption onto organic or aqueous surfaces enabling the hydrophobic region oriented towards the centre while hydrophilic region facing water. Surfactants lower the interfacial tension between immiscible fluids making them miscible, due to formation of new additional surfaces. Micelles are defined as aggregated molecules containing both hydrophobic and hydrophilic groups, with hydrophilic groups oriented towards water, while hydrophobic group oriented towards oil. The formation of micelles leads to distribution of hydrophobic compounds into the pseudo core residing in the centre thereby enhancing solubility. This leads to better dispersion od compounds and lead to increased mobility of adsorbed hydrophobic soil contaminants by decreasing the capillary forces. The minimum concentration of surfactant required to produce a maximum decrease in surface tension of a liquid is regarded as Critical Micelle Concentration (CMC).

Biosurfactants are surface active bio-compounds produced by microorganisms and are considered as alternatives to petroleum derived chemical surfactants. These green compounds have lower critical micellar concentration compared to that of synthetic ones and they lead to higher decrease in surface tension of oil-water or air-water interfaces to a very low value. This property makes microbial surfactants great froth stabilizers and emulsifiers. Microbial surfactants present various focal points over the compound ones, in particular with respect to their biodegradability, mild creation conditions, ecological compatibility, lower toxicity, high selectivity, and explicit action at extraordinary temperatures, pH, and salinities.

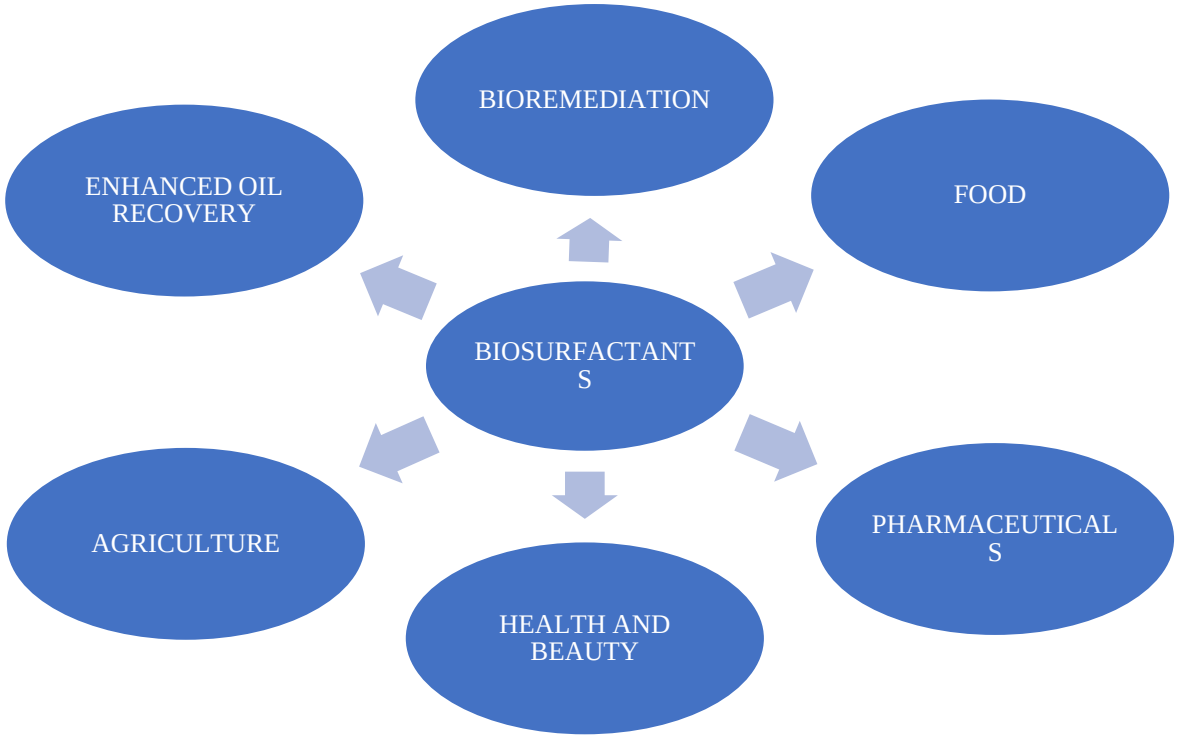


Fig 2: Applications of biosurfactants in various industries.

2. OBJECTIVE:

The target of this examination audit was to get comfortable with the properties, creation, and uses of biosurfactants in present day times. With the assistance of this audit, I hope to have a superior knowledge for biosurfactant creation and discover more applications which can be helpful for humankind.

3. BIOSURFACTANTS:

Surfactants are typically natural compounds that are amphiphilic, that means they incorporate each hydrophobic groups and hydrophilic groups. Biosurfactants are amphiphilic compounds having both hydrophilic and hydrophobic groups in it.[1] The hydrophilic region might be carbohydrate, amino acid, cyclic peptides, phosphate, carboxyl acid or alcoholic groups, while hydrophobic region comprises of a long chain fatty acid, hydroxyl fatty acids, α-alkyl-β-

hydroxy fatty acids etc. Other than bringing down the fluids surface pressure, these moieties can likewise incredibly affect the interfacial conduct and mass exchange, as they likewise bring down the interfacial strain between diverse fluid stages on the interfacial limit existing between immiscible stages.[11] Microbial surfactants possess an intense ability to lower the interfacial tension and show diverse properties as emulsification, lubrication ability, phase dispersion, detergency etc.[17] They are majorly used in food, petroleum, cosmetics industries, environmental, bioremediation, environmental and even pharmaceutical industries. Surfactant molecules are amphipathic in nature that get partitioned between two phases, having varying degree of polarity. Microbial surfactants are best and productive at their CMC which can be 10-40 times lower than that of substance surfactants, in this way less surfactant is important to get a most extreme lessening in surface pressure. Microbial surfactants are handily corrupted and are commonly considered as low or non-poisonous mixes. Microbial surfactants are known to segment at interfaces of liquid stages with particular polarities and hydrogen holding, in this way influencing the attachment of microorganisms. The presence of biosurfactant in a media can be detected by various techniques using colorimetric analysis, emulsification index determination, drop collapsing test and thin layer chromatography.

4. PRODUCTION:

Biosurfactants are obtained from non-exhaustible renewable sources thus having high surface activities, along with high specificity and the ability to function under extremes of conditions. Generally produced by aerobically growing microorganisms utilizing feedstocks as source of carbohydrates, fats etc. Biosurfactants are actively secreted into the culture medium and are supposed to aid in growth of microbes, by facilitating transport of solutes that are insoluble, across the cell membrane. They are usually non-ionic or anionic moieties and have both the lipophilic as well as hydrophobic groups.

Both high and low molecular weight biosurfactants are derived from microorganisms. Low molecular weight biosurfactants includes glycolipids like trehalose, fructose lipids, sophorolipids while peptidyl lipids include surfactin, polymyxin, etc. Surfactin is a biosurfactant produced by *Bacillus subtilis*, which possesses amphiphilic structure and serve as a potent inhibitor of bacterial and tumour growth, and are associated in lowering the surface

tension of the fluids. High molecular weight biosurfactants on the other hand are amphiphilic polysaccharides which are concerned in providing a stable emulsion and do not lower the interfacial tension.[21] Due to their ability of producing of stable emulsions they facilitate in strong adhesion of bacteria to hydrophobic surfaces. Most of the biosurfactants are obtained from *Arthrobacter*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Acinetobacter calcoaceticus*, *Candida lipolytica*, *Corynebacterium*, *Nocardia*, *Bacillus subtilis*, *Bacillus licheniformis*, *Candida spp.*, etc. Majority of biosurfactants are produced from substrates which are insoluble in water.

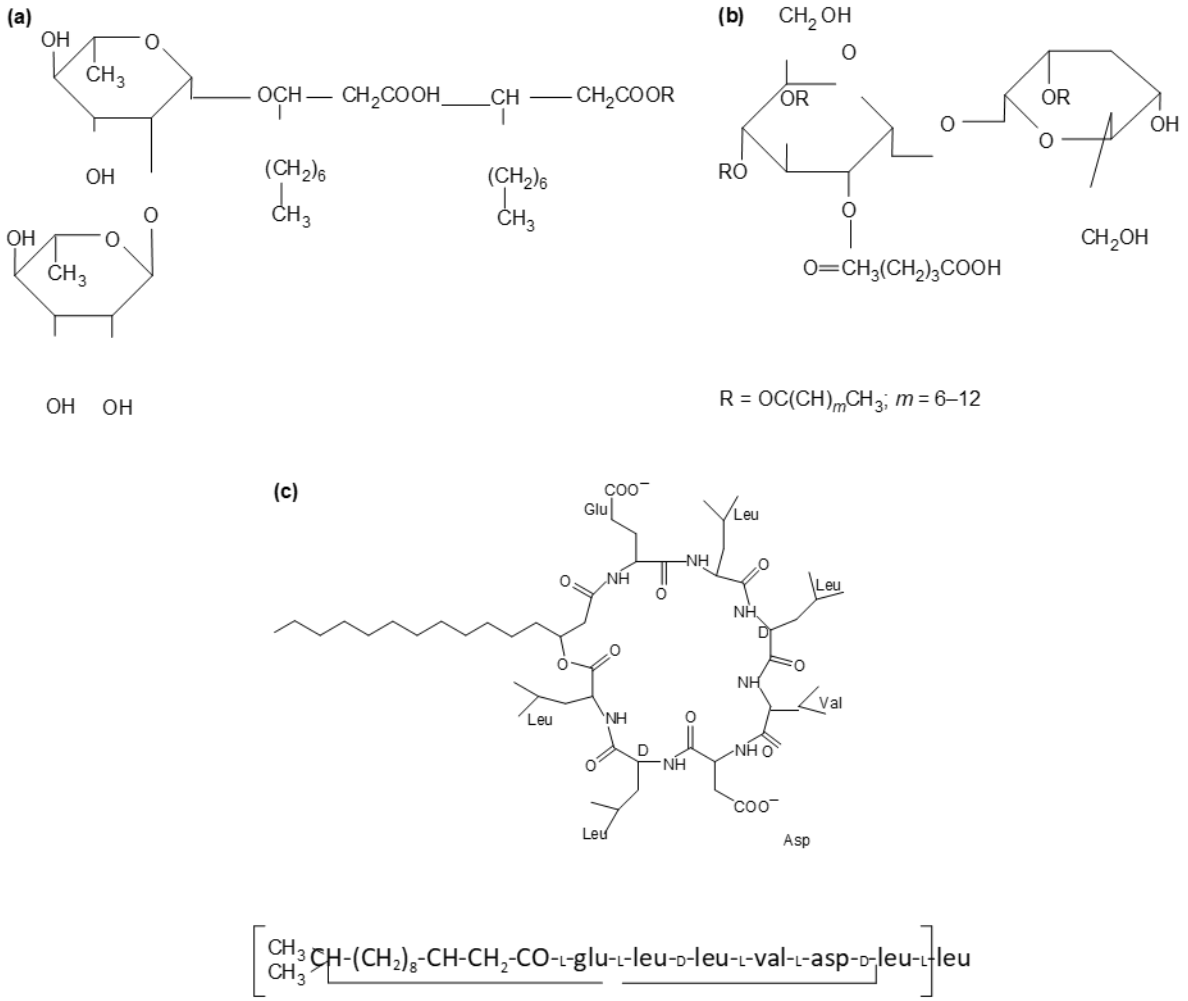


Fig 3: (a) Structure of dirhamnolipid. (b) Structure of trehalose lipid. (c) Surfactin structure

Researchers have obtained biosurfactants by growing a culture of *Candida lipolytica* on groundnut oil. Similarly, *Candida glabrata* was grown on vegetable oil to produce biosurfactants. Similarly, rhamnolipids were also produced from low cost carbon sources using

Pseudomonas aeruginosa like soybean, cottonseed, corn oil etc. Also, rhamnolipids were obtained using restaurant waste oil in bioreactor configuration using the strain *Pseudomonas aeruginosa.* Another low-cost medium was reported having Cassava waste water and waste cooking oil to obtain rhamnolipids.[30] Endophytic fungi are also been used to obtain biosurfactants, they are found in tropical areas on trees like *Piper hispidum*, which act as a potent source for ultimate production of biosurfactants.[8] The biosurfactant derived from *Candida utilis*, has low cytotoxicity, high antioxidant activity along with thermal stability, which makes it a suitable choice to be utilized in food industries. The best portrayed microbial surfactants incorporate Glycolipids and lipopeptides. *Pseudomonas aeruginosa* produce rhamnolipids (example of glycolipids),[19] trehalolipids created by *Rhodococcus erythopolis*, sophorolipids delivered by *Candida bombicola* and mannosylerythritol lipids (MEL) created by *Pseudozyma* yeasts.

To optimize the conditions for enhanced production of biosurfactants, metabolic pathway of the producing organism should be well known, also the chemical structure of biosurfactants should be well known too. Poultry farming waste and butter milk are found to be potential sources of nitrogen and carbon.[7] Hence this mixture was found efficient for production of SPB1 lipopeptide.

Petroleum derived synthetic surfactants happen to be the most widely used across different industries, primarily due to high cost of production of biosurfactants, also the fact that widescale production of these has not been defined yet to meet the industrial demands. This domain is being worked upon to find the ways to reduce cost of production, mainly focusing on use of alternate substates, microbial culture, culture conditions. Also use of low-cost medium can also aid in decreasing the cost of production.

A huge amount of organic waste is being produced via food, forest, municipalities and agriculture industries. Although biosurfactants are quite advantageous over synthetic surfactants they still are a bit costly to prepare. The only way to reduce their cost of production is modification in fermentation technologies and using renewable substrates and different microbial strains for production of biosurfactants. Further optimising operating parameters like temperature, pH, agitation speed and duration and efficient recovery of products, make them more efficient, but still a bit costly compared to synthetic ones. Use of low cost agro-industrial waste may overcome the issue of cost. It is necessary to develop techniques which allow easy

production and downstream processing of the product so as to be able to be used at a large scale. It depends upon the structure, composition and concentration of surfactant to choose a viable recovery method.it can be solved by using industrial by products like vegetal waste oil, like glycerol in appropriate concentrations does not inhibit growth and serves an excellent source of carbon.[22] Since huge amounts of waste generated by industries can be refined and used as excellent alternative substrates, thus producing low cost alternatives for production of surfactants as compared to that of petroleum derived surfactants.[11]

5. PROPERTIES:

Biosurfactants house certain unique properties like:

- Surface activity
- Biodegradation
- Detergency abilities
- Emulsification and de-emulsification activities
- Lubrication
- Wetting ability
- Foaming
- Solubilization
- Dispersion of phase etc.

Surface properties: Expansion of a surfactant to a given arrangement will bring down its surface strain because of the surfactant adsorption at the interface.[27] For a weakened arrangement, the more atoms adsorb at the interface, the lower the surface strain of the arrangement will be.

Hydrophilic-lipophilic balance: This boundary influences the soundness of the emulsion, speaking to the general commitment of hydrophobic tails and hydrophilic leader of the surfactant.[28] A low HLB favours water-oil microemulsions, and high worth favours oil-water microemulsions.

Critical packing parameter: To lessen the contact edge of the water with hydrocarbon chains, surfactant atoms will in general structure totals in arrangement with the chains situated to the inside and encased in the total.

Spontaneous curvature: Conglomeration can be legitimized dependent on the spontaneous bend. The favoured arch will likewise rely upon the general extent of polar and non-polar volumes.

Winsor R ratio: The proportion of the complete interaction energies (per unit zone of the interface) of the surfactant for the Oil and Water stages is known as the Winsor-R proportion. R< 1, demonstrates the water-surfactant connection is stronger than the oil-surfactant collaboration; R>1, proposing that the quality of oil surfactant cooperation is more grounded than the water-surfactant association; and R=1, the circumstance in which the communications are balanced.[3]

Self-assembly: Self-assembly comprises in the capacity of surfactant particles to self-associate in a given solvent, framing various kinds of totals and structures of colloidal measurements. These structures can be of restricted size or huge with network in one, a few measurements.

6. CHARACTERIZATION:

The characterization of structures was carried out using various spectroscopic techniques by obtaining Infrared spectra, Nuclear Magnetic Resonance was also carried out to characterize structures. Fatty acids were characterized using a characteristic reaction with diazomethane followed by final analysis using Gas chromatography and Mass spectroscopy. The results of FABMS were obtained by dissolving glycolipidic samples in glycerol to be used as probe matrix. Following it the alkaline lysis of glycolipids were carried out using reflux with 0.5 N NaOH solution for 12 hrs at 40°C. Fatty acids upon extraction with chloroform and methylation with diazomethane yielded a lipid sample for GC-MS analysis. Acid hydrolysis was carried out using refluxing of the sample with 2 N HCl for 2 and a half hours. Thin layer chromatography was carried out using different solvent systems to analyse sugar moiety. The interfacial and surface tensions of organic extract was measured using Lauda Automatic

Tensiometer TE-1 using De Nuoy ring method. Aqueous solutions here were acidified with pH 3 and 1 N HCl, then made basic with pH 9 and 1 N NaOH, the pH was recorded using Radiometer pH meter 28.

Added NaOH to the extracted biosurfactant leading to production of carboxylic acid salt of sodium, followed by washing with acetone and filtration using sintered glass. The precipitate so obtained was diluted with distilled water and was acidified using HCl for acid recovery and ethyl acetate was used for extraction. The gas filtration was performed using esterification of biosurfactant to get methyl esters of fatty acids.

The thermal analysis was performed in a thermal analyser, following successive steps of heating and cooling in an atmosphere of nitrogen.

Antioxidant activity was tested out by using an aliquot of 0.1 ml at varying concentrations of the biosurfactant having 1 ml of sulphuric acid, sodium phosphate, ammonium molybdate and subjected to water bath at a temperature of 90°C for 1 and a half hour. Optical density was recorded at 695 nm and expressed relative to a control of ascorbic acid having 100% antioxidant capacity. It was also tested using DPPH assay, which stands for 2,2-diphenyl-1-picrylhydrazyl. It was added to different tubes having different concentrations of biosurfactants and was incubated in the dark for 30 mins. Absorbance was measured at 517 nm and the percentage of inhibition activity was calculated using the formulae:

$$\%I = \frac{(Absi - Absf)x\ 100}{Absi}$$

where Absi is absorbance of control while Absf is that of biosurfactant.[6]

For Superoxide Sequestering test to check the antioxidant activity, the isolated biosurfactant was diluted using phosphate buffer, methionine solution, EDTA, riboflavin solution and nitro tetrazolium blue chloride and placed in a tube, the control had all of these except the biosurfactant. They were subjected for 15 mins to fluorescent lights, and reading was recorded at 560 nm.[6]

The cytotoxic activity of the biosurfactant was evaluated using MTT assay. (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) i.e. MTT protocol was designed using

fibroblast cells of mice and macrophage cells of mouse, kept in a culture flask having 5% CO2 and 37°C. Trypsin was used to detach the adhered cells and were then added to a 96 well plate having Dulbecco modified eagle medium, incubating this setup at 37°C with 5% CO2 for a day. Following this biosurfactant was added to this mixture under the prevailing same atmospheric conditions for 72 hours. DMEM medium alone acted as negative control, while positive control comprised of phosphate buffer. After the incubation MTT stain was added to the mixture and allowed incubation of 3 hrs. Following it, dimethyl sulfoxide was added and OD was recorded at 560 nm. Inhibition percentage was calculated by means of computer software.

Various classes of surfactants can be characterized by the charge of their head gatherings, specifically cationic (positive charge); anionic (negative charge); non-ionic (non-charged and exceptionally hydrophilic); and zwitterionic (nearness of both negative and positive charge places, and a net charge equivalent to zero).[1] The elements of assimilation rely upon the diffusion coefficient of the surfactant. As the interface is made, the adsorption is restricted by the dispersion of the surfactant to the interface. At times, there can exist a vivacious hindrance to adsorption or desorption of the surfactant. Such vitality hindrances can be expected to steric or electrostatic shocks. The surface rheology of surfactant layers, including the versatility and thickness of the layer, assume a significant job in the solidness of froths and emulsions.[29]

Microbial surfactants can be sorted by their method of activity, sub-atomic weight and general physicochemical properties. microbial surfactants are commonly sorted by their synthetic strategy and sub-atomic weight, as low (for example glycolipids and lipopeptides) and high atomic weight (for example polysaccharides, proteins and lipoproteins) surfactants. In heterogeneous frameworks, microbial surfactants structure an atomic interfacial film that influences the wettability and surface vitality of the first surface. Other than bringing down the fluids surface pressure, these movies can likewise incredibly affect the interfacial conduct and mass exchange, as they likewise bring down the interfacial strain between diverse fluid stages on the interfacial limit existing between immiscible stages.

7. APPLICATIONS:

Commercially available biosurfactants are obtained using chemical methods from petrochemical industries. To reduce the use of chemicals, microbes and other sources have been explored for the production of surfactants. Plants synthesize saponins, humans synthesize biliary salts and glycolipids secreted by microorganisms are some examples of organic surfactants.

Since the term is being used in a broad sense, it also includes some of the by-products produced by yeasts, bacteria and some filamentous bacteria, like emulsifiers and dispersing agents, which are generally used in petrochemical industries, food and pharmaceutical industries. Surfactants are generally used in cleaning industries which produce detergents and soaps. Surfactants are also being used for bioremediation of hydrocarbon pollution and enhanced oil recovery. Biosurfactants are being used as emulsifiers in food industries. Some major applications are:

Gene transfection:

Transfecting genes into a cell is the premise of clinical quality treatment. Lipofection utilizing cationic liposomes is viewed as a promising strategy for bringing outside qualities into the focus on cells because of their high transfection productivity, low toxicity, and immunogenicity, simplicity of arrangement, and focused on application. Physicochemical properties of cationic liposomes namely, lipid pressing density, zeta potential, and shape influence the proficiency of quality transfection. The biosurfactant actuates the layer combination between the objective cells and the cationic liposomes, quickening the proficiency of quality transfection fundamentally.

It was discovered monolayers made out of L-α-dipalmitoyl phosphatidylcholine (DPPC) containing MEL-A had more prominent film ease than those containing just DPPC. MELs are structurally classified into four types Mel a, Mel b, Mel c and Mel d. these variations are derived by the organism are the carbon source used. Mel has a property of self assembly that can be

used in chain delivery and drug encapsulation processes.[12] It was observed a higher unsaturated fat proportion liposome had the option to combine the plasma film yet didn't convey DNA into the core, while a lower unsaturated fat proportion liposome neither intertwined with the plasma layer nor conveyed DNA into the core.

As drug delivery agents:

They show properties like emulsification, frothing, detergency and scattering, help discover their application as medication conveyance vectors.[16] Rhamnolipids and sophorolipids can be blended in with lecithin to get ready biocompatible microemulsions in which the stage conduct is practically harsh toward changes in temperature and salt fixation, in this manner making them alluring for corrective and medication conveyance applications.[1] Microemulsions acquired utilizing microbial surfactants are thermodynamically steady and their isotropic frameworks that structure immediately, notwithstanding their drawn-out soundness, simple arrangement and high solubilization limit are viewed as exceptionally encouraging fluid vehicles for future medication conveyance frameworks.[13] The consolidation of an emulsion into a gel expands its strength and proficiency when contrasted with other topical medication conveyance frameworks.

Micro-emulsion systems:

The basic components to create a microemulsion-based colloidal DDS contain a watery stage, an oil stage, a surfactant and typically a co-surfactant or co-dissolvable.[23] These structures can exemplify or potentially solubilize hydrophobic or hydrophilic medications within the sight of a scattered stage inside its basic centre, in this manner dividing the scattered stage from the constant stage. These frameworks are thermodynamically steady and display high solubilization limit and ultralow interfacial strains of oil and water, accordingly making them attractive for medicate conveyance applications.[18]

Silver nanoparticles have been orchestrated utilizing a quick microbial surfactant interceded amalgamation, by blending the surfactant and AgNO3 arrangements, trailed by NaBH4 and incredible mixing. Fluid arrangements of AgNO3, sanitized biosurfactant, n-butanol, and n-heptane were overwhelmingly mixed until homogeneous converse micelles were framed. At that point, NaBH4 was utilized to frame other opposite micelles. The two converse micelle arrangements were blended and a short time later ethanol was added to break switch micelles. The silver nanoparticles were hastened from the arrangement and disengaged by centrifugation. Rhamnolipids have been effectively used to integrate circular nickel oxide nanoparticles. Unsaturated fats have been proposed to assume a twofold job in the blend of nanoparticles, by settling O/W emulsions in this way adjusting the decreasing gatherings on the external side; and additionally, by diminishing metal salts into nanometals.

In production of nano-particles:

Nanoparticles are portrayed by their novel size and stable shape. The accessible procedures are capital serious, produce perilous squanders and flimsy nanoparticles with diminished focused on action. To follow greener bio-handling microbial surfactants are being used as another option. Gold nanoparticles are by and large progressively utilized in the field of medication and quality conveyance, directed treatment and imaging advances. Its helpful applications incorporate enemy of HIV action, hostile to angiogenesis, antimalarial movement, against ligament action and biohydrogen creation. Microbial surfactants can be utilized for elite nanomaterial creation, since they effectively structure an assortment of fluid precious stones in watery arrangements. Analysts balanced out the gold and silver nanoparticles delivered by surfactin. At pH 7 the nanoparticles were uniform in size, while they were anisotropic at pH 5 and 9. Organic combination of gold and silver nanoparticles were additionally completed utilizing the microorganisms *Bacillus subtilis*[1]. Gold nanoparticles were blended both intra- and extracellularly, while silver nanoparticles were solely shaped extracellularly. The nanoparticles were balanced out by surface-dynamic particles, to be specific surfactin or different biomolecules discharged by B. subtilis. Surfactin created by *Bacillus amyloliquefaciens* KSU-109 was likewise utilized for the combination of cadmium sulphide nanoparticles which stayed stable as long as a half year. Purged rhamnolipids from *P. aeruginosa* strain BS-161R were utilized to blend silver nanoparticles showing great anti-

infection movement against both gram +ve and - ve microorganisms. A glycolipid microbial surfactant delivered by *Brevibacterium casei* MSA19 was utilized as a stabilizer for the combination of steady and uniform silver nanoparticles. The production of nanoparticles is either intra or extra cellular.

Biofilm disruption:

Bacteria's possess the ability to adapt to their environment and express themselves accordingly. Some gram +ve and gram +ve bacteria show a unique phenomenon known as Quorum sensing by which they can communicate with each other and sense their own cell density. This ability of bacteria has been involved in formation of biofilms, although it further depends upon the nutritional environment available to bacteria to carry out QS activity. During the biofilm formation and maturation event the cells attached to the surface start to aggregate into microcolonies, which are surrounded by few cells referred to as water channels. Biofilms in food industries act as a prominent source of contamination and disease. Therefore, use of biosurfactants to disrupt the adherence of microbial cells on the surface prevent formation of biofilm on food surface and thus their spoilage is prevented. The use of surfactin and rhamnolipids in particular decreased the adhesion of microbial cells on the polypropylene surfaces.[26] Biosurfactants may also be used in health and hygiene products to prevent biofilm formation in the oral cavity.

Microbial surfactants or biosurfactants possess the ability of anti-adhesion and biofilm degradation. Biofilms produced by many fungi and bacteria are degraded by synthetically derived enzymatic surfactants like lauryl-glucose. *Pseudomonas aeruginosa* derived rhamnolipids, are a class of surfactants which are efficiently used in biofilm disruption. The overproduction of rhamnolipids inhibits biofilm production by blocking cellular aggregation and secondary colonization onto the preformed biofilms. They also disperse cells from biofilms.

The biofilms produced by *Pseudomonas aeruginosa* were allowed to form on the flow cells which acted as a growth chamber for the biofilm. The chamber was supplied with oxygen and nutrients from a medium flask containing 50% TSB using a peristaltic pump. The spent

medium was collected in a waste container. The air bubbles could have disrupted the process of biofilm formation, so they were confined from the tubing using a bubble trapper, and incubated this at 30°C for 48hr. For the analysis of biofilm production in flow conditions, a Bio Flux system having the ability to acquire image from the specialized cells housed within it, was used. To facilitate the growth of biofilms the microfluid channels were primed with 50% TSB, following which they were loaded with 10^7 CFU from an overnight incubated microbial culture of *Pseudomonas aeruginosa*[2]. The cells were allowed to adhere to the plate by allowing an incubation of 48hrs at 30°C. After the formation of biofilm following the incubation period, the planktonic cells were removed and PBS along with different treatments (containing rhamnolipids 0.4 g/L, caprylic acid 0.1 g/L, a combination of rhamnolipid and caprylic acid, SDS 0.8 g/L, a combination of SDS and caprylic acid) were added to the plate for 30 mins. The cells were stained using LIVE/DEAD cells to check the growth of biofilm.

The effects of different treatments were determined on the biofilm produced upon cover slips by observing under a microscope and used fluorescence microscopy to determine the cells attached to the coverslips, which were stained using the bacterial viability kit, which helped the visualisation of microcolonies and individual cells. It was observed that biofilm produced by the bacteria was inhibited in the presence of rhamnolipids as depicted by reduction in the active cell number and appearance of reddish-brown fluorescent cells. Addition of adjuvant like caprylic acid alone had no effect ton biofilm dispersion. Addition of caprylic acid with rhamnolipid had an enhanced effect on biofilm degradation, also this combination is quite effective even at low concentrations.

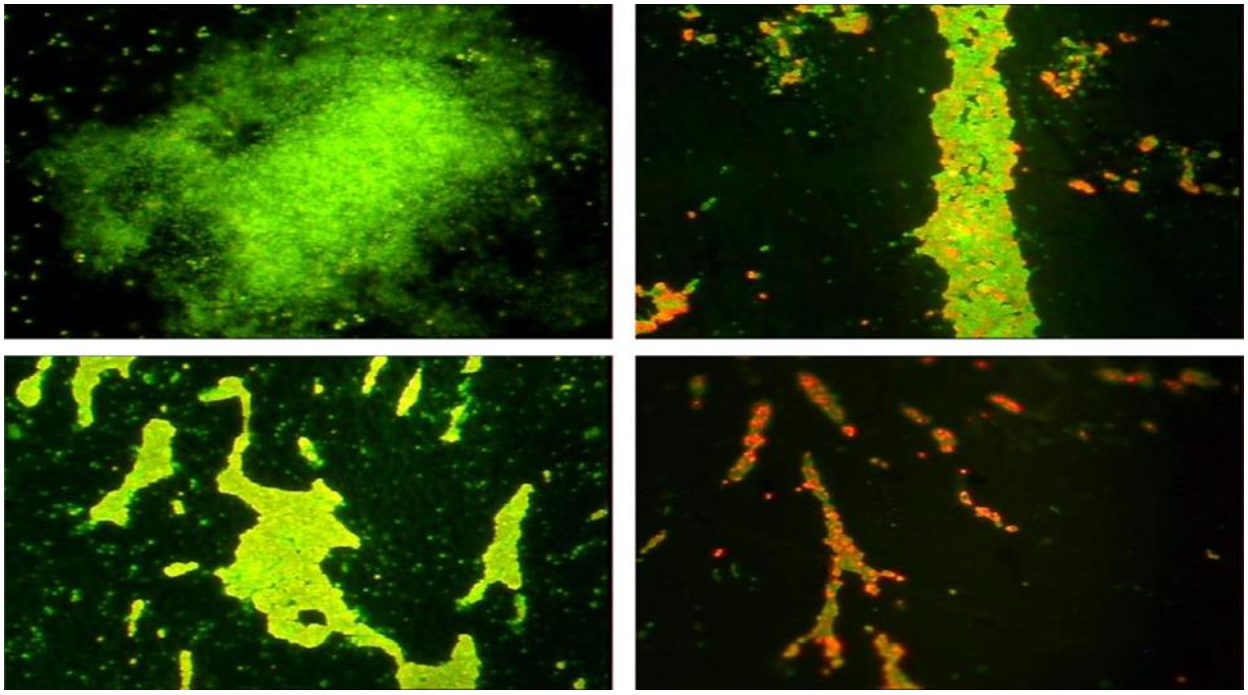


Fig 4: (a) Biofilm formation under Control

(b) Biofilm formation under the presence of rhamnolipid at a concentration of 0.4 g/L

(c) Biofilm formation under the presence of caprylic acid at a concentration of 0.1 g/L

(d) Biofilm formation under the presence of a combination of rhamnolipid (0.4 g/L) and caprylic acid (0.1 g/L).

To determine the effects of different treatments on biofilm disruption upon flow cells, rhamnolipids and caprylic acid were used. The cells were stained using the LIVE/DEAD bacterial viability kit and observed under confocal microscope. The biofilm was allowed to grow for about 2 days in the continuous flow mode. After about 30 minutes of treatment with rhamnolipid along with caprylic acid, the biofilm showed remarkable disintegration at its most important position. It was assumed to be due to the synergistic effect of rhamnolipid and caprylic acid.

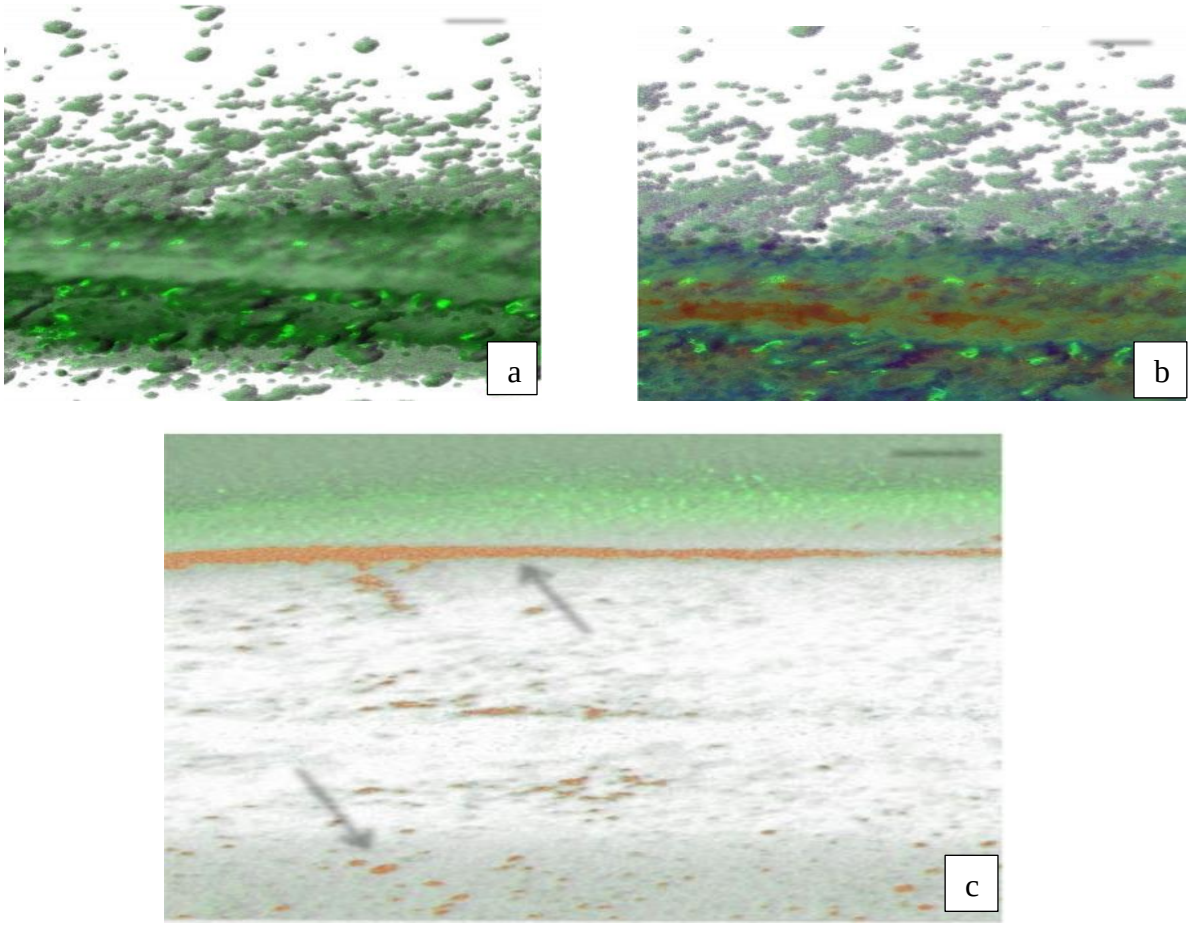


Fig 5: (a) Depicts the effect of rhamnolipid on cell viability.
(b) Depicts a significant effect due to rhamnolipid and caprylic acid treatment
(c) Depicts the compromised portion of biofilm where the cells are disrupted.

Biofilms are heterogenous structures displaying a high degree of resistance to antibiotics and biocidal compounds. Rhamnolipids have been associated to enhance the transport of bacteria through columns due to steric hinderance due to the contact between the surface and the bacteria. Rhamnolipids had been tested with various strains, media, etc. but they always tend to disrupt cell to cell adherence and biofilm disruption. The increased efficiency of biofilm disruption when rhamnolipid is used in combination with caprylic acid maybe due to synergistic effect. The rhamnolipids seem to removes the extracellular polymeric substances and microcolonies thus altering the biofilm environment and making cells more sensitive to intervention of caprylic acid which traverse through the cell membrane and causing cell death. The dispersal of biofilm may also occur due to the mechanical breakage of biofilms due to shear forces. SDS the anionic surfactant exhibits bactericidal activity against majority of oral

bacteria by penetrating the cell membrane and lysing the cell. Since SDS at a concentration greater than CMC causes protein unfolding, suggesting that SDS mediated disruption of the biofilm is due to denaturation of proteinaceous adhesions of the matrix. SDS when combined with caprylic acid had no effect. This was due to the shielding effect of caprylic acid thus protecting the cell membrane from the action of SDS, and therefore SDS is unable to disrupt the biofilm. Therefore, Rhamnolipids were proven to be the efficient antimicrobial agents in the presence of caprylic acid at a pH 5, as they induce cell death and lead to disruption of biofilms, even at low concentrations as compared to that of conventional methods.[24]

As anti-oxidants:

Mannosylerythritol lipids are versatile biosurfactants having interfacial and biochemical properties. MEL-C possesses free radical ion scavenging activity and have the highest antioxidant activity thus serves the highest protection, and are actively used in skin care cosmetics manufacturing. Similar activity is shown by RW1 a biosurfactant derived from *Bacillus subtilis,* proving a natural alternative to antioxidants.

As anti-adhesives:

Numerous biosurfactants display antimicrobial properties, as well as antiadhesive properties. Rhamnolipids and surfactin were shown to possess antiadhesive properties against *Listeria monocytogenes*, *Staphylococcus aureus* on polystyrene surfaces. Similar antiadhesive activity was shown by Lunasan produced by *Candida sphaerica* against many strains of *Streptococcus*, *Staphylococcus*, and *Candida* on plastic tissues.[25] These properties of biosurfactants serve their use as coating agents or in cooking utensils to reduce fouling, also in dairy industries. They are also being utilized as probiotics like *Lactobacillus acidophilus* strain.[20]

In food industries:

In a quest to find natural sources for obtaining biosurfactants rather than those obtained from genetically modified plants, many natural resources are being explored, mostly microbial sources as they are inexhaustible. An emulsion is a heterogenous system which has at-least one immiscible liquid dispersed in another one in the form of droplets. Their stability can be enhanced by using surfactants. Emulsification imparts, texture, consistency and dispersion patterns to food products. An emulsifier stabilized the emulsion by managing the clustering of globules.[14]

Additives are compounds having no nutritional value, but are added to modify, physical, chemical and biological properties during manufacturing, packaging and transport. Additives provide properties like thickening gelling, stabilizing and emulsifying. Glyceryl monostearate, a synthetic additive is widely used in food industries.[3]

Emulsifiers are generally surface-active agents which aid in emulsion formation due to their ability to reduce interfacial tension and stabilize the emulsion. Low molecular weight amphiphiles are used here to provide stability to various food products as beverages, dressings, sauces etc. Emulsifiers such and lecithin and gum Arabic derived from plants are being used as emulsifiers but they suffer some issues as functional limitations like use of microwaves. Lecithin is employed for production of cocoa powders which are a common ingredient for many desserts. Many of the modern-day food products like mayonnaise, butter, cream, salad dressings are produced using emulsions. Therefore, natural resources are being explored to produce bio-emulsifiers, e.g. one from *candida utilis.* Manno-proteins produced via *Saccharomyces cerevisiae* stabilizes water oil emulsion and is used to produce mayonnaise, butters etc. Most of the biosurfactants produced from yeasts and bacteria are operational at wide range of pH and temperature and are therefore used instead of conventional emulsifiers. Microbial surfactants are also used to provide texture, improve shelf life, and modify rheological properties of dough. In ice cream formulations they enhance texture, delay staling and stabilize fats.

Microbial biosurfactants are also utilized for making cookie formulations. The dough for the cookie was prepared in 3 different ways. Standard had all the normal formulations, while one of the formulations had biosurfactant replacing 50% of the pasteurized egg yolk of the standard formulation, while other formulation saw 100% replacement of pasteurized egg yolk with the biosurfactant, and they were ultimately baked.[10] Physical characteristics of the cookie was characterized after baking. Shape, texture, diameter, thickness, and spread ability were measured. Texture analyser was used to record the texture profile of the cookie dough before baking, while only firmness could be recorded after baking them. The protein content in both the alternative formulations was lower compared to that of standard formulation, since biosurfactant used here was a carboxylic acid derivative from *Candia utilis* and lacked proteins. Since the formulation which replaced egg yolk by 100% had high lipid contents, which happens to be the reason due to which energy formulation of this formulation was high.

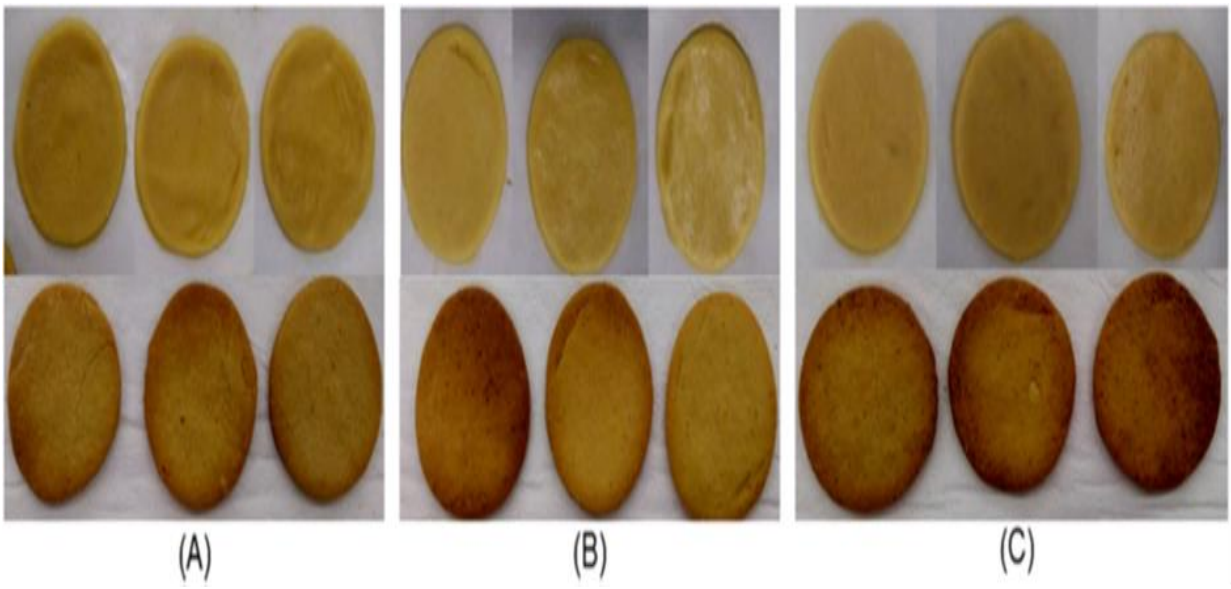


Fig 6: Cookies before and after being baked.

(a) Standard Formulation
(b) Formulation having 50% replaced egg yolk with biosurfactant
(c) Formulation having 100% replaced egg yolk with biosurfactant

Biodegradation:

Surfactants increase the access of the microorganism to low solubility compounds also compounds having recalcitrance, during the biodegradation process. Compounds being less soluble i.e. with high hydrophobicity get bonded strongly to organic matrix and are not desorbed easily to be available for degradation. During the hydrocarbon degradation, low molecular weight hydrocarbons are degraded first leaving recalcitrant compounds. Since surfactants increase the solubility in water and leads to better mass transfer, they are used to enhance biodegradation of hydrocarbons. To facilitate diesel hydrocarbon biodegradation, a suitable biosurfactant is assessed by assessing its physico-chemical properties, its biodegradability and its effect on the rate of biodegradation.[5] For selection purposes, environmental fate and toxicity was assessed by using K_{OC} and EC_{50} using a QSAR model. K_{OC} is defined as the soil organic carbon-water partition coefficient which is the ratio of chemical mass adsorbed on the soil per unit mass of the organic carbon of the soil divided by the equilibrium concentration of chemical in aqueous solution. EC_{50} is the half maximal effective concentration which is that concentration of a toxic compound which induce a response halfway between the maximum and baseline value, and is used to determine toxicity. QSAR is Quantitative structure activity relationship, a process using which the chemical structure of a molecule is correlated with a defined property like biological activity etc. Respirometric analysis was used to assess the biodegradability of the surfactants, using Biochemical oxygen demand apparatus. It was used to calculate the ratio of actual BOD to theoretical BOD. Solid phase respirometric tests were carried out to obtain, biodegradation of surfactants in soil samples.

The mobilities and the residence time of surfactant within the soil is affected by biodegradability, and sorption characteristics. For being efficient in biodegradation the surfactant must be less toxic and persistent, and must not have affinity towards soil, to allow proper distribution into the soil. Non-ionic surfactants are more biodegradable and less toxic as compared to other.

Bioremediation:

The level of relationship between natural and inorganic toxins is represented by the complex physical-concoction communications at interfaces. This relationship includes the sorption of toxins on the soil surface followed by their sequestering into the matrix of the soil, forming a Non-Aqueous Phase liquid (NAPL). NAPL are natural compounds which are insoluble in water thereby acting as a long-term pollutant, they are used in a continuous manner in water phase to replace dissipated concentrations, thereby decreasing the availability of contaminating particles to get biodegraded.[4] Bioremediation is a technique to enhance the degradation of biological compounds to lower the effect of toxins. Bioaugmentation is the practice of adding cultured microbes to facilitate degradation of pollutants, supplemented by using surfactants to facilitate desorption of pollutants lead to enhanced degradation of hydrocarbons. Surfactants are used to recover secondary oil during oil washing, and also in cleaning of oil pipes. Many synthetic and biosurfactants are employed for desorption purposes. Biosurfactants are not majorly used for bioremediation due to their high cost of production, but it may be overcome by using cheaper substrates for the microorganisms producing them like, industrial oil waste and agro-industrial wastes. Some of the major sources of biosurfactant production are *Pseudomonas aeruginosa, Corynebacterium, Nocardia, Bacillus subtilis, Bacillus licheniformis, Candida spp*., etc. The quality and quantity of nitrogen and carbon present in the substrate and the soil greatly determines the kind of biosurfactant produced. Limited nitrogen leads to increased production of biosurfactants aiding in bioremediation, therefore many bioremediation systems are not supplied with nitrogen to increase the microbial activity and lead to increased production of biosurfactants. Biosurfactants may be produced in the presence of oils and hydrocarbons.

Addition of hydrophobic organic substances in the culture media favours the isolation of hydrocarbon degrading bacteria from sites contaminated by oil, and are able to produce biosurfactants.[15] Aliphatic and aromatic hydrocarbons are used as a source of carbon for this purpose. The presence of organic compounds and metallic pollutants in the soil are the major cause of soil pollution. Organic hydrocarbons include Polycyclic aromatic hydrocarbons (PHA), Polychlorinated biphenyls (PCB), out of which PHA are more common due to it being involved in crude oil processing. Transport of pollutants in the soil is a function of non-linear rate limited biodegradation and sorption. Majority of hydrophobic contaminants bind to organic fractions in the soil due to sorption. Compounds like humic (like humic acid, humic)

and nonhumics (like proteins and waxes) are involved in the process of sorption.

The process of degrading pollutants in the soil depends upon physico-chemical and biological interaction of the pollutants and other biological factors. Degradation by means of microbial activity is in turn controlled by many factors like availability of contaminants to the microbes, pH, water, aeration, nutrients, temperature etc. Biodegradation can be enhanced by having a detailed insight of the metabolic activities of the microorganism. Microorganism form a stable oil in water emulsion which leads to increased oil degradation, thereby enhancing the availability of nutrients to the microorganisms. This phenomenon is achieved in natural systems by utilisation of autochthonous surfactant bio-population which lead to production of stable emulsions. Biosurfactants are able to solubilize the natural organic materials sorbed into the soil. Monorhabdolipid acid are utilized to remove NAPL which stays as a residue, while some *Rhodococcus* strains were used to degrade oil from sand etc. Endosulfan present in the soil was degraded by means of biosurfactant produced by *Bacillus subtilis*. Bio emulsifier alasan is used to increase the solubility of PAH, therefore leading to many folds increased in degradation and solubilities.

Soil is cleaned up using various techniques using soil exaction and disposal to landfill, phytoremediation, also plants immobilize the metals preventing their vertical or horizontal movement, thereby reducing the groundwater pollution. Microbes also have the ability to bind and form complex with association with the pollutants, thereby require more efforts and difficulties in degrading pollutants. Therefore, microorganisms can be used to remove heavy metals, by means of alkylation, or sulphur reducing bacteria is also used to remove heavy metals. Synthetic surfactants are toxic to degrading microorganisms therefore microbial surfactants are used for degradation of oil spills. Composting systems are used to increase the oxygen transfer and thereby reduce the pollutants in soil in a time of some months. An efficient way to enhance crude oil degradation in oil polluted environments is the introduction of hydrocarbon-oxidizing bacteria with high oxygenase activity, like Acinetobacter. Many complexes isolated from biosurfactant produced by bacteria, are isolated using methyl tertiary-butyl ether following sonication.

The main reason why the organic and metallic pollutants remain is soil for so long without being degraded is dependent on many factors like, they are not able to degrade them due to it being not available to them, also microorganism might not be able to carry out the essential

catabolic reactions, or inadequate interaction of the pollutants with the environment and the microorganism. Therefore, fungi and bacteria involved in the production of biosurfactants are important as they tend to solubilize the hydrophobic contaminants, facilitating their easy degradation. It was observed by keeping the contaminated sites devoid of Nitrogen, to enhance the activity of microbes degrading the soil pollutants.

Agriculture:

The health and productivity of plant crops are monitored on a regular basis to be sure about the quality of the food being obtained, and its availability to be able to meet the increasing demands of the growing population. Metabolic compounds referred to as green surfactants are produced by actinomycetes, yeast, fungi etc. Epiphytic and endophytic microbes are involved in biosurfactant production and they aid seed germination, inhibit the action of phytopathogens and as biocontrol agents for bioremediation. Since, we are trying to avoid the use of pesticides on plants to obtain chemically free plant products, rhizospheric bacteria are being explored that secrete metabolites which increase the yield of plant product. *Bacillus* and *Pseudomonas* are the majority of bacteria in Rhizobacteria group, which secrete metabolites having versatile applications as plant growth promoters, fungicidal agents like siderophores, phenazines, pyrrol nitrin, cyclic peptides, compounds such as biosurfactants and enzymes like chitinase and glucanase which possess hydrolysing activities.[9] These green compounds have lower critical micellar concentration compared to that of synthetic ones and they lead to higher decrease in surface tension of oil-water or air-water interfaces to a very low value. Rhamnolipids and lipopeptides are the majorly studied biosurfactants, which have found tremendous application in agricultural fields, along with other industries like pharmaceuticals, cosmetics, petrochemicals, food etc. Since they house amphipathic structures, due to which they promote seed germination, reduce the growth of phytopathogens and tend to induce systemic resistance in the plants.

The Rhizosphere portion of many cereals were used like rice, sorghum, millets, legumes like chickpea, groundnut, oil crops like sunflower", castor, grass etc were obtained from different districts were used for isolating the bacteria. They secrete metabolites which tend to promote plant growth and also act as antifungal. This ability was screened testing for Ammonia

production, by incubating bacterial isolates with 10 mL of peptone water for 48 hrs and 28-30°C. After incubation, 1 ml of culture broth was transferred to other tube and mixed with 1 ml of Nessler's reagent. Phosphate solubility was assessed by using Pikovskaya's agar medium having tricalcium phosphate. Phytase activity was assessed using phytic acid medium, following incubation for 2-4 days at 28-30°C temperature. After incubation zone of hydrolysis around the colonies was observed as a sign of confirmation. Isolates of the bacteria were tested for their antifungal activity. A culture of *F. oxysporum f. sp. ricini* was cultured on potato dextrose agar.

$$I\% = \frac{(C - T) \text{ x } 100}{C}$$

Where I= % inhibition of microbial growth

C= Radial growth of fungus recorded in the control plate

T= Radial growth of fungus recorded in the plate having bacteria.

All the bacteria were tested for ammonia production, antifungal activity, ability to solubilize phosphates and the capability to produce Indole Acetic Acid, via various experimental setups described above. The antifungal ability of bacteria against *F. oxysporum f. sp. ricini* was in between 72-80%. 67% of *Pseudomonas sp.* while 58% of *Bacillus sp.* possessed PGP traits.[9]

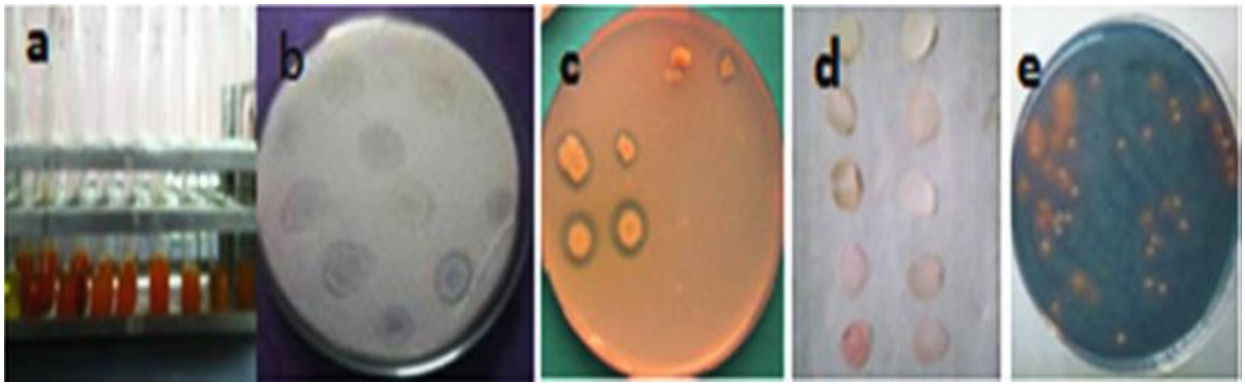


Fig 7: Different PGP traits tested.
(a) Ammonia production
(b) Solubilization of phosphate
(c) Phytase activity
(d) Indole acetic acid production
(e) Production of siderophore

It was observed that crude biosurfactant containing rhamnolipid and iturin, showed fungicidal activity against *F.oxysporum f.sp. ricini.*

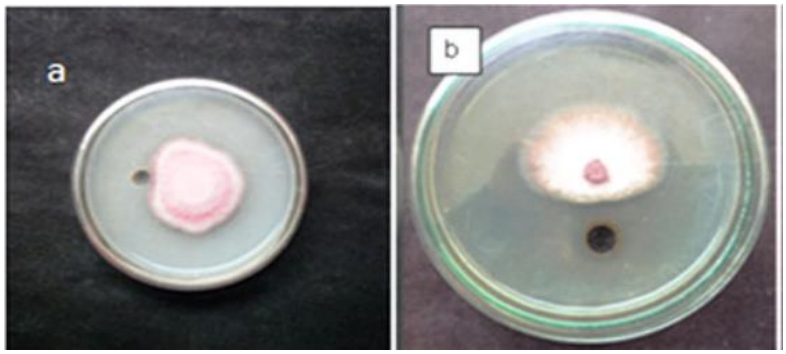


Fig 8: Antifungal activity of the biosurfactant against the chosen fungi.
(a) F.oxysporum f. sp. ricini inhibited by means of lipopeptide
(b) F.oxysporum f. sp. ricini inhibited by means of rhamnolipids

Rhizobacteria have been known to have plant growth promoting activity, alongside which they also depict strong antifungal or fungicidal activities making them a preferable choice as bioinoculants and in agriculture. Crop yield and sustainable agricultural conditions still prevail due to the regular application of chemicals which also pollute the environment. To overcome this shortcoming, bacterial metabolites which are non-toxic, tend to inhibit the growth of fungal pathogens and enhance seed germination are suitable alternatives for chemical compounds.

8. CONCLUSION:

Biosurfactants have certain unique properties like, surface activity, biodegradation, detergency abilities, emulsification and de-emulsification activities, lubrication, wetting ability, foaming, solubilization, dispersion of phase etc. Due to this diversity in properties they are used in a wide array of industries like petrochemical, petroleum, coal, metallurgical and mining industries, dairy, cosmetics, pharmaceuticals, food, agricultural and fertilizer, cosmetics, food and beverages etc. These compounds have been majorly obtained from bacteria and this is well documented, while obtaining these compounds from fungi is also possible, though there is less data on this subject. Many tropical species of plants both in India and Brazil have been used to isolate numerous endophytic microorganisms which produce biosurfactants. They are not used

at industrial scale, since their effect needs to be first determined by an experimental setup in greenhouse conditions and actual field studies, following which it can be stated if they can act as potential alternatives against the chemical agents.

9. FUTURE PERSPECTIVE AND CHALLENGES:

Microbial surfactants are non-ionic at low pH esteems, and anionic at high pH esteems because of the nearness of carboxylic gatherings. The total of surfactants in lamellar courses of action can happen on the off chance that one of the following conditions are watched. High surfactant focuses lead to a lamellar fluid crystalline stage, while twofold followed amphiphiles regularly structure bilayer sheets. After shutting, these sheets structure vesicles. Microbial surfactants can possibly be utilized in the targeted drug delivery. Additionally, pH-delicate liposomes containing rhamnolipids and di-oleoyl-phosphatidyl-ethanolamide have been depicted as effective frameworks for cytoplasmic conveyance of particles into cells. There is a critical need to investigate microbial frameworks to acquire surfactants and use them as effective drug delivery systems. Industries are seeking to find natural alternatives for biosurfactant production, to be utilized at industrial scale. Since currently biosurfactants are economically bit costly to prepare, we need to find ways to decrease the cost of production. Through the application of specialized cost-effective testing and discussion we might find a breakthrough to allow the use of biosurfactant at a large scale.

Since they are costly to produce therefore research found that the bacterial culture (producer of biosurfactant) could be grown using poultry waste flour and buttermilk, waste cassava fry oil, agro-industrial waste etc, thus serving as low cost alternative for producing the biosurfactants. Also, *Piper hispidum* was also identified as a potential alternative source for the isolation of microorganism producing biosurfactants, which can be utilized in various industries. Biosurfactants due to their higher biodegradability, biocompatibility and low toxicity, can be optimized by tweaking fermentation conditions, to obtain biosurfactants at an affordable cost and we might be able to produce them at a large scale.

10. REFERENCES:

1) Rodrigues, Ligia R. "Microbial surfactants: fundamentals and applicability in the formulation of nano-sized drug delivery vectors." *Journal of colloid and interface science* 449 (2015): 304-316.

2) Díaz De Rienzo, M. A., P. S. Stevenson, Roger Marchant, and Ibrahim M. Banat. "Pseudomonas aeruginosa biofilm disruption using microbial surfactants." *Journal of applied microbiology* 120, no. 4 (2016): 868-876.

3) Campos, Jenyffer Medeiros, Tania Lucia Montenegro Stamford, Leonie Asfora Sarubbo, Juliana Moura de Luna, Raquel Diniz Rufino, and Ibrahim M. Banat. "Microbial biosurfactants as additives for food industries." Biotechnology progress 29, no. 5 (2013): 1097-1108.

4) Christofi, N., and I. B. Ivshina. "Microbial surfactants and their use in field studies of soil remediation." *Journal of Applied Microbiology* 93, no. 6 (2002): 915-929.

5) Franzetti, A., P. Di Gennaro, G. Bestetti, M. Lasagni, D. Pitea, and E. Collina. "Selection of surfactants for enhancing diesel hydrocarbons-contaminated media bioremediation." *Journal of hazardous materials* 152, no. 3 (2008): 1309-1316.

6) Parra, J. L., J. Guinea, M. A. Manresa, M. Robert, M. E. Mercade, F. Comelles, and M. P. Bosch. "Chemical characterization and physicochemical behavior of biosurfactants." *Journal of the American Oil Chemists Society* 66, no. 1 (1989): 141-145.

7) Zouari, Raida, Semia Ellouze-Chaabouni, and Dhouha Ghribi. "USE OF BUTTER MILK AND POULTRY-TRANSFORMING WASTES FOR ENHANCED PRODUCTION OF Bacillus subtilis SPB1 BIOSURFACTANT IN SUBMERGED FERMENTATION." *Journal of Microbiology, Biotechnology and Food Sciences* 2019 (2019): 462-466.

8) Silva, M. E. T., Sergio Duvoisin Jr, R. L. Oliveira, E. F. Banhos, A. Q. L. Souza, and Patrícia Melchionna Albuquerque. "Biosurfactant production of Piper hispidum endophytic fungi." *Journal of Applied Microbiology* (2019).

9) Bee, Hameeda, Mohamed Yahya Khan, and R. Z. Sayyed. "Microbial Surfactants and Their Significance in Agriculture." In *Plant growth promoting rhizobacteria (PGPR): prospects for sustainable agriculture*, pp. 205-215. Springer, Singapore, 2019.

10) Ribeiro, Beatriz Galdino, Bruno Oliveira de Veras, Jaciana dos Santos Aguiar, Jenyffer Medeiros Campos Guerra, and Leonie Asfora Sarubbo. "Biosurfactant produced by Candida utilis UFPEDA1009 with potential application in cookie formulation." *Electronic Journal of Biotechnology* (2020).

11) Jahan et. al. 'Biosurfactants, natural alternatives to synthetic surfactants: Physicochemical properties and applications.' Advances in Colloid and Interface Science, Volume 275, January 2020, 102061.

12) Madihalli, Chandraprasad, Harshal Sudhakar, and Mukesh Doble. "Production and investigation of the physico-chemical properties of MEL-A from glycerol and coconut water." World Journal of Microbiology and Biotechnology 36 (2020): 1-11.

13) Sadeghi et. al. 'Design and physicochemical characterization of lysozyme loaded Niosomal formulations as a new drug delivery system.' Pharmaceutical Chemistry Journal, Vol. 53, No. 10, January, 2020 (Russian Original Vol. 53, No. 10, October, 2019).

14) Choudhury, Samrat Roy, Amrita Mandal, Dipankar Chakravorty, Madhuban Gopal, and Arunava Goswami. "Evaluation of physicochemical properties, and antimicrobial efficacy of monoclinic sulfur-nanocolloid." Journal of nanoparticle research 15, no. 4 (2013): 1491.

15) Jain et. al. 'Physicochemical characterization of biosurfactant and its potential to remove oil from soil and cotton cloth.' Discipline of Marine Biotechnology and Ecology, CSIR – Central Salt and Marine Chemicals Research Institute (CSIR – CSMCRI).

16) Baferani, A. Hasani, R. Keshavarz, M. Asadi, and A. R. Ohadi. "Effects of Silicone Surfactant on the Properties of Open-Cell Flexible Polyurethane Foams." Advances in Polymer Technology 37, no. 1 (2018): 71-83.

17) Chen, Yu-Fen, Chao-Hsun Yang, Ming-Shiang Chang, Yong-Ping Ciou, and Yu-Chun Huang. "Foam properties and detergent abilities of the saponins from Camellia oleifera." International Journal of Molecular Sciences 11, no. 11 (2010): 4417-4425.

18) Ohadi, Mandana, Arash Shahravan, Negar Dehghannoudeh, Touba Eslaminejad, Ibrahim M. Banat, and Gholamreza Dehghannoudeh. "Potential use of microbial surfactant in microemulsion drug delivery system: a systematic review." Drug Design, Development and Therapy 14 (2020): 541.

19) Benincasa, M., A. Abalos, I. Oliveira, and A. Manresa. "Chemical structure, surface properties and biological activities of the biosurfactant produced by Pseudomonas aeruginosa LBI from soapstock." Antonie Van Leeuwenhoek 85, no. 1 (2004): 1-8.

20) Rodrigues, Lígia, Ibrahim M. Banat, José Teixeira, and Rosario Oliveira. "Biosurfactants: potential applications in medicine." Journal of Antimicrobial Chemotherapy 57, no. 4 (2006): 609-618.

21) Parra, J. L., J. Guinea, M. A. Manresa, M. Robert, M. E. Mercade, F. Comelles, and M. P. Bosch. "Chemical characterization and physicochemical behavior of biosurfactants." Journal of the American Oil Chemists Society 66, no. 1 (1989).

22) Fu, Xiaowei, Fengqin Feng, and Bin Huang. "Physicochemical characterization and evaluation of a microemulsion system for antimicrobial activity of glycerol monolaurate." International journal of pharmaceutics 321.

23) Feng, Chao-Hui, Juan Francisco García Martín, Cheng Li, Bao-Lin Liu, Xiao-Yan Song, Qing-Li Dong, Wei Wang, and Yong Yang. "Evaluation of physicochemical properties and microbial attributes of cooked sausages stuffed in casing modified by surfactants and lactic acid after immersion vacuum cooling and long-term storage." International Journal of Food Science & Technology 51, no. 10 (2016).

24) Lorite, Gabriela S., João M. Rocha, Noora Miilumäki, Paula Saavalainen, Tuula Selkälä, Gabriel Morales-Cid, M. P. Gonçalves, Eva Pongrácz, Cristina MR Rocha, and Geza Toth. "Evaluation of physicochemical/microbial properties and licycle assessment (LCA) of PLA-based nanocomposite active packaging."

25) Pornsunthorntawee, Orathai, Panya Wongpanit, Sumaeth Chavadej, Masahiko Abe, and Ratana Rujiravanit. "Structural and physicochemical characterization of crude biosurfactant produced by Pseudomonas aeruginosa SP4 isolated from petroleum-contaminated soil." Bioresource technology 99.

26) Huang, Hui, Qisheng Yu, Hongqiang Ren, Jinju Geng, Ke Xu, Yan Zhang, and Lili Ding. "Towards physicochemical and biological effects on detachment and activity recovery of aging biofilm by enzyme and surfactant treatments." Bioresource technology 247 (2018): 319-326.

27) Raza, Zulfiqar A., Muhammad S. Khan, and Zafar M. Khalid. "Physicochemical and surface-active properties of biosurfactant produced using molasses by a Pseudomonas aeruginosa mutant." Journal of Environmental Science and Health Part A 42.

28) Rodrigues, Lígia R., José A. Teixeira, Henny C. van der Mei, and Rosário Oliveira. "Physicochemical and functional characterization of a biosurfactant produced by Lactococcus lactis 53." Colloids and Surfaces B: Biointerfaces 49, no. 1 (2006).

29) Saini, Harvinder S., Blanca E. Barragán-Huerta, Ariel Lebrón-Paler, Jeanne E. Pemberton, Refugio R. Vázquez, Anna M. Burns, Marilyn T. Marron, Chistopher J. Seliga, AA Leslie Gunatilaka, and Raina M. Maier. "Efficient purification of the biosurfactant viscosin from Pseudomonas libanensis strain M9-3 and its physicochemical and biological properties." Journal of natural products 71, no. 6 (2008).

30) Yuan, X. Z., Y. T. Meng, G. M. Zeng, Y. Y. Fang, and J. G. Shi. "Evaluation of tea-derived biosurfactant on removing heavy metal ions from dilute wastewater by ion flotation." Colloids and Surfaces A: Physicochemical and Engineering Aspects 317, no. 1-3 (2008).

Summer training report is submitted in partial fulfillment of the requirement for the degree of Bachelor of Technology

In

BIOTECHNOLOGY

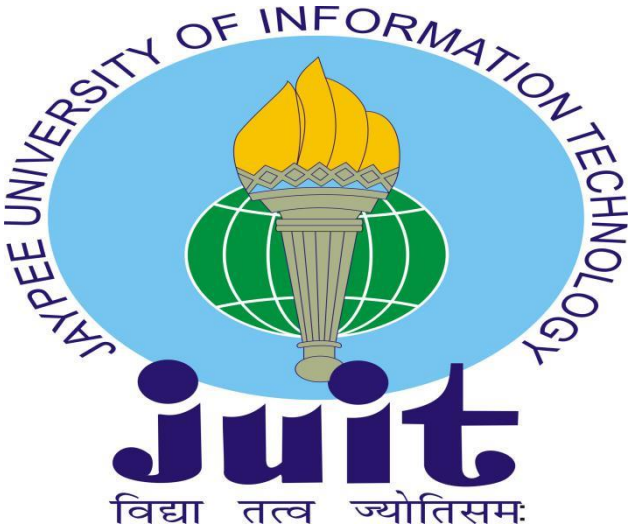
By

Ishita Kawar(171815)

Under the supervision of

Dr. Hemant Sood

to



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DECLARATION BY CANDIDATE

I hereby declare that the summer training report entitled "MICROPROPAGATION OF RHODODENDRON" submitted by me to JUIT; Waknaghat in partial fulfilment of the requirement for the award of degree of B.TECH in BIOTECHNOLOGY is a record of the bonafide summer training work carried out by me under the guidance of Dr. Hemant Sood .I further declare that the work reported in this summer training report, has not been submitted and will not be submitted ,either in part or in full, for the award of any other degree or diploma in this institute or any other institute or university.



JUIT

Signature of the guide

Dr. Hemant Sood

Wakanghat

DATE: JULY 3,2020

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TABLE OF CONTENTS

1. **INTRODUCTION**

2. **REVIEW OF LITERARTURE**

3. **REFERENCES**

INTRODUCTION

- **ABOUT THE PLANT *Rhododenron ferrugineum*:**

Rhododendron otherwise called "rose tree" is a sort of 1,024 types of woody plants in the heath family (Ericaceae), either evergreen or deciduous. It is likewise the national blossom of Nepal, where the bloom is viewed as eatable and delighted in for its sharp taste.

Rhododendron develops as shrub or little tree. It can develop from 3.9 crawls to 98 feet in stature, contingent upon the assortment.[1]

Most sorts of rhododendron have stringy root. A portion of the rhododendron species develop as epiphytes, or "air-plants" with ethereal roots. They develop by supporting on different plants and by gathering dampness and supplements legitimately from the air, while different sorts of rhododendron have evergreen leaves, while others have deciduous leaves. Evergreen sorts for the most part have huge, paddle-molded leaves. Deciduous plants frequently have little, curved leaves. Base side of leaves of certain types of rhododendron is secured with hairs or scales. Rhododendron produces pipe , chime , trumpet-molded or cylindrical blossoms. Shade of the blossoms can be white, pastel, orange, brilliant, red, pink or purple. Most sorts of rhododendron produce fragrant blossoms.

Rhododendron is otherwise called "rose tree" since it frequently creates blossoms in brackets, much the same as certain kinds of roses ("rodon" is Greek word for "rose" and "dendron" for "tree").Product of rhododendron is dry container. Ready organic product as a rule parts the long way to discharge seed.

Rhododendron is regularly utilized in arranging or for beautification of forest gardens because of fancy morphology of its leaves and blossoms. A few kinds of rhododendron are planted as supports. Dust and nectar of certain types of rhododendron contain harmful substance called grayanotoxin that can actuate harming of people and creatures. Ponies are particularly delicate to this sort of poison. Indications of inebriation incorporate stomach torment, sporadic heartbeat, automatic muscle compressions and trance state that can prompt demise.

Nectar created from nectar of specific sorts of rhododendron has psychedelic and diuretic impacts. Antiquated Greeks and Romans knew about symptoms of nectar

made of rhododendron. Rhododendron can get by as long as 100 years under ideal ecological conditions. Rhododendron are portrayed by having inflorescences with scarious (dry) perulae, a chromosome number of x=13, natural product that has a septicidal case, an ovary that is predominant (or almost so), stamens that have no members, and agglutinate (amassed) dust.

- **SPECIES ,DISTRIBUTION AND HABITAT:**

  There are in excess of 1000 distinctive regular species in the Genus (gathering) Rhododendron. Wild rhododendrons are found from ocean level to 16,000 feet in rise, and they happen in an assortment of natural surroundings, including high locales, coniferous and broadleaved forests, mild downpour backwoods, and even tropical wilderness conditions.[1,2]

  Types of the class Rhododendron are generally disseminated between scopes 80°N and 20°S and are local to territories from North America to Europe, Russia, and Asia, and from Greenland to Queensland, Australia and the Solomon Islands. The focuses of decent variety are in the Himalayas and Malaysia, with the best species assorted variety in the Sino-Himalayan area, Southwest China and northern Burma, from Himachal Pradesh, Uttarakhand, Nepal, Sikkim, Nagaland to northwestern Yunnan and western Sichuan and southeastern Tibet. Other huge zones of assorted variety are in the mountains of Korea, Japan and Taiwan.[3]

- **ECOLOGY :**

  A few types of rhododendron like Rhododendron ponticum has gotten intrusive in Ireland and the United Kingdom. R. ponticum is hard to kill, as its underlying foundations can make new shoots. Likewise, various bugs either target rhododendrons or astutely assault them.[4] Rhododendron borers and different weevils are significant vermin of rhododendrons, and numerous caterpillars will specially eat up them. Rhododendron species are utilized as food plants by the hatchlings (caterpillars) of certain butterflies and moths; see List of Lepidoptera that feed on rhododendrons. Rhododenrons species are likewise helpless against different infections some significant maladies incorporate Phytophthora root decay, stem and twig parasitic dieback, Rhododendron bud impact, (a contagious condition that makes buds turn earthy colored and dry) and not open, is brought about by the growth Pycnostysanus

azalea .moreover, rhododendrons can undoubtedly be choked by different plants or evergreen trees that grow up around them and square daylight.

- **IMPORTANCE OF PLANT:**

The business use of this blossom should be possible for the improvement of different food and pharmaceutical items can help in the accessibility of this bloom/blossom based item consistently. Thusly, this can help in the feasible improvement of provincial inborn populaces with incredible prospects of business. The plant can likewise be utilized for the improvement of lifesaving drugs and could offer colossal open doors for concocting better advertising methodologies. Rhododendron is one of the normally happening plants which have different medical advantages, for example, counteraction and treatment of sicknesses related with heart, loose bowels, the runs, detoxification, aggravation, fever, clogging, bronchitis and asthma. [5]Phenolic acids acquired from its leaves and twigs have been accounted for to have against HIV, mitigating, hostile to nociceptive exercises, and furthermore its leaves and blossoms are used for rewarding sickness, cerebral pain, diabetes, ailment, and so on.

REVIEW OF LITERATURE

- **MICROPROGATION OF *R. ferrugineum species*:**

In 1968, Dr. Wilbur Anderson started research on micropropagation of Rhododendron. [6]

Micropropagation is unquestionably by all account not the only method to engender rhododendrons. The developing of seed, layers, cuttings and unions are still generally excellent techniques.[7]This procedure offers the propagator, rhododendron reproducer and shopper the capacity to:

1. Spread plants thought about troublesome or difficult to proliferate.
2. Present new plant material all the more quickly.
3. Keep up and produce sans pathogen plant material.
4. Spread plants all year.
5. Take out the expensive support of stock plants.
6. Produce a trustworthy gracefully of plants each year.

- **STANDARD PROCEDURE FOR MICROPROPAGATION OF *R.ferrugineum* SPECIES:**

  - **Initiation:**

    1. Plants developed in pots in nursery conditions are occasionally treated and pruned for good vegetative development. This guarantees gracefully of 1 cm long unlignified shoots that can be utilized as explant material.

    2. A youthful shoot with around 15 light green leaves is cut from the mother plant. Most of the leaf is cut off, just the petiole and the leaf base are kept up onto the shoot to secure the axillary buds during cleansing.

    3. Surface sanitization is performed by washing in 70% ethanol for 30 seconds and ensuing cleansing for 15 to 20 min in 1% NaOCl, alongside a couple of drops of cleanser (for example Tween20). At long last, explants are flushed multiple times in sterile water.

    4. On sterile paper, the base of the cleaned shoot is expelled in light of the fact that it is sullied with NaOCl. The rest of the part is cut into bits of around 1.5 cm. These cuttings are planted on a level plane on duplication medium. Sterile Weck

pots or Meli-containers are the most well-known culture compartments. Axillary buds will grow and create youthful shoots (1-4 months). [5,8]

- **Multiplication** :

1. On sterile paper, shoot packs are analyzed into singular shoots, which are moved to new medium and vertically planted .

2. For standard shoot increase, 10 g/L bacto-agar, 15 mg/l 2iP and 4 mg/L IAA (indole-3-acidic corrosive) are added to BMA . Extrinsic shoots are initiated at the base of the explant.

3. Axillary shoots are incited at lower cytokinin fixations, down to 0.1 mg/L 2iP.

4. This is occasionally rehashed after each subculture cycle (generally 6-10 weeks) . Preceding possible exchange to soil, plantlets must be established.[5,8]

- **Rooting :**

1. Shoot bundles are dissected into individual shoots, on sterile paper.

2. Those shoots are transferred to a new medium promoting rhizogenesis . Rooting can take up to 2-3 months.

3. Rooted plantlet can be acclimatized.

- **Acclimatization:**

1. Expel agar cautiously from underlying foundations of plantlets (single shoots).

2. Following 3 weeks establishing in plastic seedling plate, in a mist unit of the nursery (18-20°C, relative dampness 95-100%, 16h photoperiod), plants are moved to a multi-layer developing room (21 ± 1°C, relative stickiness 75-80%, 16h photoperiod, CO2-focus 350 - 450 ppm).

3. During the accompanying 9 weeks and after acclimatization plantlets are treated normally. Suggested substrates are sphagnum peat, pH 4.0-4.5, containing 60% natural issue (acclimatization) or sphagnum peat 4: coconut fiber 1, pH 4 (ensuing development).[5,8]

- **COMPOSITION OF *R. ferrugineum*:**

Rhododendron contains minerals, for example, manganese, iron, zinc, copper, sodium, chromium, cobalt, cadmium, molybdenum, nickel, lead and arsenic. Minerals assume a crucial job in keeping up certain physicochemical ace cesses which are fundamental forever. Manganese, copper, selenium, zinc, iron and molybdenum are significant cofactors found in the structure of specific chemicals and are imperative from multiple points of view.[9] Sodium is significant in keeping up the osmotic harmony among cells and interstitial fluid.

- **TOXICOLOGY:**

Instances of rhododendron harming among people who have eaten poisonous nectar date as far back as 400 B.C. This is the main composed record of "nectar inebriation," in which 10,000 Greek fighters were influenced by eating nectar produced using rhododendron nectar. In rhododendron ponticum's unique home, the Black Sea territory of Turkey, instances of harming have been accounted for since that century too. Episodes among people in the 1980 The poisonousness found in assortments of rhododendron isn't uniform over all the plants' species, in spite of the fact that it is a trait of Rhododendron ponticum, one of the most famous assortments of the bush. It is likewise normal to family members of rhododendron, for example, different individuals from the azalea, or Ericacae, family. As a result of the synthetic substances' essence in nectar, position of apiaries close to rhododendron is hasty, as the nectar they describe may turn as poisonous thus[2]. As meager as three milligrams of nectar devoured per kilogram of body weight can demonstrate deadly. Leaves are less toxic than nectar, as a range from 100 to 200 grams of leaves would be required to truly harm a kid weighing 55 pounds.

- **Significance:**

The poisonousness originates from free phenols and diterpenes, otherwise called grayanotoxins, in the plant tissues. The creation of these is essentially a protection system by the plant against being devoured by herbivores, for example, touching creatures. The phenols are available in increasingly moved sums in more youthful rhododendron tissues, before they toughen up. The clingy sap that originates from youthful rhododendron buds is brimming with these harmful mixes and can bother

skin and eyes[1,3]. Numerous creature poisonings occur in the late-winter and pre-winter, since rhododendron stays green longer than other plant species, and presents a progressively alluring searching draw.

- **Effects:**

  Rhododendron ferrugineum(rhododendron) harmfulness is once in a while deadly to people, and manifestations normally last close to 24 hours. It brings about momentary gastrointestinal and cardiovascular issues, and the seriousness relies upon the measure of nectar or nectar ingested. Indications incorporate low circulatory strain, brought down pulse and stun, queasiness, expanded salivation and regurgitating, joined by dazedness, loss of equalization and trouble relaxing. Genuine disease and demise is progressively basic in creatures who eat rhododendron, again relying upon what amount is eaten. Ponies and elephants are two herbivores known to react seriously to rhododendron harming.

  Rhododendron toxicity is rarely fatal to humans, and symptoms usually last no more than 24 hours. It results in short-term gastrointestinal and cardiac problems, and the severity depends on the amount of honey or nectar ingested. Symptoms include low blood pressure, lowered heart rate and shock, nausea, increased salivation and vomiting, accompanied by dizziness, loss of balance and difficulty breathing. Serious illness and death is more common in animals who eat rhododendron, again depending on how much is eaten. Horses and elephants are two herbivores known to respond severely to rhododendron poisoning.

- **Treatment:**

  Detoxification cures are utilized to clear rhododendron harmfulness. These incorporate regurgitation prompting emetics when suitable for the patient, and rehashed utilization of enacted charcoal on the primary day manifestations are noted. Since the harming dries out numerous patients, liquid substitution is suggested, and other strong activities, for example, respiratory and heart backing might be required. Atropine can be endorsed to invigorate the pneumonic muscles in the event of a seriously eased back pulse.[10]

- **PHARMACOLOGY:**

Rhododendron plants (particularly R. arboretum) is a plant loaded with supplements, minerals and utilized in a wide scope of ethnomedical medicines, different pharmacological exercises have been accounted for by its mixes, divisions and concentrates, for example, antidiabetic, adaptogenic, antidiarrheal, mitigating, antinociceptive, cell reinforcement, anticancer, cardioprotective, hepatoprotective, immunomodulatory and antimicrobial which underpins its ethnomedicinal use and advantages[10]. A portion of the exacerbates that have a place with class phenolics, flavonoids, flavonoid glycosides, sterol and terpenoids have just been segregated from leaves, blossoms and bark and the rest are yet to investigate, so further examination is suggested on the sanitization and disengagement of the mixes from R. arboreum, which may include a novel or perfect remedial operator in the pharmaceutical world.



Figure: Colourful Flowers of Rhododendron

- **CONCLUSION:**

R.ferrugineum (rhododenron) species are is a widely distributed species of plant with many pharmocological benefits and mordern-day uses. Though it contains a variable amount toxin which is evident in “mad honey” made by the bees from the flower of this plant which makes it dificult to use for and limits its consumption for developing various products from it , but apart from this plant also seems to have a lot of advantages , it can be considered as one the first choices for making many rious kind of medicinal products, because of its curative or theraputic properties. The plant is rich in pytochemicals, flavanoids and other kinds of steroids which makes ita really important plant in the medicinal industries.Apart from this, rhododenron species play

an evident rom in the tea industries. This plant species when combined with certain ingredients such as mint ,green tea ,basil sea buckthorn etc. can play a major role in calming mind , relieving stress , promoting digestion and incresing appetite.This canbe achieved by either cold pressing method or by hot pressing method , for extraction of exceptional properties of theis plant species.

Hence, this plant species has a lot of potential in various sectors of medicine and food industry because of its extraordinary properties and extensive avaliability in India.

REFERENCES

Following links were referred to :

1. https://www.researchgate.net/publication/336994529_Phytochemistry_Traditional_uses_and_Pharmacology_of_Rhododendron_arboreum_A_Review
2. https://rjptonline.org/HTMLPaper.aspx?Journal=Research%20Journal%20of%20Pharmacy%20and%20Technology;PID=2019-12-9-85
3. https://www.gardenguides.com/89852-rhododendron-toxicity.html
4. https://link.springer.com/article/10.1186/s40066-019-0251-3#:~:text=Rhododendron%20is%20one%20of%20the,leaves%20possess%20effective%20antioxidant%20activity.
5. https://link.springer.com/protocol/10.1007/978-1-60327-114-1_14
6. JARS v38n2 - Micropropagation of Rhododendronsscholar.lib.vt.edu
7. https://rhodygarden.org/our-plants/rhododendrons/about-rhododendrons/
8. https://www.thethirdpole.net/2018/02/13/rhododendron-bloom-time/
9. https://scholar.lib.vt.edu/ejournals/JOTS/v38/v38n2/sanduk.html
10. https://www.britannica.com/plant/rhododendron

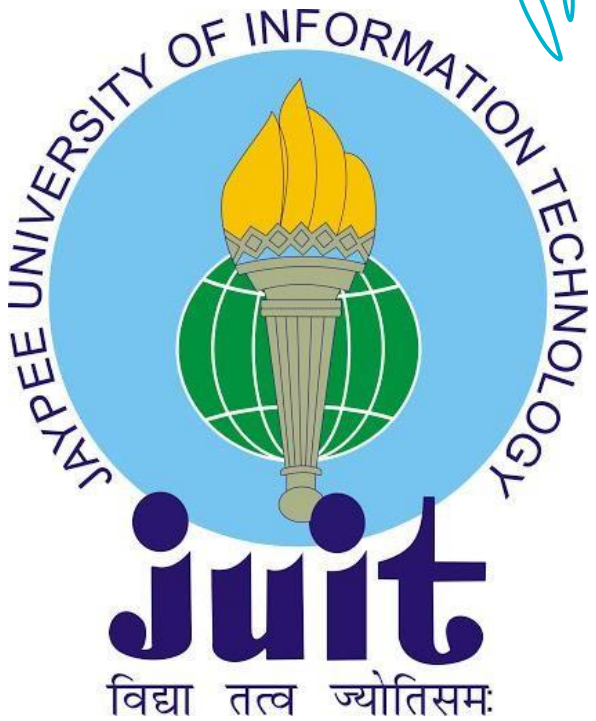
Summer Training Report

ANIMAL CELL CULTURE TECHNIQUES

Submitted By:

Ekta Choudhary (171816)

Guide:Dr. Udayabanu



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DEPARTMENT OF BIOTECHNOLOGY & BIOINFORMATICS

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CONTENTS

TOPIC	PAGE NUMBER
Introduction	3
Instrumentation	4-8
Disorder: Dementia	9-12
Basic techniques	13-17
References	18

INTRODUCTION

- For animal cell culture, the cells are taken from the organ of an experimental animal by removing directly or by mechanical or enzymatic action. These cells can also be obtained by previously made cell line or cell strain.
- The cells that are used to culture include fibroblast, lymphocytes, cells from cardiac and skeletal tissues, cells from liver, breast, skin, and kidney and different types of tumor cells.
- On the basis of number of cell division, cell culture can be divided into:
  Primary cell culture.
  Secondary cell culture & cell lines.
- History of animal cell culture:
  Animal cell culture was first successfully undertaken by Ross Harrison in 1907. Firstly, there was development of antibiotics that made easier to avoid contamination problems that plagued earlier cell culture attempts.
  Second was the development of the techniques such as the use of trypsin to remove cells from culture vessels which is necessary to obtain continuously growing cell lines.
  Lastly, by using these cell lines, scientists were able to develop standardized, chemically defined culture media that made it far easier to grow cells.
- Applications of animal cell culture:
  - ❖ Cell cultures provide a good model system for studying-
    Basic cell biology & biochemistry.
    The interaction between disease causing agents and cells.
    The effects of drugs on cells.
    The process and triggers for aging.
    Nutritional studies.
  - ❖ Toxicity testing.
  - ❖ Cancer research.
  - ❖ Virology.
  - ❖ Cell-based manufacturing.
  - ❖ Genetic counselling.
  - ❖ Genetic engineering.
  - ❖ Drug screening & development.

INSTRUMENTATION

- **Laminar air flow hood (LAF) or biosafety cabinet:**
  - ❖ LAF provide protection to the culture from any organism such as fungi, virus, bacteria under aseptic conditions by the use of high efficiency particulate air (HEPA) filters. It also protects the operator from the risk of contamination.
  - ❖ The level of contamination depends on the use of biosafety cabinet:
    Biosafety cabinet 1 (BSC 1) - it should have biosafety cabinet & efficiency of HEPA filters is 90%.
    BSC 2 - it should have closed biosafety cabinet & efficiency of HEPA filters is 95%.
    BSC 3 - it should have closed biosafety cabinet, high density, radioactive sterilization & efficiency of HEPA filters is 99.5%.



- **CO_2 incubator:**
  - ❖ It is a temporary chamber which provide appropriate environment for cell growth and development of cells. Incubator provides suitable temperature, density, moisture & pH.
  - ❖ CO_2 incubator maintain sterility of the chamber by using HEPA filters and maintain constant temp. by the use of silicon gasket on the inner door.
  - ❖ Desiccation of the media can be prevented & osmolarity can be maintained in CO_2 incubator.



- **Cooling centrifuge:**
  - ❖ Centrifuge is an instrument used in the separation of particles from a solution on the basis of their size, shape, density, viscosity of the medium & rotor speed using the principle of centrifugal force.
  - ❖ Cooling centrifuge is used in the preparation of the cells for cryo-preservation.

- **Refrigerator:**
  - ❖ A domestic refrigerator is required for cell culture laboratories for storing reagents, media & cells at 2-8 degree centigrade (for small labs).
  - ❖ Whereas, a cold room is required for the storage of cells in case of large laboratories.

- **Cryo-storage container:**
  - ❖ The cells lines in continuous culture are likely to suffer from genetic instability due to the increase in passage number so it is essential to prepare working stocks of the cells.
  - ❖ This working stock of the cells is preserved in the cryogenic storage.

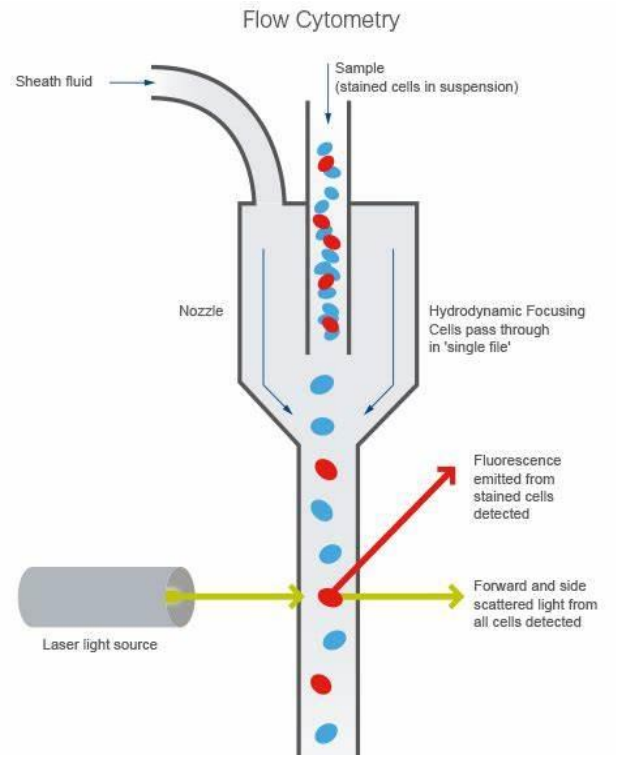
- **Liquid nitrogen container:**
  - ❖ It provides a long-term storage with low liquid nitrogen evaporation.
  - ❖ Types of liquid nitrogen container:
    Vapour phase – minimizes the risk of explosion with cryo-storage tubes.
    Liquid phase – have longer static holding time.

- **Haemocytometer:**
  - ❖ It is an instrument used for the estimation of cell number & viability.
  - ❖ It has two parts:
    Neubauer's slide – has counting scales on each quadrant & the depth of the scales is 0.1mm.
    Coverslip – used to keep the liquid sample in perfect shape into a flat layer of even thickness.



- **Water bath:**
  - ❖ Water bath is a device which maintains water at constant temperature used for the thawing of the cells directly taken out from the freezing media or liquid nitrogen.
  - ❖ It prevents the cells from any mechanical damage due to the temperature fluctuation. Temperature of water bath is 5-100 degree centigrade.

- **Flow cytometry:**
  - ❖ It is used to analyze the characteristics of the cells on the basis of laser technique.
  - ❖ Mainly used for the analysis of the expression of cell surface & intracellular molecules.
  - ❖ Flow cytometry is used for the characterization of different cells from a homogenous mixture.





- **Microscope:**
  - ❖ Inverted microscope – it is designed with the light source & condenser lens above the specimen. However, the objective & turret of the microscope is on the bottom.
    The objective focus the light to produce a real image and it is used to observe any contamination in the cell culture.
  - ❖ Dissecting microscope – also known as stereo microscope, having long working distance between 25 & 150mm. It has low magnification ability and one can manipulate the specimen even performing a small dissection under the microscope.
    Light specimens can also be observed.

- **Glasswares & plastic wares:**
  - ❖ Beaker.
  - ❖ Pipette.
  - ❖ Measuring cylinder.
  - ❖ Horizontal & vertical flask:
    T25
    T75
    T100
  - ❖ Petri-plate.
  - ❖ Microscopic slides.
  - ❖ Coverslips.
  - ❖ Cell culture plates.

- **Other equipment includes:**
  - ❖ Aspiration pump.
  - ❖ pH meter.
  - ❖ Roller racks.
  - ❖ Syringes & needles.
  - ❖ Waste containers.
  - ❖ Media, sera & reagents.
  - ❖ Cell cubes.
  - ❖ Bioreactors.

DISORDER: DEMENTIA

Dementia is the loss of cognitive functioning – thinking, remembering and reasoning and behavioral abilities to such an extent that is severe enough to affect daily functioning. Dementia ranges in severity from the mildest stage to the most severe stage when a person completely depends on others for basic living activities.

It is more common in old age people who are 85 or above, though it is not normal part of aging. Alzheimer's disease is the most common cause of dementia in older people whereas, frontotemporal disorders is more common in middle aged than older adults.

Types of dementia:

- Alzheimer's disease.
- Frontotemporal disorders.
- Lewy body dementia.
- Vascular dementia.
- Mixed dementia.

SYMPTOMS OF DEMENTIA:

Cognitive changes:

- Memory loss, which is usually noticed by a spouse or someone else
- Difficulty communicating or finding words
- Difficulty with visual and spatial abilities, such as getting lost while driving
- Difficulty reasoning or problem-solving
- Difficulty handling complex tasks
- Difficulty with planning and organizing
- Difficulty with coordination and motor functions
- Confusion and disorientation

Psychological changes:

- Personality changes
- Depression
- Anxiety
- Inappropriate behavior
- Paranoia
- Agitation
- Hallucinations

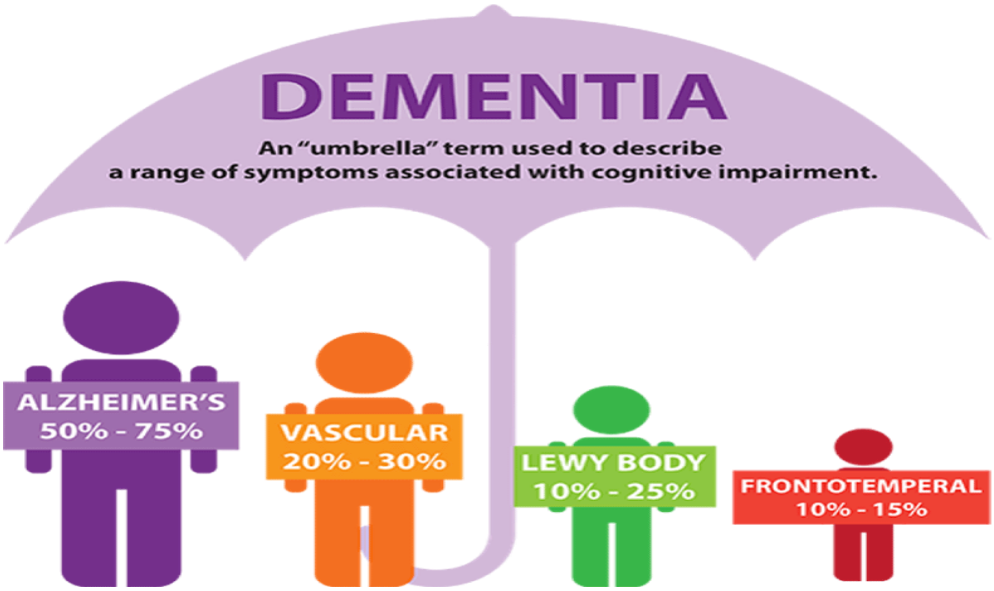
CAUSE OF DEMENTIA:

It is caused due to damage or loss of nerve cells and their connections in the brain. Depending on the area of the brain that's affected by the damage, dementia can affect people differently and cause different symptoms.

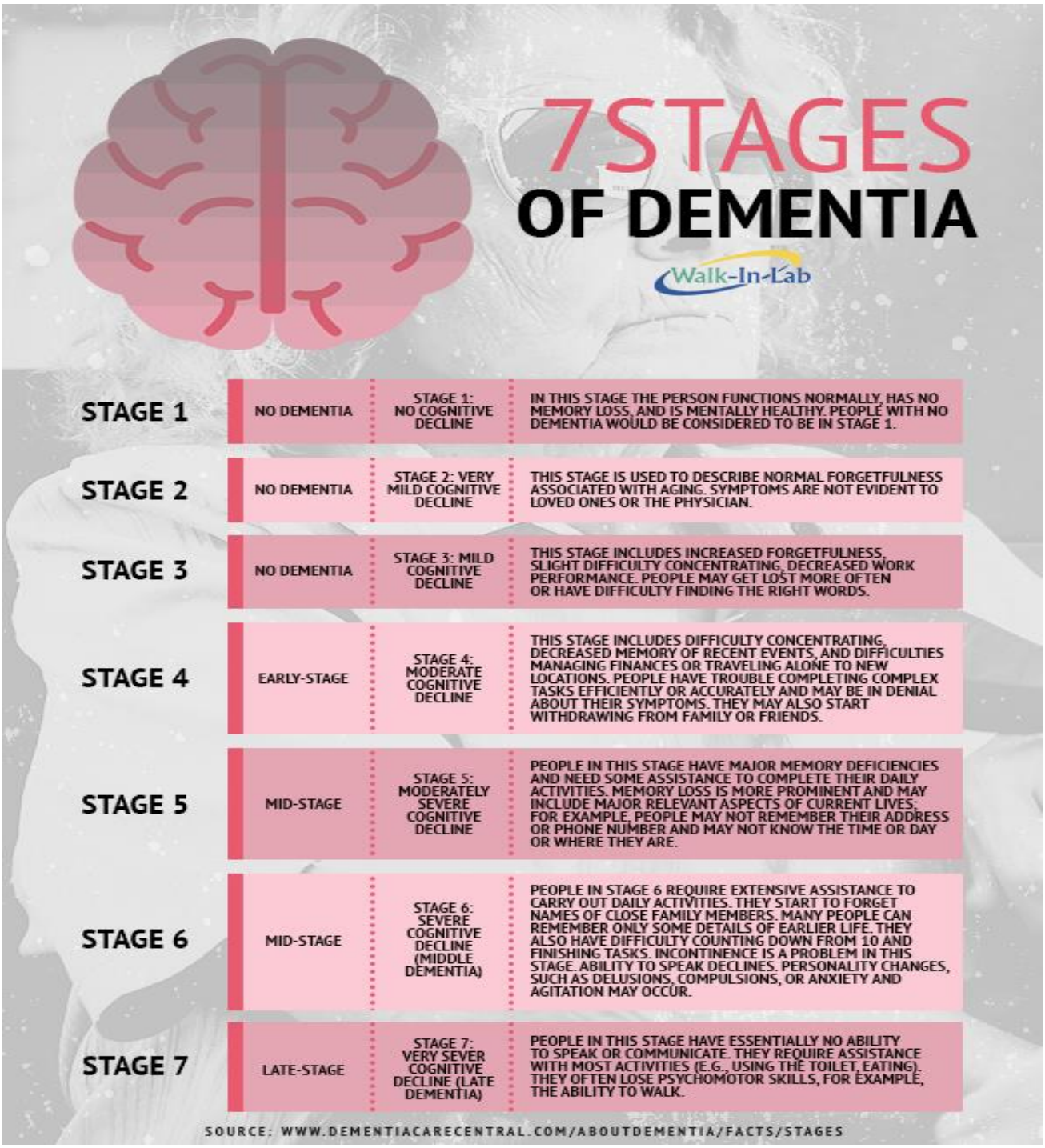
Reversible causes:
Causes of dementia that can be easily reversed include hypothyroidism, vitamin B12 deficiency, Lyme disease & neurosyphilis.

Irreversible & progressive causes:

- **Alzheimer's disease**: it is the most common cause of dementia and accounts for 50-80% of cases of dementia. The common symptoms include short term memory loss and word finding difficulties. A person suffering from Alzheimer's disease have plaques & tangles in brain. These plaques are clumps of protein called beta-amyloid whereas, tangles are made up of tau protein. As a result, these clumps damage healthy neurons and the fibers connecting them.
- **Vascular dementia**: it is the second most common cause of dementia arising due to damage in the vessels that supply blood to the brain. It accounts for at least 20% of dementia cases. The common symptoms are difficulties with problem-solving, slowed thinking, focus and organization.
- **Lewy body dementia**: it is caused due to the abnormal deposition of a protein called alpha-synuclein in the brain. These deposits are called Lewy bodies which affects chemicals in the brain. It can occur alone or along with other brain disorders. Common signs and symptoms include acting out one's dreams in sleep, visual hallucinations and problem with focus & attention.
- **Frontotemporal dementia**: caused due to damage in the brain's frontal and temporal lobes. The damage causes difficulties in thinking and behaviors controlled by these parts of the brain. Symptoms include unusual behaviors, emotional problems, trouble communicating, difficulty with work or difficulty with walking.



SEVEN STAGES OF DEMENTIA:



DIAGNOSIS:

There is no one test for diagnosis of dementia. Dementia may be diagnosed on the basis of medical history, a physical examination, laboratory tests, and the characteristic changes in thinking, day-to-day function and behavior associated with each type. Doctors can determine that a person has dementia with a high level of certainty. But it's harder to determine the exact type of dementia because the symptoms and brain changes of different dementias can overlap. In some cases, a doctor may diagnose "dementia" and not specify a type. If this occurs it may be necessary to see a specialist such as a neurologist or gero-psychologist.

Test used to diagnose dementia includes:

- Cognitive & neuropsychological tests – used to assess memory, problem solving, language skills, math skills, and other abilities related to mental functioning.
- Laboratory tests – testing person's blood and other fluids and checking levels of various chemicals, hormones & vitamins can help to find cause of symptoms.
- Brain scans – used to identify strokes, tumors and other problems that can cause dementia. Most common scans are computed tomography (CT) scan, MRI (magnetic resonance imaging) and positron emission tomography (PET).
- Genetic tests – these tests can help to find if a person is at risk of suffering from dementia.

TREATMENT:

Treatment of dementia depends on its cause. In case of most progressive dementias, there is no cure or treatment that slows or stops its progression. Though there are drugs that may temporarily improve symptoms.

Some of the ways that might help to prevent dementia (not sure) are:

- Keep mind active
- Be physically & socially active
- Quit smoking
- Get enough vitamins
- Manage cardiovascular risk factors
- Treat health conditions
- Maintain a healthy diet
- Get quality sleep

BASIC TECHNIQUES

TRYPSINIZING CELLS:

It is the process of cell dissociation using a proteolytic enzyme called trypsin which breaks down proteins to dissociate adherent cells from the vessel in which they are cultured.

Requirements:

Water bath, fresh media (DMEM), T-75 flask, PBS solution, isopropyl alcohol (for sterilization), tissues, pipettes, conical tubes, trypsin, waste beaker.

Methodology:

- Place the appropriate media in warm water bath at 37ºC for 5-10 mins.
- Then inside the sterilized hood place T-75 flask and PBS solution.
- Aspirate the media (10 ml pipette) in the T-75 flask and discard.
- Aspirate 10 ml of PBS to the flask and let sit for 1-2 mins.Swirl gently afterwards.
- Then, aspirate the PBS from the flask and discard.
- Aspirate 1ml of trypsin and put into the flask.Swirl around so that the trypsin covers the entire flask.
- Remove trypsin from the flask and discard.
- Therefore, place the flask in incubator for 5 mins.
- Add 10 ml of DMEM media onto the flask. Pipette it up and down to make sure all the cells get dispersed. Media turns cloudy.
- Aspirate the media from flask and transfer to a 15ml conical tube.
- Cells can be passaged in another flask, counted via hemocytometer or cryopreserved for further experimentation.

ASEPTIC TECHNIQUES:

- Always wear personal protective equipment (PPE), closed shoes, glasses.
- Review MSDS before handling any media or reagent.
- Hands should be washed properly before and after the experiment.
- Use 70% ethanol for sterilization of laminar flow cabinet as well as equipment and reagent bottles.
- Avoid over-crowding, confusion and maintain proper setup.
- While handling pipettes, do not touch it with anything that is non-sterile.Discard the pipette after one use or if contaminated. Do not reuse.
- Do not open anything outside the culture hood.

PASSAGING CELLS:

- Sterilize the hood and equipment properly.
- Examine culture properly for signs of contamination or deterioration.
- For removal of adherent cells, remove spent medium from the culture flask.

- Rinse flask with salt solution such as DPPS (not containing Mg2+ or Ca2+ as these inhibit cell dissociation reagent). Then, remove the salt solution.
- Add cell dissociation reagent such as TrypLE Express (cell dissociation enzymes; substitute for trypsin). Make sure that the reagent covers the entire cell sheet by gentle swirling. Also, lightly tap on flask surface to make sure that cells detach.
- With the help of microscope, it can be made sure that cells have detached. They appear round after getting detached from substrate and move around when flask is moved (when using TrypLE, inactivation is done by dilution whereas for trypsin, a serum is required).
- Transfer cells to a conical tube and centrifuge to remove residual dissociation reagents.
- Discard the medium with the help of a pipette and resuspend pellet in warm complete growth medium.
- Remove small suspension sample for cell counting. Trypan blue is used to calculate ratio of live (remains white due to intact membrane) to dead (blue) cells.
- Based on cell count, amount of additional media to be added is calculated for optimal seeding density. Media is added to cells, and the suspension is then pipetted into a fresh flask.
- Tightly cap if caps are vented and loosely if not for adequate gas exchange and minimal contamination. Transfer the cells to incubator.
- For passaging suspension cells, remove a small sample from cultured cells and count in the same manner as done for adherent cells.
- Based on cells count, additional fresh media is added to the flask. For proper gas exchange, minimum and maximum of capacity of flasks is considered. This helps in proper mixing and gas flow while shaking in incubator.
- After every three weeks, gently spin the cells, remove spent medium and replace with fresh media for eliminating cells debris and metabolic waste.

CULTURE PREPARATION & PLATING:

- HEK-293 cells (human embryonic kidney cells from 293rd experiment of Frank Graham) were cultured in tissue culture flasks and maintained between 10% and 90% confluency (number of cells) in a humidified, 37 °C, 10% CO2 incubator.
- Current density of cells is determined with the help of a microscope. Cell culture medium is removed from the cells and cells are washed once with PBS
- For a T-75 flask, 2 ml TrypLE trypsin is added to detach cells from the plate and allowed to be incubated for 2 mins. After incubation, it is verified that all the cells are detached with the help of a microscope (cells appear floating).
- Trypsinization is stopped by adding 10ml of assay medium which is pipetted up and down to disperse cells. Then, cell suspension is transferred to a conical tube.
- Cell number in solution is quantified by a hemocytometer to determine the concentration of cells for subsequent assays.
- The suspension is centrifuged at 500g for 5 mins at 18 °C. The supernatant is discarded and the pellet is resuspended in assay medium to achieve a final conc.” of 1*106 cell/ml.

- The cells are then pipetted into a 96-well plate. Incubate the plate for 4 hours at 37 °C in 10% CO2 incubator. After incubation, assay reagents are added to the plate and stimulated cell activity is determined.

CELL COUNTING:

A hemocytometer is a device used for counting cells. It is a modified microscopic slide containing two identical wells or chambers into which a small suspension of cell culture is pipetted.

Each chamber of hemocytometer is divided into a grid pattern consisting of 9 large squares. Generally, cells are counted in 4 corner squares and the center square. In these squares, cells touching the top and left boundaries are counted whereas those touching the bottom and right are excluded.

Procedure:

- 100 µL of cell suspension is added to a microfuge tube. Dilute the cell suspension with 100 µL of Trypan Blue.
- Load the prepared sample in both wells under the coverslip.
- Place under the microscope and observe.
  (dead cells allow the dye to pass through its membrane and appear blue whereas live cells do not and hence appear clear)

Formulas:

- Percentage of viable cells= (Number of viable cells/ Total number of cells) *100
- Average number of cells per square= number of viable cells/ squares counted
- Dilution factor= final volume/ volume of cell suspension
- Concentration (viable cells/ ml) = average number of cells per square * dilution factor * 10^4

PREVENTING CONTAMINATION:

- Wear personal protective equipment restricted to the cell culture lab.
- Disinfect gloves prior starting working and between working steps.
- Make sure to place the required items in the biosafety cabinet prior to working but avoid overcrowding. Sterilize every glassware, equipment or tool to be used with 70% ethanol and then place it in the cabinet.
- Water bath increases the risk of germ transfer. Therefore, it should be cleaned on a regular basis. Bactericides and fungicides are added to the water for proper removal.
- Work with one cell type at a time and disinfect the cabinet surface between work steps.
- Open and reseal sterile packages inside the cabinet only.
- Avoid opening the incubator doors for too long.
- Place cap sideways on the work surface so that it is not in contact with the air flow as well as the floor.
- Make sure not to touch the pipette tip something unsterile.
- Use petri dishes with handling rings preferably for easy transportation, stacking and culturing.

CRYOPRESERVATION:

The preservation of cells is an extremely important aspect of cell culture. The only effective means of preservation of animal cells is by freezing, which can be accomplished with either liquid nitrogen or by employing cryogenic freezers. The freezing process involves slowly reducing the temperature of prepared cells to -30 to -60°C followed by a transfer to temperatures less than -130°C. Once at ultralow temperatures, the cells are biologically inert and can be preserved for years.

FBS (Fetal Bovine Serum) contains a large amount of growth factors which facilitate cell survival and proliferation and lower number of antibodies that can bind to cells in cell culture.

DMSO (Dimethyl Sulfoxide) prevents intracellular and extracellular crystal formation in cells during the freezing process.

Isopropanol provide controlled rate freezing of cells.

Requirements:

Pre-chilled freezing media (90%FBS, 10% DMSO), container filled with isopropanol.

Procedure:

- For adherent cells, conditioned media is aspirated off and discarded.
- Attached cells are washed with PBS by gentle swirling and then PBS is discarded.
- TrypLE is added to detach the cells from the flask. Medium is added.
- Collect suspension in 15ml centrifuge tubes. Then centrifuge.
- Discard the supernatant and resuspend pellet in appropriate volume of freezing medium for optimal cell density.
- Transfer 1ml of suspension solution in each cryovial.
- Freeze the cells at -80 °C overnight. Then store in liquid nitrogen permanently.

Precautions:

- No inactivation is required when using TrypLE.
- Small sample is collected for cell counting. Viable cells should be more than 90%. Only healthy cells should be frozen.
- Amount of freezing medium to be added depends on number of cell and concentration in each vial.
- Use a container such that the temperature of the cells drops by 1 °C/min. This decreases cell damage.
- Always wear proper PPE while handling liquid nitrogen
- All steps should be carried out quickly and carefully to minimize temperature changes, and under appropriate medium formulation and freezing density.

THAWING OF CELLS:

Requirements:

Pre-warmed medium, cell culture flask.

Procedure:

- Remove cells from liquid nitrogen quickly and place them on dry ice bath.

- The cells are then thawed in a 37 °C water bath quickly. Remove from water bath when a small chunk of ice remains in the vial. The ice chunk melts when the vials are moved to culture hood from water bath.
- Transfer the contents of vial into a centrifuge tube with a sterilized pipette.
- Add 10 ml of pre-warmed cell culture medium to the centrifuge tube.
- Centrifuge the cells to remove the freezing medium containing DMSO. Discard the supernatant. Resuspend the pellet in 10ml complete pre-warmed medium.

Precautions:

- DMSO and cell culture freezing media are toxic. Always wear appropriate PPE and refer to MSDS.
- Perform each step carefully and quickly. Ensure appropriate temperature, medium formulation and seeding density.
- Ready the culture hood before removing cells from liquid nitrogen.
- Do not submerge the vial while thawing in water bath.
- Add the pre-warmed media drop-by-drop and then gradually increase the amount to prevent osmoticshock.
- Do not centrifuge the cells if the cell line is too delicate.
- Medium volume, flask size and number of flasks plated will depend on the number of cells frozen in the vial and the optimal seeding density for the cells.
- Ensure proper distribution of cells on the flask surface.

SUBCULTURE:

- Prepare space and materials carefully. Label the glassware with proper date, cell type, etc.
- Check cells before sub-culturing. There must be 80% confluency along with presence of mitotic cells.
- After removal of culture media, 9ml of Trypsin/ EDTA solution is added and flask is rocked. All of the 9 ml of Trypsin/ EDTA is removed and fresh Trypsin/ EDTA (3ml) is added. Incubate flask till all the cells become round (1-20 mins depending upon cell type). Confirm dissociation of cells. Remaining adherent cells can be removed by gentle tapping of the flask.
- 9 ml of trypsin neutralizer is added to the flask to avoid over trypsinization.
- Transfer suspension to a 15 ml centrifuge tube. Add trypsin neutralizer again to remove remaining cells and transfer this to the 15 ml centrifuge tube again.
- Centrifuge the suspension at 180g for 7 minutes. Discard the supernatant. Resuspend pellet in 12 ml of supplemented medium (or as per experiment).
- Count the number of cells and dilute as per the appropriate seeding density with supplemented medium.
- Incubate till further use. (Long term incubation with high trypsin concentration damage cells by removing cell surface proteins and thus kills the cells)

REFERENCES

- https://www.biotechnologynotes.com/animals/animal-cell-culture-history-types-and-applications/671
- https://microbeonline.com/animal-cell-culture-introduction-types-methods-applications/
- https://www.slideshare.net/SubhalaxmiSwain1/equipments-used-in-animal-cell-culture
- https://www.mayoclinic.org/diseases-conditions/dementia/symptoms-causes/syc-20352013
- https://www.nia.nih.gov/health/what-are-frontotemporal-disorders
- https://en.wikipedia.org/wiki/Dementia#Causes
- https://www.walkinlab.com/blog/wp-content/uploads/2018/10/info-graphic-7-stages-of-dementia.jpg
- https://alkalisci.com/cell-culture-flasks-vented.html
- https://www.youtube.com/watch?v=CMRKKl9XSDU
- https://www.youtube.com/watch?v=6vchql21tEE
- https://www.youtube.com/watch?v=7hEUmLz1Ew0
- https://www.youtube.com/watch?v=nr1tV_LuqJk
- https://www.youtube.com/watch?v=pP0xERLUhyc
- https://www.youtube.com/watch?v=P4dTbKVDIZ4
- https://www.youtube.com/watch?v=tCNtKrxlZPs
- https://www.youtube.com/watch?v=4HxqQOHifkU
- https://www.youtube.com/watch?v=k2PMEET4Smo

SUMMER TRAINING REPORT

ON

FERMENTATION TECHNOLOGY

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Under the Supervision

of

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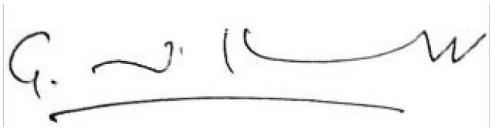
July, 2020





OBJECTIVE 1- To acknowledge the working and components of a bioreactor.

Theory: Bioreactor- It is a flask type structure which has the advantage of controlling environmental conditions and it also provide cell and microbial plant cultivation under sterile conditions. It consist of following parts;

- **Agitator-** It is used to carry out mixing of the contents present in the reactor in order to keep cells in perfect homogenous condition for better transport of nutrients and oxygen.
- **Baffle-** It is mainly used to prevent the vortex formation in the reactor as it can change the centre of gravity of the system and consumes additional power.
- **Sparger-** It supplies oxygen to the growing cells and it also helps in mixing the contents which results in less usage of power.
- **Jacket-** It helps in keeping the temperature of bioreactor down by providing water and removing extra heat from its surface.

- **Basic protocol for the operation of bioreactor:**
  - **Temperature Measurement and Control-** Temperature measurement is carried out by either using thermocouple or Pt-100 sensor which send signal to the temperature controller. Measured value is compared with set point which is entered in the controller, depending on it heating or cooling of the bioreactor is activated slowly to decrease the error.
  - **pH measurement and control-** pH measurement is carried out using autoclavable pH probe. Before using pH probe it needs to be calibrated with the two buffers used in the bioreactor cultivation experiment. Measured pH is compared with the set point which then activated the acid or alkali to bring the measured value close to the set point.
- **Identification of pH controller settings for Bio-Engineering AG:**

i. **Bioreactor-** A suitable control action setting is required for the addition of certain concentration of acid/alkali which can give quick action to measured value around the set point. It is also noted that activation of alkali/acid is done in a phased manner, this ensures adequate mixing of acid/alkali in the broth before next instalment is added. On/off time of the controller has to be adjusted by separate experiments and will depend on the buffering capacity of the broth. It is essential to maintain these settings before the start of the experiment in order to have efficient control.

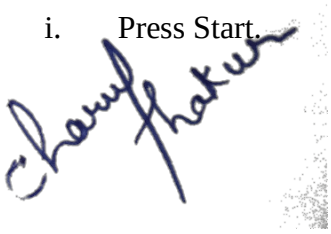
ii. **Dissolved oxygen controller-** It is measured by a dissolved oxygen probe. In this probe is to be calibrated for its zero and 100% values.

iii. **Foam control-** It controls the foam which arises due to the organic compound and the broth is vigorously agitated to keep the cells in suspension and ensure efficient nutrient transfer from the dissolved nutrients and oxygen.

Procedure:

- **To understand the significance of each part of the bioreactor;**

i. Press Start.



ii. **Speed control system-** Mainly used to provide mixing of reactor contents. Set the upper limit and actual speed then press RUN.

iii. **Gas Supply System-** It supplies air which serves as the source of the oxygen to the growing cells. Enter value and run.

iv. **Temperature Control System-** It is used to maintain the cultivation temperature in the bioreactor. Measure the value and compare it with the set point.

v. **pH measurement and control system-** Enter pH value and set point . Press run. Measure the pH and compare it with the set point.

vi. **Dissolved Oxygen Measurement and Control-** Enter value of dissolved oxygen levels and press run. Using the magenta sensor, compare the value with the set point and depending on the error the controller action is activated.

vii. **Foam Control System-** It is used to remove the foam from the system as it can lead to heavy losses to the system. It is detected by red sensor and anti foam is triggered It is added slowly so that only minimum amount is added. Over addition of antifoam may create serious problem.

OBJETIVE 2: Determination of characteristics of pH controller of Bio- Engineering AG fermenter

Theory: The pH control method is dependent on various parameters of factors such as density, viscosity and strength of acid and bases etc. Faulty settings of these parameters will lead to delayed control response. It is possible to design the controller according to the above parameters.

- **Description of the pH controller;**
  i. **pH/mV potentiometer-** It enables the adjustment of the slope of pH electrode by calibration.
  ii. **Asymmetry potentiometer-** It adjust the zero mV point of the pH signal.
  iii. **Temperature potentiometer-** It manually control temperature coefficient of pH electrode.
  iv. **Set point potentiometer-** Set pH or mV.
  v. **P-band potentiometer-** Adjust the width of the P-band potentiometer. Low P band translates to strong amplification.
  vi. **TON/TOFF potentiometer-** Adjust the opening and closing of the valve by keeping both the potentiometer at the same value which will lead to the linear transfer function.

Procedure:

i. Switch 1 connected to pH.
ii. Switch 5 and switch 8 to hand.
iii. Adjust 4 to the temperature of the solution.
iv. Dip the electrode in standard buffer of pH 7 & adjust until pH comes at 7.
v. Clear the electrode and dip it in buffer (pH 4).
vi. Adjust 3 till the meter reads at 4 pH.

OBJECTIVE 3: 15 L Bioreactor Manual

- **Preparation for sterilization**
  - Media was prepared and added to the reactor.
  - The functioning of probes was verified and electrolytes in pH and DO probes refilled.
  - Probes were inserted into the reactor.
  - Air outlet filter was used to maintain pressure equilibrium in and outside the reactor.
- **For Autoclaving**
  - The reactor was now placed inside the horizontal Autoclave,
  - Pressure was maintained in the jacket at 15psi by keeping valve in fast mode.
  - Closed the autoclave lid; adjusted valve in sterile mode.
  - Waited for maintaining equilibrium at 15 psi in reactor and jacket.
- **For login to controller**
  - Switched on the controller and a screen appeared
  - After that a home screen will appeared. Pressed view button on home page and entered into System engineer.
  - A login screen appeared. Pressed login and specified password. Pressed enter button.
- **For priming tubes**
  - Attached the autoclaved reactor and pipes to controller. Went to home page and pressed main menu.
  - Tubing prime control button was selected on the main menu.
  - Primed all the tubes for alkali, acids and antifoam.
  - Went to main menu and entered into manual controller. All the pumps and valves were controlled manually.
- **Setting parameters set points**

  <u>Temperature</u>
  - Pressed main menu and entered the temperature.
  - Specified temperature set point and pressed enter button.

  <u>Stirrer setting</u>
  - Went to the main menu and entered into stirrer settings.
  - On stirrer setting screen, pressed cascade speed limit button.
  - On cascade limit screen, the upper and lower speed limit cascade will appeared.
  - Set the upper stirrer speed limits and pressed enter.
  - Set the lower speed limit cascade and pressed enter.
  - Entered into stirrer settings and pressed stirrer set point button.
  - Wrote stirrer set point and pressed enter button.

  <u>pH setting</u>
  - On main menu, pressed pH settings and entered into pH set point.
  - Set pH point and pressed enter.

DO settings

- On home page, entered into DO settings. Then press DO set point button.
- Set DO point and pressed enter button.

❖ **Switched on controllers and ran fermentation**

1. On the home page, pressed menu button. Inside the menu, pressed start/stop all the controllers.
2. Then pressed start all controllers.
3. Then ran fermentation.
4. All the profiles of parameters i.e. pH, DO and temp were monitored by entering into respective controller sections on home page.
5. On completion, harvested the entire fermentation broth from the reactor.

OBJECTIVE 4: Biopolymer Production by Microbes

❖ **Basic Requirements**

Microorganism: *R. eutropha NRRL B14690*. The culture was maintained on nutrient agar slants at about 5ºC.It requires being sub cultured every month.

Media preparation [shake flash cultivation:

- For mineral salt medium: 2.0 g/L (NH4)2SO4, 2.0 g/L KH2PO4, 0.6 g/L Na2HPO4, 0.2 g/L MgSO4.7H2O, 20 mg/L CaCl2, 10 mL/L trace metal solution, 0.1 g/L yeast extract is to be used.
- For trace metal solution: 1.3 mg/L ZnSO4.7H2O, 0.2 mg/L FeSO4.7H2O, 0.6 mg/L (NH4)6Mo7O24.4H2O and 0.6 mg/L H3BO3.
- Fructose is used as a carbon source in concentration of 40 and 10 g/L for production media and inoculum development, respectively. Fructose, yeast extract and salt solutions are to be sterilized separately at 121ºC and then aseptically reconstituted at room temperature prior to inoculation.
- The pH of the resulting broth needs to be adjusted to 7.0 with 2N NaOH/2N HCl.

Bioreactor cultivation:

- Seed culture was prepared in a 1 L Erlenmeyer flask containing 200 mL media. Batch cultivation was then carried out at 30ºC in a 7 L LF-1523 Bioengineering (Bioengineering AG, Switzerland) bioreactor containing 4 L of media.
- The reactor was sterilized in-situ at 121ºC for 20 min, cooled and then inoculated with 5% inoculum (v/v).
- Culture pH needs was maintained at 7.0 by automatic addition of acid or base by pH–mV controller M 7832 N.
- Dissolved oxygen concentration was maintained at 30% saturation value by manually adjusting the speed of the agitator and/or airflow rate.
- Samples were withdrawn at regular intervals and analysed for biomass, PHB and residual nutrients.

❖ **Protocol for operation of simulator**

- Bioreactor:

The Bioreactor portion shows different components which described the purging of the sterile from the sparger and rotation of the impeller. The impeller is bottom driven. This arrangement is possible with Bioengineering AG Switzerland Bioreactor. This kind of agitation gives more space on the lid because of which there is no overcrowding of different inlet ports & sensors and it is particularly useful when flame is used to connect acid /alkali pipes and when transfer of inoculum is done to the reactor. The constant temperature water flows in the jacket of the reactor (marked green) to maintain the temperature of the reactor.

- Run Simulation:
  After entering the necessary details, RUN Simulation button was pressed and the graph and table for X, S, P vs time was printer on the screen.
- Out put Graph :
  The graph described the kinetic profile of different fermentations.
- Save Results:
  Pressed on the save button.
  Results were saved in the form of an Excel Sheet where all the values of kinetic profile were tabulated.

OBJECTIVE 5: Acetone-Butanol-Ethanol Production

❖ **Basic Requirements -**

- Culture - *Clostridium acetobutylicurn* strain ATCC 824 was used for production of Acetone-Butanol-Ethanol.
- Medium requirements - A standard culture media with respect to ammonium sulfate and yeast extract for the specific glucose concentrations has to be used in this study while maintaining the same concentrations of minor nutrients. It typically consists of the following components in g/L: glucose, 50; ammonium sulfate, 9.0; yeast extract, 11.0**;** K2HP04, 0.8; KH2P04 0.8; MgS04, **0.3;** MnS04 .H20, 0.02; NaCI, 0.02; FeS04 . 7H20, 0.02; and L-cysteine, 0.5. Temperature 37ºC, pH 4.5 or 6.0 .
- Flask and Bioreactor development - Heat shocks the spores kept up in RCM by putting the test tube in a bubbling water shower (100ºC for one minutes). This is to be trailed by cooling to 4ºC for 3 minutes. The temperature of the cylinder is standardized to room temperature for 60 minutes. The 3% inoculum is to be moved into 15 mL hungate top test tubes containing 10 mL of the RCM. The test tube containing the spore arrangement was saved for spore actuation at 37ºC in an anaerobic container for 20-24 hours. Satisfactory development for ensuing exchange of the inoculums was portrayed by the beginning of gas creation. 3 % inoculums were moved into a fluid glucose medium (50 g/L) in a shake flagon. Following 10 hours of development, tests were pulled back from the way of life jar each hour. The pH of the inoculum was not permitted to fall underneath 4.6 by manual expansion of 0.1 N NaOH. The suitable planning for vaccination (14-15 hours) was distinguished by the way of life corrosive break point through the examination of extracellular items by gas chromatography. A 3 % inoculum is

moved to the fermenter containing cleaned 50 g/L glucose medium at pH 4.6 Before immunization the fermenter was sparged in the head space by Nitrogen. The nitrogen sparging proceeded until the gases were being created by the way of life. The way of life was permitted to develop in a clump mode.

- **Analytical protocols -**
  - Dry wieght - 20 ml sample of the fresh fermentation stock is centrifuged at 10,000 g and 4ºC for 15 minutes. The supernatant is solidified in a profound cooler for extracellular metabolite and glucose examination. The biomass is washed multiple times with equivalent measure of refined water. The pellet is re-suspended in 10-15 mL of refined water, moved to a preweighed aluminum dish and dried in a stove at 100ºC for 24 hours. In the wake of cooling the aluminum dish to room temperature in a desiccator the dry load of the cells is estimated.
  - Glucose - Glucose concentration was determined by DNS method.
  - Solvent and Acid concentration- This was done by Gas-liquid Chromatography.
- **Protocol for operation -**
  - Bioreactor - The Bioreactor portion represents the various parts it likewise depicts the cleansing of the sterile air (if it's not too much trouble see the air channel noticeable all around delta) from the sparger and pivot of the impeller. The impeller is base driven. This sort of plan is conceivable with BioEngineering AG Switzerland Bioreactor. This sort of unsettling gives more space on the top so that there is no congestion of various bay ports and sensors and it is especially helpful when fire is utilized to interface corrosive/salt funnels and when move of inoculum is done to the reactor. The consistent temperature water streams in the coat of the reactor (stamped green) to keep up the temperature of the reactor.

The Simulation was run to understand the basic working and result formation.

OBJECTIVE 6: Propanoic Acid Production

- **Basic Requirements -**
  - Culture - *Propionibacterium acidipropionici* ATCC 4875.
  - Medium Requirements - Engineered medium is to be utilized for the arrangement of inoculum. 100 mL (20 g/L lactose) medium with the accompanying organization is to be utilized: 1 g yeast separate, 0.5 g trypticase, 0.025 g K2PHO4, 0.005 g MnSO4, 2 g lactose. pH is to be acclimated to 6.5 with 3 N NaOH/HCl. For sanitization, lactose and rest of the medium parts (basal medium) are to be autoclaved independently at 121º C and 15 psig for 20 min. Blend the two arrangements aseptically under laminar flow hood.
  - Inoculum Preparation - 20 mL of the engineered medium is to be taken in a 100 mL serum bottle, Cap it by an elastic plug and seal by aluminum top by crimper. Prior to immunization, N2 is to be sparged through the serum bottle for around 15 min. A leave valve with sterile channel must be given at the cup outlet to forestall development of extreme weight inside it. Vaccination is to be finished

utilizing a two days old inclination development rejected in 1 mL sterile refined water. A uniform suspension is to be made in the water before aseptically moving the inoculum to the serum bottle with the assistance of a sterile syringe. Development is to be done at 30º C in a shaker (Adolf Kuhner AG, Basel, Switzerland) kept up at 150 rpm. Utilize sterile syringes to pull back samples. Move the inoculum at around 40 h utilizing 6% (v/v) inoculum.

- Bioreactor Cultivation - Start fermentation in a bioreactor at an underlying grouping of lactose (utilizing) 50 g/L (7-l (Bioengineering, Switzerland) glass reactor) working volume 5 liter. Autoclave the fermentor with refined water in it, in situ. In the wake of autoclaving, when the temperature drops down to 60º C, the water is to be evacuated through the examining port by applying N2 pressure. Keep flushing the headspace of the reactor with nitrogen gas to keep up anaerobiosis all through the fermentation. The instigator is to be kept at 150 rpm. Control the temperature at 30±1 ºC and keep up the pH at 6.5±0.1 via programmed expansion of clean 6 N NaOH. A pH estimation of 6.5 has been accounted for to be appropriate for propionic corrosive amassing (Hsu and Yang 1991). Develop the inoculum in a specially designed 500-ml serum flagons (headspace flushed with nitrogen gas). Aseptically immunize the bioreactor containing 5 l of medium with 250 ml of 1-day-old log-stage culture. Gather 10 mL fluid samples at standard stretches Measure the optical thickness and rotator the rest of the volume of the sample at 10,000 g for 20 min. Store the supernatant at – 20 ºC for HPLC examination to build up the item focuses.

❖ **Analytical Protocol -**

- Biomass Estimation - Biomass estimation is done by the measurement of optical density.
- Substrate/Product Estimation - For estimation of product formed HPLC technique is used.

The Simulation was run to understand the basic working and result formation.

OBJECTIVE 7: 1, 3 Propanediol Fermentation

❖ **Basic Requirements -**

- Culture - *Clostridium diolis* DSM 15410 (previously known as *Clostridium butyricum* DSM 5431)is used for 1,3-PD production.
- Modification for maintaining Ideal condition - Customary Erlenmeyer flasks (500 ml) must be changed for completing anaerobic development outside the anaerobic tent. The mouth size (30 mm) is decreased to 10 mm and flasks are furnished with an edge to encourage fixing with elastic and aluminum tops by methods for a crimper. Sparge nitrogen gas in the carafes to cleanse out the dissolved oxygen of stock and keep up anaerobic conditions.
- Medium Requirements - Build up the inoculum in 120 ml serum bottles which contain 50 ml clean medium having arrangement (per liter): unadulterated glycerol 20 g; K2HPO4 3.4 g; KH2PO4 1.3 g; (NH4)2SO4 2 g; MgSO4.7H2O 0.2 g; CaCl2.2H2O 0.02 g; FeSO4.7H2O 5 mg; Yeast extricate 2 g; Trace component

arrangement (TES) 2 ml. The follow component arrangement (per liter) comprised of: 70 mg ZnCl2; 0.1 g MnCl2.4H2O; 60 mg H3BO3; 0.2 g CoCl2.2H2O; 20 mg CuCl2.2H2O; 25 mg NiCl2.6H2O; 0.9 ml HCl (37%). Sparge the jugs with nitrogen and hatch immunized jugs at 330C and 150 rpm in an orbital incubator shaker. Move aseptically exponentially developing culture from the serum bottle (24 h) to sterile nitrogen gassed medium in an uncommonly altered 500 ml Erlenmeyer carafe containing 100 ml medium. Brood the vaccinated flasks in an orbital shaker at 330C and foment at 150 rpm for 12 h after which utilize the effectively developing culture from the carafe as inoculum for the bioreactor.

- **Fermentation Bioreactor Setup -** Batch development of C. diolis is completed in a 3.7 L bioreactor (Bioengineering AG, Switzerland) (working volume 1.5 L) utilizing measurably improved nutrient medium formula. The medium comprises (per liter): unadulterated glycerol 54.45 g; K2HPO4 3.21 g; KH2PO4 2.75 g; (NH4)2SO4 2 g; MgSO4.7H2O 0.2 g; CaCl2.2H2O 0.02 g; FeSO4.7H2O 5 mg; Yeast extricate 2 g; Trace component solution (TES) 2 ml. The follow component solution (per liter) comprised of: 70 mg ZnCl2; 0.1 g MnCl2.4H2O; 60 mg H3BO3; 0.2 g CoCl2.2H2O; 20 mg CuCl2.2H2O; 25 mg NiCl2.6H2O; 0.9 ml HCl (37%). Disinfect bioreactor and tubing via autoclaving at 1210C and 15 psi for 40 minutes. Utilize 10% (v/v) effectively developing culture from the shake flagon as inoculum for the bioreactor. Control medium pH in bioreactor at 7.0 via programmed expansion of 2N NaOH/HCl through corrosive/base peristaltic siphons. Upset the medium in the bioreactor utilizing a level sharp edge turbine impeller turning at 150 rpm and keep up temperature at 330C by coursing chilled water utilizing FP 50 chiller (Julabo, Germany). Sparge nitrogen gas at 0.5 vvm in the bioreactor to give anaerobic conditions during the fermentation. Pull back samples at ordinary time frames h from the bioreactor and break down for biomass, lingering glycerol and 1,3-PD.

❖ **1,3-PD MODEL EQUATIONS:**

The model consists of a system of differential material balance equations which describe the batch dynamics of growth & 1,3-PD production. These equations are summarized below:

$$\mu = \mu max (S/S + KS) [1- (S / Sm)a] [1- (P/Pm)b] \quad (1)$$

$$qs = - \{(1/Ymax) \mu + m\} \quad (2)$$

$$qp = K1\mu + K2 \quad (3)$$

where μ- specific growth rate, qs - specific substrate consumption rate, qp- specific product formation rate, Sm- critical substrate concentration, m- maintenance energy constant, Pm- critical product concentration.

Daily Report

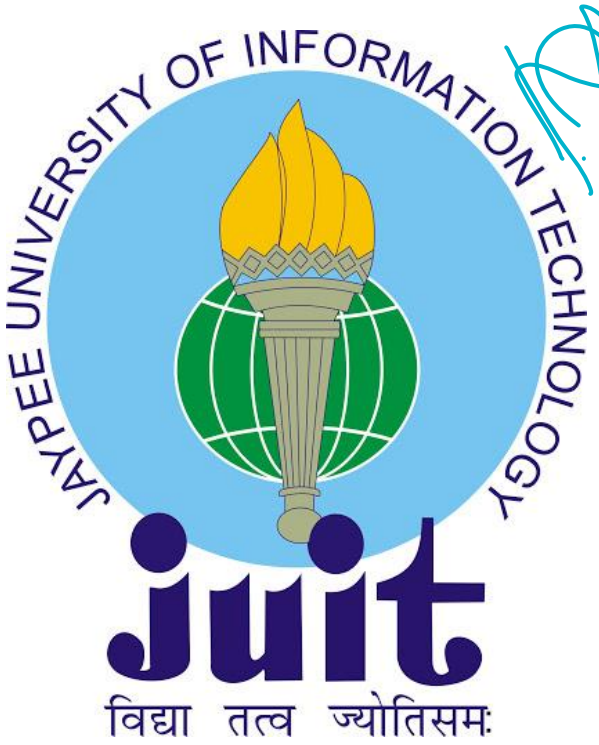
Summer Training

ANIMAL CELL CULTURE TECHNIQUES

Submitted By:

Rachita Gupta (171818)

Guide: Dr. Udayabanu



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CONTENTS

TOPIC	DATE	PAGE NUMBER
Summary	May 16-18, 2020	3
Instrumentation	May 19- June 1, 2020	4-12
Disorder- Alzheimer's	June 9-10, 2020	13-16
Basic Techniques	June 14-17, 2020	17-23
References	--	24

SUMMARY

Saturday, May 16, 2020

- Cells are taken from the organ of an experimental animal directly or by mechanical or enzymatic method. The cells can also be obtained by previously made cell line or strain such as fibroblasts, lymphocytes, cardiac or skeletal tissues. Removed cells are then grown in vitro in a controlled, favorable environment.[1]
- Used in research and diagnosis (specifically, viral infection)
- Cell culture begins with a primary culture aiming at achieving confluence, that is formation of monolayer of cell in a culture flask supplemented the required nutrients and growth factors. The cells are then passaged or sub cultured from the primary to secondary and subsequence to tertiary, until a continuous cell line is established. [1]
- Animal cell culture offers suitable model systems for investigating the following factors: [2]
  • Drug screening and development.
  • Mutagenesis and carcinogenesis.
  • Normal physiology and biochemistry of cells.
  • Potential effects of drugs and toxic compounds on the cells.
  • Vaccine production.
  • Examining drug metabolism.
  • Cytotoxicity.
  • Antibody production.
  • Investigating gene function.
  • Development of artificial tissues (e.g. artificial skin).
  • Production of biological compounds (e.g. therapeutic proteins).

Monday, May 18, 2020

- The polio vaccine was the first commercial product generated using mammalian cell cultures (primary monkey kidney cells).
- Broadly, animal tissue culture can be divided into two categories: [2]
  • Cultures that allow cell–cell interactions and encourage communication or signalling between cells → organ, histotypic and organotypic cultures.
  • Cultures in which cell–cell communication or interactions are lost or the signalling between them is missing → cultures in monolayers or suspension.

The first culture that is established from the in vivo environment is called the primary culture. This primary culture can be sub cultured many times to develop cell lines. Cell lines are generally immortalized or transformed cells, i.e. cells that have lost control over division, because of mutations or genetic alterations, or because a primary cell was transfected with some genes that immortalized the cells. [2]

INSTRUMENTATION

Tuesday, May 19, 2020

- Equipment used in cell culture technologies include: [3]
  - Hoods/ laminar flow/ biosafety cabinet
  - Incubators (CO_2 incubators)
  - Microscope (inverted)
  - Autoclave
  - Water purification devices
  - Medium filtration devices
  - Automated cell counters
  - Liquid nitrogen storage tanks
  - Water bath (circulating)
  - Centrifuge
  - Refrigerator and freezer (-20°C)
  - EVOS imaging systems
  - Electroporation instrumentation
- Aseptic work area is the top-most requirement
- Consultation with engineers and institutional biosafety officers for installation of proper requirement is required.
- Materials required are:
  - Reagents
  - Media
  - Cells
  - Serum (purified growth factors/ hormones)
  - Cell culture plasticware
  - Glassware
- Additional equipment required: [3]
  - Aspiration pump (peristaltic or vacuum)
  - pH meter
  - Roller racks
  - Confocal microscope
  - Flow cytometer
  - Cell culture vessels (flasks, petri dishes, etc)
  - Pipettes and pipettors
  - Syringes and needles
  - Waste containers

Wednesday, May 20, 2020

1. Hoods/ laminar flow/ biosafety cabinets:

The laminar stream hood gives an aseptic work territory while permitting the control of irresistible sprinkles or mist concentrates created by numerous microbiological systems.
Classes of laminar flow hoods: [3]

1. Class I: Class I laminar stream hoods offer critical degrees of security to research facility work force and to the earth when utilized with great microbiological procedures, however they don't give societies insurance from defilement. They are comparative in structure and wind stream qualities to synthetic smoke hoods.
2. Class II: Class II laminar stream hoods are intended for work including BSL-1, 2, and 3 materials, and they additionally give an aseptic domain important to cell culture tests. A Class II biosafety bureau ought to be utilized for taking care of possibly perilous materials (e.g., primate-determined cultures, virally contaminated cultures, radioisotopes, cancer-causing or harmful reagents).
3. Class III: Class III biosafety cupboards are gas-tight, and they give the most elevated feasible degree of assurance to work force and the earth. A Class III biosafety bureau is required for work including known human pathogens and other BSL-4 materials.

Laminar stream hoods shield the workplace from dust and other airborne contaminants by keeping up a consistent, unidirectional progression of HEPA-sifted air over the work territory. Contingent upon its plan, an even stream hood gives assurance to the way of life (if the air streaming towards the client) or to the client (if the air is attracted through the front of the bureau by negative pneumatic stress inside). Vertical stream hoods, then again, give huge assurance to the client and the cell culture.

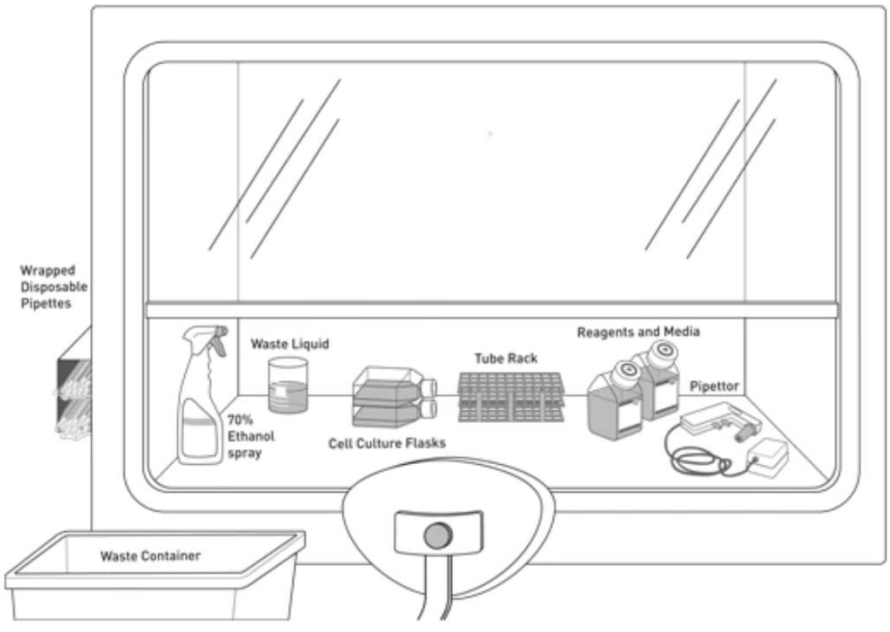


Fig1: The fundamental format of a cell culture hood [3]

2. Incubators:

The reason for the incubator is to give the proper condition to cell development. Visit cleaning of the incubator is fundamental to stay away from defilement of cell cultures. There are two essential sorts of incubators, dry and moist CO 2 incubators. Dry incubators are increasingly conservative, yet require the cell societies to be

brooded in fixed jars to forestall vanishing. Putting a water dish in a dry incubator can give some mugginess, however they don't permit exact control of environmental conditions in the incubator. Damp CO2 incubator are increasingly costly, however permit predominant control of culture conditions. They can be utilized to incubate cells refined in Petri dishes or multiwell plates, which require a controlled environment of high stickiness and expanded CO 2 pressure. [3]

Thursday, May 21, 2020

3. Water purification devices:

Commonly used purification techniques include; distillation, ion exchange, activated carbon, microporous filters, ultrafiltration, reverse osmosis, elix continuous deionization and ultraviolet (UV) radiation. [4]

It is imperative to acquire a decision of water characteristics that go from essential evaluation, for basic washing and flushing, to ultrapure for the most basic science and systematic applications, for example, HPLC and electrochemistry. Water quality required in lab is of three types: [5]

i. Type I (ultrapure) lab water: for molecular biology techniques, mammalian and bacterial cell culture, electrophoresis, qualitative analysis, etc.
ii. Type II lab water: for buffer and media preparation, glassware washing/ rinsing, histology, ELISA, dilution and reagent preparation, etc.
iii. Type III lab water: for autoclave feed, sterilizer feed, etc.

Water purification systems that are commonly used are: [3]

i. Barnstead water purification systems: pure and ultrapure water is obtained. With adaptable frameworks structured accurately for certain applications, and various water types from a solitary arrangement.
ii. Large Central Water Purification Systems: produces laboratory grade high purity water from tap water and cover a performance range from 40 l/h to 15,000 l/h.
iii. Point-of-Use Water Purification Systems: includes Type 1 ultrapure, Type 2 pure, reverse osmosis systems and stills, in addition to a full line of cartridge and filter systems.

4. Media filtration devices:

Media feeds and procedure buffers expect filtration to ensure against the presentation of microbes, infections, endotoxins and particulates that can debase and compromise forms.

Media takes care of expect filtration to diminish microscopic organisms and to give extra assurance from conceivable viral tainting. In the event that microorganisms are not decreased from media takes care of before they are added to the fermenter, the microbes can enter the procedure and ruin the maturation. [6]

Additionally, serum enhancements might be added to development media to help cell development. As the serum gets from an animal source, viral pollution is consistently a chance. The option of a viral decrease filtration step only preceding option of serum-containing development media to the aging vessel gives included insurance. Therefore, following techniques/ devices are used for filtration: [6]

i. **Retention of particulates and microorganisms utilizing high log reduction value (LRV) membrane filters**: LifeASSURE PLA arrangement channels will give a significant level of confirmation that all microscopic organisms are decreased from liquids with low (< 1CFU/1 ml)

bioburden levels. LifeASSURE PLA arrangement channels are developed of Nylon 6,6 film created by a procedure called multi-zone microporous layer innovation. The procedure of film throwing brings about a multi-zone microporous structure contained inside a solitary, nonstop film layer. The multi-zone structure contains open pores for prefiltration and more tight pores for controlled molecule and bacterial maintenance.

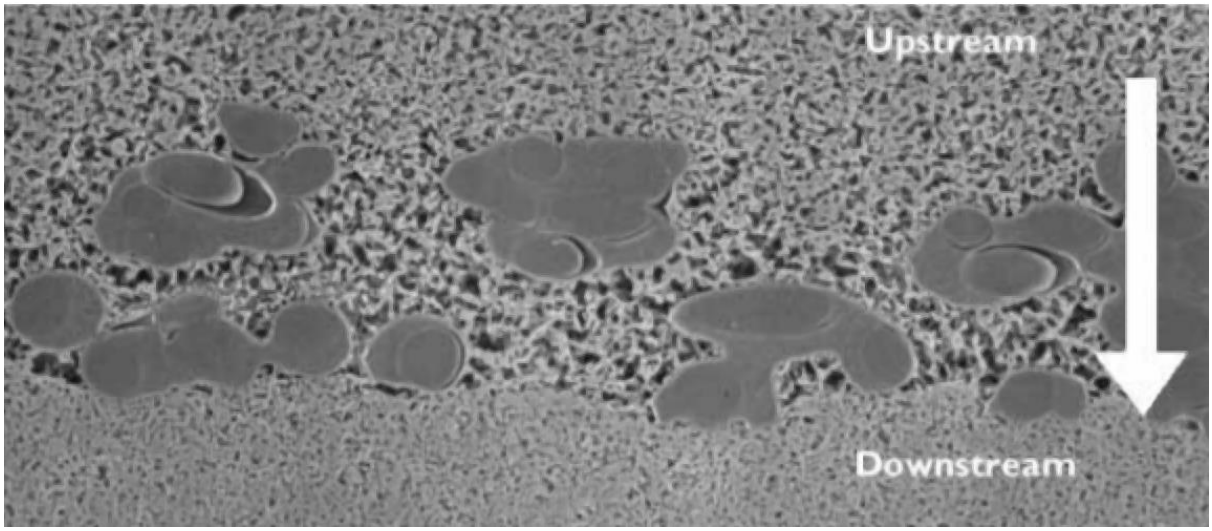


Fig2: LifeASSURE™ PLA Series Filter Membrane Structure [6]

Friday, May 22, 2020

ii. **Absolute bacteria retention and endotoxin reduction**: For the most significant level of sterility confirmation of media feeds and cushion arrangements, 3M Purification Inc's. LifeASSURE™ SP 0.20-micron, cleaning grade, outright evaluated channels are suggested. LifeASSURE SP arrangement channels are approved for total maintenance of *B. diminuta* at challenge levels more than 107 living beings for every cm2 channel region. LifeASSURE SP arrangement channels are additionally valuable for decrease of endotoxins from watery liquids. These channels are developed with two layers of decidedly charged Nylon 6,6 film. The fixed pore structure gives supreme, size-avoidance based maintenance of *B. diminuta*, while the positive surface charge gives upgraded maintenance of littler, contrarily charged molecule. Endotoxins are contrarily charged lipopolysaccharide sections of Gram-negative bacterial cell dividers. The improved endotoxin decrease by positive charge depends on electro kinetic collaboration. [6]

iii. **Virus reduction from serum-based media feeds with Zeta Plus™ VR Series Filters:** Zeta Plus™ VR arrangement channels offer a simple method to furnish extra popular leeway confirmation with an expendable, single utilize sterilizable channel cartridge. Zeta Plus VR arrangement channels are a group of profundity filtration cartridges and cases, built of cellulosic media which holds infections by particle trade adsorption. They are made out of high territory process channel helps implanted in a cellulose fibre profundity channel framework.

During the assembling procedure, a cationic charge modifier is synthetically bound to the network part, framing a changeless, interconnected, unbending profundity channel with emphatically charged electro kinetic catch destinations. The subsequent permeable profundity channel structure is a convoluted system of adsorptive stream channels fit for holding sullying infections by anion trade adsorption. [6]

iv. **Filtration of extreme pH and solvent buffer solutions with 3M Purification Inc. Betafine™ PEG & PPG Series Filters:** These channels offer particulate decrease to 0.20 micron and are built with a slope thickness polypropylene design. The slope thickness structure contains bigger pores at the upstream channel side with logically littler pores around the downstream channel side. This structure augments contaminant limit guaranteeing long channel life. Betafine PEG and PPG arrangement polypropylene channel medium is creased utilizing strategy called Advanced Pleat Technology. [6] This technique for development guarantees that the creasing procedure and media bolster materials cooperate to offer longer support life than standard spiral crease development.

Tuesday, May 26, 2020

5. Automated Cell Counters:

A cell counter/ hemocytometer is fundamental for quantitative development energy, and an extraordinary bit of leeway when more than a few cell lines are refined in the research center. It is a cell checking stage outfitted with best in class optics and picture investigation programming for fast appraisal of cells in suspension. With fluorescence capacity—brightfield and two discretionary fluorescence channels—analysts can tally cells, screen fluorescent protein articulation, and measure cell practicality. [3]

6. Storage Tanks:

A cell culture research center ought to have capacity territories for fluids, for example, media and reagents, for synthetic compounds, for example, medications and anti-infection agents, for consumables, for example, dispensable pipettes, culture vessels, and gloves, for crystal, for example, media containers and glass pipettes, for specific hardware, and for tissues and cells. Dish sets, plastics, and specialized gear can be put away at encompassing temperature on racks and in drawers. A few media, reagents, and synthetic substances are touchy to light; while their ordinary research center use under lit conditions is endured, they ought to be put away in obscurity or enclosed by aluminum foil when not being used. [3]

i. **Refrigerator:** For little cell culture research facilities, a local fridge (ideally one without an auto defrost cooler) is a sufficient and reasonable bit of gear for putting away reagents and media at 2–8°C. For bigger research centers, a virus room limited to cell culture is progressively suitable. The fridge or the virus room is cleaned routinely to evade defilement.

ii. **Freezer:** Most cell culture reagents can be put away at – 5°C to – 20°C; in this manner a ultradeep cooler (i.e., a – 80°C cooler) is discretionary for putting away most reagents. A local cooler is a less expensive option in contrast to a research facility cooler. While most reagents can withstand temperature motions in an auto defrost (i.e., self-defrosting) cooler, a few reagents, for example, anti-toxins and proteins ought to be put away in a cooler that doesn't auto defrost.

iii. **Cryogenic storage (liquid nitrogen):** Cell lines in ceaseless culture are probably going to experience the ill effects of hereditary insecurity as their entry number increments; hence, it is basic to get ready working loads of the cells and save them in cryogenic capacity. Try not to store cells in – 20°C or – 80°C coolers, in light of the fact that their reasonability rapidly diminishes when they are put away at these temperatures. There are two fundamental sorts of

fluid nitrogen stockpiling frameworks, vapor phase and liquid phase, which come as wide-necked or restricted necked stockpiling compartments. [3]

- Vapor stage frameworks limit the danger of blast with cryostorage tubes, and are required for putting away biohazardous materials.
- The fluid stage frameworks typically have longer static holding times, and are accordingly progressively affordable.
- Thin necked holders have a slower nitrogen vanishing rate and are increasingly practical.
- Wide-necked compartments permit simpler access and have a bigger stockpiling limit.

Thursday, May 28, 2020

7. Circulating Water Bath:

Circulating baths are constant temperature water baths that enable rapid heating and cooling of samples by constantly circulating water. Efficient temperature maintenance can be performed over a wide range of temperatures. [7] Circulating water baths are perfect when temperature consistency and control are especially basic, for example, when working with catalysts and in serological applications. these elite baths highlight a chip control and incorporate a removable treated steel peak spread, diffuser plate, and elastic duck.

8. EVOS Imaging Systems:

Planned by researcher for scientists, EVOS magnifying instruments fuse high-goals cameras, brilliant and carefully controlled LED light solid shapes, interfaces organized for ease of use that permit you to catch dazzling, distribution quality pictures and information. The EVOS magnifying lens are created to live up to the present desires for picture quality, UI communications, information age speed and adaptability, and end-client esteem. The efficient obtaining highlights, splendid LED block light and high-res cameras empower age of distribution quality pictures and information. The EVOS magnifying lens frameworks are particularly adaptable and perfect for an expansive scope of imaging applications, conveying wonderful pictures and information in the blink of an eye. [8]

Advantages of EVOS Cell Imaging frameworks include:

i. Adaptability and execution
ii. Minimized, ergonomic structure
iii. Scientist structured incorporated programming

Saturday, May 30, 2020

9. Electroporation Instrumentation:

Electroporation is a physical transfection strategy that utilizes an electrical pulse to make brief pores in cell layers through which substances like nucleic acids can go into cells. It is a profoundly productive procedure for the presentation of remote nucleic acids into numerous cell types, including microscopic organisms and mammalian cells. [9]

Host cells and chose atoms are suspended in a conductive arrangement, and an electrical circuit is shut around the blend. An electrical pulse at an improved voltage and just enduring a couple of microseconds to a millisecond is released through the cell suspension. This upsets the phospholipid bilayer of the film and results in the development of transitory pores. The electric potential over the cell film at the same time ascends to permit charged atoms like DNA to be driven over the layer through the pores in a way like electrophoresis.

The significant downside of electroporation is generous cell demise brought about by high voltage pulses and just halfway effective layer fix, requiring the utilization of more prominent amounts of cells contrasted with chemical transfection techniques.

The Neon® Transfection System is a second-generation transfection framework that utilizes an electronic pipette tip as an electroporation chamber. The plan and execution of the Neon® electronic pipette transfection chamber brings about expanded cell suitability and transfection productivity contrasted with conventional cuvette-based electroporation frameworks. The framework was intended for electroporation of mammalian cells, however it has discovered application for other cell types, for example, insect cell cultures and parasites. The structure of the electroporation chamber disperses the current similarly among the cells and keeps up a steady pH all through the chamber; these key advantages increment cell suitability drastically. [9]

Monday, June 01, 2020

10. Aspiration Pump:

Aspirators are frequently utilized for the expulsion and removal of fluids. The goal siphon makes a vacuum in the assortment bottle, which pulls in fluids because of the differential weight. The fluid is gathered in the jug, and can be discarded when full. [10]

Types of aspiration pump include:

i. **Peristaltic:** Peristaltic siphons are exceptionally flexible research facility machines, taking into account yearning with programmed administering, yet in addition give the component of opposite stream. Turn around stream considers different apportioning and suctioning activities which are appropriate for precisely administering fluids extending in various thickness from watery answers for medium syrups. These peristaltic siphons occupy negligible seat top room to permit more space for activity while likewise permitting the siphons to be set in minimized spaces, for example, seethe hoods. These siphons use the mechanics of positive dislodging, considering more noteworthy precision and estimation with insignificant loss of test. Planned with a rotor which packs an adaptable cylinder conveying test, the peristaltic siphon moves both example and air at a consistent rate at encompassing weight towards the outlet. [11]

ii. **Vacuum:** Vacuum siphons give sans oil vacuum siphoning. Diminishing procedure filtration times by giving high force vacuum attractions to suction arrangements, vacuum siphons are productive devices in any lab. Supporting high stream rates to speed up and diminish activity times, the vacuum siphons are intended to be light weight and effectively moved between workstations as well as all through security hoods and substance rage hoods found in numerous lab spaces. Giving premium programmed administering and variable speed settings, these siphons can deal with numerous applications. These applications incorporate vacuum filtration, degassing, impregnation, drying chambers, turning evaporators, refining, gel dryers and gas diagnostic frameworks. [11]

11. Glassware and Plasticware:

i. Beaker
ii. Pipette
iii. Measuring Cylinder
iv. Horizontal and vertical flask:
   - T-25→ maximum of 10ml medium
   - T-75→ maximum of 50ml medium, holds $7.5*10^6$ cells
   - T-100
   - T-150→ maximum of 100ml medium, holds $15.0*10^6$ cells
   - T-225→ maximum of 200ml medium, holds $22.5*10^6$ cells

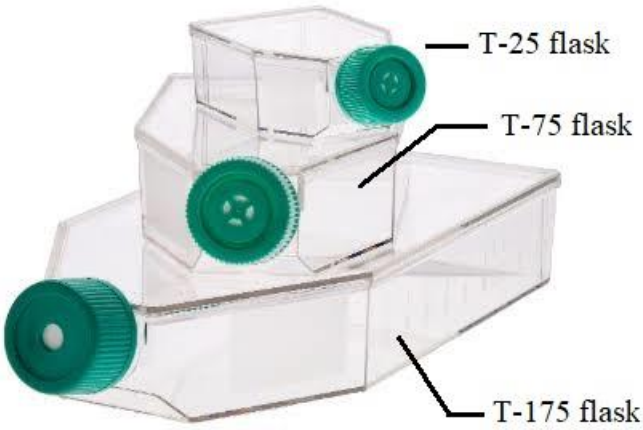


Fig3: Flask of different surface areas used for cell culture [18]

v. Petri plate
vi. Microscopic slides
vii. Coverslips
viii. Cell culture plates

12. Flow Cytometer:

Flow cytometry provides a rapid, sensitive and accurate analytical means to monitor hybridoma cell cultures. The use of glow cytometry has enabled us to study the changes in DNA, RNA, protein, IgG, mitochondrial activity and cell size that take place during the growth cycle of batch culture. [12] The fundamental rule of flow cytometry is the entry of cells in single record before a laser so they can be identified, tallied and arranged. Cell parts are fluorescently labelled and afterward energized by the laser to radiate light at different frequencies, recognized by the locators.

Tuesday, June 09, 2020

Disorder: Alzheimer's Disease

Alzheimer's disease is a progressive disorder that causes brain cells to waste away (degenerate) and die. Alzheimer's disease is the most common cause of dementia — a continuous decline in thinking, behavioral and social skills that disrupts a person's ability to function independently.[13] It happens when plaques containing beta amyloid cells form in the brain. As symptoms worsen, it becomes harder for people to remember recent events, to reason, and to recognize people they know. [14]

Origin:

The ailment was first depicted by Dr. Alois Alzheimer, a German doctor in 1906. Alzheimer had a patient named Auguste D, in her fifties who experienced what appeared to be a psychological sickness. In any case, when she passed away in 1906, an examination uncovered thick deposits, called neuritic plaques, outside and around the nerve cells in her cerebrum. Inside the cells were wound strands of fiber, or neurofibrillary tangles. Since, Dr. Alois Alzheimer was the principal individual who found the malady, AD was named after him. [15]

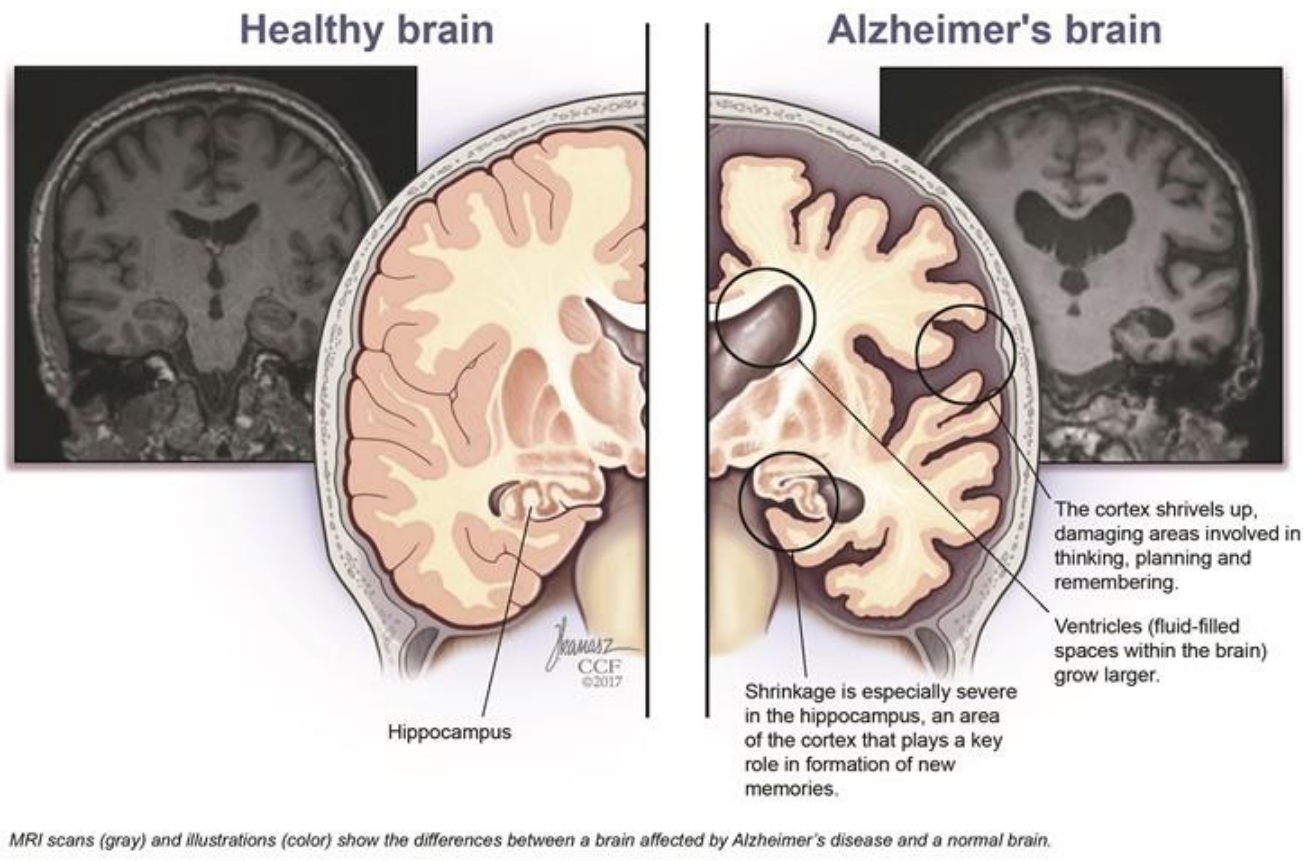


Fig4: healthy brain vs AD brain [16]

Symptoms: [14]

1. Diminished capacity to take in and recall new data, which can lead, for instance, to:

- dreary inquiries or discussions
- losing individual things
- overlooking occasions or arrangements
- getting lost on a recognizable course

2. Hindrances to thinking, complex entrusting, and practicing judgment, for instance:

- poor comprehension of dangers
- powerlessness to oversee funds
- poor dynamic capacity
- powerlessness to design perplexing or consecutive exercises

3. Hindered visuospatial capacities that are not, for instance, because of vision issues. These could be:

- failure to perceive countenances or regular articles or to discover protests in direct view
- powerlessness to utilize basic apparatuses, for instance, to situate garments to the body

4. Impeded talking, perusing and composing, for instance:

- trouble considering regular words while expressing, delays
- discourse, spelling, and composing blunders

5. Changes in character and conduct, for instance:

- bizarre temperament changes, including fomentation, aloofness, social withdrawal or an absence of intrigue, inspiration, or activity
- loss of sympathy
- urgent, fanatical, or socially unsatisfactory conduct

Wednesday, June 10, 2020

Diagnosis: [14]

- There is no single test for Alzheimer's illness, so specialists will take a gander at the signs and side effects, take a clinical history, and preclude different conditions before making a determination.
- They may likewise check the individual's neurological capacity, for instance, by testing their equalization, detects, and reflexes.
- Different evaluations may incorporate a blood or urine test, a CT or MRI output of the cerebrum, and screening for despondency.
- Here and there the side effects of dementia are identified with an acquired issue, for example, Huntington's illness, so hereditary testing might be finished.
- Subsequent to precluding other potential conditions, the specialist will complete subjective and memory tests, to survey the individual's capacity to think and recollect.
- Hereditary Test:
  - At times, hereditary testing might be proper.
  - A **gene known as the APOE-e4 (Apolipoprotein E)** is related with higher odds of individuals beyond 55 years old years creating Alzheimer's.

- Utilizing this test early could demonstrate the probability of somebody having or building up the malady. Be that as it may, the test is disputable, and the outcomes are not so much solid.
- Later on, developing organic tests may make it conceivable to evaluate for biomarkers in individuals who might be in danger of Alzheimer's.

Causes: [14]

Like a wide range of dementia, Alzheimer's is brought about by brain cell death. It is a neurodegenerative disorder, which implies there is dynamic synapse passing that occurs after some time. In an individual with Alzheimer's, the tissue has less and less nerve cells and associations. Examinations have demonstrated that the nerve tissue in the mind of an individual with Alzheimer's has small deposits, known as plaques and tangles, that development on the tissue. The plaques are found between the perishing synapses, and they are produced using a protein known as beta-amyloid. The knot happens inside the nerve cells, and they are produced using another protein, called tau.

Factors that increase the risk include:

- undergoing severe or repeated traumatic brain injuries (TBI)
- exposure to some environmental contaminants, such as toxic metals, pesticide, and industrial chemicals
- Neurochemical factors like acetylcholine, somatostatin, substance P., norepinephrine

Biochemical Markers: [17]

1. **Neuroimaging biomarkers**: Widely investigated neuroimaging biomarkers of AD incorporate brain atrophy, amyloid plaques, hyperphosphorylated tau, glucose hypometabolism, unusual cerebral blood stream, neuronal movement, and local cerebrum metabolites. Imaging modalities used to identify these markers incorporate positron emanation tomography (PET), magnetic resonance imaging (MRI), magnetic resonance spectroscopy (MRS), electroencephalography (EEG), and single-photon emission computed tomography (SPECT). Cerebrum decay (brain atrophy) estimated by MRI is presently being considered as a substantial biomarker of mild cognitive impairment (MCI), and may likewise be helpful for preclinical identification of AD.

2. **Genetic biomarkers:** Varieties in three qualities—amyloid precursor protein (APP), presenilin1 (PSEN1), and presenilin2 (PSEN2)— have been recognized as causal factors in EOAD (beginning stage AD). Along with three familial qualities (APP, PSEN1, PSEN2), APOE accounts 30–half of heritability of AD. Each of the four qualities were recognized by hereditary linkage examination and positional cloning. A couple of low-penetrance quality variations in AD have been distinguished, including APOE4, SOLR1, TOMM40, BIN1, CLU, ABCA7, CR1, PICALM, MS4A6A, CD33, MS4A4E, and CD2AP. Of these, APOE4 is the most emphatically connected with LOAD (late beginning AD), yet the connection shifts with ethnicity, age, and sex. Other nongenetic hazard factors,

for example, age and past head injury, have been embroiled in LOAD and have been appeared to cause changes in miRNA expression and posttranslational alterations that influence molecular signalling.

3. **Cerebrospinal Fluid (CF) biomarkers:** Cerebrospinal fluid (CSF) biomarkers for Alzheimer's disease (AD) include Aβ1–42, total tau (t-tau), and phosphorylated tau-181 (p-tau). Reduced levels of CSF Aβ1–42 and increased levels of t-tau and p-tau indicate an AD diagnosis. Because cerebrospinal fluid (CSF) can only be collected by lumbar puncture, CSF-based biomarkers of AD may not lend themselves to diagnostic screening applications or routine use in elderly patients.

4. **Peripheral fluid-based biomarkers:** Blood-based AD biomarkers may give a superior, less obtrusive option for AD screening, early determination of AD, and continue testing to evaluate treatment viability. Two basic ways to deal with finding and creating fringe liquid-based AD biomarkers are lipidomics and proteomics. The best explored AD blood-based biomarkers are the Aβ peptides Aβ1–40 and Aβ1–42; tau proteins; fiery proteins C-responsive protein (CRP), antichymotrypsin, macroglobulin, interleukins, TNF-α, supplement factors, homocysteine, clusterin, APOE, and serum amyloid protein (SAP).

5. **Cell-based biomarkers:** Cytomic or cell-based AD biomarker approaches involve multiparametric assessment of functional, morphological, and antigenic differences between cells isolated from peripheral systems from individuals with or without AD. The most widely researched peripheral cells for assessment of AD biomarkers include blood cells (lymphocytes, red blood cells, platelets, and leukocytes), skin fibroblasts, retinal nerve cells, and buccal cells.

BASIC TECHNIQUES

Sunday, June 14, 2020

Trypsinizing cells: [21]

It is the process of cell dissociation using trypsin, a proteolytic enzyme which breaks down proteins, to dissociate adherent cells from the vessel in which they are being cultured. When added to a cell culture, trypsin breaks down the proteins which enable the cells to adhere to the vessel.

Requirements: water bath, fresh media (DMEM), T-75 flask, PBS solution, isopropyl alcohol (for sterilization), tissues, pipettes, conical tubes, trypsin, waste beaker.

Methodology:

1. Place the appropriate media in warm water bath at 37ºC for 5-10 mins.
2. Place T-75 flask and PBS solution inside the sterilized hood.
3. Aspirate the media (10 ml pipette) in the T-75 flask and discard.
4. Aspirate 10 ml of PBS to the flask and let sit for 1-2 mins. Swirl gently afterwards.
5. Aspirate the PBS from the flask and discard.
6. Aspirate 1ml of trypsin and put into the flask.
7. Swirl around so that the trypsin covers the entire flask.
8. Remove trypsin from the flask and discard.
9. Place the flask in incubator for 5 mins.
10. Add 10 ml of DMEM media onto the flask. Pipette it up and down to make sure all the cells get dispersed. Media turns cloudy.
11. Aspirate the media from flask and transfer to a 15ml conical tube.
12. Cells can be passaged in another flask, counted via hemocytometer or cryopreserved for further experimentation.

Aseptic Techniques: [22]

1. Always wear PPE, closed shoes, glasses
2. Review MSDS before handling any media or reagent
3. Wash hands properly before and after the experiment. This removes potential contaminants such as bacteria and dead skin cells.
4. 70% ethanol is used for sterilization of laminar flow cabinet as well as equipment and reagent bottles as well.
5. Place everything at its respective position to avoid over-crowding, confusion and disruption of air flow. Proper setup allows easy, fast and sterile work environment.

6. While handling pipettes, make sure that it does not touch anything non-sterile such as outside of reagent bottles. Discard the pipette after one use or if contaminated. Do not reuse.
7. Do not open anything outside the culture hood.

Passaging Cells: [19]

Sub-culturing, also called passaging cells, is the removal of medium and transfer of cells from a previous culture into fresh growth medium, a procedure that enables the further propagation of the cell or cell strain.

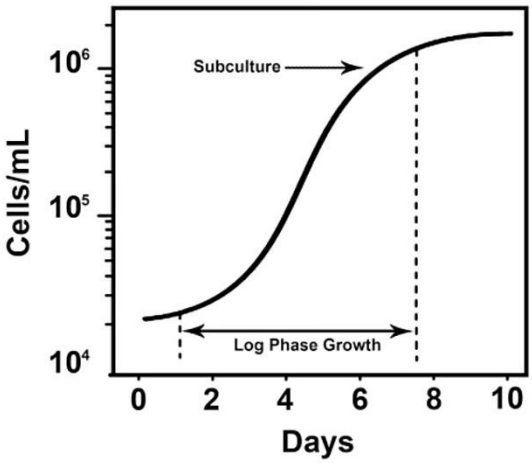


Fig5: Cell Cycle graph depicting appropriate cell density required for passaging [19]

1. Sterilize culture hood and equipment properly.
2. Check culture carefully for signs of contamination or deterioration.
3. For removal of **adherent cells**, remove spent medium from the culture flask.
4. Rinse flask with salt solution such as DPPS (not containing Mg^{2+} or Ca^{2+} as these inhibit cell dissociation reagent).
5. Remove the salt solution.
6. Add cell dissociation reagent such as TrypLE Express (cell dissociation enzymes; substitute for trypsin). Make sure that the reagent covers the entire cell sheet by gentle swirling. Also, lightly tap on flask surface to make sure that cells detach.
7. With the help of microscope, it can be made sure that cells have detached. They appear round after getting detached from substrate and move around when flask is moved.
   Note: when using TrypLE, inactivation is done by dilution whereas for trypsin, a serum is required.
8. Transfer cells to a conical tube and centrifuge to remove residual dissociation reagents.
9. Discard the medium with the help of a pipette and resuspend pellet in warm complete growth medium.
10. Remove small suspension sample for cell counting. Trypan blue is used to calculate ratio of live (remains white due to intact membrane) to dead (blue) cells.

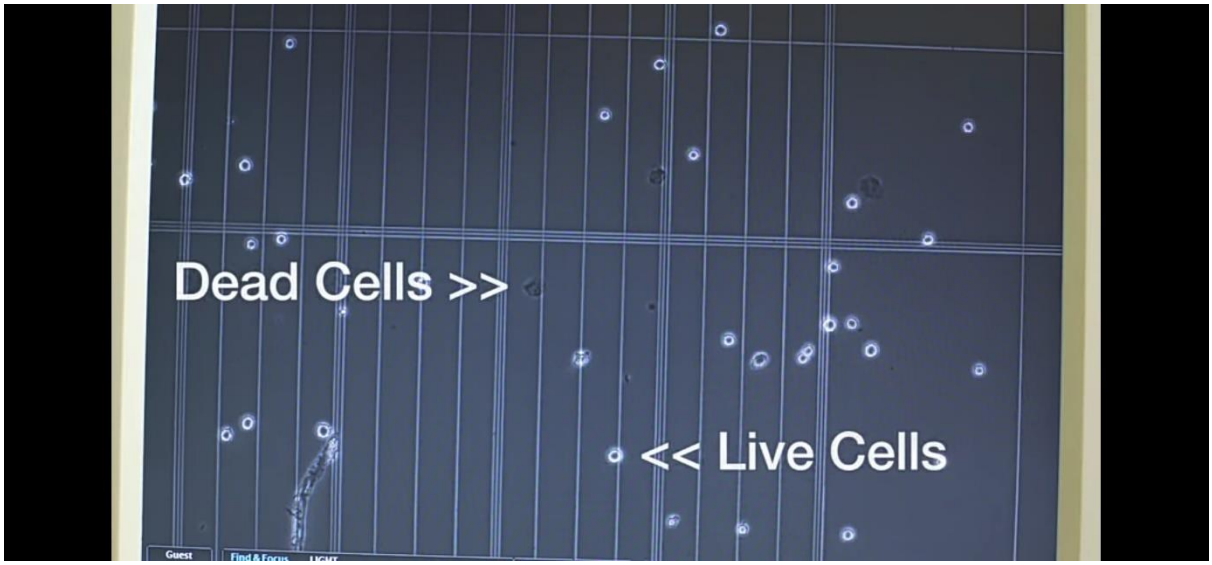


Fig6: cells observed in hemocytometer after staining with trypan blue [19]

11. Based on cell count, amount of additional media to be added is calculated for optimal seeding density.
12. Media is added to cells, and the suspension is then pipetted into a fresh flask.
13. Tightly cap if caps are vented and loosely if not for adequate gas exchange and minimal contamination.
14. Transfer the cells to incubator.
15. For passaging **suspension cells**, remove a small sample from cultured cells and count in the same manner as done for adherent cells.
16. Based on cells count, additional fresh media is added to the flask. For proper gas exchange, minimum and maximum of capacity of flasks is considered. This helps in proper mixing and gas flow while shaking in incubator.
17. After every three weeks, gently spin the cells, remove spent medium and replace with fresh media for eliminating cells debris and metabolic waste.

Monday, June 15, 2020

Culture Preparation and Plating: [20]

1. HEK-293 cells (human embryonic kidney cells from 293rd experiment of Frank Graham) were cultured in tissue culture flasks and maintained between 10% and 90% confluency (number of cells) in a humidified, 37 °C, 10% CO_2 incubator.
2. Current density of cells is determined with the help of a microscope.
3. Cell culture medium is removed from the cells and cells are washed once with PBS
4. For a T-75 flask, 2 ml TrypLE trypsin is added to detach cells from the plate and allowed to be incubated for 2 mins.
5. After incubation, it is verified that all the cells are detached with the help of a microscope (cells appear floating)

6. Trypsinization is stopped by adding 10ml of assay medium which is pipetted up and down to disperse cells.
7. Cell suspension is transferred to a conical tube.
8. Cell number in solution is quantified by a hemocytometer to determine the concentration of cells for subsequent assays.
9. The suspension is centrifuged at 500g for 5 mins at 18 °C.
10. The supernatant is discarded and the pellet is resuspended in assay medium to achieve a final conc." of $1*10^6$ cell/ml.
11. The cells are then pipetted into a 96-well plate according to fig7.

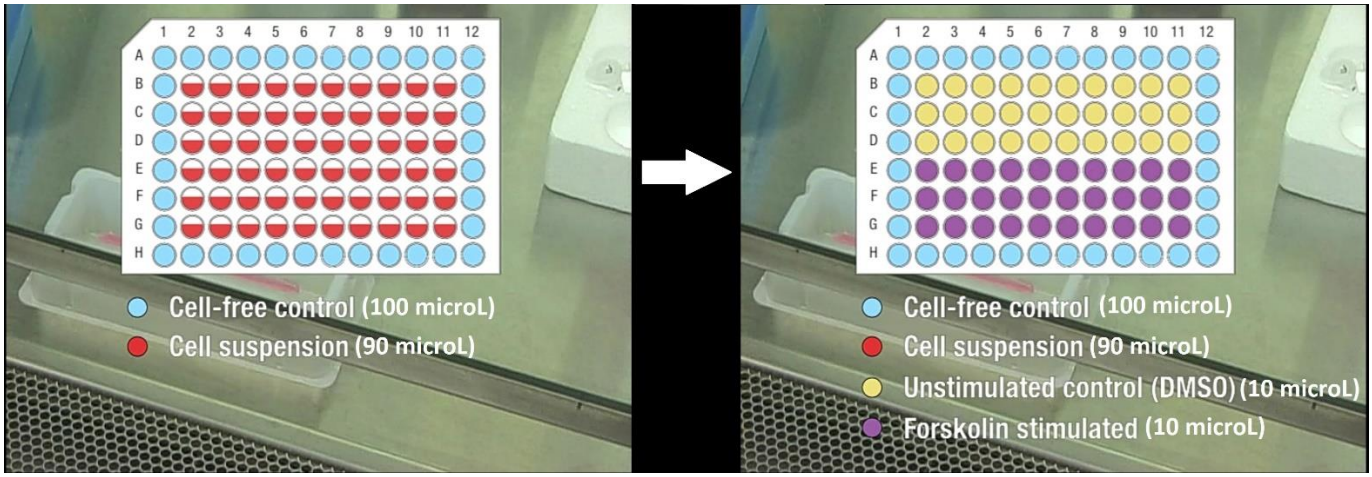


Fig7: 96 well plate prepared for culture and plating [20]

12. Incubate the plate for 4 hours at 37 °C in 10% CO_2 incubator.
13. After incubation, assay reagents are added to the plate and stimulated cell activity is determined.

Cell Counting: [23]

A hemocytometer is a device used for counting cells. It is a modified microscopic slide containing two identical wells/ chambers into which a small suspension of cell culture is pipetted.

Structure: Each chamber of hemocytometer is divided into a grid pattern consisting of 9 large squares. Each square has identical dimensions and harbor 10^{-4} ml of cell suspension. Generally, cells are counted in 4 corner squares and the center square. In these squares, cells touching the top and left boundaries are counted whereas those touching the bottom and right are excluded.

Note: do not count artifacts (structure that appear blurry or does not have a well-defined shape). Proper storage, cleaning and handling of hemocytometer reduce the chances of artifacts.

Procedure:

1. 100 µL of cell suspension is added to a microfuge tube.
2. Dilute the cell suspension with 100 µL of Trypan Blue.
3. Load the prepared sample in both wells under the coverslip.
4. Place under the microscope and observe.

Note: dead cells allow the dye to pass through its membrane and appear blue whereas live cells do not and hence appear clear.

Formulas involved:

1. Percentage of viable cells= (Number of viable cells/ Total number of cells) *100
2. Average number of cells per square= number of viable cells/ squares counted
3. Dilution factor= final volume/ volume of cell suspension
4. Concentration (viable cells/ ml) = average number of cells per square * dilution factor * 10^4

Tuesday, June 16, 2020

Preventing Contamination:[24]

1. Wear personal protective equipment restricted to the cell culture lab. PPE should be specific for the individual as well.
2. Disinfect gloves prior starting working and between working steps. Let gloves dry after that.
3. Make sure to place the required items in the biosafety cabinet prior to working but avoid overcrowding. Sterilize every glassware, equipment or tool to be used with 70% ethanol or lint-free wipes and then place it in the cabinet. Arrange everything at its designated place for fast and efficient working.
4. Color- coded and clear labeled products help organize the work space.
5. Water bath increases the risk of germ transfer. Therefore, it should be cleaned on a regular basis. Bactericides and fungicides are added to the water for proper removal.
6. Work with one cell type at a time and disinfect the cabinet surface between work steps.
7. Open and reseal sterile packages inside the cabinet only.
8. Avoid opening the incubator doors for too long. This can be achieved by installing clear glass doors which can help locate the item before opening the incubator chamber.
9. Quarantine new cells in a designated incubator until proved void of contaminants.
10. Place cap sideways on the work surface so that it is not in contact with the air flow as well as the floor.
11. Make sure not to touch the pipette tip something unsterile.
12. Use petri dishes with handling rings preferably for easy transportation, stacking and culturing.

Wednesday, June 17, 2020

Cryopreservation: [25]

Note: Label each vial with cell type, passage number and date

FBS (Fetal Bovine Serum) contains a large amount of growth factors which facilitate cell survival and proliferation and lower number of antibodies that can bind to cells in cell culture.

DMSO (Dimethyl Sulfoxide) prevents intracellular and extracellular crystal formation in cells during the freezing process.

Isopropanol provide controlled rate freezing of cells.

Requirements: Pre-chilled freezing media (90%FBS, 10% DMSO), container filled with isopropanol

Procedure:

1. For **adherent cells**, conditioned media is aspirated off and discarded.
2. Attached cells are washed with PBS by gentle swirling and then PBS is discarded.
3. TrypLE is added to detach the cells from the flask. Medium is added.
4. Collect suspension in 15ml centrifuge tubes.
5. Then centrifuge.
6. Discard the supernatant. Resuspend pellet in appropriate volume of freezing medium for optimal cell density.
7. Transfer 1ml of suspension solution in each cryovial.
8. Freeze the cells at -80 °C overnight.
9. Then store in liquid nitrogen permanently.

Precautions:

1. No inactivation is required when using TrypLE.
2. Small sample is collected for cell counting (number and % viability)
3. Viable cells should be more than 90%. Only healthy cells should be frozen.
4. Amount of freezing medium to be added depends on number of cell and concentration in each vial.
5. Use a container such that the temperature of the cells drops by 1 °C/min. This decreases cell damage.
6. Always wear proper PPE while handling liquid nitrogen
7. All steps should be carried out quickly and carefully to minimize temperature changes, and under appropriate medium formulation and freezing density.

Thawing of Cells: [26]

Requirements: pre-warmed medium, cell culture flask

Procedure:

1. Remove cells from liquid nitrogen quickly and place them on dry ice bath.
2. The cells are then thawed in a 37 °C water bath quickly.
3. Remove from water bath when a small chunk of ice remains in the vial. The ice chunk melts when the vials are moved to culture hood from water bath.
4. Transfer the contents of vial into a centrifuge tube with a sterilized pipette.

5. Add 10 ml of pre-warmed cell culture medium to the centrifuge tube.
6. Centrifuge the cells to remove the freezing medium containing DMSO.
7. Discard the supernatant. Resuspend the pellet in 10ml complete pre-warmed medium.

Precautions:

1. DMSO and cell culture freezing media are toxic. Always wear appropriate PPE and refer to MSDS.
2. Perform each step carefully and quickly. Ensure appropriate temperature, medium formulation and seeding density.
3. Ready the culture hood before removing cells from liquid nitrogen.
4. Do not submerge the vial while thawing in water bath.
5. Add the pre-warmed media drop-by-drop and then gradually increase the amount to prevent osmotic-shock.
6. Do not centrifuge the cells if the cell line is too delicate.
7. Medium volume, flask size and number of flasks plated will depend on the number of cells frozen in the vial and the optimal seeding density for the cells. Viable cell count can also be considered for this.
8. Ensure proper distribution of cells on the flask surface.

Subculture: [27]

1. Prepare space and materials carefully. Label the glassware with proper date, cell type, etc.
2. Check cells before sub-culturing. There must be 80% confluency along with presence of mitotic cells.
3. After removal of culture media, 9ml of Trypsin/ EDTA solution is added and flask is rocked. All of the 9 ml of Trypsin/ EDTA is removed and fresh Trypsin/ EDTA (3ml) is added. Incubate flask till all the cells become round (1-20 mins depending upon cell type). Confirm dissociation of cells. Remaining adherent cells can be removed by gentle tapping of the flask.
4. 9 ml of trypsin neutralizer is added to the flask to avoid over trypsinization.
5. Transfer suspension to a 15 ml centrifuge tube. Add trypsin neutralizer again to remove remaining cells and transfer this to the 15 ml centrifuge tube again.
6. Centrifuge the suspension at 180g for 7 minutes.
7. Discard the supernatant. Resuspend pellet in 12 ml of supplemented medium (or as per experiment)
8. Count the number of cells and dilute as per the appropriate seeding density with supplemented medium.
9. Incubate till further use.
   Note: Long term incubation with high trypsin concentration damage cells by removing cell surface proteins and thus kills the cells.

REFERENCES

1. Hudu, Shuaibu Abdullahi, Ahmed Subeh Alshrari, Ahmad Syahida, and Zamberi Sekawi. "Cell culture, technology: enhancing the culture of diagnosing human diseases." *Journal of clinical and diagnostic research: JCDR* 10, no. 3 (2016): DE01.
2. Bhatia, Saurabh, Tanveer Naved, and Satish Sardana. "Introduction to Pharmaceutical Biotechnology, Volume 3; Animal tissue culture and biopharmaceuticals." *Introduction to Pharmaceutical Biotechnology, Volume 3; Animal tissue culture and biopharmaceuticals, by Bhatia, Saurabh; Naved, Tanveer; Sardana, Satish. ISBN: 978-0-7503-1348-3. IOP ebooks. Bristol, UK: IOP Publishing, 2019* (2019).
3. https://www.thermofisher.com/in/en/home/references/gibco-cell-culture-basics/cell-culture-equipment/basic-laboratory-equipment.html
4. https://www.biocompare.com/Lab-Equipment/19628-Laboratory-Water-Purification-Systems-Lab Water/#:~:text=Commonly%20used%20purification%20techniques%20include,and%20ultraviolet%20(UV)%20radiation.
5. evoqua.com/en/brands/IPS/Pages/Laboratory-Water.aspx
6. https://www.bioprocessonline.com/doc/filtration-of-cell-culture-growth-media-and-0001
7. https://www.fishersci.com/us/en/browse/90088140/circulating-baths
8. https://www.thermofisher.com/in/en/home/life-science/cell-analysis/cellular-imaging/cell-imaging-systems.html?gclid=Cj0KCQjwz4z3BRCgARIsAES_OVdIuPQWJ6b609BsII7W5KQCUed0ACfW2AhvIghbUJbX6PmcvLKUYOUaAluhEALw_wcB&ef_id=Cj0KCQjwz4z3BRCgARIsAES_OVdIuPQWJ6b609BsII7W5KQCUed0ACfW2AhvIghbUJbX6PmcvLKUYOUaAluhEALw_wcB:G:s&s_kwcid=AL!3652!3!429011377326!p!!g!!evos%20imaging%20system&cid=bid_pca_iie_r01_co_cp1359_pjt0000_bid00000_0se_gaw_bt_lgn_ins
9. https://www.thermofisher.com/in/en/home/references/gibco-cell-culture-basics/transfection-basics/transfection-methods/electroporation.html
10. https://www.welchvacuum.com/en-in/applications/aspiration-cell-culture#:~:text=Aspiration%20(Cell%20Culture),-Contact%20Us&text=How%20can%20we%20help%20you%3F&text=In%20biochemistry%2C%20microbiology%20and%20cell,due%20to%20the%20differential%20pressure.
11. https://www.pipette.com/laboratory-vacuum-pumps
12. Al-Rubeai, Mohamed, A. N. Emery, and S. Chalder. "Flow cytometric study of cultured mammalian cells." *Journal of biotechnology* 19, no. 1 (1991): 67-81.
13. https://www.mayoclinic.org/diseases-conditions/alzheimers-disease/symptoms-causes/syc-20350447#:~:text=Alzheimer's%20disease%20is%20a%20progressive,person's%20ability%20to%20function%20independently.
14. https://www.medicalnewstoday.com/articles/159442
15. https://www.slideshare.net/sanilmlore/alzheimers-disease-29439517
16. https://www.keepmemoryalive.org/brain-science/alzheimers-brain
17. Khan, Tapan. *Biomarkers in Alzheimer's Disease*. Academic Press, 2016.
18. https://alkalisci.com/cell-culture-flasks-vented.html
19. https://www.youtube.com/watch?v=CMRKKl9XSDU
20. https://www.youtube.com/watch?v=6vchql21tEE
21. https://www.youtube.com/watch?v=7hEUmLz1Ew0
22. https://www.youtube.com/watch?v=nr1tV_LuqJk
23. https://www.youtube.com/watch?v=pP0xERLUhyc
24. https://www.youtube.com/watch?v=P4dTbKVDIZ4
25. https://www.youtube.com/watch?v=tCNtKrxlZPs
26. https://www.youtube.com/watch?v=4HxqQOHifkU
27. https://www.youtube.com/watch?v=k2PMEET4Smo

A project report submitted in partial fulfilment of the requirement for the degree of Bachelor of Technology

In

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS BY

VITASTA JALALI

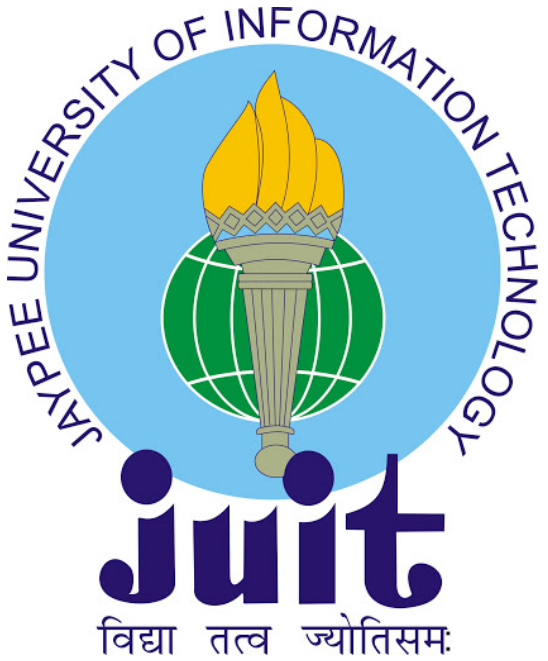
171819

Under the supervision of

Dr. Sudhir Syal

Professor and Head department of biotechnology and bioinformatics

to



JAYPEE UNIVERSITY OF INFORMATION AND TECHNOLOGY, WAKNAGHAT, SOLAN – 173234, HIMACHAL PRADESH

CANDIDATES DECLARATION

I hereby declare that the work presented in this report entitled "**STUDY ON ATCC (AMERICAN TYPE CULTURE COLLECTION)**" in the partial fulfilment of the requirement for the degree of Bachelor of technology in biotechnology department is an original record carried under the guidance of Dr. Sudhir Syal.

VITASTA JALALI

(171819)

This is to certify that the above statement made by the candidate is true to the best of my knowledge.

NAME OF THE SUPERVISER:

Dr. Sudhir Syal

Professor and Head department of biotechnology and bioinformatics

ACKNOWLEDGEMENT: - The guidance from mentor and Jaypee university of information technology is acknowledged.

Here we are beginning with ATCC and a little about long haul parasitic protection that how it is done for example various techniques for it.

ATCC (AMERICAN TYPE CULTURE COLLECTION)

ATCC: - It is a chief worldwide natural materials asset and measures associations whose missions centers around obtaining, verification, creation, protection, improvement and dissemination of standard reference microorganisms, cell lines, and different materials. While keeping up customary assortment materials, ATCC grows top notch items, norms, and administrations to help logical exploration and discoveries that improve the wellbeing of worldwide populaces.

KIND OF CULTURE PRESERVATION DONE

- >buffers and strains

- > Cryopreservation

- > Media

Web based ORDERING STEPS

1. Create profile
2. Establish client account
3. Place a request
4. Track your requests

It offers open and private-division associations in accomplishing redid answers for overseeing natural materials.

For the executives a few focuses are to be followed: -

- >Authentication and portrayal examine

- >Storage and cryopreservation

- >Data the executives, request satisfaction and conveyance

- >Intellectual property the executives

- >Regulatory and legitimate consistence

- >cold chain the executives

- >off-site biorepository the executives

It works through our all venture procedure for example from starting request, plan and inception of the venture to the biobanking and appropriation of your natural materials.

ATCC'S EXTENSIVE COLLECTION

In excess of 3400 nonstop cell lines accessible by species, tissues/infection type and flagging pathways.

Tumor cell and atomic boards, for malignant growth research commented on with quality change and sub-atomic profiles.

More than 18000 bacterial strains helpful in industry applications examine advancement.

In excess of 3000 human and creature infections.

Parasites and yeast speaking to more than 7600 species.

More than 1000 genomic and engineered nucleic acids.

More than 500 microbial societies suggested as quality control reference strains.

Instructive REQUIREMENTS

Scientists: - four year college education in a science related field and 2-5 years of important experience.

SENIOR BIOLOGISTS: - 4 to 8 years of significant experience + four year certification in science field. Experience working with infections and cell culture is must.

Client care REPRESENTATIVE: - least secondary school certificate degree and 4 years of client care understanding.

Store TECHNICIANS: - secondary school certificate degree or GED. 1-4-year involvement in information section, dispatching/recuperation/test the executives. Experience of working with a companywide venture based framework.

Permitting ASSOCIATE: - four year college education in a natural science or business licensed innovation law.

Least 3-5 years of experience working in permit innovation.

WORKING OF ATCC

Beginning with an ATCC Bacterial Strain

ATCC bacterial strains are dispatched solidified on dry ice in plastic cryopreservation vials, as lyophilized societies in glass ampoules or serum vials, or as live societies on agar inclines or in stock medium. Endless supply of solidified societies, quickly resuscitate societies by defrosting and in this way moving societies to a fitting development medium. In the event that this is absurd, store solidified vials in fluid nitrogen fume (beneath - 130°C). Then again, the solidified material can be put away between - 70°C and - 80°C for brief periods (1 to 5

days); in any case, practicality will decay at temperatures above - 130°C. Freeze-dried societies can be put away securely at 4°C or lower. Upon receipt, rehydrate or weaken societies utilizing the proper medium and brooding conditions determined on the item sheet. Live societies ought to be moved to a suitable development medium upon receipt and hatched under the conditions determined on the item sheet

Item Sheet

ATCC bacterial strains are sent with an item sheet that contains nitty gritty data on the inception and development of materials, just as perfect development and engendering conditions. This item sheet, just as extra data, can be found on the ATCC site or can be mentioned from the ATCC Technical Service Department.

Classification Changes

Changes in scientific classification or further examination of bacterial strains may prompt an adjustment in terminology. These progressions are demonstrated on item sheets and can be discovered online on the item page. Additional data on bacterial classification changes can be found on the List of Prokaryotic Names with Standing in Nomenclature (LPSN).

Planning of Medium

Ahead of time, set up the proper medium and extra reagents essential for bacterial strain recovery and development. Guarantee that the best possible hatching conditions are prepared. Data for the definition and readiness of the media and brooding conditions for these items is accessible on the ATCC site.

Opening Glass Ampoule

All societies ought to be considered conceivably dangerous and ought to be opened by people prepared in microbiological methods working in offices with regulation prerequisites suitable for the biosafety level of the way of life. ATCC suggests that the taking care of or opening of glass ampoules be acted in an organic wellbeing bureau. On the off chance that this is beyond the realm of imagination, wear defensive garments, gloves, a face shield or wellbeing goggles, and hold the vial away from your body. Guarantee that every single void vial are cleaned before removal.

Beginning with an ATCC Bacterial Strain

Opening Double-Vial Preparations

1. Warmth the tip of the external vial in a fire.

2. Include a couple of drops of water on the hot tip to break the glass.

3. Strike the finish of the vial with a record or pencil to expel the tip.

4. Evacuate the protection and internal vial with sterile forceps.

Delicately raise the cotton plug. `

Opening Single-Vial Preparations (see graph on page 3)

1. To recoup the cell suspension from the glass ampoule, score the neck of the ampoule with a little, sterile document.

2. Sanitize the outside of the ampoule with newly arranged 70% ethanol or dunk it into a measuring glass of newly arranged 70% ethanol.

3. Wrap the ampoule inside a few folds of a sterile towel or dressing to dry remaining ethanol.

4. Working in a laminar stream hood, hold the vial upstanding and snap open the vial. Guarantee that your dressing doesn't turn out to be excessively wet with ethanol, or liquor could be sucked into the way of life when the vacuum is broken. Rehydrate the material right away.

Starting Frozen Cultures

1. Set up a sterile test tube that contains the suggested vehicle for bacterial development as recorded in the provided item sheet. Guarantee that the medium contains every single important reagent and is equilibrated for temperature and pH.

2. Defrost the example vial through delicate unsettling in a water shower that is set to the typical development temperature of that strain. Defrosting will be quick; around 2 minutes or until all ice gems have dissolved.

3. Expel the vial from the water shower and purify the external surface utilizing 70% ethanol. Follow

exacting aseptic conditions in a laminar stream hood for every further control.

4. Unscrew the head of the vial and move the whole substance to a sterile test tube containing the proper development medium. Extra test cylinders can be immunized by moving 0.5 mL of the

essential culture to extra auxiliary societies.

5. Brood societies under the suitable temperature and environmental

conditions as suggested on the item sheet.

6. Analyze societies after the suggested hatching time frame. The

hatching period will fluctuate among strains and is recorded on the item sheet

FUNGAL LONG-TERM PRESERVATION

Cryopreservation method: - a cryoprotectant utilized that is glycerol (forestall arrangement of ice gems and advance cell endurance) or DMSO put away in liq nitrogen at - 196'c.

- >Slant culture strategy: - 100% feasibility in half glycerol as long as two years and 86.66% as long as 30 months at 4'c.

- >Slide cut culture technique: - 100% of organisms have recovery limit as long as two years of safeguarding at 4'c.

Lyophilization: - otherwise called freeze drying, it is a safeguarding technique accomplished through lack of hydration. It includes freezing at a temperature underneath - 40*C and afterward controlled drying under vacuum.

It happens in a few stages: -

- >firstly, it is refined utilizing acceptable aseptic procedure ideally on non-specific media without expansion of anti-infection agents.

- >after development cell suspension is made in cryopreservation support.

- > then it is exposed to freeze drying under - 40*C and afterward controlled drying under vacuum.

- >then it is put away at 4* to 10*C and tried normally for suitability.

- > then they get by for approx. 20 years.

Paraffin strategy: - clean fluid paraffin is poured over the inclination of culture and put away upstanding at room temperature, the layer of paraffin guarantees anaerobic conditions and forestalls parchedness of medium. this strategy assists with saving society for quite a long while.

Safeguarding in D/W: - In this parasitic fitting are cut with sterile propylene move tubes at that point move to cryovials containing approx. 2ml sterile d/w and afterward put away at RT, parasites conservation for 10 yrs.

Protection on paper: - spore framing growths are put away on bits of sterile channel paper at RT or 6'c for 5-15 yrs.

- >Pieces of agar containing fruiting bodies are set on sterile channel paper in petri dish.

- >dried in desiccator under vacuum.

- >stored at RT.

Agar incline societies: -

- >All microbiology research facilities save miniaturized scale living beings on agar incline.

- >The agar inclines are immunized and brooded until great development shows up.

- >They are then secured with clean mineral oil to a profundity of 1 cm over the tip of inclination surface.

- >The inclines are hatched for 24hr or more and are then put away in cooler.

- >These societies are intermittently moved to new media.

NAMING OF FUNGI

Each species has two names a generic or genus and a specific name eg:Amanita muscaria.

1) Genus name is commence with a capital letter and specific one is followed in lower

case.

2) Species name is either underlined or italicize and is followed by the reference of that person who have first described the particular species variant.
3) Then different genus are grouped into families with members having same features eg: as mentioned above Amanita muscaria and Amanita australis are of same family i.e. Amanitaceae.(family name always end with -aceae)
4) Groups of family are then gathered into orders with broader likeness which all end with -ales. Thus, Amanitaceae belong to the orders Agaricales along with the Agaricaceae(common edible mushroom Agaricus campestris belongs)
5) Orders are then grouped into subclasses or class, which end with either mycetidae or mycetesAAQa for the latter.
6) Evolutionary tree produces this structure.

We mainly focused on ATCC in it we focused on types of culture preservation, online ordering steps, management, extensive collection, educational requirements, working.

LEARNING OUTCOME

We studied about ATCC so we came to know that it is the largest culture collection organization in the world which collects, stores, and distributes standard reference microorganisms, cell lines and other materials for research and development. we also learned that what is the process of online ordering first we have to make a profile then customer account has to be established then we can place an order and later we can track it too. Management is done in such a way that cultures originality is maintained, storage and cryopreservation, data is managed for cultures being stored. ATCC has extensive collections of cultures i.e. like there are more than 1000 genomic and engineered nucleic acids, more than 7600 parasites and yeast species, 3400 nonstop cell lines, more than 18000 bacterial strains helpful for industrial applications. Then we learnt about the requirements that are needed for the various jobs in the organisation. About its working we learned that

- ➔ Bacterial strains are dispatched solidified on dry ice in plastic cryopreservation vials as lyophilised societies in glass ampoules or serum vials or as live societies on agar inclines or in stock medium. and then they are stored in fluid nitrogen fume, then again put in between -70 and -80*C for brief periods. Live societies are then moved to a suitable development medium and it is hatched under the conditions determined on the item sheet.
- ➔ Important data is sent along with bacterial strains.
- ➔ Changes in scientific classification or further examination may prompt an adjustment in terminology. This progress is demonstrated on item which is on online page.
- ➔ Medium is set up with extra reagents for bacterial strain recovery and development.

- ➔ Then glass ampoules are opened by people prepared in microbiological methods working in offices with regulation suitable for biosafety level of the way of life.

We also learnt about some methods for long term preservation of fungi and we also learned about the naming of fungi that how it is done.

PROTEOMIC TECHNOLOGY, TECHNIQUES AND USAGE

Summer training report submitted in partial fulfillment of therequirement for the degree of Bachelor of Technology

In

Biotechnology and Engineering

By - Naveeta Karar

Roll no- 171820

Under the Supervision of:
Dr. Jitendra Vashisht

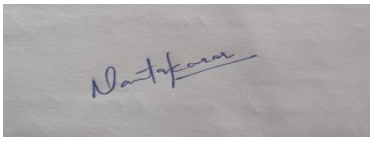


Department of Biotechnology and Bioinformatics & Engineering and Information Technolology.

Jaypee University of Information Technology,
Waknaghat, 73234, Himachal Pradesh, INDIA

CANDIDATE'S DECLARATION

We hereby declare that work presented in this report entitled "*PROTEOMICS TECHNOLOGY, TECHNIQUES AND USAGE"* in partial fulfilment of the requirements for the award of degree in *Bachelor of Technology* in the *Department of Biotechnology and Bioinformatics* [BT & BI] from Jaypee University of Information Technology Waknaghat, Solan, H.P. is an authentic record of my own work carried out under the supervision of Dr. Jitendra Vashistt Assistant Professor in Department of BT & BI. This is to certify that the above statement made is true to best of my knowledge.



Naveeta Karar (171820)



Dr. Jitendraa Vashistt
(Assistant Professor in the Department of Biotechnology and Bioinformatics)

ACKNOWLEDGEMENT

The satisfaction that accompanies with the successful completion of any task would be incomplete without the mention of people whose ceaseless cooperation made it possible, whose constant guidance and encouragement crown all efforts with success. I am very much grateful to my project supervisor Dr. Jitendraa Vashistt for the constant push and kind-heartedness which eventually lead to the final completion of the report.

Naveeta Karar (171820)

ABSTRACT

Proteomics is the analysis of the entire protein complement of a cell, tissue, or organism under a specific, defined set of conditions. Most Proteomic discoveries and efforts to date have been mainly directed towards the areas of cancer research, drug and drug target discoveries and biomarker research. It includes the analysis and categorization of overall protein signatures of a genome. Mass spectrometry with LC-MS-MS being widely used equipment is the central among current proteomics and the requirement of skilled personnel substantially increase the costs, therefore limit their wider use especially in the developing world.

INTRODUCTION:

What is proteomics?

- Proteomics is the study of composition, structure, function and interaction of the proteins directing the activities of each living cell.
- Biomarkers detection might allow identification of patients who would benefit from further evaluation.
- Proteome analysis provides a non-invasive, fast diagnostic tool for patient with various diseases.
- Proteomic technologies can be applied for an unbiased examination to detect novel biomarkers that could play a critical role in treatment monitoring and prognosis.
- The proteome also fluctuates from time to time, cell to cell and in response to external stimuli.
- Proteomics in eukaryotic cells is complex due to post translational modifications, which arise at different sites by numerous ways.
- Fluctuations in gene expression level can be determined by analysis of transcriptome or proteome to discriminate between two biological states of the cell. Microarray chips have been developed for large-scale analysis of whole transcriptome.
- Proteins are effectors of biological function and their levels are not only dependent on host translational control and regulation. Thus, the proteomics would be considered as the most relevant data set to characterize a biological system.
- The conventional techniques for purification of proteins are chromatography based such as ion exchange chromatography, size exclusion chromatography and affinity chromatography. For analysis of selective proteins, enzyme linked immunosorbent assay and western blotting can be used. These techniques may be restricted to analysis of

few individual proteins but also incapable to define protein expression level.

- The vast majority of proteomics is based on the bottom-up protocol, where the complex mixture of proteins from a cell, tissue, or organisms is enzymatically digested into a very large mixture of peptides.

Proteins can be organized in four structural levels:

- Primary: The amino acid sequence, containing members of a twenty-unit alphabet.
- Secondary: Local folding of the amino acid sequence into alpha helix and beta sheets.
- Tertiary: 3D conformation of the entire amino acid sequence.
- Quaternary: Interaction between multiple small peptides or protein subunits to create a large unit.

Understanding the proteome allows for:

1. Characterization of proteins
2. Understanding protein interactions
3. Identification of disease biomarkers

<u>Branches of proteomics:</u>

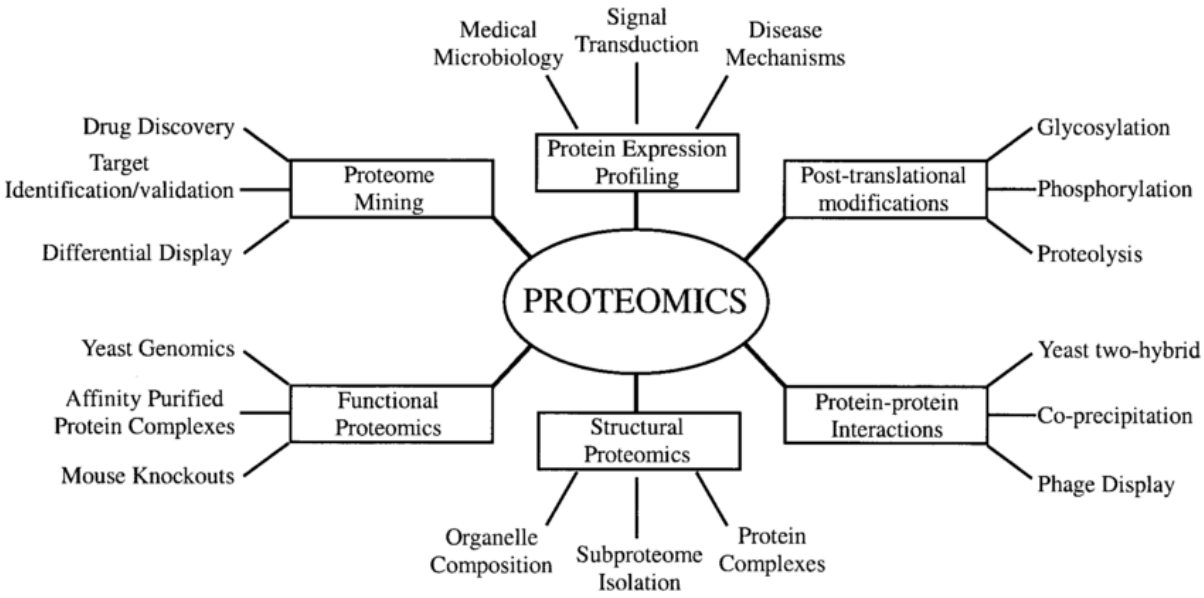
1) Structural proteomics: helps to identify discovered genes and drug interaction. Structural analysis can also show where drugs bind to proteins and where protein interacts with each other. Technologies such as crystallography, X-ray, NMR spectroscopy.

2) Expression proteomics: helps to identify the main gene in a particular sample. Protein found only in a diseased sample may represent a useful drug target and diagnostic marker. Technologies such as 2D- PAGE and mass spectroscopy.

3) Interaction proteomics: analysis of protein interactions. Characterization of protein-protein interactions and helps to determine protein functions and also show how protein assembles in large complexes.

<u>Techniques used in Proteomics</u>:

- Mass spectroscopy: Proteomic separation technique, gel-based or gel-free, a mass spectroscopy is always the primary tool for protein identification.
- Blotting.
- Microarray technology.
- SILAC(stable isotope labeling with amino acids inside culture): Requires no chemical manipulation, the amount of labeled proteins requires for analysis using SILAC technique is far less than that with ICAT.
- ICAT(isotope coded affinity tag): Extremely helpful to detect peptides with low expression levels.
- Protein microarray: multiplex immunoassays that measure hundreds of known proteins in complex biological matrices.
- Two dimensional electrophoresis(2DE)
- Multidimensional protein identification technology(Mud PIT)
- Fluorescence 2D Difference Gel Electrophoresis(2D-DIGE): allow the quantitative comparative analysis of three samples using a single gel.
- Isobaric Tag for Relative and Absolute Quantitation(iTRAQ): Relative and absolute quantification of proteins.



FACTORS THAT AFFECT THE PROTEOME OF A CELL

Physiology, interactions, temperature, stress, pharmaceutical substances, culture conditions, genome (cell specific gene expression).

WHY PROTEOMICS?

- Proteomics is the large-scale study of proteins and Proteins are the vital parts of living organisms, with many functions.
- The proteome is the entire set of proteins that is produced or modified by an organisms or system. Proteomics has enabled the identification of ever increasing number of protein.
- Proteins represent the actual functional molecules in the cell. When mutations occur in the DNA, it is the proteins that are ultimately affected.
- The proteome is also very dynamic. Most of our cells contain the same genome regardless of the environmental conditions, cell type, and development stage. And the proteome is much more complex than either the genome or transcriptome because each protein can be chemically modified in different ways to synthesis. Many proteins have carbohydrate groups added to them. Others are acetylated, phosphorylated and methylated.
- The proteome provides 1000-folds more cellular information than the genome, there are 23,000 human genes, 100,000 transcripts, and over 20 million protein variants.
- Because of translational levels of cellular control, transcriptional, not every gene is transcribed and not every RNA is translated.
- Proteins are preferred targets for therapeutic agents and diagnostic tests. Immunoassays are easy, quick, and cost effective.
- Identify and function of a protein is defined by its unique sequence of amino acids connected through peptide bonds. Most human diseases involve changes in the composition or functions of proteins in one form or another.

METHODS UTILISE IN PROTEOMICS:

Three methods for separation of complex protein or peptide samples are preferred in proteomics:

Sodium dodecyl sulfate- polyacrylamide gel electrophoresis (SDS-PAGE), denaturing polyacrylamide gel electrophoresis, two-dimensional gel electrophoresis, and high-performance liquid chromatography.

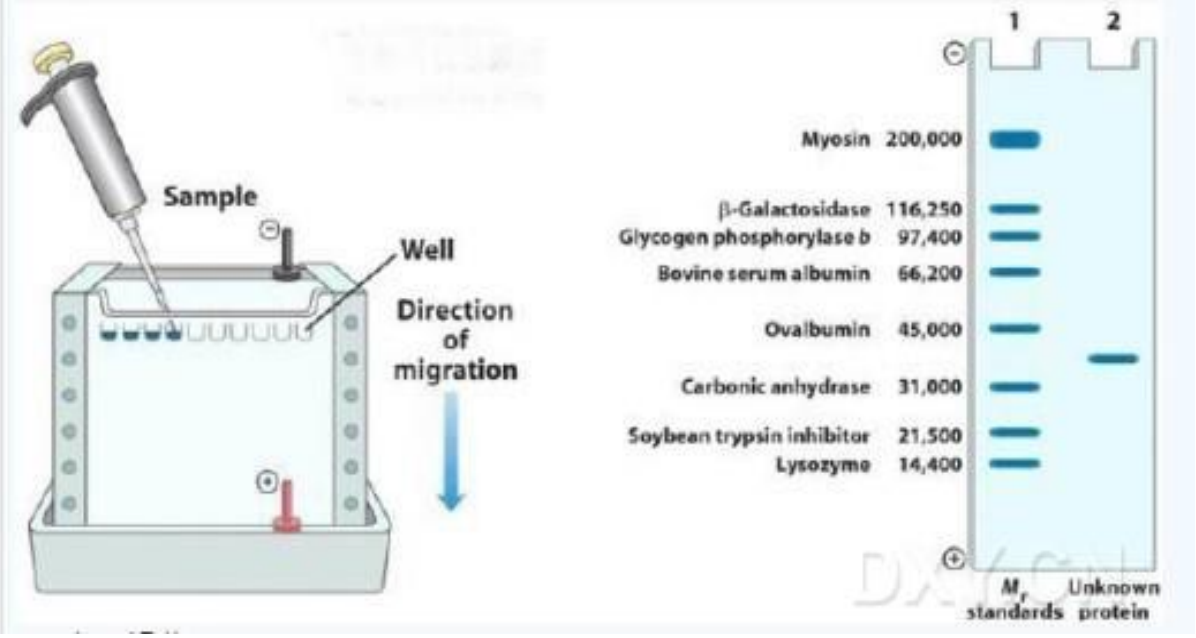
- PAGE (Polyacrylamide gel electrophoresis) is one of the most frequently

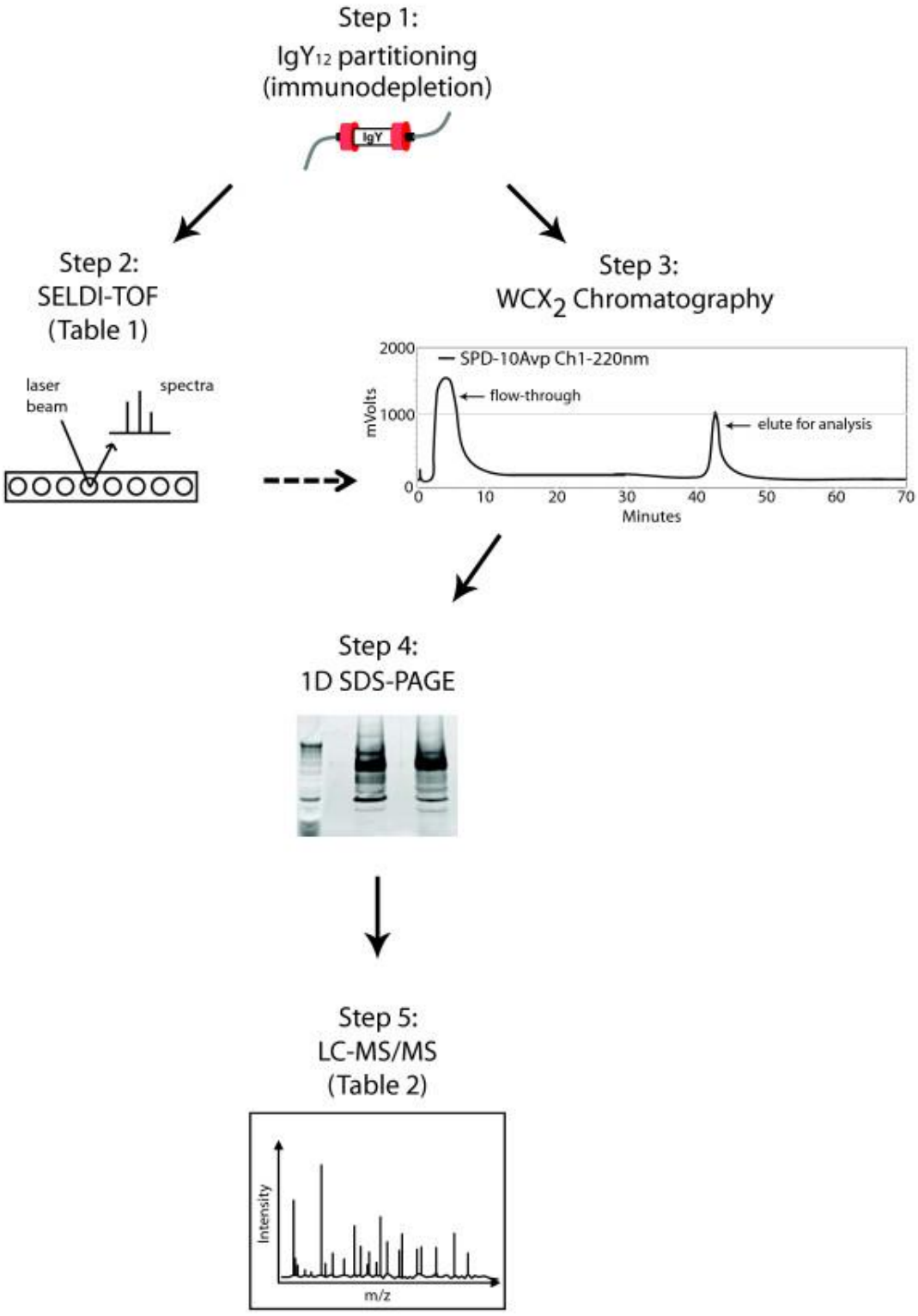
techniques for separating macromolecules including DNA, RNA and proteins. No protein separation technique is more widely used than SDS-PAGE, mostly due to its simplicity, reproducibility, acceptable instrument and consumable expenses. This method separates proteins based on their size or primary structure, but not amino acid sequence. SDS-PAGE can be used to check the purity of samples and to estimate the molecular weights for unknown proteins**.**

- Two dimensional- PAGE is primary technique for proteomics. It separates thecomplex mixture of sample using two different properties of the proteins. Proteins are separated by the pI value and relative molecular weight. Two dimension- PAGE techniques which are capable of separating up to10,000 proteins in a single gel. The two dimensional is successfully applied for the characterization of post-translation modifications, mutant proteins and evaluation of metabolic pathway.

- High-performance liquid chromatography: High performance liquid chromatographic technique that can separate a mixture of compounds, it yields high performance and high speed compared to traditional columns chromatography because of the forcibly pumped mobile phase.

FLOW CHART FOR DESIGNING A PROTEOMICS EXPERIMENT:


Sample
Well
Direction of migration
1
2
Myosin 200,000
β-Galactosidase 116,250
Glycogen phosphorylase b 97,400
Bovine serum albumin 66,200
Ovalbumin 45,000
Carbonic anhydrase 31,000
Soybean trypsin inhibitor 21,500
Lysozyme 14,400
M_r standards
Unknown protein



Flow chart presenting experimental design of proteomic analysis combining immunodepletion, ion exchange chromatography and 1D SDS-PAGE

CONCLUSION: I have learned the basics of techniquesutilized in proteomicsby various online modules and consultation with my teacher. As I have learned the principle and

functionality of these techniques, will utilized in future for my experimental work.

REFERENCES:

What is proteomics?
https://doi.org/10.10.1093/chromsci/bmw167

Why proteomics ?
https://www.news-medical.net

Methods utilize in proteomics.
https://www.sciencedirect.com

Flow chart design of proteomic experiment.
https://www.researchgate.net

Proteomic methods
https://link.springer.com

https://en.m.wikepedia.org

https://onlinelibrary.wiley.com

https://www.sciencedirect.com

https://www.nature.com

https://www.biocompare.com

Daily Report of Summer Training submitted in partial fulfillment of the

requirement for the degree of

Bachelor of Technology in

Biotechnology

By

JigyasaBatra (171821)

Under the supervision of

Dr. M. Udayabhanu

to

DEPARTMENT OFBIOTECHNOLOGY AND BIOINFORMATICS

Jaypee University of Information Technology Waknaghat, Solan- 173234, Himachal Pradesh

Contents

- Animal Cell Culture ; Summary
- Instrumentation
- Animal Cell culture Media
- Type 2 Diabetes Mellitus
- Basic Techniques

ANIMAL CELL CULTURE: SUMMARY

1. Definition

Cell Culture can be defined as removal of cells or tissues from the organism and then cultivated in the stimulated environment with optimum growth conditions.[1]

Cell Culture is used in variety of biological processes like Recombinant technologies and genetic manipulations.

2. Requirements

The following provisions must be available in the laboratory-[2]

- Preparation and sterilization
- Aseptic Handling
- Centrifugation
- Cell Counting
- Microscopy
- Incubation
- Storage at Room Temperature, -20ºC, 4ºC and 196ºC

3. Laboratory Design

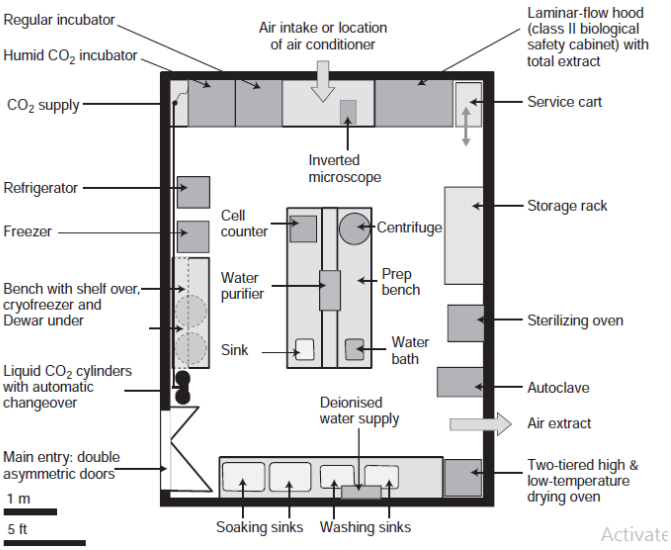


Fig 1: Layout for Small Tissue Culture Laboratory[2]

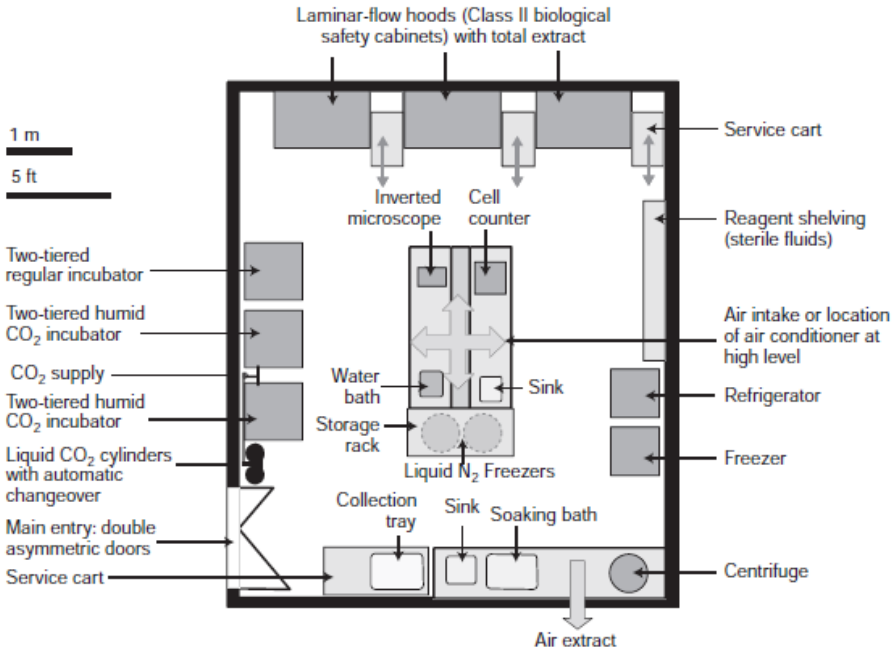


Fig 1: Layout for Medium Sized Tissue Culture Laboratory[2]

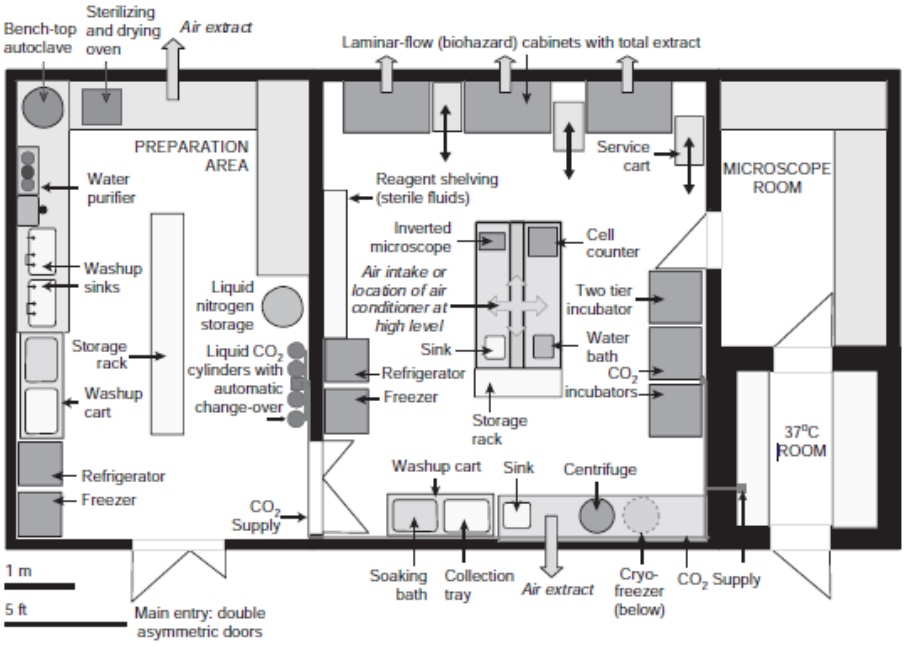


Fig 3: Large Size Tissue Culture Laboratory

4. Major Developments in Cell Culture

a) Inhibition of contaminants with use of Antibiotics.
b) Use of trypsinization for preventing adherent cells to subculture.
c) Using chemically defined culture media.

5. Terminologies

a) Primary Cell Culture- Cell will divide and grow in a culture media after removing from the organism.
b) Cell Line- Continuous propagation of cells when subcultured from primary cell culture.
c) Anchorage dependency- Cells grow as monolayer adhering to the substrate.
d) Passaging / Subculturing – The process of splitting the cells
e) Finite Cells- When the cells have finite lifespan.
f) Continuous Cell lines- When the cells can grow up to infinite life span.

6. *In-vitro* Propagation and Cultivation of Cells

Formation of Monolayer of Primary Culture on the substrate containing required media and nutrients.[1]



After achieving confluence cells are then subcultured or passaged from primary to secondary culture then tertiary and then subsequently till the achievement of continuous cell line.[1]

7. Types of Tissue Culture

a) Cell Culture: Tisue is detached from an explants generally enzymatically and then grown in cell suspension and then can be cultured as a monolayer or suspension culture
b) Explant Culture: It is the method of growing tissue or cell outside the organism with the use of broth or agar medium.
c) Organ Culture: The entire organ or an embryo is excised and cultured

INSTRUMENTATION

Tissue Culture Laboratory Equipment[2,3]

1. Laminar Flow Hood or Biological Safety Cabinet- It is an essential equipment used to maintain containment and aseptic environment.
2. Inverted Microscope- It is used for viewing and assessing cell cultures and samples.
3. Hemocytometer Slide- Specialized slide used for counting cells.
4. Cell Counter- It is an automatic electronic cell counter preferable over Hemocytometer.
5. Refrigerator and Freezer- It is used for storage of media, nutrients and cell culture at required temperatures.
6. Sink- It is needed for washing.
7. Vacuum / Periplastic Pump- It is essential for withdrawing fluids from flask and for filter sterilization.
8. Centrifuge- It is essential as needed for centrifugation of cells for the purpose of removal of trypsin or other preservatives.
9. Incubator- Needed for controlling humidity and CO_2.
10. Liquid Nitrogen- It is needed for long term cryopreservation.
11. Pipettor(s)- Essential for accurately dispensing small volumes.
12. Hot Room- It is used for incubation of large number of flasks and stirrer cultures.
13. Shelves and trolleys- It is used for storing and transporting glassware.

Preparation Area[2,3]

1. Water Purifier- It is essential for water is used for media preparation.
2. Weighing Balance- It is essential for weighing reagents and media nutrients unless all media and reagents purchased are ready to use.
3. pH Meter- It is essential for measuring pH or prepared media and reagents.
4. Conductivity Meter and Osmometer- It is essential for quality checking of media.
5. Automatic Dispenser- It is used for dispensing required amount of liquids.
6. Walk-in-Cold Room or Large Refrigerator- It is needed for bulk long term storage of media and nutrients.

7. Water Bath with Shaker- It is essential for cell dissociation and trypsinization.,

Sterelization[2]

1. Sterilizing Oven- It can also be used as drying Oven. It is used for sterilization of glassware and heat resistant plastic ware.
2. Steam sterilizer (autoclave, pressure cooker)- It is used for sterilizing slable liquids and solutions.
3. Filter Sterilization- It is used for heat liable materials.
4. Phase contrast or Fluorescence Microscope- It is used for high power observation of cells.
5. PCR Thermal cycler- It is used for Polymerase chain amplification of DNA or RNA (in RT -PCR).

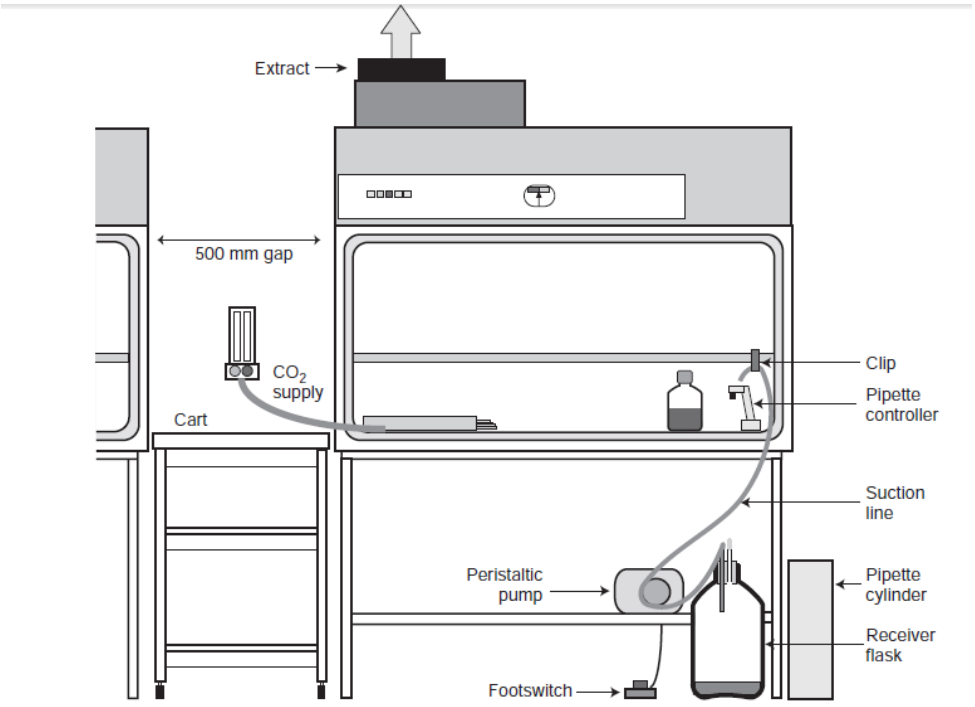


Fig 4: Laminar Flow Hood

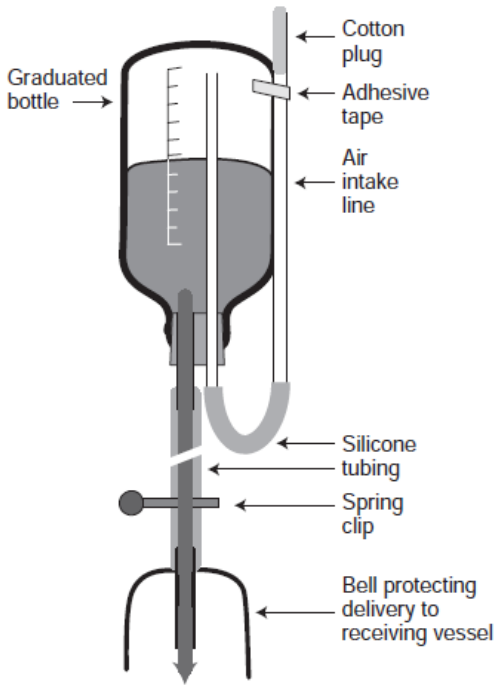


Fig 5: Graduated Bottle Dispenser

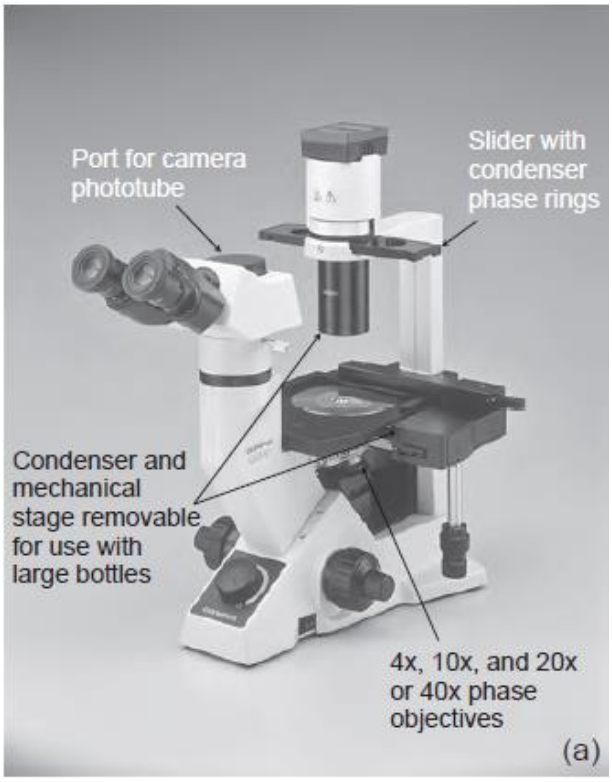


Fig 6: Inverted Microscope



Fig 7: Culture Chambers

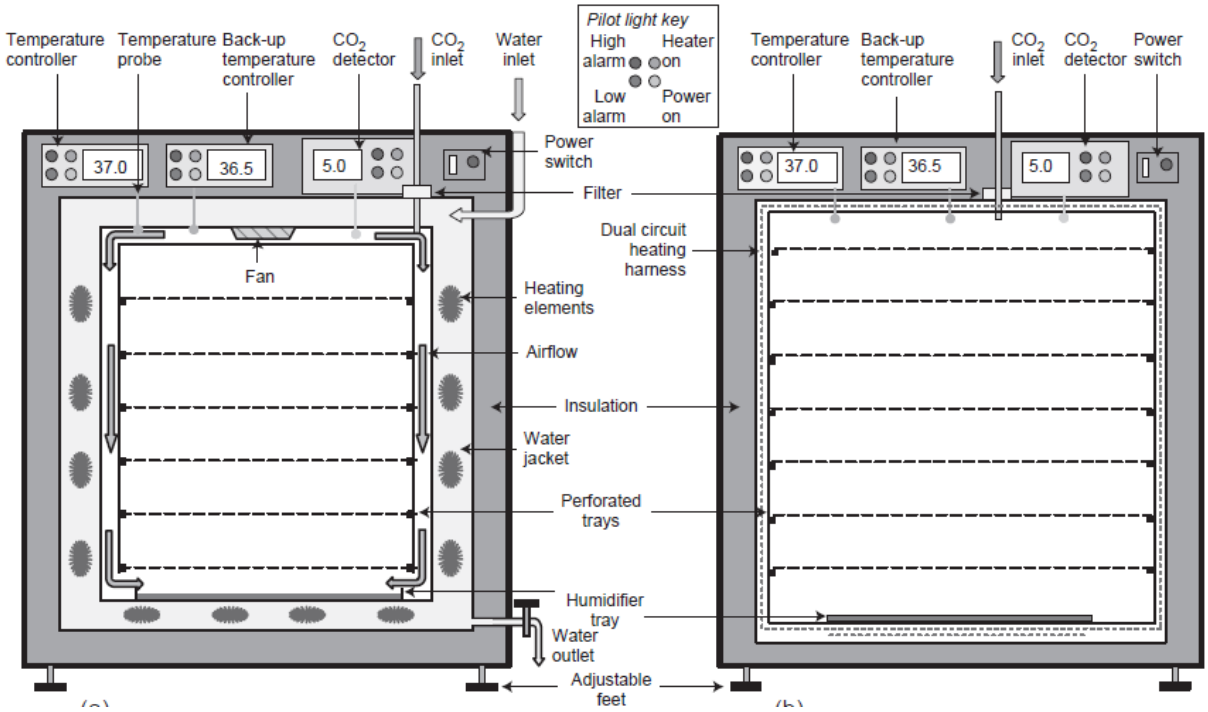


Fig 8: CO_2 Incubator Design



Fig 9: Water Purifiers



Fig 10: Bench top Autoclave

ANIMAL CELL CULTURE MEDIA

There are two type of Cell Culture Media-

1. Natural Media- It contains only natural biological substances like serum, plasma and embryo extract.[4]

   For Example- Plasma isolated from heparanized blood, hormones or serum, bone marrow extract and extract from embryo,spleen or liver, and amniotic or pleural fluid.
2. Synthetic Media- It contains only basal media or supplements like hormones, serum and growth factors.[4]

   For example- Serum of human bovine or equine, human source components, crude protein fractions

Important Components of Commercial Culture Media

1. DMEM- It is the modified medium from Basal Medium Eagle (BME) and contains High Glucose - 4 mM L-glutamine 4500 mg glucose/L 1500 mg/L sodium bicarbonate.
2. RPMI- It contains great amount of phosphate and modified to consist of 2 mM L-glutamine, 10 mM HEPES, 1 mM sodium pyruvate
3. McCoy- It is a general purpose media consisting of High Glucose, L-glutamine, Bacto-peptone, Phenol Red, HEPES with or without Sodium Pyruvate.

   There are also many other media like M 2, Nutrient Mixture F-10, Nutrient Mixture F-12 and many more.

TYPE 2 DIABETES MELLITUS (DM)

Type 2 Diabetes mellitus (DM), the most common type of diabetes, is the condition in which the body develops resistance to insulin. It can be characterized by hyperglycemia, insulin resistance, hyperinsulinemia and other insulin related deficiencies.[5] There are many factors including lifestyle and genetic that determines Type 2 DM. The prominent aspect of life style that causes this disease is obesity.[6] The other factors of lifestyle can be smoking, consuming alcohol and sedentary lifestyle.[7]

The genetics has found to have prominent relation with Type 2 DM. There are certain genes involved in the development of type 2 DM like TCF7L2, CDKAL1, HHEX, PPARG, FTO, WFS1, KCNJ11, LC30A8, NOTCH2, , FTO, IGF2BP2, and SJAZF1.[8]

Metabolomics is the study of alterations related to metabolism that may lead to disease propagation.[9] The high sensitive and high resolution studies like Mass Spectrometry may help in detecting thousands or hundreds of metabolites and changes associated in the specific region.[9]In some researches there are certain metabolites that are found be positively related with Type 2 DM.These metabolites are mannose, galactose, uric acid, oxalic acid, glucaric acid-1, sorbitol, 4-lactone, galacticol, 3-methyl-2-oxopentanoic acid and 2-hydroxybutyric acid .[10]

Some researches also revealed that bases on serum butyrylcholinesterase levels or brain derived neurotrophic factor helps in identifying Type 2 DM can also be determined based on cholinesterase level which also may link their association with alzheimer's disease.[11]Hence these enzymes can also be called as biomarkers for type 2 diabetes.[11]

ANIMAL CELL CULTURE PROCEDURE

Cell Counting Using Hemocytometer

Hemocytometer is a deviceused to count cells in a culture. It is modified slide containing two two identical wells into which small volume of cell suspension is pipetted.



Fig 11: Hemocytometer Slide[12]

1. The cell suspension is first diluted with trypan blue dye, which helps in distinguishing living and dead cells.
2. The dye passes through the membrane of dead cells which will then appear blue under the microscope.
3. Living cells will exclude and will appear mostly clear. Then both the chambers were loaded with cell suspension under the coverslip.
4. Then the Hemocytometer was placed under observation in the inverted microscope.

Each pattern is divided into a grid pattern, consisting of nine large squares. Each square has the same dimentions and contains 10^{-4} mL of suspension.

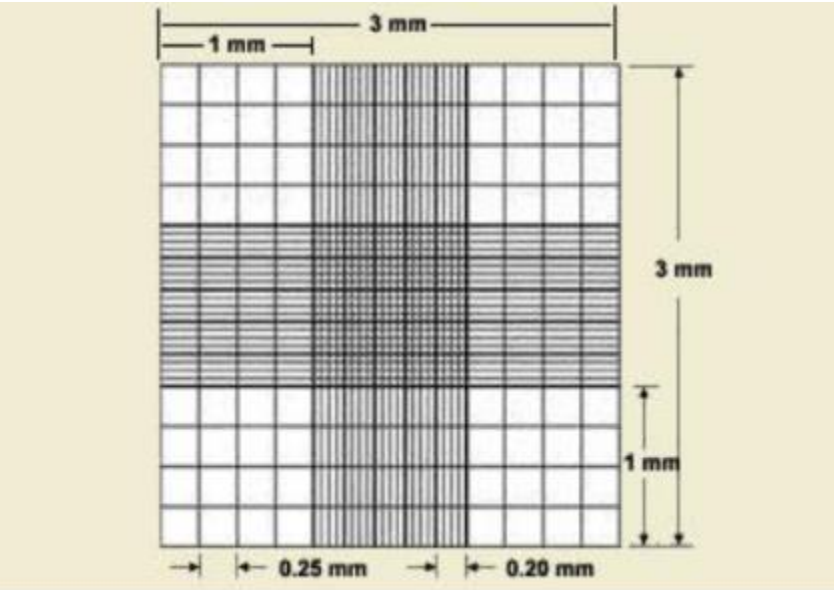


Fig 12 : Hemocytometer Slide grid view[12]

The several Calculations can be made through the following Formulas-

1. Percentage of Viable Cells = (Number of Viable Cells/Total Number of Cells)*100
2. Average Number of Cells per Square = Number of Viable cells/Total number of squares
3. Dilution Factor = Final Volume/ volume of cells
4. Concentration (viable cells/ml) = Average number of cells per square*Dilution Factor*10^{-4}

Aseptic Techniques

1. Cell culture heavily depends on keeping the cultures free from microorganism contamination. This can be accomplished by keeping proper sterile environment by following all the guidelines under sterile techniques.
2. Always wear Personal Protective Equipment (PPE) while working in a laboratory and close toed shoes.
3. Hands should be properly washed before the cell culturing laboratory work to remove the dead skin microorganisms or particles for they can be potential source of contamination.
4. 70 % ethanol can remove the microorganisms that can contaminate the cultures.

5. Biosafety Cabinate should be cleaned before and after the use. Spaying Alcohol should not be used where the flame is being used due to fire hazard.
6. All the items to be kept inside must be pre-sterelized with alcohol.
7. Always enter your hands inside the hood with the arms in forward motion. Media and reagents must be kept sterile by only touching them with sterile objects.
8. Pipette aid should be kept in the right side for it is easy to control the same with the right hand.
9. When one is opening the new pipette packet it should be ensured that it should not touch any non sterile object.
10. It should be ensured that all the media, supplies and reagents must be opened inside the hood. Each pipette should be used one time and then discarded or washed if using glass pipettes.

Culture Preparation

1. Cells were taken from a flask containing tissue culture at 10-90% confluency in a humidified 37ºC , 10% CO_2 incubator.
2. The density of the cells should be confirmed by observing them under microscope.
3. Cell culture medium should be removed from the cells and cells should be then washed with PBS one time.
4. Then trypsin solution should be added according to 2ml for a T75 flask to detatch the cells from the flask.
5. The cells are then incubated with trypsin solution for 2 minutes . After the incubation time the cells should be observed under Microscope to check if they all are detached and all clumps should be dispersed.
6. Trypsinization should then be stopped by adding 10ml of Assay Medium per T75 flask.
7. Cells in assay medium then dispersed by pipetting up and down.
8. Cells suspension should then be transferred to a conical tube.
9. A hemocytometer then can be used to quantify the number of cells in a solution. Cells are counted in order to determine their concentration for subsequent assays.

10. Cells are then centrifuged at 500*q for 5 minutes at 18ºC. after centrifugation supernatant should be removed and the pallet cells are resuspended to maintain 1 million cell/ml in assay medium.
11. The cells are then pipetted into 96 well plate with boundaries consisting of cell-free contol. The remaining wells should contain half of the samples as cell suspension with DMSO for unstimulated control and the other half as cell suspension with forskolin solution for stimulation.
12. The plate should then be incubated at 37ºC and 10% CO_2 for 4 hours.
13. After incubation assay should be added to the plate and observed for the stimulated cell activity.

Subculturing (or Passaging) of Primary Cells

1. All the ,materials needed should be sterilized and kept inside the hood.
2. Reagent volumes should be adjusted as per the required size of culture vessel using for subculturing.
3. Confluency should be checked under the microscope for it should have 80% concfluency and should contain mitotic cells.
4. All the culture media should be discarded and trypsin EDTA should be added.
5. The flask should be shacked so that trypsin should present at all the surface.
6. Then immediately remove the trypsin EDTA solution and fresh EDTA solution should be added.
7. Cells should be incubated under the room temperature until it becomes rounded in shape.
8. The remaining adherent cells should be disloadged by wrapping the flask very gently.
9. The over trypsinization should be prevented. Following detachment trypsin nutrilizer should be added.
10. Cells should then be transferred to the conical tube.
11. The cells are then centrifuged at 180g for 7 minutes.
12. The supernatant should then be removed very carefully.
13. The pellet should then be resuspended in the supplemented medium.
14. The cells are then gently pipette up and down for mixing in the suspended solution.

15. The concentration of the cells should then be determined by microscope.
16. The cells should then be diluted in the suspension medium and new culture vessel should be seeded at appropriate density and returned to the incubator.

References

1. Hudu, ShuaibuAbdullahi, Ahmed SubehAlshrari, Ahmad Syahida, and ZamberiSekawi. "Cell culture, technology: enhancing the culture of diagnosing human diseases." *Journal of clinical and diagnostic research: JCDR* 10, no. 3 (2016): DE01.
2. Freshney, R. Ian. *Culture of animal cells: a manual of basic technique and specialized applications*. John Wiley & Sons, 2015.
3. Oyeleye, O. O., S. I. Ola, and O. G. Omitogun. "Basics of animal cell culture: Foundation for modern science." *Biotechnology and Molecular Biology Reviews* 11, no. 2 (2016): 6-16.
4. Yao, Tatsuma, and Yuta Asayama. "Animal-cell culture media: History, characteristics, and current issues." *Reproductive medicine and biology* 16, no. 2 (2017): 99-117.
5. Maitra A, Abbas AK. Endocrine system. In: Kumar V, Fausto N, Abbas AK (eds). Robbins and Cotran Pathologic basis of disease (7th ed) 2005. Philadelphia, Saunders; 1156-1226.
6. Barlow, Sarah E. "Expert committee recommendations regarding the prevention, assessment, and treatment of child and adolescent overweight and obesity: summary report." *Pediatrics* 120, no. Supplement 4 (2007): S164-S192.
7. Hu, Frank B., JoAnn E. Manson, Meir J. Stampfer, Graham Colditz, Simin Liu, Caren G. Solomon, and Walter C. Willett. "Diet, lifestyle, and the risk of type 2 diabetes mellitus in women." *New England journal of medicine* 345, no. 11 (2001): 790-797.
8. Olokoba, Abdulfatai B., Olusegun A. Obateru, and Lateefat B. Olokoba. "Type 2 diabetes mellitus: a review of current trends." *Oman medical journal* 27, no. 4 (2012): 269.
9. Laakso, Markku. "Biomarkers for type 2 diabetes." *Molecular Metabolism* 27 (2019): S139-S146.
10. Savolainen, Otto, BjörnFagerberg, MadsVendelbo Lind, Ann-Sofie Sandberg, Alastair B. Ross, and GöranBergström. "Biomarkers for predicting type 2 diabetes development—Can metabolomics improve on existing biomarkers?." *PLoS One* 12, no. 7 (2017): e0177738.

11. Gedela, Srinubabu, AllamAppa Rao, and Narasimha Rao Medicherla. "Identification of biomarkers for type 2 diabetes and its complications: a bioinformatic approach." International Journal of Biomedical Science: IJBS 3, no. 4 (2007): 229.
12. https://www.researchgate.net/publication/323013975_Hemocytometer_Calculator

Summer Training Report

on

INNOVATIONS MADE SO FAR IN COVID-19 VACCINES

Submitted in partial fulfillment of

BACHELORS OF TECHNOLOGY

By

KIRTI ARORA (171823)

UNDER THE SUPERVISION OF

DR. RAHUL SHRIVASTAVA



DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY WAKNAGHAT, SOLAN

TABLE OF CONTENT

TITLE	PAGE NO
Declaration	**3**
Acknowledgement	**4**
Introduction	**5**
General stages for the Development Cycle of Vaccines	**8**
Coronavirus Vaccine Tracker (Vaccine made so far in clinical evaluation)	**10**
Coronavirus Vaccine Tracker (Vaccine made so far in Pre-clinical evaluation)	**16**
App helping Social Distancing	**19**
References	**20**
Reference Manager & EndNote	**21**
Conclusion	**22**

DECLARATION

We hereby declare that the summer training work entitled "Innovations made so far in COVID-19 Vaccines" has been solely submitted to the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Wakhnaghat, under the guidance of our supervisor **DR. RAHUL SHRIVASTAVA.**



Name: **Kirti Arora (171823)**



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Date – 3rd July

ACKNOWLEDGEMENT

I take this opportunity to express our first and foremost gratitude to our "DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS" for the confidence bestowed upon us and entrusting our project title "**Innovations made so far in COVID-19 Vaccines.**"

At this juncture, with proud privilege and profound sense of gratitude we feel honored in expressing our deepest appreciation to **Dr. Rahul Shrivastava,** for being a lot more than just a supervisor and going beyond the call of duty in our guidance, support, advice, and motivation throughout. He has been the source of inspiration of come what may; these issues cannot bring you down. Sincere thanks for his insightful advice, motivating suggestions, invaluable guidance, help and support in successful completion of this summer training Project and also for his constant encouragement and advice throughout our project work.

Special thanks to our parents for their infinite patience and understanding for the constant support and most importantly God, who in his mysterious ways, always made things work out in the end.

In gratitude,

Kirti Arora (171823)

INTRODUCTION

What is COVID-19?

It stands for Coronavirus disease-2019 Coronaviruses (CoV) are a family of virus that causes illness in human ranging from the Common Cold to more severe diseases. Covid-19 is new strain of virus and it is 95% similar to SARS virus, known as Novel Coronavirus according to **WHO (World Health Organizations)**

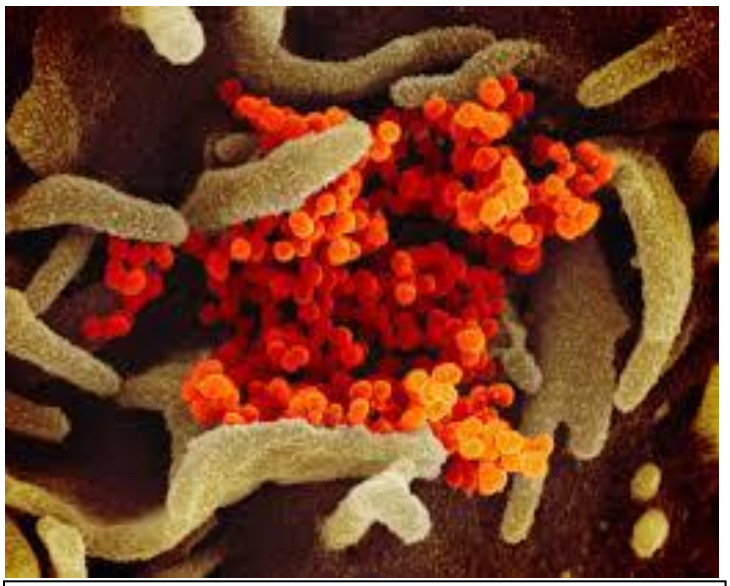
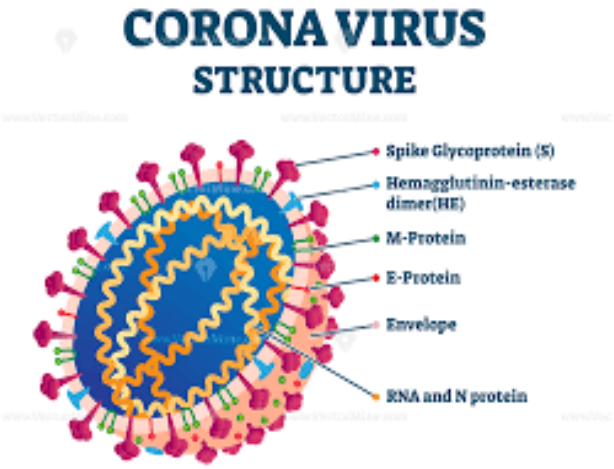


Fig: Electron microscope image of SARS-CoV-2 (orange). NATIONAL INSTITUTE OF ALLERGY AND INFECTIOUS DISEASE

Anatomy of virus:

The Covid-19 virus has several features we may be able to target with drugs to break it down and stop its entering into the cells of Host.



Some vaccines work against the Spike Glycoprotein as ChAdOx1 (university of Oxford) and some are working against the RNA such as Moderna.

Virus lives longer on negatively Charged Surfaces.

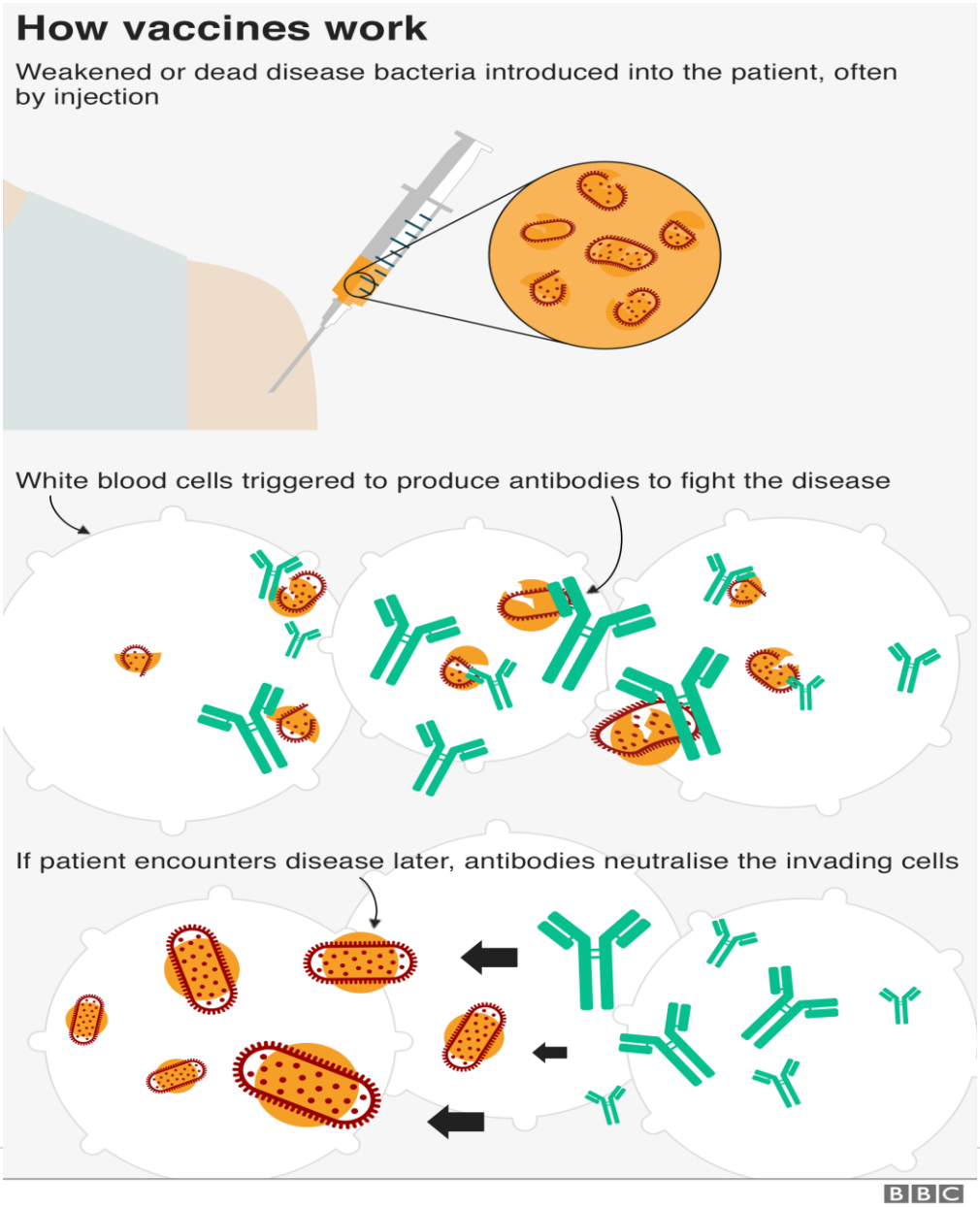
Evolution of COVID-19 infection with transformation to a Pandemic:

- The first case of coronavirus disease 2019 (COVID-19) likely occurred from a zoonotic transmission in china in December 201, linked to a large seafood market that also traded in live wild animals (Wuhan).
- The causative virus, Severe Acute Respiratory Syndrome Coronavirus 2(SARS-CoV-2) designated as a novel virus COVID-19.
- This is the third acute infectious disease caused by coronavirus infection in this Century, after Sudden Acute Respirator Syndrome (SARS) and Middle East Respiratory Syndrome (MARS).
- It has got a high Human to Human transmission capability and rapidly spread from China to other parts of the World.
- By 24 March 2020, SARS-C0V-2 had infected more than 381,000 people across 195 countries/regions and killed more than 16,000: a pandemic as declared by the World Health Organization. **Tay MZ et al 2020**

Mode of transmission in current Pandemic

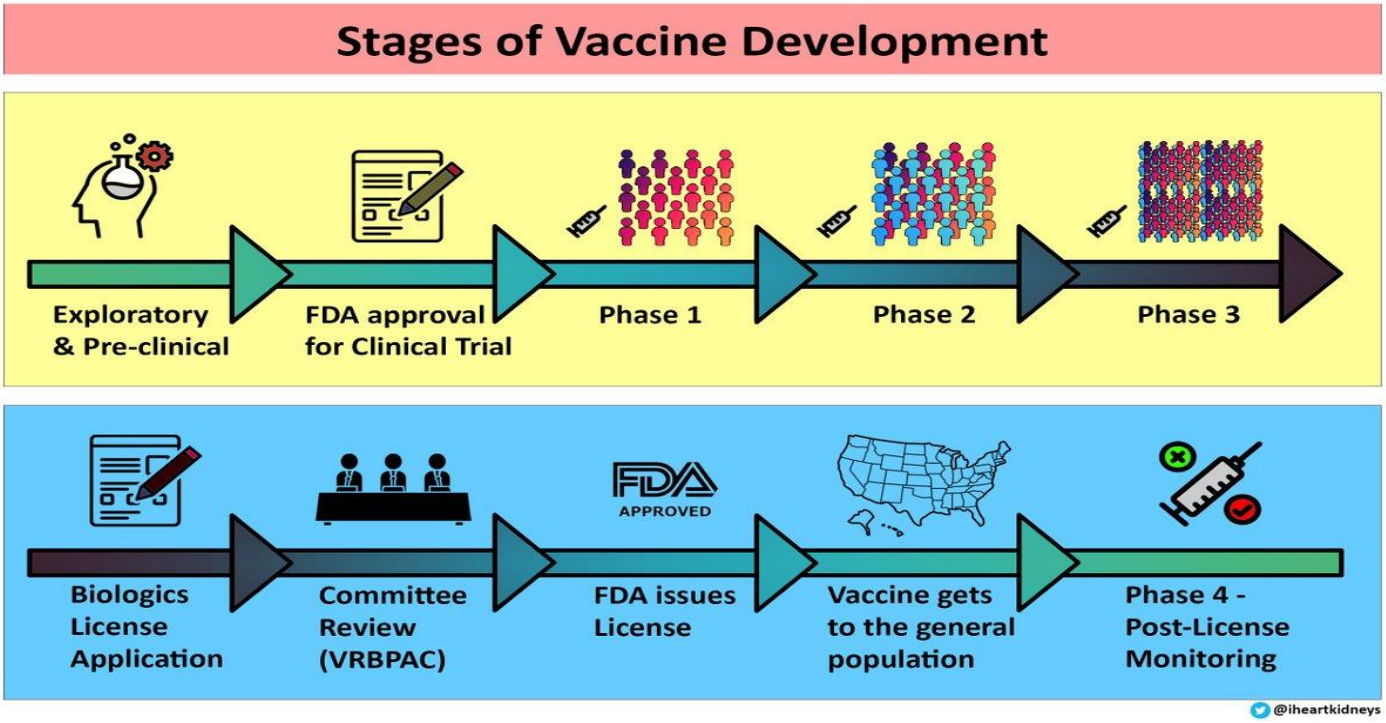
1. Human to Human through Respiratory Aerosols, Sputum, blood, body fluids. (Contagious).
2. Through formite & surfaces of furniture/cloths/utensils/packages etc.
3. Faeco-oral route (Nouri-Vaskeh M 2020)
4. Air Conditioning & air handling units spreading Aerosols (Lu J et al 2020).
5. Spread through surfaces of packages, furniture and other objects.

Location of the virus COVID-19	Time of Survival
Aerosol	**≤ 3 hours**
Plastic material/ Packages	**≤ 2 to 3 Days**
Cardboard	**≤ 1 to 2 Days**
Stainless Steel	**≤ 2 to 3 Days**
Copper	**≤ 4 hours**



(BBC)

GENERAL STAGES OF THE DEVELOPMENT CYCLE OF VACCINE



Exploratory stage

(Research phase to identify natural & synthetic antigens to combat the disease)

Pre-clinical Stage

(It involves testing candidate vaccine on animals such as mice, guinea pigs & monkeys to check immune response)

Clinical development

(It has three phases of human trial- During the phase 1 on small groups for vaccine trial, Phase 2 Clinical study is expanded and vaccine is given to people who have characteristics similar to those for whom the new vaccine is intended, phase 3 vaccines is given to thousands of people and tested for efficacy and safety)



Regulatory review and approval

(If a vaccine has passes through all the stages then submit a Biologics License Authority (BLA) to FDA)

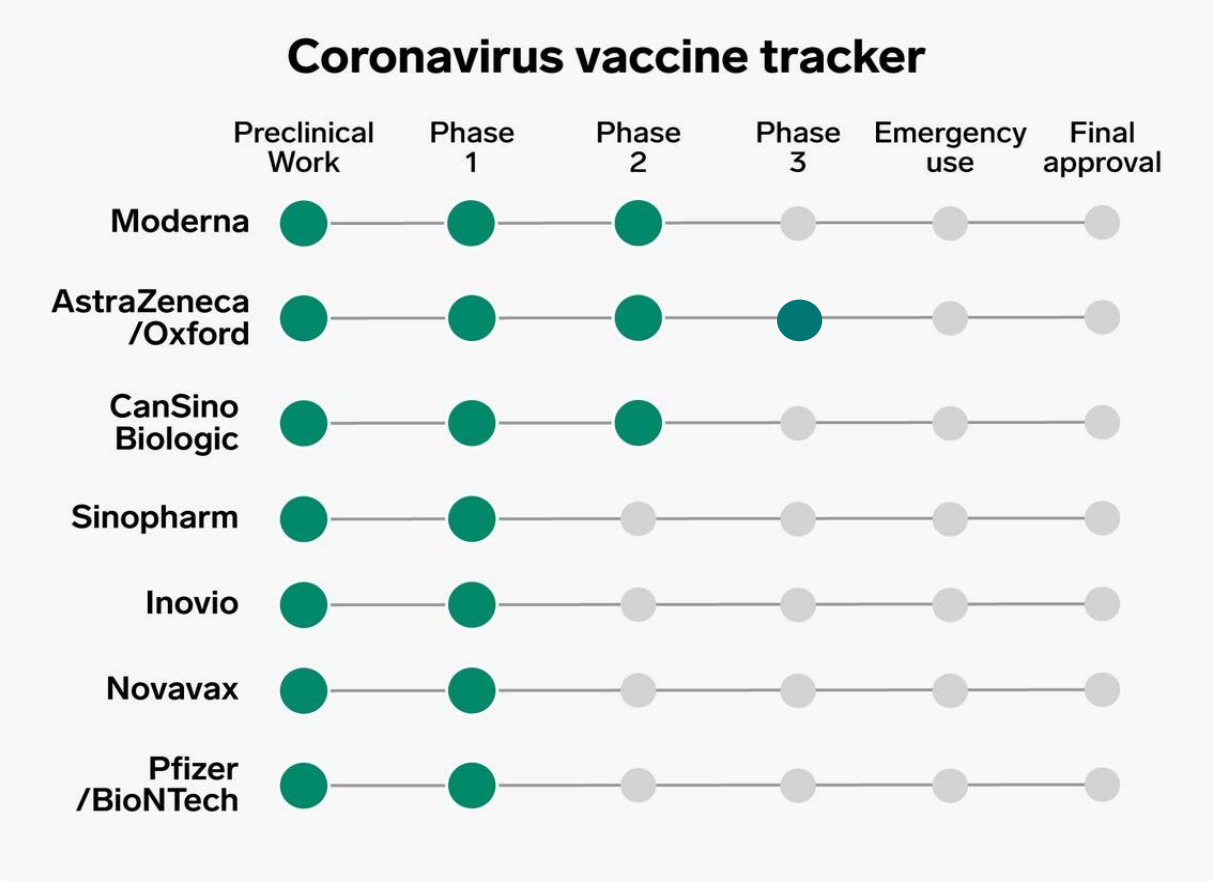


Manufacturing and Quality Control

(After all the stages move into manufacturing stages, but constant monitoring of the process and quality control measures must be put in place)

Lastly, vaccine production should comply with the current Good Manufacturing Practice standards to ensure constant quality and safety of vaccine.

(**The Hindu)**



VACCINES MADE SO FAR

18 candidate vaccines in clinical evaluation as on 2nd July (WHO)

- **University of Oxford/ AstraZeneca:** The first vaccine of the World that has entered into the Trial Phase 3. Reports from the trail shows it is safe even for people with weak immune system.

Platform: Non-Replicating Viral Vector

Type of Candidate vaccine: **ChAdOx1-5**



ChAdOx1 nCoV-19 is made from a virus (ChAdOx1), which is a weakened version of common cold virus (Adenovirus) that has been genetically changed so that it is impossible for it to grow in humans. Genetic material has been added to the ChAdOx1 construct that is used to make spike glycoprotein from COVID-19 this spike protein is responsible to bind to

ACE2 receptors in human cells to gain entry to the cells and cause infection.

By vaccinating with ChAdOx1 body recognize and develop an immune response to the spike proteins.

(University of Oxford)

- **CanSino Biological Inc. / Beijing Institute of Biotechnology:** Those patients who received a single dose of the vaccine produced certain immune cells, called T cells, within two weeks. Antibody needed for immunity peaked at 28 days after the inoculation and has entered the phase 2.

  Platform: Non-Replicating Viral Vaccine

  Type of Candidate Vaccine: Adenovirus type 5 Vector

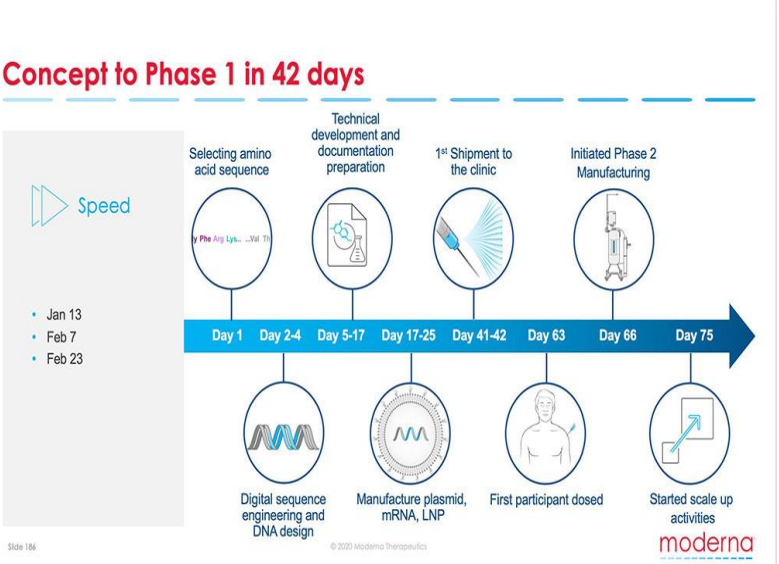
  Ad5-nCov is a genetically engineered vaccine candidate with the replication defective adenovirus type 5 as the vector to express SARS-CoV-2 spike protein, which prevents the disease. **(The Indian Express)**

- **Moderna/ NIAID:** is set to move in the second phase of vaccine trial in the month of July.

  Platform: RNA

  Type of candidate vaccine: **LNP-encapsulated mRNA (mRNA-1273)**

  mRNA vaccines work closely mimicking nature by delivering mRNA to the body's cell, which produce antigenic proteins which remembered by the immune system. In the future body is able to recognize the virus.



(Moderna)

- **Wuhan Institute of Biological Products (Sinopharm):** The vaccine has entered in Phase II trial.

  Platform: Inactivated

  Type of Candidate vaccine: Inactivated vaccine using non living viruses that lost disease causing capacity to stimulate the immune system to develop an immune response.

- **Beijing Institute of Biological Products (Sinopharm):** The vaccine has entered in Phase II trial.

  Platform: Inactivated

  Type of Candidate: Inactivated vaccine.

- **Sinovac:** It is a Chinese firm entered in Phase ½ trial (reached the final stage of human testing).

  Platform: Inactivated

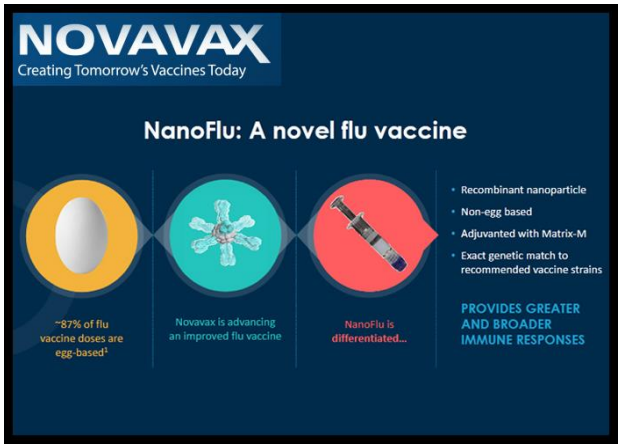
  Type of Candidate vaccine: Inactivated+ alum

  The vaccine, an old fashioned formulation consisting of a chemically inactivated version of the virus and they also provides strong evidence that the virus is not mutating in a way that would make it resistant to a COVID vaccine. **(The Indian Express)**

- **Novavax (NVX-CoV2373):** is an American Vaccine development company and entered in Phase ½ stages.

  Platform: Protein Subunit

  Type of candidate vaccine: Full length recombinant SARS CoV-2 glycoprotein nanoparticle technology



platform to generate antigen from coronavirus spike protein and adjuvanted with Matrix M to enhance the immune responses.

(Drug development)

- **BioNTech/ Fosun/ Pharma/Pfizer:** It uses an innovative gene-based technology known as mRNA and it has entered in ½ phase trials (early stage of human trials). They develop four vaccine candidates each representing different combination of mRNA.

  Platform: RNA

  Type of candidate vaccine: **3 LNP-mRNAs**

  (Pfizer)



- **ICMR & Bharat Biotech Limited (Covaxin):** It gets approval for human trials and entered in phase 1 of trials and it has successfully cleared the pre-clinical testing on animals such as guinea pigs and mice.

  The collaboration with ICMR and NIV and NIV isolated a strain of novel Coronavirus from asymptomatic Covid-19 patient and transfer to the Bharat biotech Limited.

  Candidate: **Covaxin**

  Type of candidate vaccine: Inactivated (uses the dead virus) injected into a human and no replication is there since it is killed virus and mounts an immune response towards the virus.

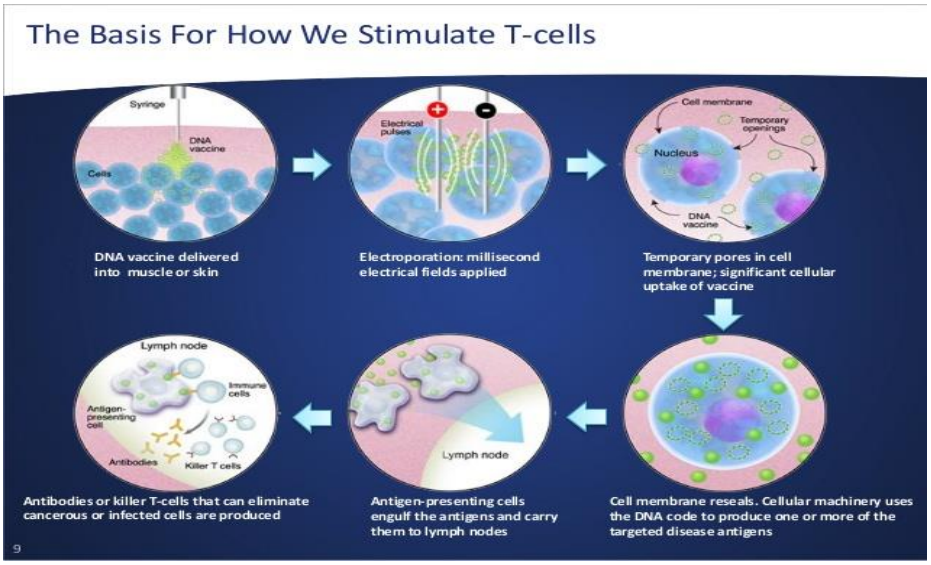
  (The Indian express)

- **Institute of Medical Biology, Chinese Academy of Medical Sciences:** It gets approval for early-stage clinical trials with randomized, Double-blind, placebo-controlled phase.

  Candidate: Inactivated

  Type of candidate Vaccine: Inactivated

- **Inovio Pharmaceuticals (INO-480):** It gets promising results from the preclinical studies in mice and guinea pigs and entered in Phase 1 trials.



  It is the only nucleic acid based Vaccine that is stable at room temperature for more than a year and doesn't to be frozen in transport and for storage purpose. This vaccine works on transferring DNA into cells, where it is translated into proteins then later activates an individual's immune system which generates a robust targeted T cell and expresses a monoclonal antibody production.

  Platform: DNA

  Type of candidate vaccine: DNA vaccine with electroportation.

- **Genexine Consortium:** It is a Korean biotech firm DNA vaccine pipeline GX-19. It has entered in phase 1 trial which express SARS-CoV-2 S protein antigen.

  Platform: DNA

  Type of candidate vaccine: **DNA Vaccine** **(WHO)**

- **Gamaleya Research Institute:** They developed two forms of vaccine-Liquid & powder for injections and it has entered in phase 1 trial.

  Platform: Non-Replicating Viral Vector

  Type of candidate vaccine: Adeno-based

- **Clover Biopharmaceuticals Inc./ GSK/ Dynavax:** It has entered in Phase 1 trial and it has the resembling like SARS-CoV-2 Spike protein (synthetic protein native like spike protein) and combined with an adjuvant.

  Platform: Protein Subunit

  Type of Candidate Vaccine: Native like Trimeric subunit spike protein vaccine.

- **Anhui Zhifei Longcom Biopharmaceuticals/ Institute of Microbiology, Chinese Academy of Sciences:** It has entered in phase 1 trial (Human trial)

  Platform: Protein Subunit

  Type of Candidate Vaccine: Adjuvanted recombinant protein (RBD- Dimer)

- **Imperial College London:** It has entered in phase 1 trial and this drug is based on new self-amplifying RNA technology which artificially creates the spike protein that boost the immunity against the virus.

  Platform: RNA

Type of candidate Vaccine: LNP-nCoVsaRNA

- **Curevac:** It has entered in clinical Phase 1 trial after getting approval from German Health Authority Paul- Ehrlich- Institute and FAMHP and uses nucleotides without chemical Modifications in the mRNA to generate a strong immune response which encodes for the spike proteins and is made up of lipid nanoparticles.

  Platform: RNA

  Type of candidate Vaccine: mRNA **(Clinical trials arena)**

- **People's Liberation Army (PLA) Academy of Military Sciences/ Waivax Biotech:**

  China's third approval for the second phase of clinical trials with the CanSino for Chinese troops.

  Platform: RNA

  Type of Candidate Vaccine: mRNA

132 candidate vaccines in preclinical evaluation according to WHO (World Health Organization) such as Zydus Cadila, Johnson & Johnson, Panacea Biotec, Merck and many more as on 2nd July (WHO)



- **Monoclonal antibodies by Utrecht University-** The Monoclonal antibodies that are made in humans and in the mice can be isolated by fuse B-cells (single) with leukemic cells (hybridomas) to make them immortal and tested whether

they make an antibody that would recognize the target.

When a monoclonal-like [antibodies that] we have generated is given to patients it does its work immediately, and much faster that the body could make its own antibodies.

(The Hindu)

☐ **Blood Plasma Transfers (Convalescent Plasma) -** People who recovered from COVID-19 have neutralizing antibodies to the disease in their blood.

Blood collected from the fully recovered patients (COVID)

Regular Withdrawal Process, ↓ test for other pathogen

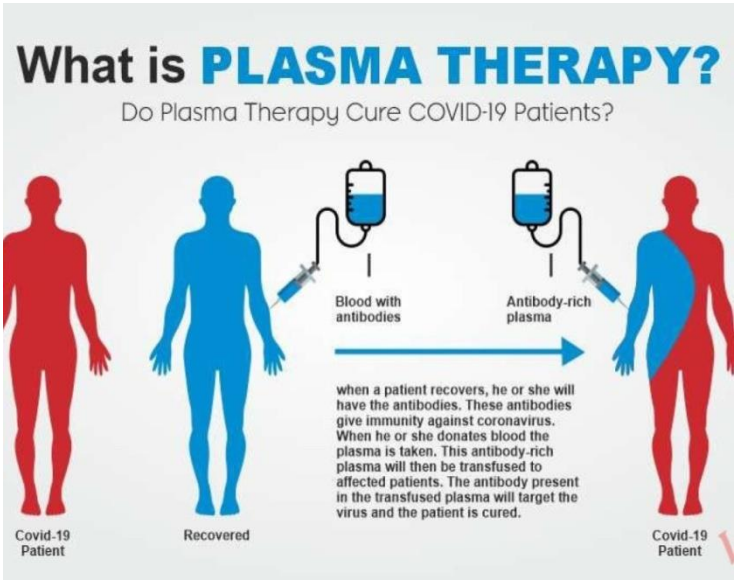
If safe

↓

Then Extract plasma

↓

Transfusion



↓

In Patients & help then to fight against the virus.

(The Hindu)

☐ Stem cells by Abu Dhabi Stem Cell Center (ADSCC)-

Peripheral blood ; The small number of stem cells that make their way from the bone marrow to the circulating stem cells are taken from the patients veins.



↓

Stem cell is separated from the blood

↓

Nebuliser turns the lipid medicine into a mist which is then breathed into lungs

↓

Stem cell mist covers damaged lung cells, encouraging them to repair themselves.

(www.ADSCC.com)

☐ **Thailand's mRNA vaccine-** Proceeded to test its novel vaccine on monkeys after seeing positive results on mice.

The Thai vaccine uses messenger RNA, which prompts body cells to produce antigens, molecules on the surface of viruses that spur the immune system into action.

(www.Times.com)

☐ **Tobacco vaccine by Tobacco Production Company-**They are on the pre-clinical trial stage.

They are making of an experimental vaccine based on proteins from tobacco leaves. **(Times)**

Apps helping Social Distancing and avoiding close contact with infected persons

- Aarogya Setu App
- Crowdless -Devised by Lanterne, a UK start up, it uses satellite data and artificial intelligence technologies to identify where people are congregating across the Globe.
- Sodar App by Google
- Mobility Trend Report by Apple

REFERENCES

- https://www.who.int/docs/default-source/coronaviruse/novel-coronavirus-landscape-covid-
- The Hindu Newspaper
- The Indian Express Newspaper
- https://www.bbc.com/news/world-48186856
- http://www.ox.ac.uk/news/2020-05-22-oxford-covid-19-vaccine-begin-phase-iiiii-human-trials
- https://www.modernatx.com/modernas-work-potential-vaccine-against-covid-19
- https://publichealthonline.gwu.edu/blog/producing-prevention-the-complex-development-of-vaccines
- Attended Webinar by NIT, Jalandhar on Innovations against COVID-19: Opportunities for Start-ups in Health Care Sector.

Reference Manager and End Note

These will allow you to manage references in research work quite efficiently specially employed by research students and researchers who are battling their citations and references in their research papers; there are some tools which may make our task easier.

Research Manager is software employed by scholars and authors for recording and bibliographic citations and for project references. It performs three basic functions- searching, storing and writing. The research management software packages contains database by which full bibliographic references are often added and selectively added. In Modern reference Management packages integrated with word processors in order that reference list are often added automatically in appropriate format from a web bibliographic database like Web of Science, Pub Med, NCBI, Google Scholar and one can import the small print from bibliographic database. Several Advantages of Research managers is inserting references depending on the journal specifications which include the utilization of brackets, parenthesized, commas, author name and lots of more, aid to make bibliographies, automatically add the references and citations.

Example- Mendeley, EndNote, RefWorks and lots of more

EndNote it's one among the references management software packages which used for bibliographies and references while writing. It keeps all the references and every one reference related materials during a personal library and one can easy share their references also with EndNote moreover; one can synchronize their references also like with their pc, a web library, telephone also. Several Advantages of EndNote- find full text for references in only one click, add references automatically and link updating to your work, search hundred of online resources for references and pdfs, provide write or read only access to your library & build your bibliography using the newest references type.

CONCLUSION

The Great Hope in the control of any infectious Disease is always a **Vaccine.** A vaccine can be in the weakened or inactivated form administered to humans that will protect them from infectious disease by supplying specific antibodies to them, while not making a person actually sick from it such as in the Bubonic Plague (Black Death), **Small Pox, Polio** (The only Disease that has been completely eradicated because of the **effective one time vaccine** was developed), Spanish Flu (The Great Pandemic of 1918-19), H1N1 Influenza. The COVID-19 pandemic has seen renewed efforts for the development of vaccine and several candidates are at various levels of processing and in the trial stages. In such a scenario an effective vaccine must overcome all the issues related to COVID-19 and will be a most effective tool to combat against the CORONAVIRUS.

Training report

Topic:Genotyping of single nucleotide polymorphisms by applying TARMS-PCR method.

By ayush tyagi 171824

Introduction

Cancer is the uncontrolled development of strange cells anyplace in a body. There are more than 200 kinds of cancer. Anything that may make an ordinary body cell grow anomalous possibly can cause cancer; general classes of cancer-related or causative specialists are as per the following: concoction or poisonous compound exposures, ionizing radiation, a few pathogens, and human hereditary qualities. Cancer side effects and signs rely upon the particular sort and grade of cancer; albeit general signs and indications are not unmistakable the accompanying can be found in patients with various cancers: weakness, weight reduction, torment, skin changes, change in entrail or bladder work, uncommon dying, constant hack or voice change, fever, bumps, or tissue masses. Even though there are numerous tests to screen and possibly analyse cancer, the clear analysis is made by assessment of a biopsy test of suspected cancer tissue. Cancer organizing is regularly dictated by biopsy results and decides the cancer type and the degree of cancer spread; arranging additionally assists parental figures with deciding treatment conventions. When all is said in done, in most organizing techniques, the higher the number allotted (for the most part between 0 to 4), the more forceful the cancer type or increasingly far reaching is the cancer in the body Single nucleotide polymorphisms (SNPs) are one of the most well-known kinds of hereditary varieties in the human genome. SNPs in qualities that manage DNA bungle fix, cell cycle guideline, digestion and resistance are related with hereditary powerlessness to cancer. Understanding the instruments basic the impacts of SNPs that bring about cancer weakness is basic to understanding the atomic pathogenesis of different cancers. From a clinical point of view, SNPs are likely indicative and helpful biomarkers in numerous cancer types. SNPs are situated in various locales of qualities, for example, advertisers, exons, introns just as 5'-and 3' UTRs. Along these lines, modifications in quality articulation and their impact on cancer defencelessness change contingent upon the area of the SNPs. The advertiser area SNPs influence quality articulation by changing advertiser action, interpretation factor authoritative, DNA methylation and histone adjustments. The exonal SNPs influence cancer helplessness by smothering quality interpretation and interpretation. SNPs in intron areas create graft variations of transcripts and advance or disturb official and capacity of long non-coding RNAs (lncRNAs). SNPs in the 5'-UTR influence interpretation, though SNPs in the 3'-UTR influence microRNA (miRNA) authoritative. SNPs in districts that are situated a long way from the real qualities diminish or improve quality interpretation through long-extend cis impacts. In this precise survey, we examine the hereditary and epigenetic instruments that

underlie the SNP-related cancer defencelessness and the possible utility of SNPs as cancer biomarkers.

Methodology

Different types of DNA extraction methods

Synthetic or arrangement-based DNA extraction technique:

Various kinds of natural and inorganic arrangements are utilized in the synthetic or arrangement based DNA extraction method.The steps of the DNA extraction continue as before in all the sorts of DNA extraction methods.SDS, CTAB, phenol, chloroform, isoamyl liquor, Triton X100, guanidium thiocyanate, Tris and EDTA are a few normal synthetic concoctions utilized in the arrangement based DNA extraction method.The arrangement based (additionally called compound) DNA extraction strategy is partitioned into natural dissolvable based DNA extraction and inorganic dissolvable based DNA extraction.The natural dissolvable based DNA extraction technique depends on the utilization of natural substances, for example, phenol and chloroform. Because of the unsafe idea of the phenol and chloroform, the technique is restricted.Nonetheless, phenol-chloroform DNA extraction strategy is perhaps the best strategy among all.Among the inorganic DNA extraction, two are generally mainstream: utilization of proteinase K and utilization of salt.The proteinase K DNA extraction strategy encourages high DNA yield however the strategy is tedious. Likewise, if not kept up well in a virus chain, the proteinase K cannot be used for a more drawn out timeframe. The lower steadiness of the chemical is another significant issue in this method. Salting out DNA extraction strategy is more secure than the PCI technique. The utilization of salts, for example, sodium chloride, potassium acetic acid derivation and ammonium acetic acid derivation helps in the DNA extraction.However, the strategy is progressively forceful in mix with proteinase K.Use of the distinctive salt in DNA extraction can expand the yield yet the virtue isn't adequate.

Phenol-chloroform strategy for DNA extraction:

This strategy is probably the best technique for DNA extraction. The yield and nature of DNA acquired by the PCI strategy is excellent on the off chance that we perform it well. The strategy is additionally called as a phenol-chloroform and isoamyl liquor, PCI technique for DNA extraction.The significant synthetic concoctions of PCI DNA extraction strategies are lysis cushion, Phenol and chloroform.The lysis support contains Tris, EDTA, MgCl2, NaCl, SDS, and different salts. Here the segments of lysis cushion help in lysis of cell layer just as the atomic envelope. The protein part of the cell denatured with the assistance of chloroform and phenol which are natural in nature.

Job of synthetic compounds:

Tris: DNA is pH delicate, Tris cradle keeps up the pH of the arrangement. Additionally, it communicates with the lipopolysaccharides of the cell film and makes them porous, this will help in lysis of the cell layer.

EDTA: EDTA is a chelating operator and can be utilized to square DNase movement. DNase is a chemical which lyses the DNA. Be that as it may, each chemical expected cofactor to work appropriately. The chelator EDTA hinders the action of DNase by obstructing the cofactor restricting site. It will work best in blend with Tris.

SDS: Sodium dodecyl sulfate is an anionic cleanser which helps cell film and atomic envelope to tear open.

NaCl: the Na+ particle of NaCl makes the ionic bond with the negative charge of DNA and kill it. It will help DNA meets up and shield from denaturation.

MgCl2: by and large, it secures the DNA. MgCl2 hinder the negative charge of the lipoproteins of the cell film. After the lysis of cell, there is no compartment in the cell consequently it ensures DNA by blending in with other cell organelles.

Phenol: it hastens the protein polluting influences.

The SDS expels the negative charges from the amino corrosive and upsets the affirmation of a protein. In this manner, the protein loses its structure and balanced out by utilizing the SDS.The blend of phenol, chloroform and isoamyl liquor helps in the expulsion of protein. After centrifugation, the phenol settles in the base of the cylinder and DNA in the fluid stage while the denatured protein stays between the two layers as a whitish cloud.So care must be taken to gather nucleic corrosive from this strategy. The gathered nucleic corrosive is accelerated with the assistance of chilled liquor (isoamyl liquor). We can add salt too to build the yield of the DNA. At last, the DNA is broken up in TE cradle. Due to the utilization of the natural solvents, this technique is additionally named as a natural dissolvable based DNA extraction method.The PCI strategy for DNA extraction is generally acknowledged. Indeed, even the scientific divisions trust PCI technique instead of a Kit strategy. The amount of DNA gets by PCI strategy is high. We can acquire 800 to 900 ng of DNA with incredible quality.If we set up all synthetic compounds well indeed and perform it truly we can generally get a decent outcome by this method.However, the measure of test required for PCI DNA extraction is high. It is hard to separate DNA from the examples, for example, hair and nail. Additionally, the virtue of DNA turns into a significant issue if not performed well

An enzymatic technique for DNA extraction:

All things considered, this strategy is a mix of a salt technique just as enzymatic strategy. Here the extraction cushion is utilized before going further on enzymatic digestion.The extraction support structure may differ from lab to lab, in any case, the significant segments are Tris, EDTA, NaCl, sodium lauryl and SDS. Here phenol, chloroform or isoamyl liquor is not utilized. Rather, the chemical proteinase K is used for processing the sample.The test is brooded with proteinase K for 2 hours this will process all the protein present inside the sample.Immediately after the proteinase K assimilation, the example is accelerated by chilled liquor. By centrifuging test, all other cell flotsam and jetsam are evacuated. At long last, the DNA pellet is broken up in TE buffer.This strategy for DNA extraction is fast and simple. We can utilize prepared to utilized DNA extraction cushion. Indeed, even the yield is high. In any case, the nature of DNA is a significant worry for this method.We had secured an

entire article on this technique. Peruse it here: Proteinase K DNA extraction strategy

Strong stage DNA extraction strategy:

These days all the DNA extraction units accessible depend on the exceptional science of the strong/fluid stage DNA extraction.The silica is the strong substance which ties with DNA during cleansing alongside it, various arrangements are utilized to filter the DNA.The strong stage silica is one of them.The primary bit of leeway of silica gel-based DNA extraction is that it is quick and gives "PCR prepared DNA" for the downstream applications. No extraction or precipitation steps are required accordingly this technique is prevalent among all.

Silica section based DNA extraction technique

The silica section based DNA extraction technique is exceptionally novel and not quite the same as other DNA extraction methods.In the PCI or proteinase K strategy we need to rotator test ordinarily and need to gather watery stage or pellets relying on the progression of extraction. Some of the time we need to gather fluid stage or some of the time we need to gather pellets.The silica-put together DNA extraction technique works with respect to the one of a kind science of communication among silica and DNA. An emphatically accused silica particles tie of the contrarily charged DNA and hold it during centrifugation.The technique was first portrayed by McCormick in 1989. In any case, the thought was created in 1979, when silica was utilized in DNA cleansing by Vogelstein.Different kinds of DNA extraction strategies The picture speaks to the general procedure of Spin section technique for DNA extraction.The silica-based strong stage DNA extraction strategy is presently monetarily accessible and it is most routinely utilized in indicative research centers. In light of its great quality DNA yield and negligible straightforward working framework, it is broadly accepted.The lysis support breaks the cell layer and the atomic envelope. The proteinase K processes all the protein.In the absolute initial step, the example is brooded with a phone lysis cradle or called a DNA extraction buffer.Along with it, a modest quantity of proteinase k is added to the example. The various debasements are expelled by centrifugation. Here the DNA stays limited with silica and different contaminations goes through the silica column.Now the DNA can be washed twice for improving the virtue in it. The fluid stage contains the polluting influences are disposed of by disposing of the assortment tube.Finally, the DNA is broken up into the TE cradle. The technique is quick solid, precise and devours less time when contrasted with other methods.Other DNA extraction strategies are DNA extraction utilizing the anionic pitches, attractive dot DNA extraction strategy and CsCl thickness inclination DNA extraction strategy.

DNA extraction utilizing the anionic pitches:

The Chelex the result of Bio-Rad research centers is the best case of the anionic pitch utilized in the DNA extraction.The emphatically charged chelex ties to the contrarily charged phosphate of DNA and aides in the extraction of DNA. In any case, at times a few contrarily accuses contaminants additionally meddle of DNA extraction by authoritative with the anion.The chelex is comprised of the styrene-divinylbenzene copolymers. The strategy for utilizing chelex as an anionic pitch for

DNA extraction was first depicted by Walsh et al., in the year 1991, the example they had utilized was the blood.Another sap utilized by Seligson et al., was the diethylaminoethyl.In this technique, the segment of the cylinder is loaded up with positive tars. The phone lysate goes through the framework and DNA ties to the decidedly charged resins.By applying the low fixation salt cushion, proteins and different debasements or trash are washed off and just DNA stays into the matrix.In the last advance filling the grid with the high focus salt support the DNA is eluted from the tars and accelerated utilizing the alcohol.The technique is additionally called as DNA extraction through anion trade chromatography.

DNA extraction by metallic beads:

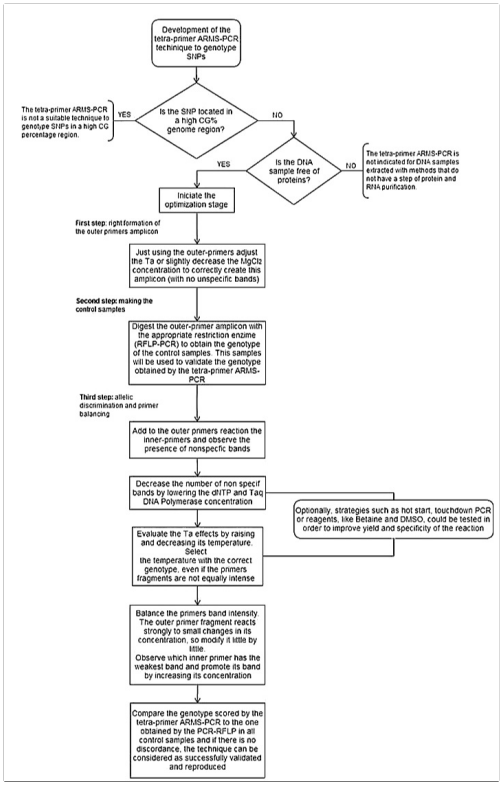
Decidedly charged attractive globules draw in the contrarily charged DNA. The DNA is isolated under the attractive field. DNA extraction cushion is required in this procedure also.Different sorts of DNA extraction methods Graphical portrayal of virtue versus time utilization of various strategies for DNA extraction.

CsCl thickness inclination strategy for DNA extraction:

In this technique, the DNA is isolated dependent on the thickness of it with the centrifugation.In the rapid centrifugation, at the isopycnic point where the thickness of the DNA and the slope (CsCl) become same, the DNA band will appear.However, the strategy is monotonous and difficult to proceed as it required hello there speed centrifugation (10,000 to 12,000rpm) for more than 10 hours.Still, the plasmid DNA can be secluded more effectively than the supercoiled DNA.Another significant impediment of the thickness angle centrifugation is the utilization of the cancer-causing EtBe in the DNA extraction.The EtBr intercalates between the strands of DNA and isolates supercoiled DNA from the non-supercoiled.

The tetra-primer amplification refractory mutation system-polymerase chain (T ARMS-PCR) response is a straightforward and conservative strategy to genotype single-nucleotide polymorphisms (SNPs). It utilizes four primers in a solitary PCR and is followed just by gel electrophoresis. Be that as it may, the advancement step can be dedicated and tedious. Henceforth, we propose to exhibit and examine basic strides for its turn of events, in an approach to give valuable data. Two SNPs that gave distinctive enhancement conditions were chosen. DNA extraction techniques, toughening temperatures, PCR cycles conventions, reagents, and primers fixation were likewise investigated. The utilization of tetra-primer ARMS-PCR could be debilitated for SNPs in DNA districts wealthy in cytosine and guanine and for tests with DNA not filtered. The liquefying temperature was viewed as the factor of more noteworthy impedance. Nonetheless, little changes in the reagents focus altogether influence the PCR, particularly MgCl2. Adjusting the inward primers band is additionally a key advance. Along these lines, to adjust the inward primers band, power is critical to see which one has the most vulnerable band and advance its band by expanding its fixation. The utilization of tetra-primer ARMS-PCR goes to the desires for current genomic research and permits the investigation of SNPs in a quick, solid, and minimal effort way.

Results and conclusion

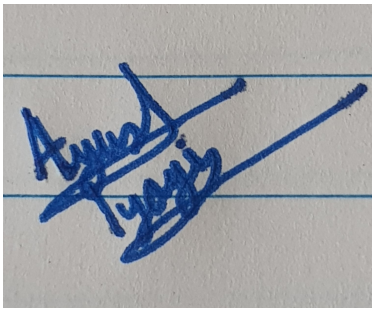


Flowchart representation of critical steps during the tetra-primer ARMS–PCR technique development and considerations about its use



Student Signature

Supervisor Signature



Report Submitted in Fulfillment of Summer Internship of

Introduction to Chemical Pharmacology

BACHELORS OF TECHNOLOGY

by

NEHA VERMA (171825)

UNDER THE SUPERVISION OF

Dr. Rahul Shrivastava

July-2020

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY
WAKNAGHAT,

SOLAN

TABLE OF CONTENT

TITLE	PAGE NUMBER
Declaration	3
Acknowledgement	4
Abstract	5
Introduction	6-15
Objectives	16
References	17
Reference Manager and Endnote	18

DECLARATION

I hereby declare that the Summer Internship work entitled **"Introduction to Chemical Pharmacology"** has been solely submitted to the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Wakhnaghat, under the guidance of our supervisor **Dr. Rahul Shrivastava**



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Date - 5th July

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I take this opportunity to express my first and foremost gratitude to our "DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS" for the confidence bestowed upon me and entrusting our project title "Introduction to Chemical Pharmacology."

At this juncture, with proud privilege and profound sense of gratitude I feel honored in expressing my deepest appreciation to **Dr. Rahul Srivastav,** for being a lot more than just a supervisor and going beyond the call of duty in my guidance, support, advice, and motivation throughout. He has been the source of inspiration of come what may, these issues cannot bring you down. Sincere thanks for his insightful advice, motivating suggestions, invaluable guidance, help and support in successful completion of this Summer Internship Project and also for his constant encouragement and advice throughout.

Special thanks to my parents for their infinite patience and understanding for the constant support and most importantly God, who in his mysterious ways, always made things work out in the end.

In gratitude,

Neha Verma (171825)

ABSTRACT

This report predicts the summary of clinical pharmacology, which again involves pharmacokinetics(what the body does to the drug) and pharmacodynamics(what the drug does to the body). They are highly interactive, kinetics affects the dynamics but in many cases when a system is affected by a drug, you can have a feedback loop that may change kinetics. So studies are ongoing for all drugs at different phases of development to understand how variability and pharmacokinetic parameters such as adsorption, distribution, elimination, and the overall exposure affects the pharmacodynamics response.

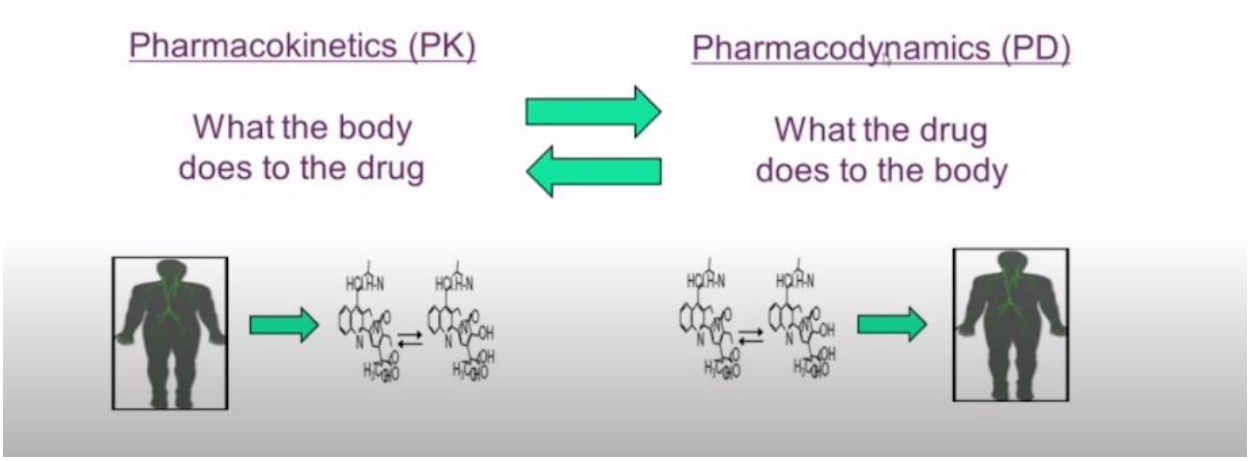
INTRODUCTION

WHAT IS CLINICAL PHARMACOLOGY

It has two basic parts Pharmacokinetics and Pharmacodynamics.

Pharmacokinetics is what the body does to the drug.

Pharmacodynamics is what the drug does to the body i.e. what are the effects of drug on the body such as efficacy, targeting and toxicity.

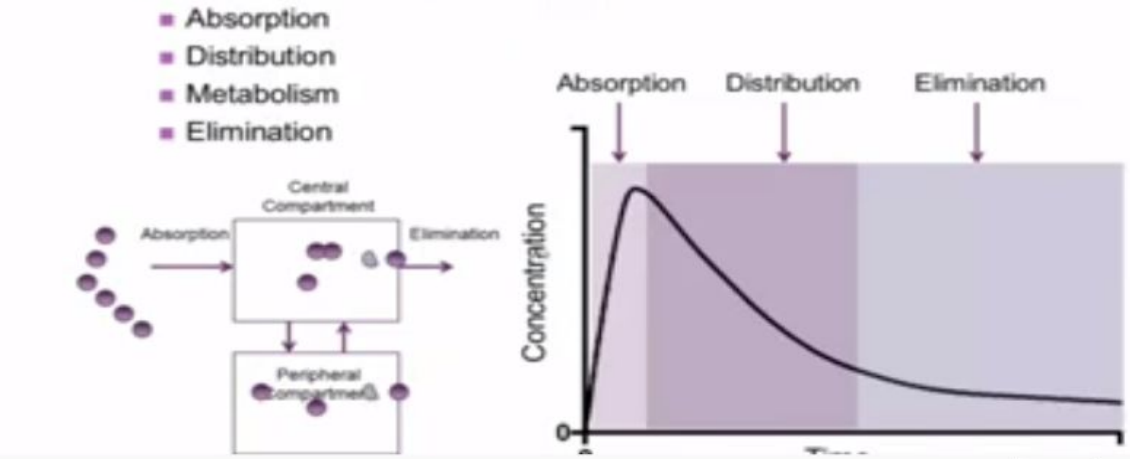


Pharmacokinetics

We can explain pharmacology mathematically.It is basically the drug's journey through the body, and how the drug is handled by the body.

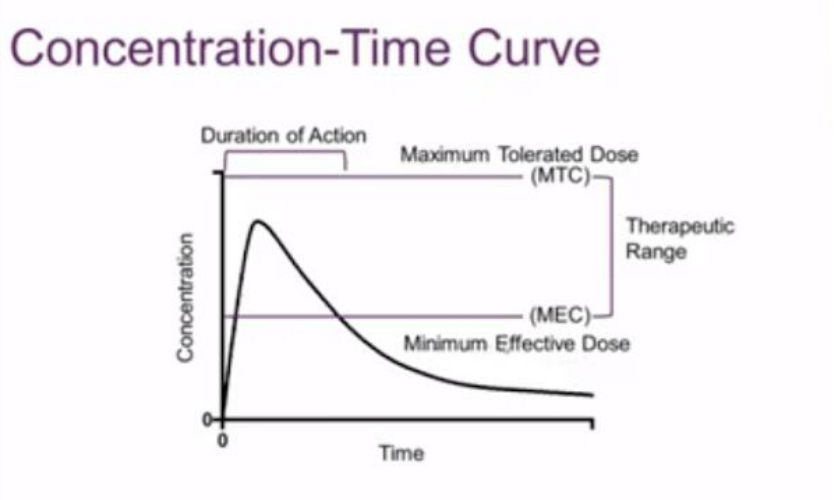
There are four different basic processes to pharmacokinetics , which is called ADME - adsorption, distribution, metabolism, elimination.

When a drug is dosed orally or IV, it goes into the central compartment, which is adsorption phase. It then goes to the peripheral compartment which is the distribution phase. And lastly the drug is eliminated which is the elimination phase.

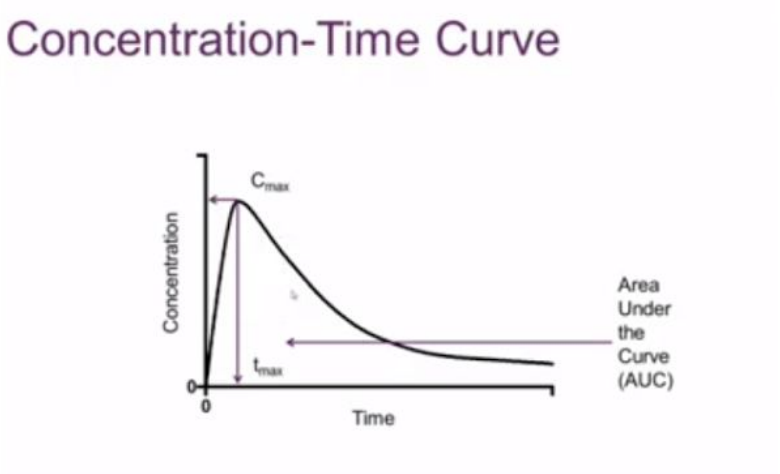


Following graph depicts the concentration vs time curve which is involved in chemical studies, time on the x-axis and concentration on the y-axis.

It shows Minimum Effective Dose i.e. the exposure and Maximum Tolerated Dose I.e. therapeutic range



Some important terms such as Cmax I.e. maximum concentration, Tmax which is the time at the maximum concentration and AUC which is the Area Under Curve which measures the overall exposure.



In this study we are going to evaluate different parameter and eventually see how they predict the pharmacodynamic response.

Routes of Administration

How can we Administer drugs to patients?

1. Parental Administration such as intravenous, intramuscular or subcutaneous injection.

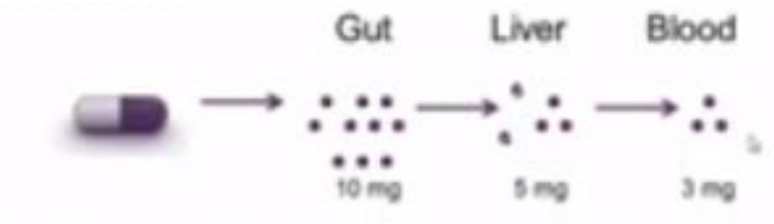
2. Oral Administration such as through capsules, tablet, suspension, or liquid.

3. Sub-lingual Administration such as tablets.

4. Local Administration such as ointments, cream, patch, suppository, inhalation.

BIOAVABILITY

It s the fraction or percentage of the drug dose reaching the systemic circulation meaning the blood exposure. So, if a dose is given orally, it goes in and it dissolves or breaks down into the gut which is then absorbed into the blood and is metabolized by liver through first-pass effect. Ultimately, what gets into the blood after the liver is what we call bio-available.



Factors affecting Distribution

The factors that affect adsorption, tissue permeability, blood flow, binding to plasma protein,binding to additional cellular component.

Protein Binding

It is related to the binding of drug to plasma proteins such as albumin, beta-globulin, and alpha-acid glycoprotein. It is important to learn that the drugs that are bound to these proteins have no effect. So, amount of drug is determined by different concentrations I.e. free drug concentration, the protein bound concentration, and affinity for binding sites.

%bound = (bound drug / bound drug+free drug) * 100

%bound drug concentration is affected or changed by following parameters:-

1. Renal failure
2. Inflammation
3. Malnutrition
4. Fasting
5. Drug interactions

Elimination

There are 3 different metabolism

1. Enzymatic metabolism: The goal is to enhance the elimination from body. The enzymatic metabolism mostly occurs in liver by reactions that increases the water solubility. The metabolites are then secreted back into the blood where they are eliminated from body. There are different phases of enzymatic metabolism .The phase 1, which is making drug more hydrophillic, phase 2 metabolism involves conjugation and make it more water soluble so that it is eliminated.

2. Renal elimination: It is of two types

a) Filtration these are small, no protein bound molecules, which move through the renal glomerulus and renal tubule and gets eliminated through urine.

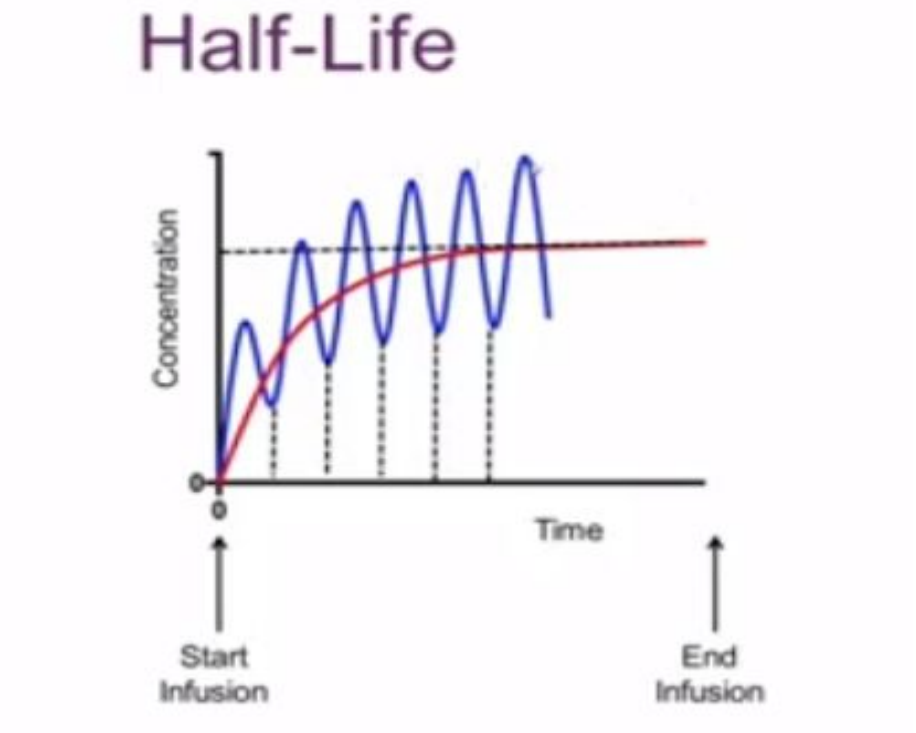
b) Secretion where the drugs are actively secreted into the renal tubules and are also eliminated in urine.

3.Cellular Elimination: This type of elimination is for complex drugs such as for nano-particles, conjugates, and biologics(antibodies or antibody drug conjugates).Active cells of monocytes and macrophages or phagocytic cells clear the complex agents.

Half life

An important pharmacokinetic parameter is Half Life which means the time it takes for half the drug to be administered.

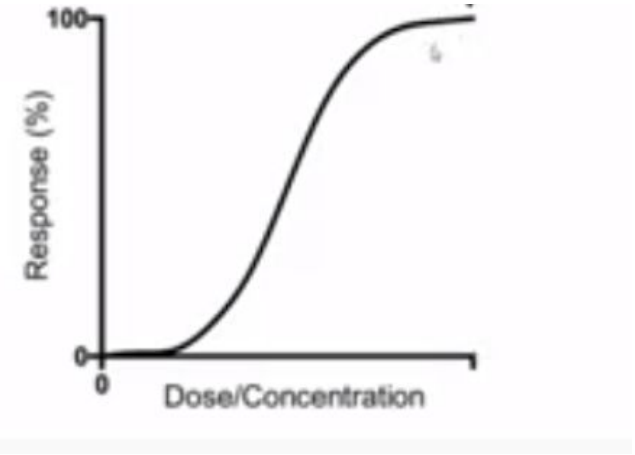
So each drug has its own half life that needs to be characterized. So if you are giving repeated doses of a drug, how long it takes to get into a stable state is half life.



Pharmacodynamics

It is the opposite of pharmacokinetics, it is what the drug does to the body. It is related to drug's destination or purpose and involves efficacy and toxicity I.e. Therapeutic index, Sites of action, Affinity of receptors.

Following graph shows when you give a dose or concentration of a drug measured in pharmacokinetics studies, the degree of response goes from zero upto 100 percent and you get a sigmoidal curve and once you reach a point where giving more or higher concentration of drug, you get no more added effects that can occur. You just get off targeted effects or toxicity. So different drugs will have different concentration vs response relationships as related to which drug will be more effective.

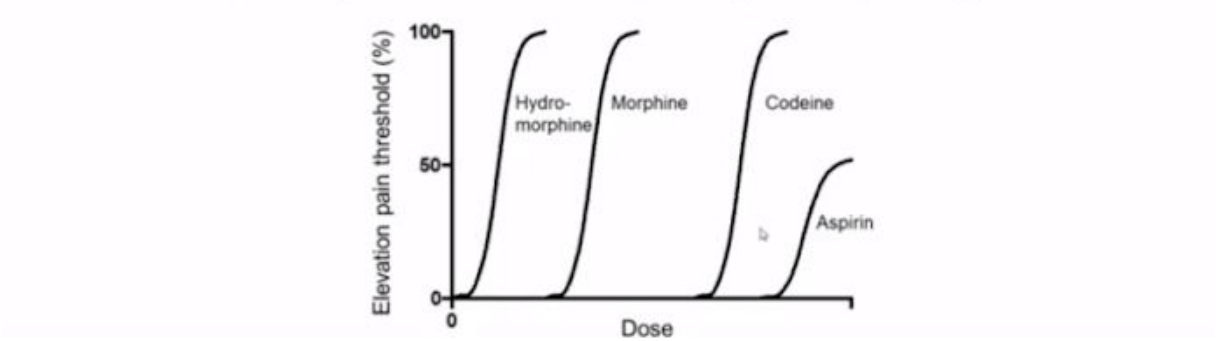


Potency

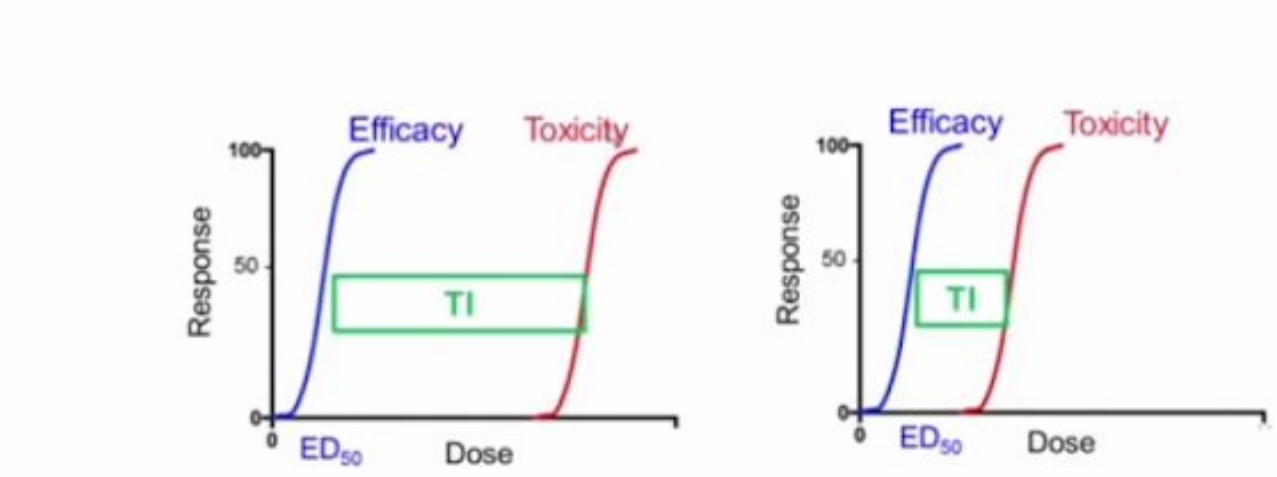
It is a dynamic term related to the relative strength and response for a given dose. The effect of concentration or a dose needed to elicit half the maximum dose or response, is EC50 or ED50 and potency is inversely related to ED50 or EC50.

The following graph shows relation between the dose or exposure of a particular drug and elevation or treatment of pain from zero to a hundred percent.

As the potency curve move to the left that means these drugs are more potent, or as it moves to right it means these agents are less potent.



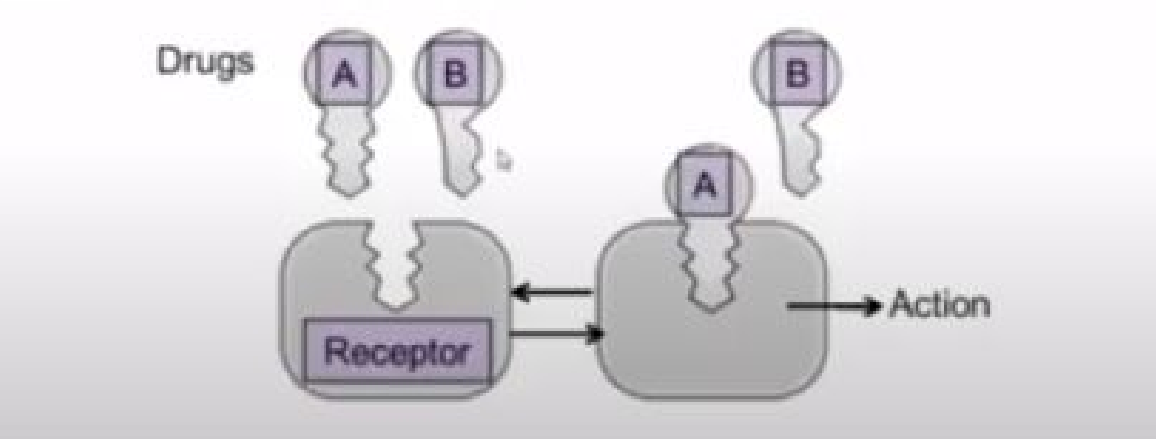
Therapeutic index is a very important pharmacodynamic term. Therapeutic index is related to the toxic or lethal dose at 50%. An easier way to think about therapeutic index is to look at the range or distance between what is required for efficacy or what is required for toxicity.And by looking at the dose or exposure vs response relationship, the efficacy curve represented by blue and toxicity curve represented by red line. The distance or exposure range between what causes efficacy and what causes toxicity is called therapeutic range. The graph below on left has wide therapeutic index which is a good characteristic of drug.



Molecular Mechanism Of Action

In pharmacodynamics there is different molecular mechanism of action. Drug must bind to a specific sit to elicit a response, called the drug receptor site interaction. There is many different targets for these receptors and interactions- lipids, nucleic acids, proteins which are mostly receptors and many of those have not been fully characterized. So basically it is a lock and key analogy.

Below is the diagrammatic representation of molecular mechanism of action. Here, we need a drug, either drug A or drug B to bind to the receptor to achieve a response. If drug a binds, it achieves a response or action that is going on. SO in this following method multiple drug bind to multiple target to elicit a pharmacologic response.



There are different types of interactions or agents I.e. agonists and antagonists. Drug interaction occurs when an agonists and antagonist are dosed together.

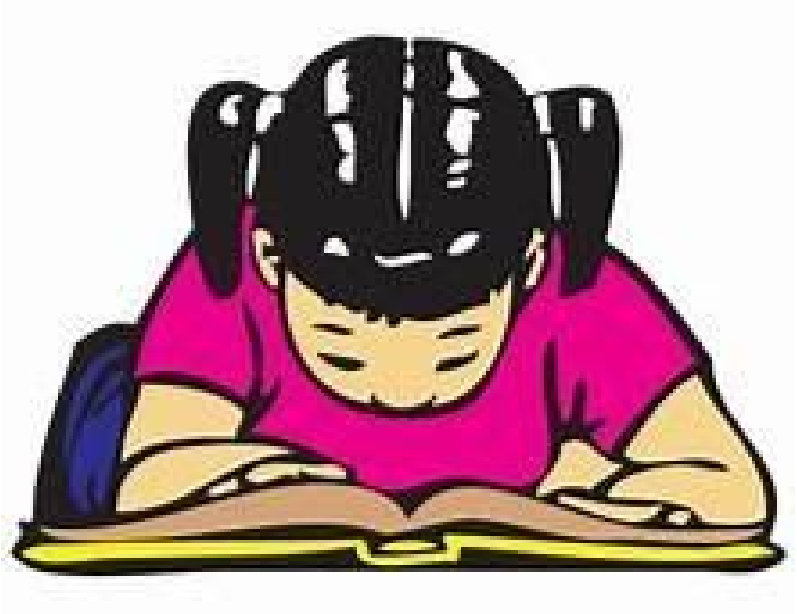
Agonists

It binds to receptor and cause effect, eg. Blood pressure change, pain reduction. Agonists are driven by affinity and intrinsic activity.

Antagonist

These binds to the receptor but there is no measurable cellular or physiological change that occurs. It blocks the usual receptor and it can also reduce the effect of an agonists. They do have affinity but no intrinsic activity.

OBJECTIVE



1. To describe how drugs are developed and where clinical pharmacology studies are performed.
2. To study what involves Pharmacokinetics which involves adsorption, distribution, metabolism, elimination of drugs.
3. The definition of Pharmacodynamics as related to key terms such as dose response relationships including receptors and actions of drug targeting.
4. To predict how individual variability in Pharmcokinetics affect Pharmacodynamics such as drug afficacy or drug toxicity.

REFERENCES

1. A. DiMasi, L. Feldman, A. Seckler, A. Wilson, "**Trends in risks associated with new drug development: success rates for investigational drugs"**, 87 (2010), pp. 272-277

2. A. DiMasi, H.G. Grabowski, R.W. Hansen "**Innovation in the pharmaceutical industry: new estimates of R&D costs",** J Health Econ, 47 (2016), pp. 20-33

3. P.K. Owens, E. Raddad, J.W. Miller, J.R. Stille, K.G. Olovich, N.V. Smith, et al. "**A decade of innovation in pharmaceutical R&D: the Chorus model"**, 14 (2015), pp. 17-28

4. F. Sams-Dodd "**Target-based drug discovery: is something wrong?"**
Drug Discov Today, 10 (2005), pp. 139-147

5. F. Prinz, T. Schlange, K. Asadullah "**Believe it or not: how much can we rely on published data on potential drug targets?"**, 10 (2011), pp. 712-714

6. T.J. Hwang, D. Carpenter, J.C. Lauffenburger, B. Wang, J.M. Franklin,A.S. Kesselheim "**Failure of investigational drugs in late-stage clinical development and publication of trial results"**, 176 (2016), pp. 1826-1833

PRODUCTION OF DISEASE-FREE POTATOES VIA MERICLONING

Report submitted in fulfillment of Summer Training for

BACHELORS OF TECHNOLOGY

IN

BIOTECHNOLOGY

By

YUKTI (171826)

UNDER THE SUPERVISION OF

DR. HEMANT SOOD

May-June (2020)

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY WAKNAGHAT,

SOLAN

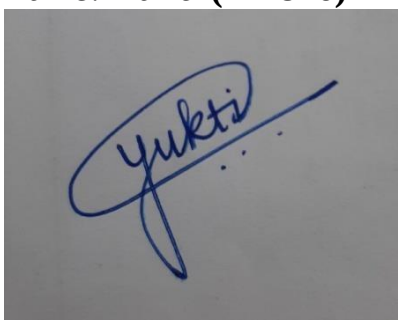
TABLE OF CONTENT

CHAPTER NO.	TITLE	PAGE NO.
	DECLARATION	3
	SUPERVISOR'S CERTIFICATE	4
	ACKNOWLEDGEMENT	5
CHAPTER 1	INTRODUCTION	6-10
CHAPTER 2	REVIEW OF LITERATURE	11-14
CHAPTER3	MATERIAL AND METHODS	15-17
CHAPTER 4	CONCLUSION	18-19
	REFERENCES	20-21

DECLARATION

I hereby declare that the summer training work entitled "**PRODUCTION OF DISEASE-FREE POTATOES VIA MERICLONING**" has been solely submitted to the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat have carried out under guidance of supervisor **DR. HEMANT SOOD.**

Name: **Yukti (171826)**



Department of Biotechnology and Bioinformatics

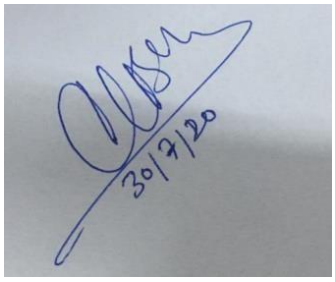
Jaypee University of Information Technology, Solan

Waknaghat.

Date: 02/07/2020

SUPERVISOR'S CERTIFICATE

This is to certify that the summer training work titled "**PRODUCTION OF DISEASE-FREE POTATOES VIA MERICLONING**" by **Yukti** during May-June 2020 in fulfillment for the summer training in Plant tissue culture in Biotechnology of Jaypee University of Information Technology, Solan has been carried out under my supervision. This work has not been submitted partially to any other University or Institute for the award of any degree or appreciation.

Signature of Supervisor - 

Name of Supervisor **- Dr. Hemant Sood**

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Date: 02/07/2020

ACKNOWLEDGEMENT

I take this opportunity to express my first and foremost gratitude to my "DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS" for the Confidence bestowed upon me and entrusting my training titled "**PRODUCTION OF DISEASE-FREE POTATOES VIA MERICLONING**".

At this juncture, with proud privilege and profound sense of gratitude, I feel honored in expressing my deepest appreciation to **Dr. Hemant Sood,** for being a lot more than just a supervisor and going beyond the call of duty in my guidance, support, advice, and motivation throughout. She has been the source of inspiration. Sincere thanks for her insightful advice, motivating suggestions, invaluable guidance, help and support in successful completion of this summer training and also for her constant encouragement and advice throughout my summer training.

In gratitude,

Yukti (171826)

CHAPTER 1

INTRODUCTION



Micropropagation is a practice of rapidly multiplying mother plant material to produce a large number of offspring using plant tissue culture techniques. It is the multiplication of genetically identical copies of individual plants. Micropropagation can be done sexually or asexually.

One of the approaches of Micropropagation is through Meristem Culture, also known as Mericloning. Mericloning is producing identical plants by Micropropagation of apical meristem or auxiliary buds. It is asexual means of culturing or is vegetative culturing of a plant. Apical meristem is the tissues present at extreme ends/tips of shoot. It is about mm of diameter and 0.25-0.3 mm in length. It is isolated by applying a V-shape cut. Morel and Martin (1952) were the first to use this technique for virus eradication of Dahlia.

It is a complicated process which consists of 5 stages:-

1. **Stage 0**:- In this stage, selection and growth (maintenance) of stock plants (mother plants) for about 3 months under controlled conditions is done.
2. **Stage 1**:- Here, initiation and establishment of culture is done in a suitable medium. Selection of appropriate explant which can be organs, shoots or axillary buds is being done.
3. **Stage 2**:- Multiplication of shoots or rapid embryo formation from explant.
4. **Stage 3**:- Rooting of the shoots is done.
5. **Stage 4**:- Establishment of plantlets in sterilized soil for hardening under greenhouse environment.

Different approaches can be used such Meristem culture; Callus culture; Suspension culture; Embryo culture; Protoplast culture etc. Temperature range appropriate for Micropropagation is between 20°C-28°C. Lower light intensity is more appropriate.

Advantages of Mericloning:-

1. High plant propagation rate.
2. Irrespective of seasonal variations, Micropropagation can be carried out whole year.
3. Lack of vascular tissue.
4. Plants that are highly heterozygous and cannot be stored as genetic resource, there meristem can be used for in vitro storage.
5. Production of disease-free plants.
6. High auxin concentration.

Disadvantages of Mericloning:-

1. Difficulty in isolation.
2. Low survival rate.
3. Long regeneration time for explants.

The plant chosen to carry forward the training is ***Solanum tuberosum*** (Potato).

Solanum tuberosum

- *Solanum tuberosum* is a perennial plant which belongs to the family Solanaceae. It is starchy tuber which is a root vegetable.
- All parts of the plant (including the fruit) except the tubers contain the toxic alkaloid solanine and are thus inappropriate for human consumption.
- Plants which are propagated from the tubers (having at least 1-2 eyes) are clones whereas those that are produced from seeds give a wide range of varieties.

- More than 5000 potato varieties are present worldwide whereas the major species is a tetraploid with 48 chromosomes.
- The potato genome has 12 chromosomes which have 860 million base pairs. It is a medium-sized plant genome.
- A raw potato has 79% water, 17% carbohydrates (88% is starch), 2% protein, and contains negligible fat.
- Insects that commonly cause potato diseases or damage the plants are the potato tuber moth, the green peach aphid (*Myzus persicae*), the potato aphid, mites, etc.
- There are about 40 insect species infectious to potato. The following are the major potato's diseases that a grower must be concerned about:-
    - ✓ Potato leafroll virus: The leaves of the potato plant roll; may become pale and chlorotic. The tuber may get internal net necrosis. Spreads by aphid feeding.
    - ✓ Potato Virus Y: The severity of symptoms depends on the variety of potato. The viral strain PVYN cause necrosis in tubers. There are cases with no, mild or severe symptoms.
    - ✓ Late Blight (*Phytophathora infestans*): It is one of the most famous potato diseases. It is a fungal disease which spread through air current.

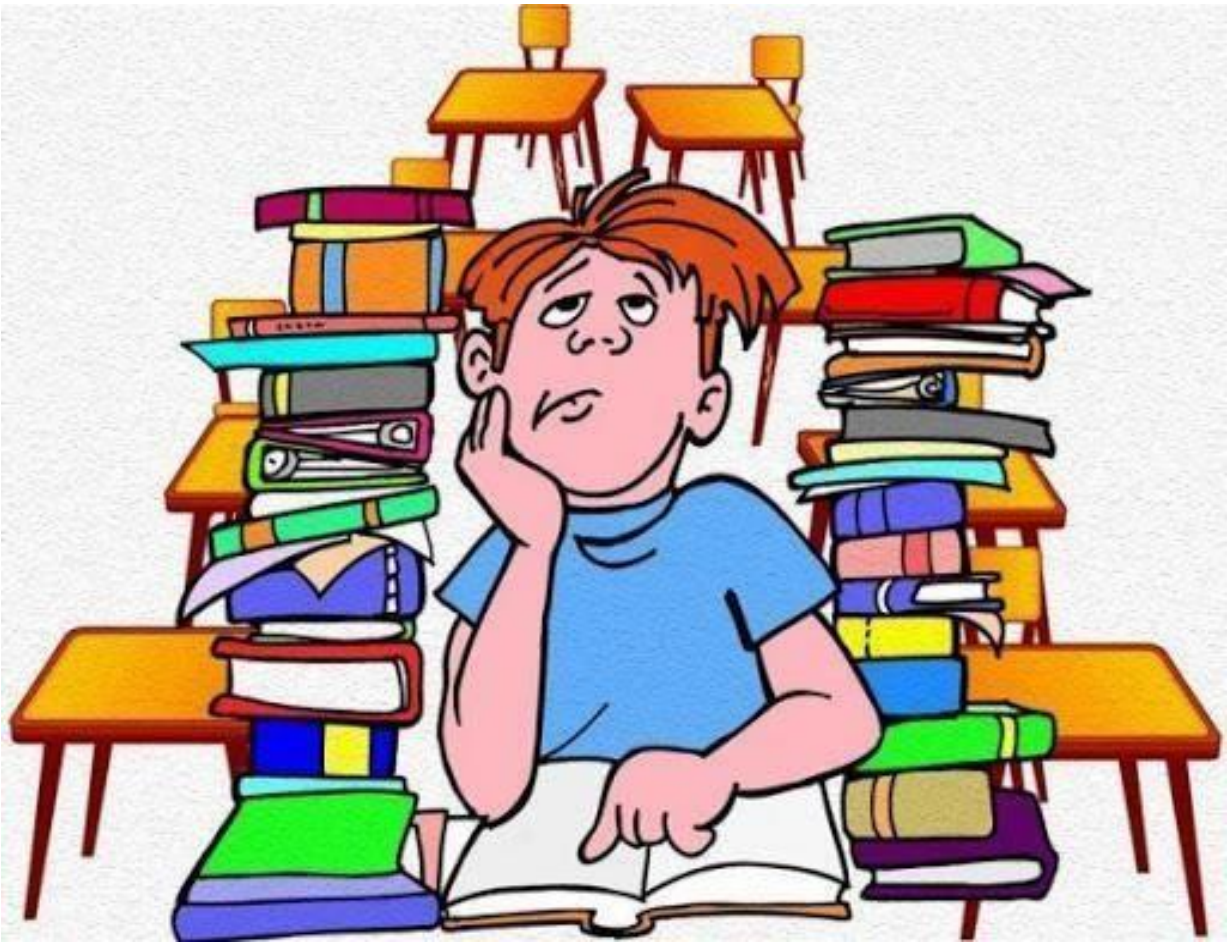


<u>Figure 1:</u> (1) Potato with PVY; (2) Late Blight of Potato

Production of disease-free potato is very important for commercialization of this crop as these diseases are carried forward in next growing season. These diseases can also affect other Solanaceae plants such as tomatoes. Transfer of virus from one generation to another in seed tubers makes it a major limitation.

CHAPTER 2

REVIEW OF LITERATURE



1. **<u>Detection and Identification of Viruses in Potatoes</u> :**
   Viral detection and identification is very important for eradication of the virus. The virus is diagnosed by the symptoms making it an important factor. The virus must be diagnosed at an early stage and with accuracy for crop management. To isolate virus, study its symptoms and level of infection, transmission of virus from infected tissue to healthy one is the only procedure. Electron microscopy is the method which determines the shape and size of virus. Cross-reactivity of antisera against virus is used for classification of plant viruses. Virus can be identified by sequencing a part of genome which requires isolation and cloning of that part of genome. Nucleic acid probes and viral nucleic acid related techniques can be used.

   (A. Gera and S. Marco)

2. **<u>Major In Vitro Techniques for Potato Virus Elimination and Post Eradication Detection Methods</u> :**
   Meristem culture is major in vitro techniques used for viral elimination in seed tubers. It can be solely used or can be used in association with other techniques such as cryotherapy (of shoot tip), chemotherapy (e.g. - Ribavirin), electrotherapy or thermotherapy (temperature and viral RNA silencing are related; low temperature preferred). It is shown that potato virus elimination depends on type of virus infecting the potato, antiviral agent used to eradicate the virus, duration of heat treatment and potato cultivar. Real time RT-PCR or ELISA can be used for detection of viral elimination rate.

   (H. Gong, C. Igiraneza and L. Dusengemungu)

3. **<u>Virus free potato tuber seed production through Meristem culture in Tropical Asia</u> :**

   Four widely cultivated varieties of potato of Bangladesh which are Diamant, Multa, Lalpakri and Cardinal is cultured using apical Meristem. The Meristem culture were proliferated for shoot production and root induction in MS and $MS_{\circ}$ medium which consists of different types and concentration of phytohormones. Medium having 0.5 mg l^{-1} GA_3+0.04mg l^{-1} KIN was the best medium found for establishing Meristem. Use of IBA in concentration 0.5mg l^{-1} has been recommended for shoot and root proliferation from primary Meristem considering all the treatments. DAS-ELISA test was done to find out virus-free potatoes which were further used for Micropropagation of potato tubers. Shoot induction was found to be best in medium having 2.0 mg l^{-2} GA_3 while the root induction was observed best in medium having combination of 0.1 mg l^{-1} GA_3 and 0.1 mg l^{-1} KIN. These plantlets were then acclimatized and were successfully grown in filed. All the potatoes grown using this method were virus-free.

   (S.A. Hossain et al.)

4. **<u>Production of Virus Free Potato Plants Using Meristem Culture from Cultivars Grown under Jordanian Environment</u> :**

   The percentage of infection from Potato Virus Y in three varieties of potato cultivars found in Jordan was 21.4% for Spunta, 15.7% for Alaska and 12.8% for Safrane cultivars.

   0.5 mg/l IBA supplemented medium gave best results for shoot and root induction. ELISA test along with RT-PCR was used to detect the virus-free plantlets. These plantlets were acclimatized and gave 90% success rate in Spunta and 80% success rate in Alaska and Safrane.

   (M. Miassar Al- Taleb et al.)

5. **Determination of Virus-free Potato Planting Materials by Positive Selection and Screening of tubers from Seed Stores in the Western Highlands of Cameroon :**

There was a random collection of leaves from asymptomatic plants. The plants from which leaves were collected were marked and after four weeks tubers were collected from these plants. These were tested using DAS-ELISA for six viruses, i.e, PLRV, PVY, PVA, PVX, PVS and PVM out of which five were found to infect leaves and four were found to infect tubers. Tubers were free from PVA and PVX while leaves were free from only PVA. PVM was found most in tubers whereas PLRV was found least. As the size of the tuber increases, there is a significant decrease in the rate of infection. Thus, size of potato tubers can tell a farmer about a healthy tuber.

(A.P. Njukeng et al.)

6. **In vitro Micropropagation of potato (*Solanum tuberosum* l). cultivars :**

Use of various sterilization processes was done to disinfect potato sprouts which were isolated from two genotypes such as Excuisita and Bergerac. The sterilization process that gave highest survival rate was of 1% $HgCl_2$. Apical Meristem was isolated from these sprouts in which further shoot was induced and then rooting was done. Excuisita gave higher shoot length while Bergerac gave higher shoots per plant.

(D. Xhulaj and B. Gixhari)

CHAPTER 3

MATERIALS AND METHODS (according to Literature)



Materials

- Different potato varieties having different viral infections for conducting experiments
- GA_3, KIN and IBA in different concentrations
- Murashige and Skoog medium
- Pantothenic acid
- For surface sterilization:-
  - 70% C_2H_5OH
  - Mercuric chloride($HgCl_2$) solution in different concentrations
  - Sodium hypochlorite
  - Tween20
  - Savlon

Methods

- 0.5-1cm sprouts surface sterilized for 15-20 min under tap water

↓

Sprouts sterilized by dipping in 70% C_2H_5OH and $HgCl_2$ for 30 seconds

↓

Washed several times with autoclaved distilled water

↓

Isolated apical meristems were cultured in MS medium supplemented with 3% sucrose, plant hormone, 0.6% agar, 2ppm Pantothenic acid and 0.25ppm GA_3

↓

Cultured in growth room having temperature 25±1°C; relative humidity of 50%; photoperiod of 16/8 hour light/dark and illumination of 50µmol m^2 s^{-1}

↓

After 30 days, healthy cultures were selected

↓

Healthy cultures were induced for shoot proliferation

↓

Rooting was done and plantlets were acclimatized

- 25-30 days old seedlings isolated and used as explants

↓

Clean shoot tips excised and sterilized using savlon and tween20

↓

Washed with autoclaved distilled water 2-3 times

↓

Washed explants with 0.1% $HgCl_2$ with gentle shaking for 2-8 min and washed with distilled water3-5 times

↓

The isolated meristems placed on Filter Paper Bridge in test tube having liquid MS medium containing IBA, GA_3 and KIN

↓

Developed meristems were inoculated on medium for shooting for 3-5 days after 3-4 weeks of inoculation of primary meristem

↓

Virus indexing was done using double antibody sandwich ELISA

↓

Virus-free plantlets were selected and further root was induced by incubating at 25±2°C and a photoperiod of 16 hours.

↓

After 3-4 weeks these plantlets were acclimatized and were virus-free

CHAPTER 4

CONCLUSION

- The potato tubers which were produced by meristem culture and other plant tissue culture techniques were mostly virus-free and had a high success rate.

- Serological techniques were used mostly for virus detection.

- ELISA and RT-PCR are also used for detection of virus.

- Meristem-cultured potato plants gave virus-free tubers. As we know viruses are associated with vascular system of plants and as growth is very fast in new meristem so vascular tissue is not developed in it so far. We know virus moves through vascular system and thus it cannot reach the meristem making virus-free.

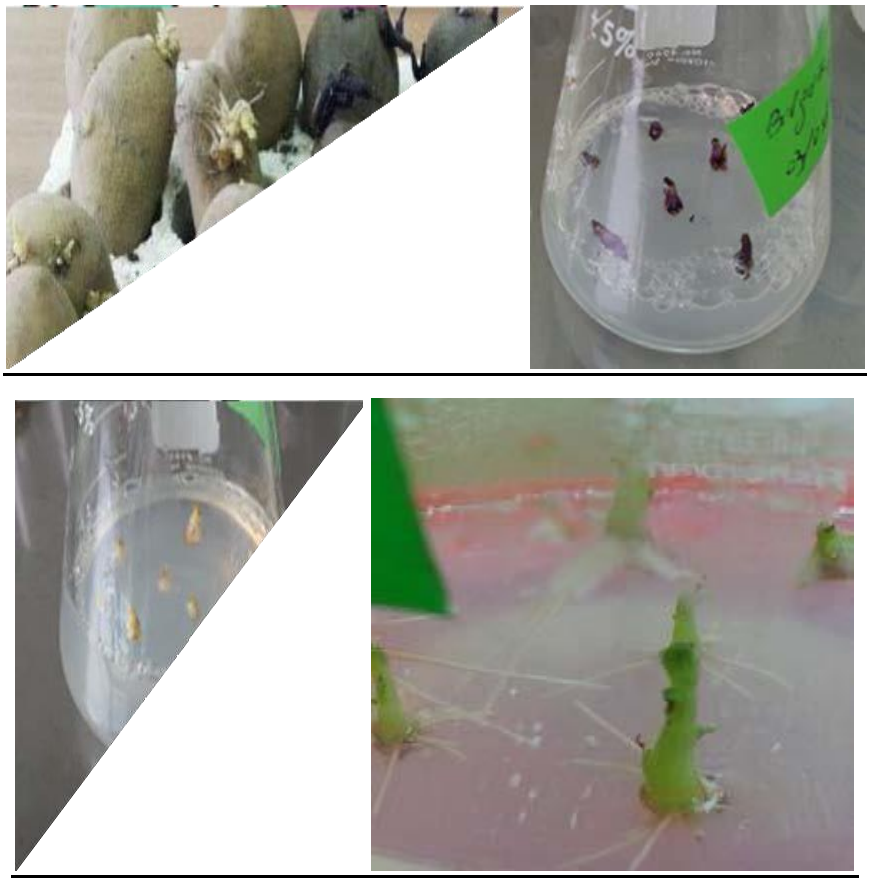


Figure 2: **(1) Effect of GA_3 for rapid sprout formation; (2), (3) and (4) Explant proliferation in MS medium**



Figure 3: **Initial stage of large-scale propagation of a virus-free cultivar in the greenhouse. Cuttings from these mother plants are used to produce the first crop of tubers in an isolated field**

REFERENCES

[1] S.A. Hossain et al., "Virus Free Potato Tuber Seed Production Through Meristem Culture in Tropical Asia," *Asian Journal of Plant Sciences*, vol. 2, no. 8, pp. 616-622, 2003.

[2] M. G. CHEWACHONG et al., "Determination of Virus-free Potato Planting Materials by Positive Selection and Screening of Tubers from Seed Stores in the Western Highlands of Cameroon," *African Crop Science Conference Proceedings*, vol. volume 8, pp. 809-815, 2007.

[3] M.F. Clark and A.N. Adams, "Characteristics of the microplate method of enzyme-linked immunosorbent assay for the detection of plant viruses," *Journal of General Virology*, vol. 34, pp. 475-483, 1977.

[4] J.F. Shepard and L.E. Claflin, "Critical analysis of the principles of seed potato certification," *Annual Review Phytopathology*, vol. 13, pp. 271-298, 1975.

[5] G.Leobenstein et al., "Virus and virus-like diseases of potatoes and production of seed potatoes ," *Kluwer Academic Publishers*, pp. 271-283, 2001.

[6] G. Haliloglu and H. Boston, "Nucleotide Sequence Analysis for assessment of Variability of Potato Leafroll Virus and Phylogenetic Comparisons," *Journal of Biological Sciences*, vol. 2, no. 9, pp. 582-586, 2002.

[7] A. Chandelier et al., "RT-PCR ELISA Tests on Pooled Sample Units for the Detection of Virus Y in Potato Tubes ," *Journal of Virological*

Methods, vol. 91, pp. 99-108, 2001.

[8] S.E. Coleman and D. Donelly W.K. Coleman, "Potato Microtuber Production and Performance:a review," *Am. J. of Potato Research*, vol. 80, pp. 103-115, 2003.

[9] R.S. Modawi and M.M. K.G. Abd Elaleem, "Effect of Cultivar and Growth Regulator on in vitro Micropropagation of Potato (Solanum tuberosum L).," *American-Eurasian Journal of Sustainable Agriculture*, vol. 3, no. 3, pp. 487-492, 2009.

[10] R. Anjum et al, "Field evaluation and enzyme-linked immunosorbent assay detection of potato leaf roll virus, potato virus X and potato virus Y in potato germplasm.," *Journal of Agricultural Science*, vol. 9, no. 7, p. 229, 2017.

[11] R. Gracia and F. Lozoya-Saldana J. Abello, "Electrotherapy and shoot tip culture eliminate potato virus X in plants," *Americal Journal of Potato Research* , vol. 73, no. 4, pp. 149-154, 1996.

[12] C. Igiraneza and L. Dusengemungu H. Gong, "Major In Vitro Techniques for Potato Virus Elimination and Post Eradication Detection Methods. A Review," *American Journal of Potato Research*, vol. 96, pp. 379-389, March 2019.

[13] D. Xhulaj and B. Gixhari, "IN VITRO MICROPROPAGATION OF POTATO (Solanum tuberosum L). CULTIVARS," *Agriculture & Forestry*, vol. 64, no. 4, pp. 105-112, 2018.

CHROMATOGRAPHIC TECHNIQUES USED FOR ARGINASE PURIFICATION

Training report (2020) in the fulfilment of

BACHELORS OF TECHNOLOGY IN BIOTECHNOLOGY

BY

YASHKIRTI GARG (171827)

UNDER THE SUPERVISION OF

DR. SAURABH BANSAL





DEPARTMENT OF BOTECHNOLOGY AND BIOINFORMATICS

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TABLE OF CONTENT

SERIAL NO.	TITLE	PAGE NO.
1.	Acknowledgement	3.
2.	Enzyme	4.
3.	Characteristics of organisms producing arginase	6.
4.	Culture conditions	7.
5.	Methods of purification ➢ Gel filtration ➢ Ion exchange ➢ Affinity	8.
6.	Enzyme activity assay	15.
7.	References	18.

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Thank you



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ENZYME ARGINASE

It is an enzyme that contains manganese. The reaction catalysed by arginase is **arginine + H_2O → ornithine + urea.** In the urea cycle, arginase catalyses the fifth and the last step aiding to the disposal of the harmul ammonia from the mammalian body. [1]

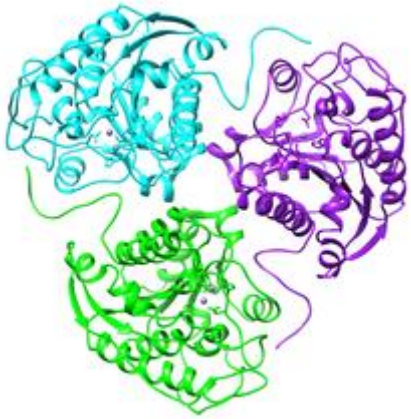


FIGURE1: RIBBON DIAGRAM OF HUMAN ARGINASE1 TRIMER. PDB ENTRY 2pha [2]

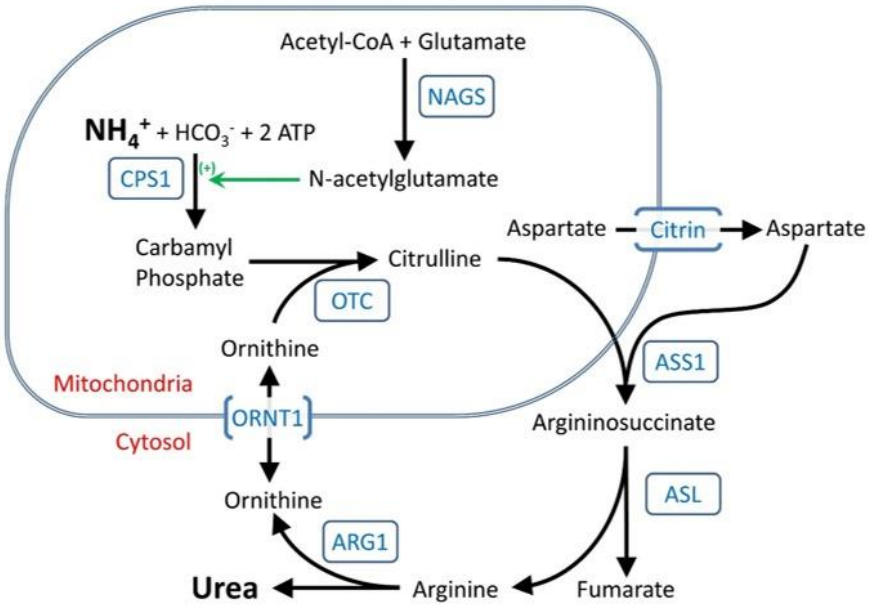


FIGURE2: THE UREA CYCLE [2]

ABBREVIATIONS IN FIGURE 2.

Carbamoylphosphate synthetase I (CPS1)

Ornithine transcarbamylase (OTC)

Argininosuccinic acid synthetase (ASS1)

Argininosuccinic acid lyase (ASL)

Arginase (ARG1)

N-acetyl glutamate synthetase (NAGS)

Ornithine translocase (ORNT1)

Two isoenzymes of arginase exist: [1,2]

Arginase I (ARG1): Present in the cytoplasm of hepatocytes

Arginase II (ARG2): Present in the mitochondria of several tissues of kidney, prostate, macrophages, lactating memory glands, and brain.

Sources of arginase: Arginase is found in bacteria *(Helicobacter pylori, Bacillus anthracis, Bacillus subtilis, Staphylococcus aurens),* yeast, plants, invertibrates and vertebrates. It is said that it first appeared in bacteria. The tranfer of arginase to eukaryotes have been said to occour through mitochondria. In invertebrates, plants, bacteria and yeast, one form of arginase is localised. Whereas in vertebrates and other animal, the second isoform is present.

Enhanced activity of arginase:

- Will result in decrease of L-arginine levels in the body.
- Impair T cell mediated immune function.
- Allow tumor development and growth.
- Cardiovascular and nervous sytem dysfunction.

Deficiency of arginase: Referred to as arginenimia or hyperarginemia. It is a hereditary disorder and is autosomal recessive.

- Causes the accumulation of ammonia in the blood.
- Increases the toxicity of the blood.
- Can causes nervous system disorders, intellectual disability, seizures.

CHARACTERISTICS OF ORGANISMS PRODUCING ARGINASE

Characteristics	*Bacillus subtilis*	*Saccharomyces cerevisiae*
Cell type	Prokaryote	Single celled eukaryote
Gram staining	Positive	-
Cell wall	Peptidoglycan(murein), techoic acid, lipotechoic acid, proteins	Polysaccharides (beta glucan and mannon sugar polymers), chitin, mannoproteins
Cell membrane	Phospholipids and proteins	Phospholipids and proteins
Respiration	Obligate aerobe, facultative anaerobe	Aerobic and anaerobic
Shape	Rod shaped	Elliptical and ovoid
Morphology	4-10 micrometer long, 0.25-1micrometer in diameter, heavily flagellated, forms endospore.	4-10 micrometer in diameter.
Source of extraction	Upper layer of soil, gastrointestinal tract of humans and ruminants.	In fruits, insects, in humans, soil, grains, plants, and tree barks.
Pathogenic	NO	NO
Also known as	Hay bacillus, grass bacillus	Baker's yeast

THE CULTURE CONDITIONS OF ORGANISMS PRODUCING ARGINASE

[3,4]

Culture conditions	*Bacillus subtilis*
Medium composition	Bouillon agar slants. 1% peptone 0.5%yeast extract 0.3% NaCl 0.1% l arginin HCl 0.02% $MnSO_4$(pH=7)
temperature	30 Celsius
pH	7.0
Time	13 hours
Volume of medium	15Lt
Vessel/flask type	30Lt jar fermenter
Aeration	1Lt air/1 Lt medium/min
Agitation	350 rpm
Harvest	150gm wet cells from 15Lt of culture broth

Culture conditions	*Saccharomyces cerevisiae*	
Media composition ***(initially, cells transfered from difco-bacto agar slant to stalk medium)***	**Liquid stalk medium**	
	Basic culture medium Citrate buffer Vitamins Mineral salts 0.02M L- arginine	
	1st culture	**Subculture**
Temperature	30C	30C
pH		4.5
Time	24 hours	4 hours
Volume medium	A small loop of cells in 500ml od stalk medium	5-10 ml culture in 200ml medium
Vessel/ flask type	1Lt buchner flask	500 ml buchner flask
Aeration	Vigorous	Vigorous

METHODS OF PURIFICATION OF ARGINASE

GEL FILTRATION CHROMATOGRAPHY: [5, 6]

Principle and working: Gel filtration is a technique in which separation of components is based on the difference in molecular weight or size. It is also known as molecular sieve chromatography. It is often used in the purification of proteins, polysaccharides and nucleic acids.

The basic components of the gel filtration experiment are the matrix, chromatography column and the elution buffer. The matrix is the separation medium which acts as the stationary phase of the chromatography whereas the elution buffer is the mobile phase of the chromatography and flows through the matrix and out of the column. The chromatography column is a tube with the frit and the elution buffer. The packed matrix is called bed and the volume it contains is known as the bed volume.

The gel filtration matrix contains microscopic beads that had pores and internal channels. The larger the molecule, the more difficult it is for the molecule to pass through pores and penetrate through the beads. Therefore larger molecule tends to flow around and in between the beads. This is called the void volume. Smaller molecules are to say stuck moving through the channels and pores inside the beads. Therefore they take more time. As a result the larger molecules having larger molecular weight flow through the column as a faster speed and the smaller molecules with less molecular weight are eluted later. Similarly as for the shape, the molecules with more compact shape as a spherical will penetrate the beads more readily than those having elongated shape. Therefore the elongated molecules will pass the beads more easily and fast and will be eluted first.

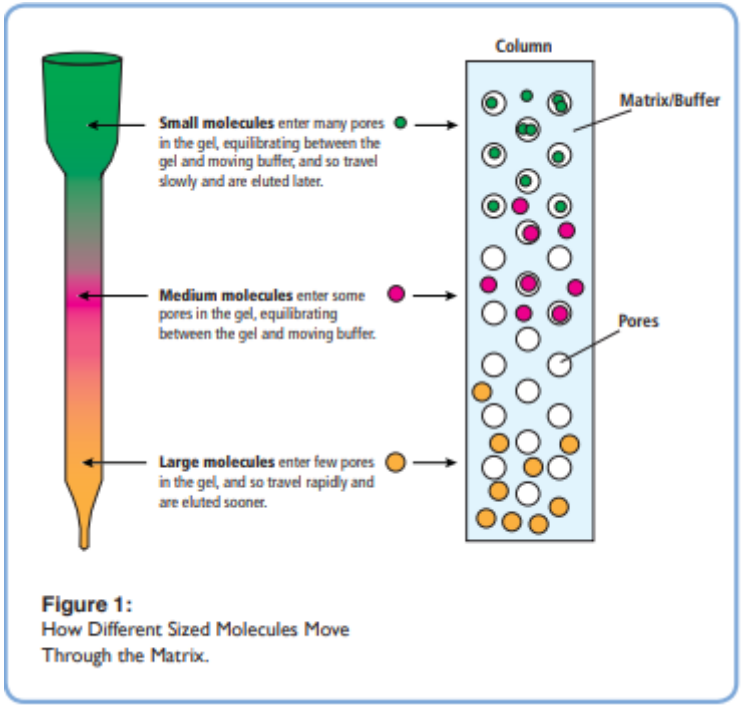
PROCEDURE:

1. Initially, a column of gel beads is set up for the gel filtration chromatography
2. The packed bed is equilibrated with a buffer.
3. At this point, a test solution is eluted through the column.
4. The particle in the test will go into or diffuse out of the porous gel network.
5. The particles that have less molecular weight will stay longer inside the column and the molecules with larger molecular weight will be passed out easily through the column.
6. In this way, the elution of molecules of different size and shape happens at various stretches. The components eluted can be identified.

APPLICATIONS:

1. It is a widely used and easily accessible method for the purification of enzymes, polysaccharides, nucleic acids, proteins etc.
2. Can enable the renaturation of denatured protein.

3. The molecular weight of the separated particle can be determined.
4. Can be used to examine the quaternary structure of purified proteins.



MOVEMENT OF DIFFERENT SIZED MOLECULE IN THE MATRIX [7]

RESINS USED IN GEL FILTRATION CHROMATOGRAPHY.

1. **Sephadex:** Sephadex is a cross linked dextran gel used for gel filtration. It is a gel being manufactured in microscopic beads form and if most commonly used in the gel filtration columns. The organic chains are cross linked to give a 3D network that gets functional group attached by ether linkages to the units of the polysaccharide chain. The fractionation properties can be altered by changing the degree of cross linking of the gel. with varying degrees of porosity; bead sizes fall in discrete ranges between 20 and 300 µm. For the purification of protein arginase by gel filtration method, sephadex-G150 was used with particle size 40-120 µm and pore size 1-**150** kDa . Certain properties are mentioned below along with some other resins.

GEL TYPE	FRACTIONATION RANGE (GLOBULAR PROTEINS)
G-10	≤700
G-75	3000-80,000
G-150	5000-300,000
G-200	5000-600,000

2. **Sephacryle:** Cross-linked co-polymer of allyl dextran and N,N'-methylenebisacrylamide. These are smaller particle sizes with narrower size distributions optimized for more efficient separations with faster flow. Gives fast and easy high-resolution results in both lab and industrial scales.

GEL TYPE	FRACTIONATION RANGE (GLOBULR PROTEINS)
S-100	~ 1×10^3 ~ 1×10^5
S-200	~ 5×10^3 ~ 2.5×10^5
S-300	~ 1×10^4 ~ 1.5×10^6
S-400	~ 2×10^4 ~ 8×10^6

TROUBLESHOOTING OF GEL FILTRATION CHROMATOGRAPHY:

SITUATION	CAUSE	REMEDY
Molecular weight or shape is not as expected	Protein has changed during storage Ionic interaction between protein and matrix	Prepare fresh samples Maintain ionic strength of buffer above 0.05M
Low recovery of activity, but normal recovery of protein	Protein may be unstable or inactive in the buffer Enzyme separated from co-factor or similar	Determine the pH and salt stability of the protein Test by pooling alliquotes from the fractions and repeating the assay
Lower yield than expected	Protein may have been degraded by proteases Non specific adsorption	Add protease inhibitors and buffers Reduce salt concentration to minimize interaction, increase pH.
Air bubbles in bed	Column packed or stored a cool temperature and then warmed up or buffer not properly degassed	Remove bubbles by passing degassed buffer through the column.
Cracks in bed	Large air leak in column	Check all connection for leaks. Repack the column if possible.

ION EXCHANGE CHROMATOGRAPHY: [8, 9, 10]

Principle and working: Ion chromatography is a process that allows the separation of ions and polar molecules based on their affinity to ion exchangers. The principle of separation is thus by reversible exchange of ions between the target ions present in the sample solution to the ions present on the ion exchangers.

Two types of ion exchange chromatography are present:

- **Anion exchange chromatography:** It is used for the separation of substances based on their charges using a positively charged group. The solution gets coated with positively charged counter ions. The anion exchange resin will bind to the negatively charged molecule and displaces the counter ion. The strength of binding between the substance and the resin is based on the strength of the negative charged substance. DEAE cellulose is an anion exchanger resin.
- **Cation exchange chromatography:** It is used when the molecule of interest is positively charged. The resins get coated with the negative charge and the positively charged molecules bind to it. SP sepharose is an example of the cation exchanger resin.

PROCEDURE:

1. The chromatography column is clamped on the stand in an upright position.
2. The buffer is drained into the column and let it to drain out completely. The column resin was left to settle down
3. 1 ml. Equilibration buffer is added to the column and is allowed to drain. This step is repeated again.
4. The protein extract was loaded into the column. (arginase)
5. The column was washed with equilibration buffer around four times to remove any unbound protein. 2ml of was fraction was collected as the buffer drains
6. The sample was eluted with a salt gradient: equilibration buffer, elution buffer, and a high salt buffer.
7. 1ml of gradient elution buffer was added to the column
8. 1ml of fraction was collected into the tube that drained out.
9. Protein concentration was determined by spectrophotometer.

APPLICATIONS:

1. IEC can be used for the separation and purification and analysis of charged molecules, such as proteins, enzymes, nucleotides, antibiotics and vitamins etc.
2. To determine the base composition of nucleic acids.
3. Most effective method for purification of water. Water is usually softened for drinking purposes.

RESINS USED IN ION EXCHNAGE CHROMATOGRAPHY

Sepharose: It is a crosslinked, beaded form of Agarose (a polysaccharide extracted from seaweed). It is used in the chromatographic separation of biomolecules. The gel structure of sepharose is stabilized by hydrogen bonding and not by cross linking. This makes it not ideal for usage with dissociating media like urea.

GEL TYPE	MOLECULR WEIGHT
DEAE sepharose (anion exchanger)	$4 \acute{} 10^6$
Q sepharose (anion exchanger)	$4 \acute{} 10^6$
CM sepharose (cation exchanger)	$4 \acute{} 10^6$
SP sepharose	$4 \acute{} 10^6$

TROUBLESHOOT FOR ION EXCHANGE CHROMATOGRAPHY.

SITUATION	CAUSE	REMEDY
Reduced or no flow through the column	Outlet closed of pump not working	Open outlet, check pump for signs of leak
	Microbial growth in the column	Store in the presence of 20% alcohol to prevent growth. Always filter buffer
Peak of interest is poorly resolved	Sample applied incorrectly	Check bed surface and top filter for possible contamination.
	Incorrect pH buffer/ ionic strength.	Check pH and ionic strength to ensure that column was re-equilibrated after previous run.
	Column overload	Decrease sample load.
More samples are recovered than expected	Protein co-eluting with other substances	Optimize conditions to improve resolution. Check buffer conditions.
Spikes appear in chromatogram	Air bubble trapped in UV monitor flow cell	Always use degassed buffers
Peaks are small	Sample absorbs poorly at chosen wavelength	If appropriate, check absorbance range on monitor. Use a different wavelength.

AFFINITY CHROMATOGRAPHY: [12, 13]

Principle and working: It is a method of separating biochemical mixture based on a highly specific interaction between antigen and antibody, enzyme and substrate, receptor and ligand, or protein and nucleic acid.

The biological molecules present in a mixture are purified by exploiting their molecular properties i.e. the differences in the strength of interaction within the mobile phase and the stationary phase. The stationary phase in affinity chromatography consists of a support medium on to which a ligand is covalently bound. As the unrefined mixture of substance is left to pass through the chromatography column, particles that have a binding sir for the immobilized substrate bind to the stationary phase whereas all the other substances are eluted out of the column. When different non required substances are eluted, the bound target molecule is eluted by various methods as by changing the pH, ionic strength and polarity conditions.

PROCEDURE:

1. Active fractions of the protein were pooled and applied on a hydroxyapatite column having the measurements as 1.2x10cm
2. The column was earlier equilibrated with Tris-HCl buffer having pH7.5 and 10mM also containing 0.6mM Mncl2 and 10% glycerol followed by 15mL of 0.5M KCl prepared in column equilibrating buffer.
3. The flow rate of the column was adjusted to 12 ml per hour and each 1 ml fractions were collected and its proteins content and arginase activity were assayed.

APPLICATION:

1. Affinity chromatography is used to purify and concentrate a substance from a mixture into a buffering solution.
2. Reduces the amount of unwanted substances in a mixture.
3. A sensitive method for purification.

RESINS USED IN AFFINITY CHROMATOGRAPHY:

It is the most widely used resin in the column for affinity chromatography is a crosslinked (CL) beaded Agarose, which is available in 4% and 6% densities. An additional cross linking of the beaded Agarose resin can increase its ability to withstand high pressure but it will also lower its binding capacity.

Gel type	Exculsion limit
CL 4% agarose	20,000 kDa
CL 6% agarose	4000kDa
Superflow agarose	6000 kDa
Acrylamide-azlectone polymer	2000kDa

TROUBLE SHOOTING AFFINITY CHROMATOGRAPHY:

SITUATION	CAUSE	REMEDY
More activity is recovered than was applied to the column	Different assay conditions have been used before and after the chromatographic step Removal of inhibitors during separation	Use the same assay conditions for all the assays in the purification scheme.
Reduced or poor flow through the column	Clogged column filter Precipitated protein	Remove and clean or use a new column Repack the column
Back pressure increases during a run or during successive runs	Turbid samples. Precipitation of protein in the column filter or at the top of the bed	Improve sample preparation. Improve sample solubility by the addition of ethylene glycol, detergents or organic solvents. clean the filter or use the new column
Distorted bands as sample runs into the bed	Air bubble at the top of the column or in the inlet adopter Clogged or damaged net in upper adaptor	Re-install adapter taking care to avoid air bubbles. Keep particles out of samples and eluents.
Protein does not bind or elutes as expected.	Sample has not been filtered properly. Column is overloaded with sample.	Clean the column, filter the sample and repeat. Store in 20% ethanol to avoid microbial growth of any type.

ARGINASE ENZYME ACTIVITY ASSAY [14]

1. **The arginase enzyme activity from bacillus subtilis was determined by measuring the extent of arginase activity in conversion of Arginine into Ornithine.**

100uL of arginine substrate buffer
(20mM Tris-HCl, 1 mM MnCl2, 40mM arginine, pH8.4)

+

7.50-7.58 ug protein of the sample incubated for 50min at 45deg C

Qualitative method

TLC

Conducted by utilising silica gel

Standard ornithin,

Mobile phase (butanol:acetic acid:

Dichloromethanol: water in

5:3:3:3)

Quantitative method

HPLC

Samples passed through 0.45um

PVDF filter

Derivatazing with 6-

aminoquioly-N-hydroxysuccinimidyl carbonate

Separated the derivative with AccQ column

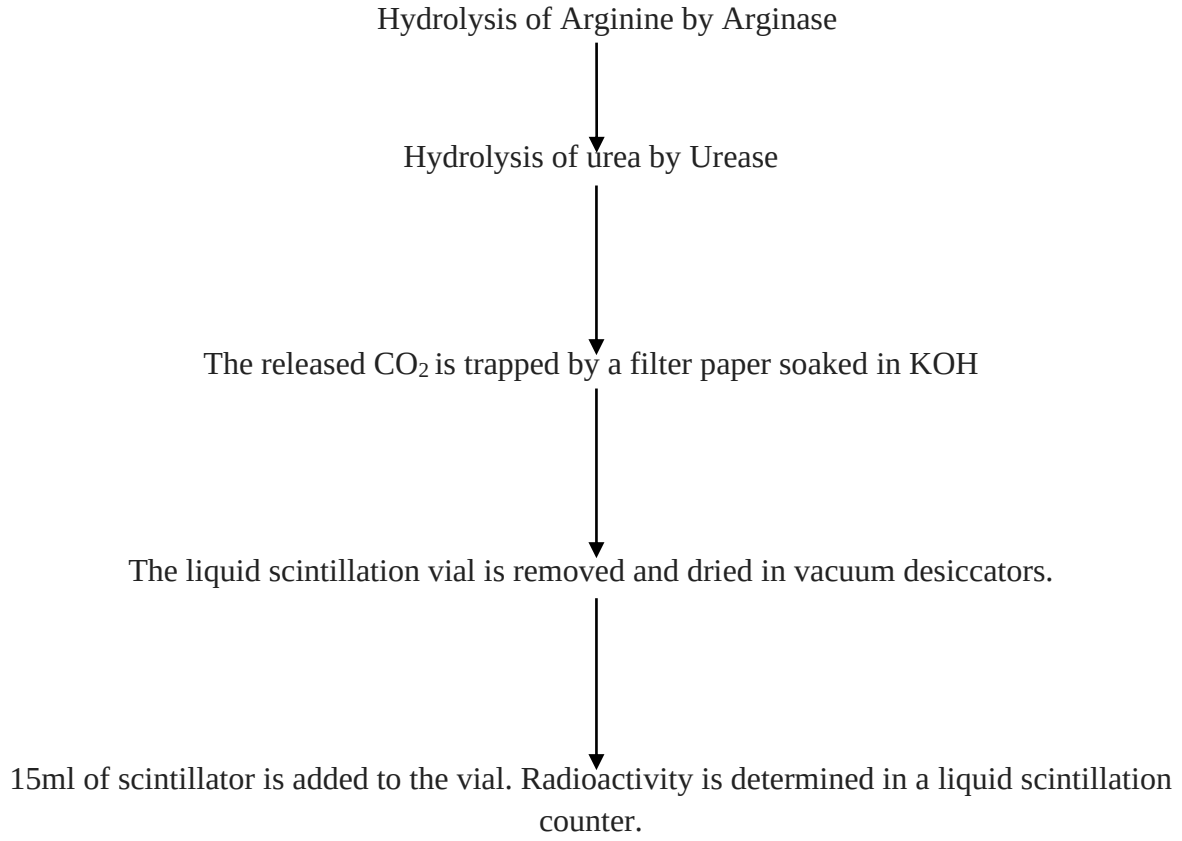
Ornithine content was calculated by referring to the standard curve.

2. Radioisotopic assay of arginase activity: [15]

This is a sensitive method used for the estimation of arginase activity, using arginine-guanido-^{14}C. The reaction is as follows



This is measured with a liquid scintillation counter. Following steps are carried out:



3. Determination of arginase activity by Ornithine-Ninhydrine reaction [16]

Erythrocytes Arginase hemolysate was prepared and the total protein was measured by the Bradford assay.

(0.25ml enzyme hemolysate + 0.5ml 100uM Arginine)



2ml of 6% Ninhydrin was added to 1 ml of filtered sample



The sample after further processing was read using a spectrophotometer at an absorbance of 505nm.

REFERENCES

1. https://en.wikipedia.org/wiki/Arginase

2. Di Costanzo L, Pique ME, Christianson DW (May 2007). "Crystal structure of human arginase I complexed with thiosemicarbazide reveals an unusual thiocarbonyl mu-sulfide ligand in the binuclear manganese cluster". *J. Am. Chem. Soc*. **129** (20): 6388–9. doi:10.1021/ja071567j.

3. Caldwell RB, Toque HA, Narayanan SP, Caldwell RW. Arginase: an old enzyme with new tricks. *Trends Pharmacol Sci*. 2015;36(6):395-404

4. Jin-Ju Yu1 , Ki-Bum Park, Su-Gon Kim1 , Suk-Heung. Expression, purification, and biochemical properties of arginase from bacillus subtilis 16. *Journal of microbiiolog.*2013; 51(2):222-228. DOI 10.1007/s12275-013-2669-9

5. P.Y. chan and E.A cossins. Arginine metabolism in saccharomyces cerevisiae. Some general properties of yeast arginase. *Plant and cell physiol.* 1973; 14:1973

6. www.chromatography.amershambiosciences.com

7. Lars Hagel. Gel filtration chromatography.*current protocols in molecular biology.*(2001); 44(1) https://doi.org/10.1002/0471142727.mb1009s44

8. http://kirschner.med.harvard.edu/

9. https://conductscience.com/ion-exchange-chromatography-protocol/

10. https://www.biochemden.com/ion-exchange-chromatography/

11. Özlem Bahadir Acikara (April 10th 2013). Ion-Exchange Chromatography and Its Applications, Column Chromatography, Dean F. Martin and Barbara B. Martin, IntechOpen, DOI: 10.5772/55744.

12. .www.microbesnotes.com

13. https://en.wikipedia.org/wiki/Affinity_chromatography

14. David S Hage, Affinity Chromatography: A Review of Clinical Applications, *Clinical Chemistry*, Volume 45, Issue 5, 1 May 1999, Pages 593-615, https://doi.org/10.1093/clinchem/45.5.593

15. Rüegg UT, Russell AS. A rapid and sensitive assay for arginase. *Anal Biochem*. 1980;102(1):206-212. doi:10.1016/0003-2697(80)90340-1

16. Nicola Carulli, Shigekoto Kaihara, Henry N.Wanger. radioisotopic assay of arginase activity. Analytial Biochemistry (1968);24; 515-522

17. Iyamu EW, Asakura T, Woods GM. A colorimetric microplate assay method for high-throughput analysis of arginase activity in vitro. *Anal Biochem*. 2008;383(2):332-334. doi:10.1016/j.ab.2008.08.016

18. https://en.wikipedia.org/wiki/Sephadex

19. https://en.wikipedia.org/wiki/Sepharose

20. http://wolfson.huji.ac.il/purification/PDF/Columns/GE_ProteinPurificTroubleshGuide.PF

21. https://www.sigmaaldrich.com/technicaldocuments/protocols/biology/ion-exchange-chromatography/troubleshooting.html

Summer Training Report

Submitted In Partial Fulfilment Of The Requirement For The

Degree of Bachelor of Technology

In

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

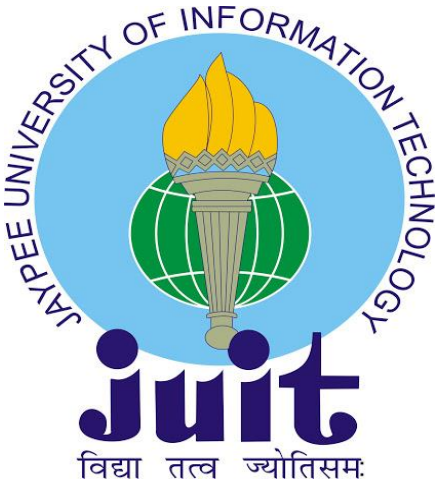
BY

Ishita Samrat (171828)

Under the supervision of

Dr. Rahul Shrivastava

to



JAYPEE UNIVERSITY OF INFORMATIONAND TECHNOLOGY, WAKNAGHAT, SOLAN – 173234,

HIMACHAL PRADESH

CANDIDATES DECLARATION

I hereby declare that the work presented in this report entitled **"ANTIBODY ENGINEERING"** in the partial fulfilment of the requirement for the degree of Bachelor of technology in biotechnology department is an original record carried over a period from 15th May to 30th June 2020 under the guidance of **Dr. Rahul Shrivastava**

Ishita Samrat (171828)



This is to certify that the above statement made by the candidate is true to the best of my knowledge.

NAME OF THE SUPERVISOR:



Dr. Rahul Shrivastava
Associate professor
Department of Biotechnology and Bioinformatics

ANTIBODY ENGINEERING

Introduction

Antibodies are Proteins that recognize and bind to a particular antigen with very high specificity. They are naturally occurring proteins associated with the immune system with a primary work to identify and neutralize infection, such as bacteria and viruses. They are capable of recognizing specific protein patterns, which makes them helpful in clinical diagnostic and therapeutic domains. Antibodies are proteins produced by the immune system to fight with pathogens and have long been appreciated for their exquisite specificity. Antibodies recognize and epitope onto antigens in order to remove them from the body. A wide range of substances are recognizes by the body as antigens, including disease-causing organisms and toxic substances

For example, insect venom. Antibodies are produced by specific white blood cells called B lymphocytes (or B cells). When an antigen binds to the B-cell surface, B cells stimulated the by antigen to divide and mature into a group of identical cells called a clone. The develop B cells, called plasma cells, discharge a large number of antibodies into the bloodstream and lymphatic system

Antibody engineering can refers to the process of using in vitro or in vivo techniques to produce human antibodies for research or clinical use. Ever since it is found, antibody engineering has grown to surround a range of production technologies and techniques. The idea to use antibodies as magic bullets to target toxins or radioisotopes to defined cell types is now obsolete. Kohler and Milstein took a major step towards this goal 25 years ago and developed hybridoma technology, thereby providing a reliable source of monoclonal antibodies (mAbs) of known specificity. However, in the recent times, there have been few antibody-based products suitable for therapy available. This delay can be chiefly explained by the fact that mouse antibodies trigger a human anti-mouse antibody response.

Active production of human antibodies began after the realization that transgenic mice could be created and utilized, which are experimental animals that contain some

human genes in their genome. More specifically, in the case of antibody engineering, they contain human antibody gene sequences.

In vitro generation followed this, antibody engineering techniques that is phage display, development of counter acting agent pieces(construction of antibody fragments), immunomodulatory antibodies, and cell free system. This allowed true engineering endeavors to carefully select genetically engineered recombinant libraries using phage display technology

By the evolution of the hybridoma technology, it became feasible to immortalize single B cells, which results in the production of infinite quantities of antibodies of a single, well-defined antigen-binding specificity, called as monoclonal antibodies. Though, the initial hybridoma-derived monoclonal antibodies were highly immunogenic in humans and murine. In order to overcome problems of the immunogenicity of rodent-produced antibodies, progresses in genetic engineering and expression systems have been used and thus it improved the ability of the antibodies to trigger human immune effector activity. The potential use of monoclonal antibodies as targeted therapeutics has been further expanded by the development of chimeric, humanized, and totally human antibodies, as well as antibodies with novel structures and functional properties. Recombinant antibody-based therapies are now used to treat a variety of diverse conditions that include infectious diseases, inflammatory disorders, and cancer. These therapies are one of the fastest growing classes of biopharmaceutical therapeutics in today’s world.

Monoclonal antibodies (mAb or moAb) are antibodies made up of identical immune cells that are all clones of a unique parent cell. Monoclonal antibodies have monovalent affinity, in that they bind to the same epitope (the part of an antigen that is recognized by the antibody). one the other hand, polyclonal antibodies bind to

multiple epitopes and are usually made by several different plasma cell (antibody secreting immune cell) lineages. Bispecific monoclonal antibodies can also be engineered, by increasing the therapeutic targets of one single monoclonal antibody to two epitopes. it is possible to produce monoclonal antibodies that specifically bind to that substance; they can then serve to detect or purify that substance.

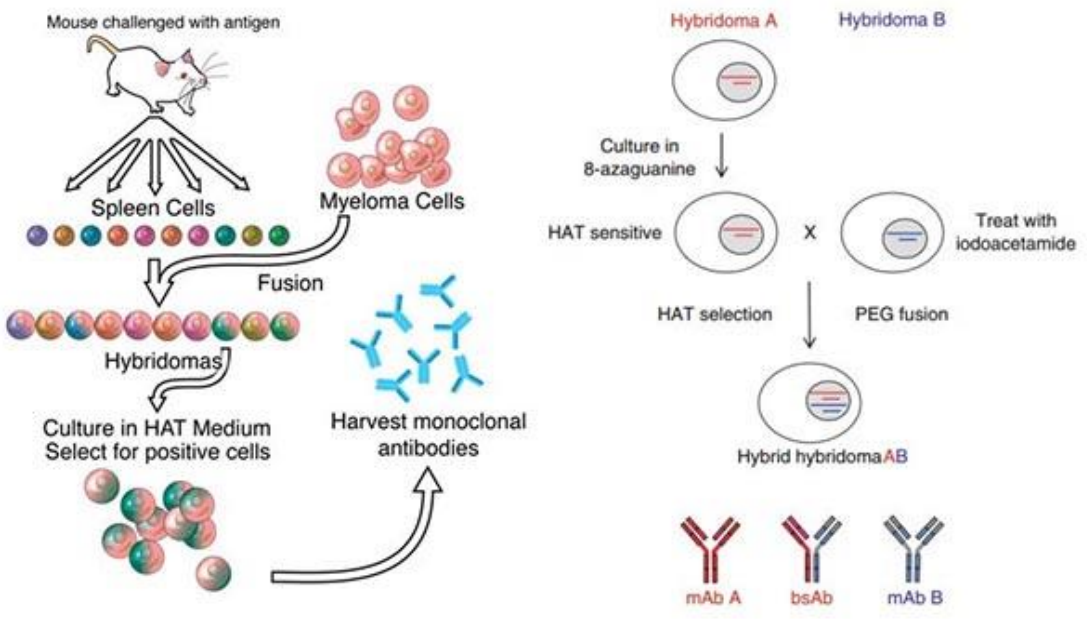


Fig: The left part of this figure shows the monoclonal antibody production by hybridoma technology. The right part of this figure shows the BsAbs production by hybrid-hybridoma technology. (Moldenhauer, G. 2011)

The first human monoclonal antibody was engineered using phage display and choosing antigen-specific binders from blood lymphocyte libraries. The transgenic animals used, mice and rabbits, were integrated with human immunoglobulin loci.

Other therapeutic solutions utilizing small molecules have sometimes not succeed where engineered antibodies have succeeded. Engineered monoclonal antibodies are capable of binding with high affinity and high specificity to molecular targets that are classically seen in diseased conditions, but this is absent in normal cells. Where the specific action is known, engineered antibodies work using several known activities.

- First, they can work by antagonistic action by hindering an interaction between a cell receptor and its ligand.
- Secondly, antibodies can obtain immune cells to the target tissue by their Fc domain, to initiate antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).
- Thirdly, they can induce apoptosis via receptors, and modulate the expression of cell-surface receptors.
- Lastly, conjugated antibodies (antibodies bound to a therapeutic drug) can aid the delivery of radioisotopes or chemotherapeutic drugs to the site of interest, minimizing side effects and maximizing efficacy.

Methods of antibody engineering:

1. Recombinant

The production of recombinant monoclonal antibodies involves repertoire cloning, CRISPR/Cas9, or phage display/yeast display technologies. Recombinant antibody engineering involves antibody production through viruses or yeast, rather than mice. These techniques depend on rapid cloning of immunoglobulin gene segments to create libraries of antibodies with slightly different amino acid sequences from which antibodies with desired specificities can be selected. The phage antibody libraries are a variant of phage antigen libraries. These techniques can be used to enhance the specificity with which antibodies recognize antigens, their stability in various environmental conditions, their therapeutic success and their detectability in diagnostic applications.Fermentation chambers have been used for large scale antibody production.

2. Chimeric antibodies/humanized antibodies

Chimeric antibodies are produced by replacing the constant regions of a mouse antibody with those of a human antibody, to such an extent antibody binds to an antigen like the original monoclonal antibody, and is recognized by the human immune system like a human protein

While mouse and human antibodies are structurally similar, the differences between them were sufficient to invoke an immune response when murine monoclonal antibodies were infused into humans, resulting in their rapid removal from the blood, as well as systemic inflammatory effects and the production of human anti-mouse antibodies (HAMA).

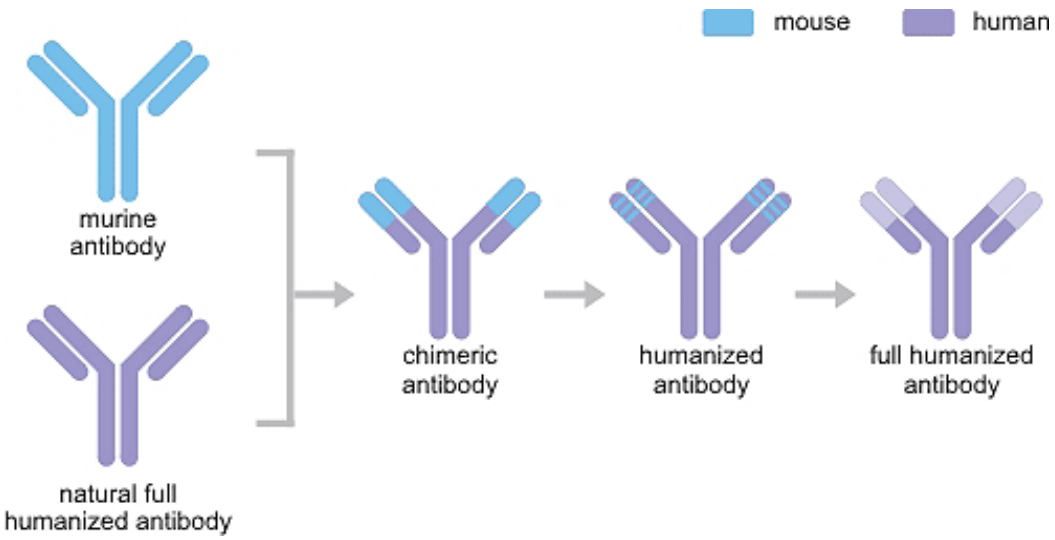


Fig: Generation of chimeric and humanized antibodies.

Recombinant DNA has been explored since the late 1980s to increase residence times. In one approach, mouse DNA encoding the binding portion of a monoclonal antibody was merged with human antibody-producing DNA in living cells. The expression of this "chimeric" or "humanised" DNA through cell culture yielded part-mouse, part-human antibodies. Production of chimeric mouse-human monoclonal antibodies.

 Chimeric mouse-human heavy- and light-chain expression vectors are produced.These vectors are transfected into Ab myeloma cells. Culture in ampicillin medium selects for transfected myeloma cells that secrete the chimeric antibody.While structurally similar, diffeences between mouse and human antibodies were sufficient to invoke an immune response when Murine monoclonal antibodies were injected into humans, resulting in their rapid removal from the blood, as well as systemic inflammatory effects and the production of Human Anti-Mouse Antibodies (HAMA). Recombinant DNA has been explored since the late 1980s to increase residence times. In one approach, mouse DNA encoding the binding portion of a monoclonal antibody was merged with human antibodyproducing DNA in living cells. The expression of this "chimeric" or "humanised" DNA through cell culture yielded part-mouse, part-human antibodies.

Applications of Antibody Engineering

Antibody engineering is used in the treatment of several diseases and many diagnostic tests. Specific cells (Maynard) are targeted using antibody technology since each antibody binds very specifically to only one type of cell or molecule. This specific binding of antibodies and antigens is responsible for the success of applications of antibody engineering. The progress in the production methods of antibodies are making it possible to generate antibodies specific to almost any antigen. Emerging applications of antibody engineering include cancer therapy and radioimmuno detection of tumors. Antibodies present many exciting possibilities to the future of medicine.

1.Diagnostic tests:

Once monoclonal antibodies for a given substance have been produced, they can be used to detect the presence of this substance. Proteins can be detected using the Western blot and immuno dot blot tests. In immunohistochemistry, monoclonal antibodies are used to detect antigens in fixed tissue sections, and in the same manner, immunofluorescence are used to detect a substance in either frozen tissue section or live cells.

2.Analytic and chemical uses:

Using the method of immunoprecipitation, antibodies can also be used to purify their target compounds from mixtures.

3.Therapeutic uses:

Monoclonal antibody therapy

Therapeutic monoclonal antibodies proceeds through multiple mechanisms, such as blocking of targeted molecule functions, inducing apoptosis in cells which express the target, or by modulating signalling pathways.

3. Cancer treatment:

Monoclonal antibodies opens up one possible treatment for cancer by binding only to cancer-cell-specific antigens and prompt an immune response against the target cancer cell. Such mAbs can be modified for delivery of a toxin, radioisotope, cytokine or other active conjugate or to design bispecific antibodies that can bind with their

Fab regions both to target antigen and to a conjugate or effector cell. Every intact antibody can bind to cell receptors or other proteins with its Fc region.

Monoclonal antibodies for cancer.

ADEPT:antibody directed enzyme prodrug therapy;

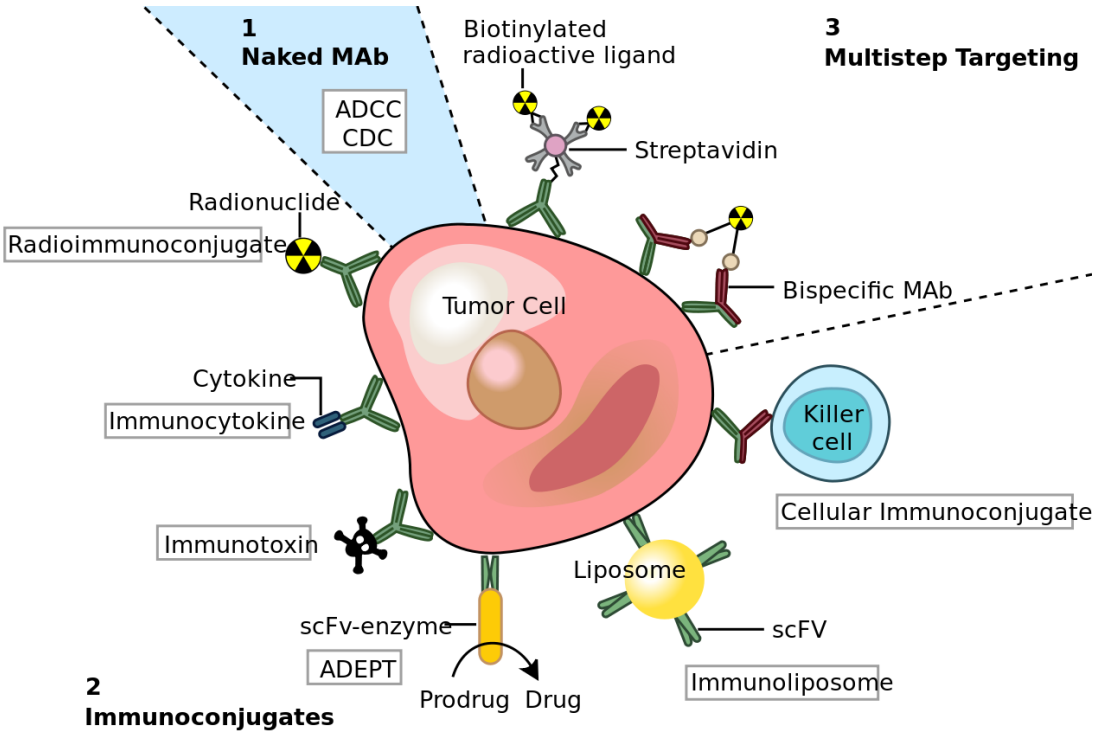
ADCC: antibody dependent cell-mediated cytotoxicity;

CDC: Complement-Dependent Cytotoxicity;

MAb: Monoclonal Antibody;

scFv: Single-Chain Fv Fragment.

MAbs approved by the FDA for cancer include:



Monoclonal antibodies for cancer. ADEPT: antibody directed enzyme prodrug therapy; ADCC: antibody-dependent cell-mediated cytotoxicity; CDC: complement-dependent cytotoxicity; MAb, monoclonal antibody; scFv, single-chain Fv fragment.

Monoclonal antibodies have come across recently to be useful for cancer therapy, with some treatments gaining FDA approval. It has been established that some antibodies bind specifically to tumor-associated antigens which are present in higher concentration on tumor cells than normal cells (Maynard). The antibodies then begin to accumulate in malignant tumor tissue which can then induct cytotoxic immune cells or can be combined with a drug delivery mechanism to deliver chemotherapy drugs. One monoclonal antibody, rituximab, is being used for the treatment of large cell lymphoma in conjunction with chemotherapy. Studies show that after one year of treatment, 69% of patients treated with rituximab in conjunction with chemotherapy were free of lymphoma in comparison with only 49% of patients treated solely with chemotherapy were free of lymphoma (Monoclonal Antibodies). The use of monoclonal antibodies for cancer treatment is very encouraging.

Cancer targeting monoclonal antibodies

One type of monoclonal antibody AVASTIN or Bevacizumab which is used to treat metastatic cancer, non-small cell lung cancer, and metastatic breast cancer Bevacizumab is a recombinant humanized monoclonal IgG1 antibody that binds to the vascular endothelial grown factor(VEGF) and inhibits its activity. This drug is able to target VEGF specifically because it contains human framework regions and complementarity determining regions of a murine antibody that specifically binds to vascular endothelial growth factor.

The bevacizumab antibodies prevents VEGF from interacting with its receptors on the surface of endothelial cells which causes the endothelial cells to proliferate and new blood vessels to form. In mice with xenotransplant models of colon cancer the drug reduced microvascular growth and slowed progression of the metastatic cancer. It has

been found that the treatment of cancer is best paired with AVASTIN and chemotherapy for best results. (AVASTIN(Bevacizumab) For Intravenous Use)

Although monoclonal antibodies have shown prominant results in the treatment of cancer, dangerous side effects can occur. In AVASTIN some dangerous side effects that have been seen are gastrointestinal perforation would healing complications, and hemorrhage. In clinical trials for AVASTIN all three dangerous side effects resulted in fatality (AVASTIN Bevacizumab:

Antibodies may be used as a more effective cancer treatment than chemotherapy in the future. Since monclonal antibodies have the ability to target cells directly that exhibit the designated antigen, this treatment may one day be used instead of chemotherapy which effects all cells in the body. Since there are still dangerous side effects of using monoclonal antibodies as treatment an antibody would have to be developed that didn't cause complications.

Autoimmune diseases:

Monoclonal antibodies used for autoimmune diseases include infliximab and adalimumab, which are effective in rheumatoid arthritis, Crohn's disease, ulcerative colitis and ankylosing spondylitis by their ability to bind to and inhibit TNF-α. Basiliximab and daclizumab inhibit IL-2 on activated T cells and thereby help prevent acute rejection of kidney transplants.

Future of Antibody Engineering:

Earlier we used to treat cancer using chemotherapy and nowadays, we use antibodies. The previously used technologies were imaging techniques such as MRI or CT Scan but in the recent times we use a new technique referred as Radioimmunodetection in

which antibodies are tagged with radioisotopes, whose presence in tissue can be detected with medical imaging scanners. Once the antibodies have been injected into the body, they target tumor cell surface marker antigens. The resulting image can detect cery small tumors and can tell more about the stage of the cancer. Using antibodies to detect the most common tumor cell surface marker, the carcinoembryonic antigen, has been shown to detect tumors as small as 0.5cm. The use of radioimmunodetection could result in earlier detection of small tumors in early treatable stages. Antibody technology is used to target a specific cell to which monoclonal antibody binds to specific cell or molecule. If this process becomes sustainable then the respective drugs are lined up into production.

The majority of engineered monoclonal antibodies currently at some stage of clinical trials are owned by small biotechnological companies. This may be expected to change with time, given the large revenues and approval ratings that by far exceed those of other small molecule drugs.

As of December 2019, 79 therapeutic monoclonal antibodies were approved by the FDA. Of those, 89% are related to oncological or immunological treatment. Following this trend, the majority of therapeutic monoclonal antibodies being considered for clinical use belong to three main areas of potential targeted treatment: oncological, immunological and anti-infective.

Current Status Of Engineered Antibodies

Current antibody drugs have progressively less adverse impacts because of their high specificity. Therefore, therapeutic antibodies have become the predominant class of new drugs developed in recent years. In the course of recent years, antibodies have become the top of the line drugs in the pharmaceutical market, and in 2018, eight of the best ten smash hit drugs overall were biologics. The worldwide therapeutic monoclonal counter acting agent showcase was esteemed at roughly US$115.2 billion out of 2018 and is relied upon to produce income of $150 billion before the finish of 2019 and $300 billion by 2025.Thus, the market for therapeutic antibody drugs has

experienced explosive growth as new drugs have been approved for treating various human diseases, including many cancers, autoimmune, metabolic and infectious diseases. As of December 2019, 79 therapeutic mAbs have been approved by the US FDA, but there is still significant growth potential. the most recent market patterns and layouts the preeminent antibody engineering technologies used in the development of therapeutic antibody drugs, such as humanization of monoclonal antibodies, phage display, the human antibody mouse, single B cell antibody technology, and affinity maturation. At long last, future applications and points of view are likewise examined.

REFERENCES:

i. https://doi.org/10.3389/fmicb.2017.00495

ii. https://www.news-medical.net/life-sciences/Antibody-Engineering-Challenges-and-Perspectives.aspx

iii. https://doi.org/10.1016/j.bioeng.2006.10.001

iv. https://www.sciencedirect.com/science/article/abs/pii/S1389034406001109

v. https://doi.org/10.1134/S0026893317060139

vi. https://link.springer.com/article/10.1007/BF02932912

vii. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5368232/

viii. https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0209509

ix. https://doi.org/10.4137%2FIJCM.S11968

Reference Manager: Reference Manager was the first commercial reference management software developed in 1982 by Ernest Beutler and his son Earl Beutler through their company Research Information Systems. It was mostly used by scholars and authors to record and utilize bibliographic citations (references). The people can share a central database of references and can have multiple users to add and edit records at the same time. There exists a feature in which one can specify for each user whether read-only or edit permissions to the database. The nearest competing package EndNote doesn't offer such functionality. Reference Manager also offers different citation templates for various reference types. Its Web Publisher allows the publication of reference databases to an intranet or internet site which makes it available for users to search and download references into their own bibliographic software.

The development of Reference Manager was abandoned in 2008 and it was taken off the shelves on 31st December,2015. Thomas Reuters (who later acquired Research Information Systems) wanted to focus exclusively on EndNote.

EndNote: EndNote is a commercial reference management software which is used to manage references, citations and bibliographies while writing articles. It keeps all the references and reference-related materials in a searchable personal library. One can also share their references with collaborators using EndNote Sync. The references can be used in word-processing documents to create formatted citations and bibliographies or independent reference lists. EndNote groups citations into "libraries" with the file extension *.enl and a corresponding *.data folder. The *.data folder contains various MySQL files with *.myi and *.myd extensions. EndNote can be installed and its features can be accessed in the Tools menu of Microsoft Word. The data is synchronized via the EndNote cloud service, with everybody having full write access to the library. EndNote also offers a web-based implementation called as EndNote Web which is integrated with the ISI Web of Knowledge.

Thomas Reuters sold EndNote to Clarivate Analytics in 2016. EndNote X7 was able to import Reference Manager databases and convert Word documents formatted with Reference Manager into EndNote formatting.

Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Training Report submitted in fulfillment of Industrial Training of

BACHELORS OF TECHNOLOGY

IN

BIOTECHNOLOGY

By

KHUSHI MAHESHWARI (171829)

UNDER GUIDANCE OF

Mr. Navdeep Soryan

Quality Assurance and Control Department at M/s Sanwaria Sweets Pvt. Ltd. (KANHA), Jaipur



JULY-2020

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY WAKNAGHAT,

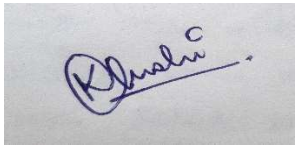
SOLAN

TABLE OF CONTENT

S.No.	TITLE	PAGE NO.
1.	DECLARATION	3
2.	SUPERVISOR'S CERTIFICATE	4
3.	CERTIFICATE	5
4.	ACKNOWLEDGEMENT	6
5.	INTRODUCTION ABOUT TRAINING ORGANIZATION	7
6.	ABOUT THE TRAINING	8
7.	WEEKLY PROGRESS REPORT 1	9
8.	WEEKLY PROGRESS REPORT 2	10
9.	WEEKLY PROGRESS REPORT 3	11-17
10.	WEEKLY PROGRESS REPPRT 4	18-25
11.	WEEKLY PROGRESS REPORT 5	26-28
12.	WEEKLY PROGRESS REPORT 6	29-34
13.	CONCLUSION	35

DECLARATION

I hereby declare that the Summer Training work entitled "Qualitative Analysis of Traditional Indian Sweets and Namkeen Products" has been solely submitted to the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology, Waknaghat have carried out under guidance of Mr. NAVDEEP SORYAN, Quality Assurance and control Department at M/s Sanwaria Sweets Pvt. Ltd. (KANHA), Jaipur.



Name: **Khushi Maheshwari (171829)**

Department of Biotechnology and Bioinformatics

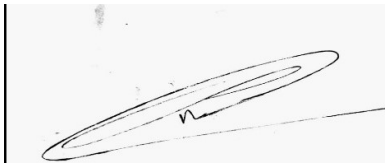
Jaypee University of Information Technology, Solan

Waknaghat.

Date: 20th July 2020

SUPERVISOR'S CERTIFICATE

This is to certify that the summer training work titled **"Qualitative Analysis of Traditional Indian Sweets and Namkeen Products"** by **Khushi Maheshwari** during 45 days in month of June and July 2020 in fulfillment for the Industrial Training has been carried out under my supervision. This work has not been submitted partially to any other University or Institute for the award of any degree or appreciation.



Signature of Supervisor

Name of Supervisor **- Mr. Navdeep Soryan**

Designation - **Quality Department (HEAD)**

F-837-838, RIICO Industrial Area, Phase-III, Sitapura,
Tonk Road, Jaipur, (Rajasthan), India-302023

Email: sanwariasweets@gmail.com

Date: 20th JULY,2020

CERTIFICATE

kanha
multi cuisine restaurant | sweets

Sanwaria Sweets Pvt. Ltd.

CIN U15433RJ2007PTC025493
Tel.: 0141-2700648, E-mail : officekanha@gmail.com

15.07.2020

TO WHOM SO EVER IT MAY CONCERN

This is to certify that Miss Khushi Maheshwari student of Jaypee University of Information Technology (JUIT), Solan, HP has successfully completed Training for 1 Month and 15 Days W.e.f. 01.06.2020 to 15.07.2020 with the Quality Assurance and Control Department at M/s Sanwaria Sweets Pvt. Ltd. (Kanha), Jaipur.

During her training she has undergone 1 project and has successfully submitted the respective report of that project. She has submitted project on:

1. **Qualitative Analysis of Traditional Indian Sweets and Namkeen Products**

The Project submitted by her was excellent and added value to the organization.

She has shown a great amount of reliability, sincerity and willingness to learn and is capable of working in a multi-sectoral team. We wish her success in all future endeavors.

For Sanwaria Sweets Pvt. Ltd.,

For SANWARIA SWEETS PVT. LTD.

Lokpal Singh
(Assistant General Manager-HR & Admin.)

A.G.M.(H.R.-ADMIN)

Regd. Office :

J-6, Himmat Nagar, Near Gopalpura Fly Over, Tonk Road, Jaipur-302018, Rajasthan

ACKNOWLEDGEMENT

I take this opportunity to express my first and foremost gratitude to Quality Assurance and control Department at M/s Sanwaria Sweets Pvt. Ltd. (KANHA), Jaipur, for the confidence bestowed upon me and entrusting the summer training titled **"Qualitative Analysis of Traditional Indian Sweets and Namkeen Products"**

At this juncture, with proud privilege and profound sense of gratitude, I feel honored in expressing our deepest appreciation to All the members Quality Department**,** for being a lot more than just a supervisor and going beyond the call of duty in our guidance, support, advice, and motivation throughout. They all been the source of inspiration of come what may; these issues cannot bring you down. Sincere thanks for the insightful advice, motivating suggestions, invaluable guidance, help and support in successful completion of this summer training and also constant encouragement and advice throughout my work.

Special thanks to our parents for their infinite patience and understanding and project partners for the constant support and most importantly God, who in his mysterious ways, always made things work out in the end.

In gratitude,

Khushi Maheshwari (171829)

INTRODUCTION ABOUT TRAINING ORGANIZATION

The Company was incorporated by the name of Sanwaria Sweets Private Ltd in 2008 within the pink city Jaipur with the motto of enriching the normal Indian culture of sweets, namkeens with a correct blend with modern technology. The Company was founded by its MD, Mr Natwar Lal Sharda. Being a commerce graduate contains a hold on facts and figures. His vision was to make a food arena where the entire family could have dined together and had all the eatables required in an Indian household. Right from the start the stress was on hygiene and quality with esteemed presentation of products so on provide customers with quality and taste of extremely high standard. Within a brief span we've grown as prominent brand catering to taste buds of many people. it's the love and trust of individuals which has allow us to grow many folds in mere short span of period.

"KANHA" – brand name of the company takes pride in amazing chain of multi cuisine, fine dining restaurants, sweet shops, bakery, hotel and banquets in the pink city.

The company is committed to provide value and satisfaction to the customers by manufacturing and supplying quality and safe products which meet their expectations in accordance with principles of HACCP and within the statutory and regulatory framework.

ABOUT THE TRAINING

It completely involves about the protocols followed and carried forward to check and keep the product safe for consumption. Variety of test are carried out to maintain the proper quality of food up to the standard mentioned in the report with the standard table upon which each and every product is checked starting from the raw material to the finished good.

Company's utmost aim is that all the sweets and namkeens are prepared in the unit with proper care and quality proven environment. They take every care to maintain hygiene and quality anytime and every time.

Company having its own lab for testing the raw materials and finished products . Its main emphasis is to produce high quality products.

Firstly , the quality process goes through the 3P cycle.

1. Purchase of raw material carefully supervised and handled.
2. Verification and analysis is conducted using various instruments and tests listed below.
3. Final stage is when the products is completely tested and regarded safe for consumption, packaging is done in hygienic condition with most modern automatic packaging technology and transported to various hubs to be sold out to the customers.

Company is goal oriented towards supplying clean, fresh and wholesome food products to suit all ages. Not only about the standard and standards but also to manufacture and market products at affordable cost to any or all and provide the food products to boost the standard of life for one and everyone.

Weekly progress report 1

Name – Khushi Maheshwari

Roll No.- 171829 (BT62)

Course- B.Tech in Biotechnology

Semester- 6

Batch- 2017-21

Date- 1st June 2020 to 7th June 2020

Topic- Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Objective of the week- Introduction about the training

Objective achieved- Quality analysis is done for both fresh and processed food products through standard protocol in the laboratory. The test provides critical and vital information about different characteristics of the food such as composition, taste, smell, ingredients etc. This information is necessary to determine the properties of the food along with the ability to produce economically ensuring the food is safe, nutritious and best to be consumed

Apart from analysis , Quality control plays an important role. It determined what standards should be maintain to ensure the quality of product according to the consumers demand and acceptance. Various physical and chemical, nutritional, microbiological parameters are used to maintain quality of product. The factors totally depend upon the flavor, aroma, texture, quantity, sugar content, fibers, peroxides, FFA etc.

This is not only the criteria but somehow it tells us about some factors regarding the quality of product (shelf life, packaging techniques, composition).

To keep ensure the quality , food laws are made related to GMP (good manufacturing practices), HACCP (hazard analysis and critical control point), factory inspections, import and export inspections, labeling, additives used in the product.

Week one was focused upon explaining the basic procedure and protocols used by the food industries to produce best quality products that completely withstand in the market with great demand and that are most importantly safe to be consumed.

Weekly progress report 2

Name – Khushi Maheshwari

Roll No.- 171829 (BT62)

Course- B.Tech in Biotechnology

Semester- 6

Batch- 2017-21

Date- 8th June 2020 to 14th June 2020

Topic- Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Objective Of the week- Enlisting of all the products manufactured in the company

Objective Achieved-

- Starting from enlisting the name of all the products and categorizing them in different heading.
- Studying about the basic ingredients used in the manufacturing.
- Processing of machines (how machines work to produce large amount of finished goods in a short duration of time)
- Packaging techniques involved (vacuum packing – to eliminate oxygen from the packet to ensure long term stability of the product after opening the packet)
- Dispatching to various branches in the town along with online and export deliveries.
- List of all the products that are manufactured in the company are mentioned below along with the tests performed.

Weekly progress report 3

Name – Khushi Maheshwari

Roll No.- 171829 (BT62)

Course- B.Tech in Biotechnology

Semester- 6

Batch- 2017-21

Date – 15th June 2020 to 21st June 2020

Topic- Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Objective of the week- Plant and lab Visit (to know about various sections of the complete plant including laboratory and day to day practices involved)

Objective achieved-

Learnt about – The machinery involved in the processing of raw material up to packaging to a final product for dispatch

The whole plant is divided into 4 blocks (EAST, WEST, NORTH, SOUTH)

- Each block is engaged in prescribed work with complete machinery and labor in a complete hygienic environment.
- Laboratory Equipment- Refractometer, Muffle furnace, Hot plate, weighing Balance, Sieve Shaker, pH meter, Soxhlet Apparatus, Dean & Stark Apparatus, Distillation Unit, Distillation Unit, Titration Station
- Detailed explanation of all the equipment with working and SOP.
- Analysis of Result with the standard Table according to FSSAI.

WEIGHING BALANCE

- Purpose- To lay down the operating procedure for weighing Balance
- Procedure
  1. Switch ON the instrument.
  2. Ensure the instrument is clean and free from dust particles.
  3. Press the red button for instrument working.
  4. For verification place minimum or maximum weight i.e., 50mg and 200gm, 50gm, 100gm.
  5. After the completion of work clean the balance plate.
  6. Switch OFF the instrument after completion of work.
- Preventive Measure
  1. Clean the balance and pan before and after use.
  2. Check the power cable and switch.



REFRACTOMETER

- Purpose- To describe the procedure for operation of refractometer.
- Procedure/Operation

1. Open the prism lock and place few drops of liquid testing sample (pil) at the temperature specified.
2. Allow the liquid to smear on the lower prism surface and quickly close the prism lock.
3. Adjust the eye piece cross wire with a knob by rotating it in a clockwise or anticlockwise directions so that the sharp demarcation line passes through its centre.
4. Sharp demarcation is produced in the form of a circle having half-light and half-dark portion.
5. A knob provided just above the prism can do fine adjustment.
6. Note down the reading from the scale with the help the magnified lens of the instrument.

- Precautions
  1. Use thermometer and water jacket with tubes provided in the instrument whenever it is required.
  2. Clean the instrument and keep under the box when not in use.
  3. Ensure that the instrument is free from dust .
  4. Ensure that all the parts including eye lens, prism and mirror are cleaned before operation.
  5. Place the instrument on the table where adequate light can be reflected through the prism.

MUFFLE FURNACE

- Purpose- To lay down the operating procedure of muffle furnace.
- Procedure
  1. Switch on the instrument.
  2. Ensure that the instrument is clean and free from dust particles.
  3. Press the push button to set the temperature and rotate the coarse knob and release the push button.
  4. The digital display shows the actual temperature of furnace and the red light of the temperature controller glows.

5. When temperature reaches at the setting point, the red light of the temperature controller automatically switched “OFF” and green light will glow. The equipment is now ready for operation.
6. Switch OFF the instrumentation after the completion for work.

- Precautions
  1. Clean the equipment after working.
  2. Check the power cable and switch.



pH meter

- Purpose- To lay down the operating procedure for pH meter.
- Procedure
  1. Ensure that pH meter is clean and dry.
  2. Switch on main power supply to instrument that display the reading.
  3. Ensure that the system is calibrated.
  4. Remove the electrode, wash with distilled water and wipe it with tissue paper.
  5. Place the electrode in pH 4.0 standard buffer solution and adjust with the help of calibration knob pH from 3.95 to 4.05. Record the pH
  6. Remove the electrode , wash with distilled water and wipe it with tissue paper.

7. Place the electrode on pH 9.2 standard buffer solution. The pH from 9.15-9.25 should display on the screen of meter.
8. Prepare new buffer solution after one month or whenever required and record.
9. If calibration of pH meter does not meet the acceptance criteria inform quality manager.
10. Do not use if it is out of calibration.

- Precautions
  1. The pH meter should be away from vibration platform.
  2. Bring the temperature of the pH buffers and samples to room temperature before beginning calibration procedure. All solution temperature should be within 2˚C±8˚C in refrigerator.
  3. While cleaning, disconnect the pH meter from the AC adaptor and unplug ant interference cable that are connected to pH meter.
  4. Don't use any solvent for cleaning.
  5. Don't touch the electrode or probe.
- Preventive Measures
  1. Check that no air bubbles in junction or scratches on the glass tip.
  2. Probe should be rinsed with distilled water between readings or with the solution to be read.
  3. Probes should be stored with a cap full of saturated KCl.
  4. Clean the electrode by emptying the fill chamber and immerse the tip in 0.1N HCl, rinse with water and immerse in 0.1N NaOH for 2 minutes.

MAGENTIC STIRRER WITH HOT PLATE

- Purpose- To lay down the operating procedure of magnetic stirrer with hot plate.
- Procedure
  1. Switch on the instrument.
  2. Ensure that the instrument is clean and fee from dust particles.
  3. The red bulb illuminate on the instrument will indicate "power ON" the instrument.
  4. Green bulb indicates the temperature of instrument (adjust by rotating temperature knob).

5. Keep the magnate inside the container which are placed on the plate and start the rotation by knob.
6. After the completion of work, remove the magnate and wash it with distilled water.
7. Switch OFF the instrument after the completion of work.

- Preventive measures
  1. Clean the plate surface.
  2. Check the power cable and switch.
  3. Thermostat cut off on set value.

HOT AIR OVEN

- Purpose- To lay down the operating procedure of Hot Air Oven.
- Procedure
  1. Switch on the instrument.
  2. Clean the instrument properly.
  3. Red bulb illuminate on the instrument will indicate “Power ON” .
  4. Green bulb indicates the temperature of instrument.
  5. Press PUSH button on display controller and set the temperature by Coarse and Fine knob by rotating.
  6. Start the analysis procedure .
  7. Green bulb display will stop when the process value (pv) attained the set value (sv).
- Preventive measure
  1. Clean the surface on oven inner side and outer side with soft cloth or tissue.
  2. Check display reading whether properly visible or not.
  3. Check that oven door is in good condition.

DOUBLE DISTILLATION UNIT

- Purpose- To lay down the operating and cleaning procedure of Distillation unit.
- Procedure

1. Connect the water inlet pipe to the tap.
2. Switch ON the main supply.
3. Keep an empty clean water container below the water outlet pipe to collect top distilled water.
4. Switch ON the distillation unit.
5. Collect about 500ml distilled water initially in the tank and discard it . After that collect the required amount of distilled water by the operating unit.
6. Analyse the distilled water i.e., hardness , TDS, pH.

- Cleaning procedure
  1. Dismantle the unit with the help of lab assistant.
  2. Put about 500ml of dilute HCl in distillation unit.
  3. Keep the HCl in unit for approx. 12 hrs.
  4. Wash away the acid with tap water very thoroughly.
  5. Start the unit and collect the water about 2 litre and discard it.
  6. Clean the unit after every 3 months or whenever required.
- Preventive Maintenance
  1. Clean the equipment after using.



Fig: SIEVE SHAKER

Weekly progress report 4

Name – Khushi Maheshwari

Roll No.- 171829 (BT62)

Course- B.Tech in Biotechnology

Semester- 6

Batch- 2017-21

Date – 22nd June 2020 to 28th July 2020

Topic- Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Objective of the week- Performing 3 Quality analysis test and learning their protocols and SOP

Objective Achieved-

- In the coming week, 3 basic tests for the analysis of moisture%, Salt% and Acidity% was carried out.
- Standard protocol was studied along with how to calculate the percent value after the test was carried out.
- Comparing the values with the standard table.
- Standard table made for the reference.

TEST 1 - Moisture Analysis

- Purpose- To estimate the moisture content in the sample.
- Reagents- Not required
- Procedure
    1. This method consist of measuring the weight loss of food material due to evaporation of water at particular temperature.
    2. Weigh accurately 10gm of sample in a pre-weighted dry test tube.
    3. Place the dish in hot air oven at 105˚C±1˚C for 4 hrs for finished products and 120˚C±1˚C for 3 hrs for raw commodity
    4. Cool in a desiccator and weigh.
    5. Repeat the process of drying, cooling and weighing till weight loss does not vary by more than 1mg.
- Calculations

$$\text{Moisture \%} = \frac{(\text{Initial sample weight} - \text{fina sample weight})}{\text{Weight of sample taken}} * 100$$



Fig: Sample taken in triplets to calculate moisture %

Test 2- Acidity%

- Purpose – To estimate the acidity % in sample.
- Reagents- 1% phenolphthalein , 0.05 NaOH
- Procedure
    1. Taking accurately 5gm of crushed namkeen sample and 0.5gm for seasoning sample into a beaker.

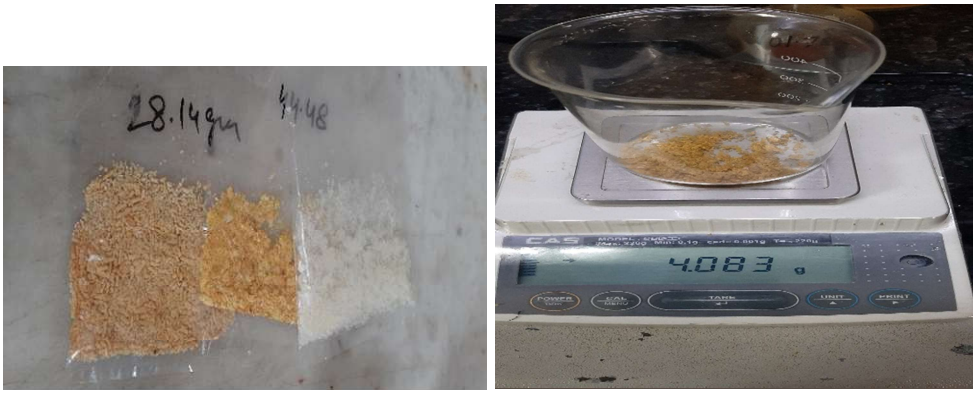


Fig: Crushed Sample Of Namkeen and Weighing 5gm sample over Weighing Balance

2. Add 100ml of distilled water to it.
3. Put few drops of 1% phenolphthalein to it as an indicator
4. Then titrate the solution with N/20 NaOH (sodium hydroxide)

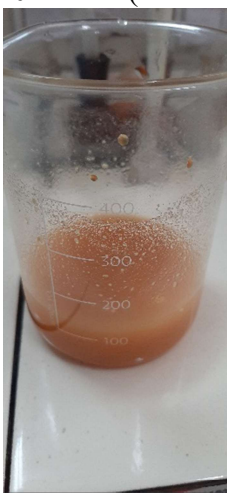


Fig: sample containing 100ml DW

5. Change in colour (pink) indicates the end pint.
6. Note the titrated value.
7. Carry out blank determination using water.

- Result- Pink Colour visible



- Calculations

$$\text{Acidity \%} = \frac{(\text{sample titer} - \text{blan titer}) * \text{Normality of NaOH} * \text{factor}}{\text{Weight of sample taken}}$$

^ Factor for Tartaric acid is 7.50, Malic Acid is 6.70 and for citric acid is 6.40

Test 3- Salt %

- Purpose – To estimate the salt % in the sample
- Reagents – Distilled water, 5% Potassium chromate indicator, 0.1N Silver Nitrate
- Procedure-
    1. Taking accurately 5gm of crushed namkeen sample and 0.5gm for seasoning sample into a beaker.
    2. Add 100ml of distilled water to it.
    3. Put few drops of 5% Potassium chromate to it as an indicator
    4. Then titrate the solution with N/10 Silver Nitrate
    5. Change in colour (reddish brown tinged persists) indicates the end pint.



    6. Note the titrated value.
    7. Carry out blank determination using water.
- Calculations

$$\text{Salt\% (total chloride)} = \frac{(\text{sample titer} - \text{blank titer}) * \text{Nof silver nitrate}}{\text{Weight of sample taken}} * 5.845$$

NAMKEEN STANDARDS

S. No.	Product Name	Moisture (max %)	Acidity (%)	Salt (%)	Fat (%)	AEF (max %)
1.	Aloo Bhujia	2	0.36 – 0.46	2.05 – 2.80	40 – 42	0.6
2.	Bikaneri Bhujia	2	0.13 – 0.23	2.15 – 2.80	42 – 44	0.6
3.	Cornflakes mixture	2	0.34 – 0.44	1.64 – 2.0	32 – 34	0.6
4.	Khatta Meetha	2	0.28 – 0.38	1.25 – 1.80	32 – 35	0.6
5.	Masti Mix	2	0.24 – 0.34	2.0 – 2.80	32- 34	0.6
6.	Moong Dal	2	0.14 – 0.24	1.73 – 2.23	21 – 24	0.6
7.	Navrattan	2	0.29 – 0.39	2.12 – 3.0	32 – 35	0.6
8.	Raita Boondi	3	0.04 – 0.14	0.19 – 0.29	42 – 45	0.6
9.	Salted Peanuts	2	0.15 – 0.25	1.5 – 2.0	42 – 45	0.6
10.	Tasty nuts	2	0.23 – 0.33	2.50 – 3.0	42 – 46	0.6
11.	Nimbu Masala	2	0.55 – 0.70	2.50 – 3.10	39 – 42	0.6
12.	Chatpat Bhel	2	0.55 – 0.65	2.0 – 2.65	40 – 45	0.6
13.	Kadke	3	0.26 – 0.36	3.11 – 3.44	32 – 35	0.6
14.	Laung sev	3	0.10 – 0.25	2.5 – 3.10	38 – 42	0.6
15.	Punjabi tadka	2	0.75 – 0.85	3.01 – 3.85	37 – 41	0.6
16.	Chirpira masala masti	2	0.25 – 0.35	2.25 – 3	32 – 36	0.6
17.	Chirpire tangy tomato	2	0.30 – 0.40	2 – 2.75	32 - 36	0.6

TRADITIONAL INDIAN SWEETS STANDARD

S. No.	Product name	Shelf Life (Days)	Moisture (%)	Weight/Pcs. (gm)
1.	Badam Barfi	6	10 - 15	22 - 27
2.	Pinni	7	10 - 16	40 - 45
3.	Badam Pista Barfi	6	8 - 12	22 - 27
4.	Chowgini ladoo	5	15 - 20	40 - 42
5.	Laju Gujia	6	6 - 12	22 - 27
6.	Doda Barfi	8	10 - 16	30 - 35
7.	Fruit Cake	10	8 - 12	15 - 20
8.	Doodh Moti Paak	6	12 - 18	22 - 30
9.	Plain Barfi	5	10 - 15	22 – 30
10.	Nariyal Ladoo	4	10 - 15	30 – 40
11.	Kaju Pista roll	6	6 - 12	14 – 16
12.	White Kalakand	2	20 - 30	30 – 35
13.	Kaju Kalash	6	6 - 12	9 – 12
14.	Kaju Katli	10	6 - 12	12 – 14
15.	Milk cake	4	10 - 15	40 – 45
16.	Dudh ladoo	5	15 - 22	40 – 42
17.	Walnut Barfi	5	12 - 18	22 – 25
18.	Kaju Rajbhar	6	6 - 12	22 – 25
19.	Kanpuriya Ladoo	6	18 - 24	36 – 38

Along with namkeen and sweet, following protocol is also applicable for all the vegetables prepared for the restaurant with appropriate temperature, sanitized and clean environment.

Raw Vegetables used are of very good quality to avoid any complains for the customer and to maintain the best standard of the food.

KITCHEN STANDARDS

S. No.	Products	Acidity	Salt	Other	Weight per ml
1.	Bhaji	0.34 - 0.44	1.8 – 2.3	All veg. in mashed form	Not applicable
2.	Chole Bature	0.38 – 0.48	1.6 – 2.3	Gravy should be more quantity than chole	Not applicable
3.	Green chutney	0.39 – 0.49	2.5 – 3.0	NA	0.9450 to 0.9460 gm/ml
4.	Red Chutney (Tomato)	0.45 – 0.55	1.8 – 2.3	NA	1.470 to 1.480 gm/ml
5.	Tikki Chhole	0.30 – 0.40	1.6 – 2.0	Gravy should be in more quantity than chole	Not applicable
6.	Tikki Pani	1.2 – 1.7	14 – 18	Brix 14 to 15	0.990 to 0.998 gm/ml
7.	Dal Makhani	0.20 – 0.30	1.4 – 1.8	Brix 12 to 16	0.4320 to 0.4330 gm/ml

8.	Dosa Masala	0.18 – 0.28	1.0 – 1.05	Black Potato Should not be in use	Not applicable
9.	Mix. Veg	0.28 – 0.38	1.6 – 2.0	Veg. are cut in standard size (1 to 2 mm)	Not applicable
10.	Paneer	0.24 – 0.34	1.5 – 2.0	Paneer Pieces are cut in standard size	Not applicable
11.	Sambher	0.25 – 0.35	0.16 –0.22	Brix 8 to 10	Not applicable
12.	Curd	0.50 – 0.65	14 – 16 TSS	Brix 20 to 25	1.1080 to 1.1095 gm/ml
13.	Coconut Chutney	0.10 – 0.14	NA	Brix 10 to 20	1.0605 to 1.0620 gm/ml
14.	Aloo Sabzi	0.30 – 0.40	1.5 – 2.0	NA	Not applicable
15.	Red Gravy	0.20 – 0.30	0.60 –0.70		
16.	White Gravy	0.05 – 0.1	0.42 –0.52		

Weekly progress report 5

Name – Khushi Maheshwari

Roll No.- 171829 (BT62)

Course- B.Tech in Biotechnology

Semester- 6

Batch- 2017-21

Date – 29th June 2020 to 5th July 2020

Topic- Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Objective of the week- Performing 3 Quality analysis test and learning their protocols and SOP

Objective Achieved-

- In the coming week, 3 basic tests for the analysis of Peroxide value, Free Fatty Acid% and Water chloride test was carried out.
- Standard protocol was studied along with how to calculate the percent value after the test was carried out.

Test 4- Peroxide value

- Purpose- To estimate Peroxide value in the sample.
  (The peroxide value of oil is the amount of peroxide present and expressed as mile equivalents of peroxide per 1000g of sample. This value gives an indication of the extent to which oil has been oxidised)
- Reagents
  1. Solvent (mix 2 volume of chloroform and 3 volume of glacial acetic acid)
  2. Saturated potassium iodide solution (dissolve 4 parts of pure potassium iodide in 3 parts of distilled water. Keep the solution in brown glass bottle)
  3. 1% Starch indicator
  4. 0.01 N Sodium thiosulphate solution
- Procedure
  1. Take 5g of oil sample in a flask
  2. Add 30 ml of solvent to it and mix well.
  3. Then add 0.5 ml of saturated potassium iodide solution, shake well and keep for 1min in dark.
  4. Now add 25ml of distilled water to the solution.
  5. If the solution is clear after the addition of starch indicator than there is no peroxide value but if the solution becomes little bit black than it indicates that there is presence of peroxide. Therefore, after the titrate the same with N/ 100 Sodium Thiosulphate using starch as an indicator and note down the titrated value.
- Calculations

$$\text{Peroxide Value (PV)} = \frac{\text{Titre Value} * \text{Normality of Sodium Thiosulphate}}{\text{Weight of sample taken}} * 1000$$

Test 5- Free Fatty Acid (FFA%)

- Purpose- To estimate the FFA % in the sample.
  (Acid value is the number of milligrams NaOH required to neutralize the free fatty acid present in one gram of oil or fat)
- Reagents- !% phenolphthalein indicator , 0.05 N NaOH , Ethyl alcohol

- Procedure
    1. Take accurately about 50ml of ethyl alcohol in a conical flask.
    2. Add few drops of 1% phenolphthalein indicator.
    3. Titrate against N/20 NaOH till light oink colour appears.
    4. Now add accurately about 20g of oil sample.
    5. Heat the content for about 3-4 minutes by periodically shaking the flask.
    6. Add 1ml of 1% phenolphthalein indicator.
    7. Titrate against N/20 NaOH till pink colour persists , note volume of N/20 NaOH used.
- Calculations

$$\text{FFA \%} = \frac{\text{Value of } \frac{N}{20} \text{NaOH used} * \text{Normality of NaOH} * 28.2}{\text{Weight of sample taken}}$$

FFA of Oleic acid =28.2

Acid value= 1.99*FFA

Test 6- Water Chloride Test

- Purpose- To check the Chloride in water.
- Reagents- 5 % Potassium Chromate indicator , 0.1 N Silver Nitrate
- Procedure

(Chloride is expressed as ppm of chloride on which basis water is classified according to the below degree of chloride)

1. Take accurately 100 ml of water sample in a conical flask after thoroughly rinsing it with distilled water.
2. Put few drops of 5% Potassium Chromate to it as indicator.
3. Then titrate the solution with N/10 Silver nitrate.
4. Change in colour (reddish brown tinged persists) indicates the end point.
5. Note down the titre value.
6. Carry out the blank determination using water.

- Calculations

$$\text{Chloride \%} = \frac{(\text{sample titer} - \text{blank titer}) * \text{N of silver nitrate} * 35.45}{\text{Weight of sample taken}} * 1000$$

Weekly progress report 6

Name – Khushi Maheshwari

Roll No.- 171829 (BT62)

Course- B.Tech in Biotechnology

Semester- 6

Batch- 2017-21

Date – 6th July 2020 to 15th July 2020

Topic- Qualitative Analysis of Traditional Indian Sweets and Namkeen Products

Objective of the week- Performing 3 Quality analysis test and learning their protocols and SOP

Objective Achieved-

- In the coming week, 3 basic tests for the analysis of water hardness , Volatile oil%, Moisture % in sample using Dean &Stark Apparatus was carried out.
- Standard protocol was studied along with how to calculate the percent value after the test was carried out.
- Along with test done in the last weeks, qualitative analysis was also done of other products as company also manufactures some bakery products and ingredients in house that are used for making dishes.
- Understanding the various tests carried out to test the quality of milk used to manufacture products in the industry.
- At the end, the whole report was compiled and certificate was issued on 15th July 2020 after completing the full time training for 1 month and 15 days i.e., from 1st June 2020 to 15th July 2020

Test 7 - Water Hardness test

- Purpose- To check the hardness in water
- Reagents- Ammonia Buffer Solution , Eriochrome Black T indicator/ One total hardness indicator tablet , 0.02 N EDTA (ethylene di- amine tetra acetic acid) solution
- Procedure

  Hardness is expressed as ppm of $CaCO_3$ on which basis water is classified according to the below degree of hardness

$CaCO_3$	Conditions
Less than 50	Soft
50 to 100	Slightly Hard
100 to 200	Hard
Above 200	Very Hard

  1. Take accurately 100ml of water sample in a conical flask after thoroughly rinsing it with distilled water.
  2. Add 1ml of Ammonium Buffer Solution.
  3. Now add an appropriate amount of the indicator or tablet.
  4. If hardness is present, A red colour will appear.
  5. Titrate slowly with standard EDTA solution, stirring continuously until the last reddish tinge disappear from the solution and a permanent blue colour is produced.
  6. Note down the titre value.
- Calculations

Hardness = Titre Value * 10ppm

Test 8- Volatile Oil %

- Purpose- To estimate the Volatile Oil% in spice sample
- Reagents- Not Required

- Procedure
  1. Take appropriate quantity of material (spices) in round bottom flask.
  2. Add appropriate quantity of distilled water in round bottom flask.
  3. Attach Clevenger apparatus with round bottom flask.
  4. Attach condenser with water pipe at inlet and outlet point for condensation process.
  5. Put the round bottom flask on heating mantle with assembled system and with supporting clamp around the neck of flask.
  6. Start the heater and water supply in inlet of condenser.
  7. Water in round bottom flask gradually begins to boil and travel upwards into Clevenger apparatus in the form of steam.
  8. Steam will be condensed in the condenser and collected at receiver end.
  9. Oil layer begins to collect on the top of the wate rat receiver point.
  10. Run the process for minimum 5 to 6 hours for complete extraction of volatile oil.
  11. To stop the distillation, turn off and unplug the heating mantle and take out the flask.
  12. Collect the volatile layer in measuring vial or tube.

- Calculations

$$\text{Volatile Oil \%} = \frac{\text{collected volatile oil}}{\text{weight of sample taken}} * 100$$



Fig: Soxhlet Unit is nowadays used for faster extraction of oils from the sample

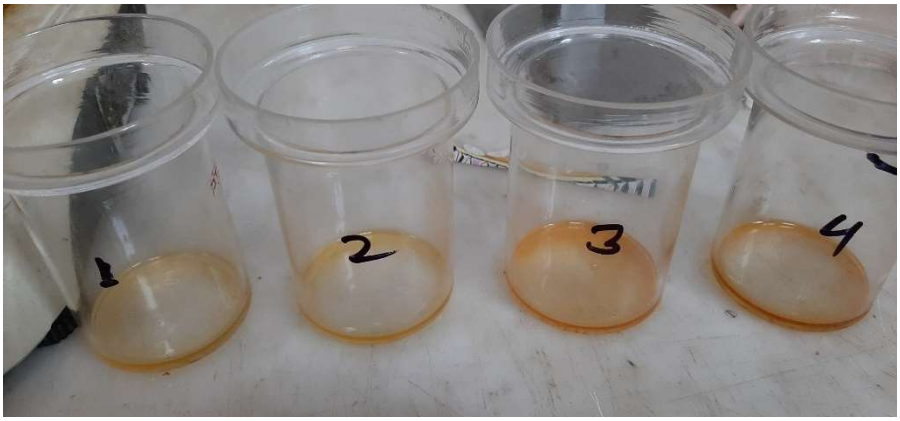


Fig: Extracted out oil from the sample

Test 9- Moisture % in spices by Dean and Stark Method

- Purpose- To estimate the moisture % in spices sample by Dean & Stark method.
- Reagents- Toluene
- Procedure
  1. Take accurately about 25g of spice sample in round bottom flask.
  2. Add appropriate amount of toluene in round bottom flask.
  3. Attach Dean & Stark apparatus with round bottom flask.
  4. Attach condenser with water pipe at inlet and outlet point for condensation process.
  5. Put round bottom flask on the heating mantle with assembled system and with supporting clamp around the neck of flask.
  6. Start the heater and water supply in inlet if condenser.
  7. Toluene in round bottom flask gradually begins to boil and moisture of spice travel upward in to Dean & Stark apparatus in the form of steam.
  8. Steam will be condensed in the condenser and collected at the receiver end.
  9. Run the process for minimum 3 to 4 hours for complete extraction of moisture.
  10. To stop the distillation, turn off and unplug the heating mantle and cool the flask.
  11. Collect the water layer in measuring vial or tube.
- Calculations

$$\text{Moisture \%} = \frac{\text{Collected water quantity}}{\text{weught of sample taken}} * 100$$

Bakery Department Standard Parameter

S. No.	Product Name	Height (cm)	Length (cm)	Width (cm)	Thickness (mm)	Total Weight (Bread +Poly) (gm)	PP Weight (gm)	Bread Weight (gm)	Total No. of pieces	Weight/ piece of Bread (gm)
1.	White Bread 175	28.8	12.8	9.7/10.1	0.04	188.2	4.29	183.9	17	9.16
2.	Atta Bread 250	35.6	11.2	9.9/10.4	0.05	276.4	6.56	269.8	11	24.03
3.	White Bread long 300	35.8	10.2	7.6	0.02	328.6	4.35	323.2	23	13.46
4.	Sandwich Bread 350	35.9	12.3	10.2	0.05	370.4	7.51	363.3	20	17.85
5.	Atta Bread 400	38.8	10.5	10.49.3/10.3	0.04	411.8	7.10	403.5	14	29.0
6.	White Bread 500	38.5	10.4	9.9/10.3	0.05	532.9	7.02	525.8	21	24.49
7.	White Bread 600	43.8	12.4	9.9/10.6	0.05	622.0	7.43	614.6	21	25.11
8.	Sandwich Bread 700	35.9	12.5	10.3	0.05	726.0	10.17	715.8	22	32.54

RAW OR PASTEURIZED MILK			
S. No.	**Test Parameter**	**Cow**	**Buffalo**
1.	Solid Not Fat	Min. 8.5%	Min. 9.0%
2.	Fat	Min. 3.5%	Min. 6.0%
3.	Skimmed Milk Adulteration	Should not be detected	Should not be detected
4.	Adulteration	Should not be detected	Should not be detected
5.	Titrable acidity	Min. 0.12 – 0.16%	

MAWA (MANUFACTURED IN HOUSE)		
1.	Moisture	25±4% (Limit in house)
2.	Titrable acidity	0.6 to 0.8% (as per IS:4883:1980)
3.	Fat	Min. 37% (as per IS:4883:1980)
4.	Total Solid	Min. 55 to 65% (as per IS:4883:1980)

PANEER / CHENNA (MANUFACTURED IN HOUSE)			
1.	Titrable Acidity	Max. 0.50% (as per IS:10484:1983)	
2.	Limit as per FSSAI, 2006	Moisture	Milk Fat
3.	Paneer/ chenna	Max. 60 to 65%	Min. 50%
4.	Medium Paneer / Chenna	Max. 60 to 65%	20.0 to 50.0%
5.	Low Paneer / Chenna	Max. 70%	Max. 20.0%

CONCLUSION

Apart from producing healthy and safe food for consumption, because of increasing competition manufacturers and owners have realized that we need to have continuous and committed efforts towards improving the product and the service quality.

Starting from the raw material, processing time, packaging , a lot of changes occur in the ingredients, taste flavor, aroma which completely gives a finished good a new dimension.

The test performed in the company are solely taken into consideration for improvement in the quality of product and to remove flaws from them because the company's aim is to provide safe, healthy and quality products to its customers and also improving upon the feedback they get from customers on how the processes can be improved to the world class quality keeping in mind-

- High Ethical Standards
- High level of courtesy
- Customer first, Company second, self-last
- Respect for privacy
- Warmth and Concern
- Empathy
- Teamwork
- Mutual Trust
- Two Way Communication
- Concern for safety, security & health of consumers

PHYTASE AND DIFFERENT CHROMATOGRAPHY TECHNIQUES USED FOR ITS PURIFICATION

TRAINING REPORT (2020) IN THE FULFILMENT OF

BACHELORS OF TECHNOLOGY IN BIOTECHNOLOGY

BY

MEGHA SHARMA (171830)

UNDER THE SUPERVISION OF

DR. SAURABH BANSAL





DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS

JAYPEE UNIVERSITY OF INFORMATION AND TECHNOLOGY

WAKNAGHAT, SOLAN

Acknowledgement

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Date : 03/07/2020

INDEX:

1. **Phytaseenxyme**
2. **Characteristics of organisms producingphytase**
3. **Culture conditions of organisms producingphytase**
4. **Protein determination and phytaseassay**
5. **Ion exchangechromatography**
6. **Gel filterationchromatography**
7. **Affinity chromatography**
8. **Refrences**

Phytase

A phytase is a type of phosphate enzyme that catalyzes the hydrolysis of phytic acid –an indigestible, organic form of phosphorous that is found in many plant tissues, especially in grains and oil seeds. (1)

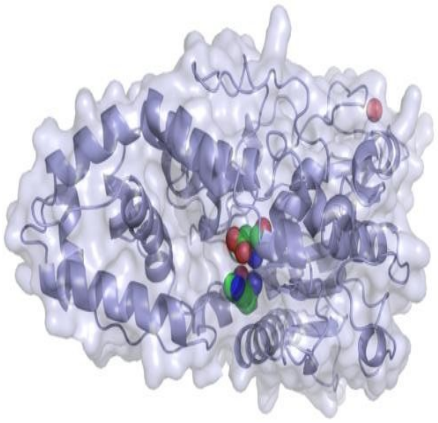

Fig 1: Phytase enzyme (2)

Applications : Phytase is utilized as a animal feed supplement to improve phosphorus nourishment and to increase the nutritive value of plants.

Phytase is basic for upgrading healthy benefit of feed and improving animal development and wellbeing**.** Phytase in poultry improves gut health. (3)

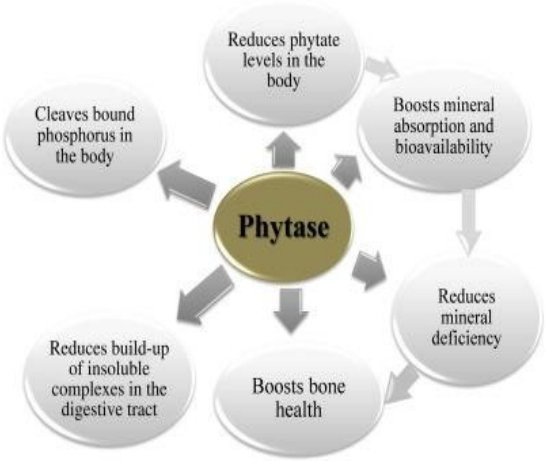

Fig 2 : Applicationofphytase(4)

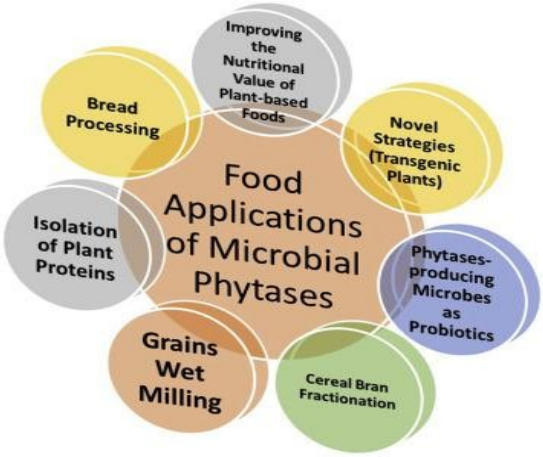

Fig 3: Food applications of microbialphytase(4)

Reaction: phytase is a phosphate enzyme that catalyzes the hydrolysis of phytic acid (myo – inositol hexakisphosphate) –and releases a unstable form of inorganic phosphorus.(5)

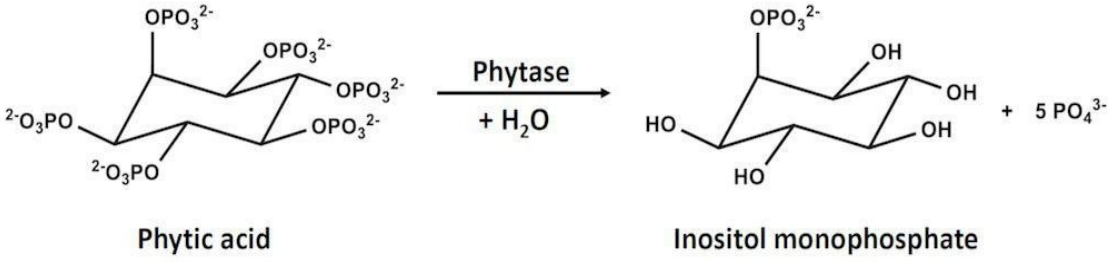

Fig 4 : Reaction of phytase (convertion of phytic acid to inositol monophosphate(5)

Sources of phytase: can get from three unique sources; plants, animal and microorganisms. Phytase is found in the gut of ruminant animals (cattle and sheep) making it possible for them to utilize the phytic acid found in grains as a source of phosphorus.
Phytase are created by yeast either normally or by forms dependent on recombinant DNA innovation utilizing diverse yeast strains.
Phytase had also reported in rice, wheat, maize, soybeans, corn seeds or oil seeds.(6)

Characteristics of organism producing phytase:

CHARACTERISTICS	***Lactobacillus coryniformis***	***Bacillus subtilis***
Gram staining	Gram positive	Gram positive
Cell wall	Teichoic acid, polysaccharides and proteins.	Peptidoglycan(murein), teichoic acid, lipotechoic acid, proteins
Cell membrane	Glycopolymers and proteins	Phospholipids and proteins
Respiration	Facultative anaerobic or microaerophilic	Obligate aerobe, facultative anaerobe
Shape	Rod shaped	Rod shaped
Morphology	0.5-1.2 micrometers by 1.0-10.0 micrometers Long, slender rods to short, coryneform coccobacillus	4-10 micrometer long, 0.25-1 micrometer in diameter, heavily flagellated, forms endospores.
Source of extraction	Dairy products	Upper layer of soil, gastrointestinal track of human and ruminants
Pathogenic	No	No

CHARACTERISTICS	***Candida melibiosica***
Kingdom	Fungi
Division	Ascomycota
Cell wall	Chitin, fibrillar polysaccharides and proteins
Morphology	Small, oval, 2-4 micrometer in diameter
Pathogenic	Yes

Culture conditions of organisms producing phytase:
(7,8)

CULTURECONDITIONS	***Bacillus subtilis***
Media composition	6% wheat bran 0.04% NH_4NO_3 0.02% $MgSO_4$ $7H_2O$ 1% casein hydrolysate 0.05%KH_2PO_4 0.04%K_2HPO_4
Phytase screening plates	1.5% D-glucose 0.5% calcium phytate 0.5%NH_4NO_3 0.05%$MgSO_4$ $7H_2O$ 0.05% KCL 0.001% $FeSO_4$ $7H_2O$ 0.01% $MnSO_4$ $4H_2O$ Agar 1.5% (Ph=7.0, incubated at 37degree Celsius for 16h)
pH	6.5
Temperature	37 degree Celsius
Volume	10 ml.
Time	16 hours.
Agitation	230 rpm.

CULTURE CONDITIONS	*Candida melibiosica*
Media composition	Liquid medium Fructose- 30.0 g/l Yeast extract- 5.0 g/l Meat peptone- 8.0 g/l 0.2 mM KH_2PO_4
pH	8.5
Temperature	28 degree Celsius
Aeration degree	50- 1000 dm^3/h
Stirring speed	300- 600 min^{-1}
Flask type	300 Erlenmeyer flask

Protein determination and phytase assay:

1)The total protein concentration was determined by the coomasive blue G -250 dye –binding assay for phytase from *Aspergillus niger.(9)*

The activity of phytase was determined under these conditions:
Temperature = 37 degree Celsius
Sodium acetate buffer = 350 micro liter
pH = 5.0
Sodium phytate = 875 nmol

Added 10 micro litter of the enzyme solution(phytase) to the assay mixture

⇩

Incubated at 37degree Celsius for 30 minutes

⇩

According to the ammonium molybdate method the librated phosphate was measured

⇩

Blanks were run by addition of the ammonium molybdate solution prior to addition of the enzyme solution to the assay mixture.

One unit of enzyme activity is defined as the amount of enzyme that liberates 1 umol of inorganic phosphate per minute under the assay conditions.(9)

Bradford protein assay: (quantitative assay)

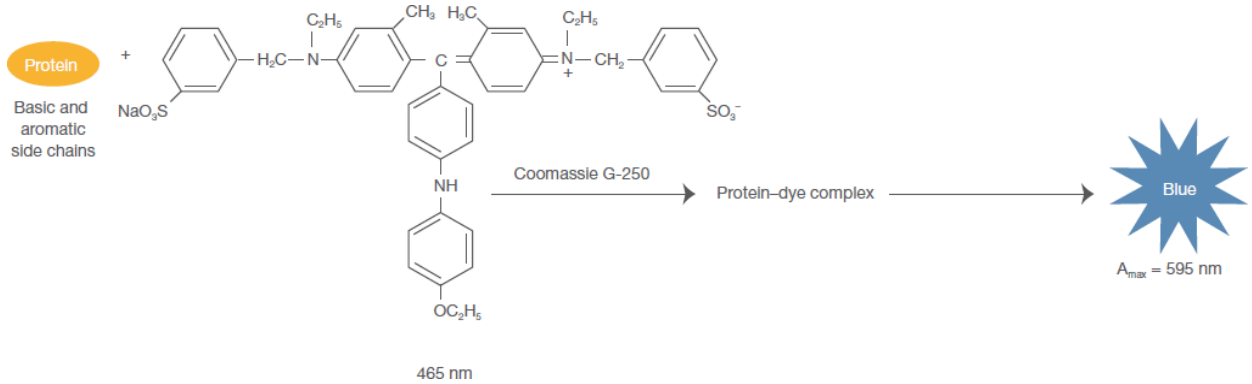

Fig 5: Reaction Bradford protein assay(10)

Add the sample(phytase) into a cuvette; dilution may be necessary

⇩

1.5 ml of bradford reagent is added into the sample

⇩

cover the cuvette with the help of a plastic paraffin film

⇩

mix it properly by gently inverting

⇩

for 10 minutes incubate at room temperature

⇩

Measure absorbance at 595 nm (11)(12)

Ion exchange chromatography

Ion chromatography (or ion exchange chromatography) is a chromatograph that seperates the particles and polar atoms depending on their charge. It works on any sort of charged particle—including proteins, nucleotides, and amino acids. Cations or anions can be isolated using this chromatography.

Principle : ion exchange chromatography relies on the attraction between oppositely charged stationary phase, known as an ion exchanger, and analyte. Ion-exchange chromatography separates molecules based on their respective charge.

The ion exchange chromatography matrix consists of positively and negatively charged ions. Essentially, molecules undergo electrostatic interactions with opposite charges on the stationary phase matrix. The stationary phase consists of an immobile matrix that contains charged ionizable functional groups or ligands. The stationary phase surface displays ionic functional groups (R-X) that interact with analyte ions of opposite charge. To achieve electroneutrality, these inert charges couple with exchangeable counterions in the solution.(13)

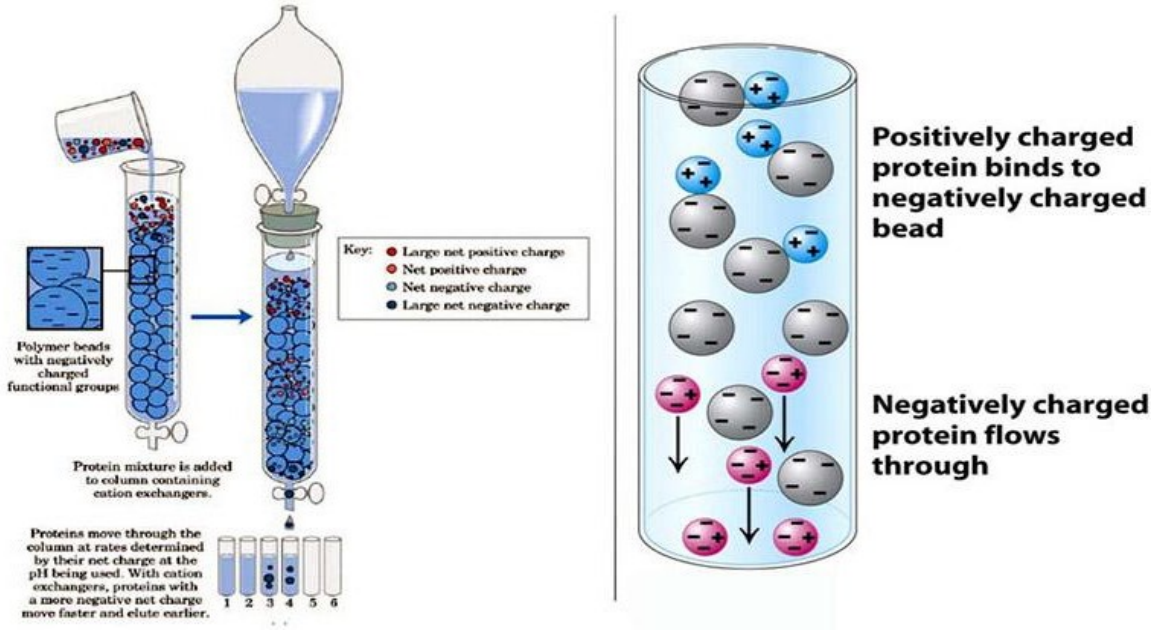

Fig 6: Ion exchange chromatography (separation on the basis of charge)(14)

This type of chromatography is further subdivided into cation exchange chromatography and anion-exchange chromatography. The molecules which are positive in charge will bind to cation exchange resins while the negatively charged molecules bind to anion exchange resins.

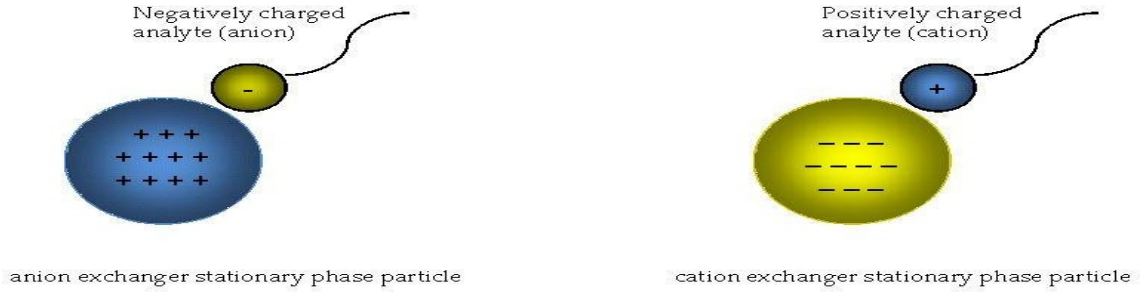

Fig 7: Cation and anion exchange (15)

Procedure :

1) Clamped the chromatography column on the stand in an uprightposition.
2) The buffer is drained into the column and and let it to completely drainout.
3) Ensured that the column resin was left to settled down in thecolumn.
4) Added 12ml equilibration buffer, and allowed it to drained out the second 1ml. (again repeated thisstep)
5) The protein extract was then loaded into thecolumn..
6) Then the column was washed with equilibration buffer for about 4 times to remove the unbound protein and collected 2ml of wash fractions as the buffer drains in the well labeled2ml collectiontubes.
7) Eluted the sample with a salt gradient: equilibration buffer, elution buffer, and a high salt buffer.
8) Added 1ml of gradient elution buffer to thecolumn.
9) Noted the change incolor.
10) Determined the protein concentration of thefractions.

Factors affecting ion exchange separation:

a) Nature and properties of ion exchangeresins
b) Nature of ion exchangeions:
    Valency ofions.
    Size of ions.
    Polarizability
    Concentration of solution
    Concentration and charge of ions
c) pH of the mobilephase
d) Ionic strength
e) Mobile phasemodifiers
f) Temperature

Resins used :

Sephadex : sephadex ion exchangers are insoluble in all solvents commonly used in liquid chromatography. They are stable in water, salt solutions, organic solvents and alkaline and weakly acidic solutions in the pH range of 2-10. The media can be autoclaved as a slurry in the salt form for 30 minutes at 120 degree Celsius and pH 7.

Description	**Functionality**	**Bead size (μ)**
Sephadex-CM C-25	Carboxymethyl	40-120
Sephadex-CM C-50	Carboxymethyl	40-120
Sephadex –DEAE A-25	2-(diethylamino)ethyl	40-120
Sephadex –DEAE A-50	2-(diethylamino)ethyl	40-120
Sephadex –QAE A-25	Quaternary aminoethyl	40-120
Sephadex –QAE A-50	Quaternary aminoethyl	40-120
Sephadex –SP C-25	Sulfopropyl	40-120

DEAE –C : diethylaminoethyl cellulose is a positively charged resin which is used in ion-exchange chromatography, a type of column chromatography, for the separation and purification of proteins and nucleic acid.

TOYOPERAL QAE-500 : It is a strong anion exchange resin for the purification of biomolecules. The resin is composed of a base material of hydroxylated methacrylic polymer beads that have been functionalized quaternary amino ethyl (QAE) strong anion exchange group.

Properties of resin:

It must be chemically stable.
It should be insoluble in common solvents.
It should have a sufficient degree of cross linking.
The swollen resin must be denser than water.
It must contain sufficient number of ion exchange groups.

Applications : To analyze base composition of nucleic acid.
Softening of hard water
Demineralization of water
To measure the additives in food and drug samples
To separate protein mixture

Advantages : costeffective
Re – usable
Low maintenance cost
Effective technique
Quick separation

Troubleshoot : (16)

SITUATION	CAUSE	REMEDY
Protein elutes later than expected or not at all	Incorrect buffer pH	Check pH meter calibration. Use a buffer pH closer to the PI of the protein.
	Ionic strength too low	Increase salt concentration in elution buffer.
	Ionic interaction between protein and matrix	Reduce salt concentration to minimize hydrophobic interaction. Increase pH add suitable detergent or organic solvent.
Reduced or noflow through thecolumn	outlet closed or pumps not working	Open the outlet, check pumps for signs of leakage
	Blocked filter, end piece,	Remove and clean or replace if possible.

	adaptor or tubing	Always filter the sample and buffer before use.
	Protein precipitation in the column caused by removal of stabilizing agents during separation	Modify eluent to maintain stability
Protein does not bind or elute as expected	Sample has not been filtered properly	clean the column, filter the sample and repeat.
	Incorrect buffer pH/or ionic strength	Check conditions required. Prepare new solutions.
Lower protein yield than expected	Protein may have been degraded by proteases	
	Adsorption to filter during sample preparation	Add protein inhibitor to the sample and buffers to prevent proteolytic digestion. Run sample through a medium such as benzamidine . fast flow to remove trypsin –like serine proteases.
		Use another type of filter
	Sample precipitates	May be caused by removal of salts or unsuitable buffer conditions.
	Hydrophobic proteins	Use denaturing agents, polarity reducing agents of detergents.
	Non –specific adsorption	Reduce salt concentration to minimize hydrophobic interaction. Increase pH, add suitable detergent or organic solvent.

Gel filteration chromatography

Gel filteration chromatography, is a chromatographic method in which molecules in solution are separated by their size, and in some cases molecular weight. It is usually applied to large molecules or macromolecular complexes such as proteins and industrial polymers.(16)

Principle :

It is a technique in which the separation of components is done based on their molecular weight or size. It is used for the purification of proteins, polysaccharides and nucleic acid.

The stationary phase which is used is a porous polymer matrix whose pores are fully filled with the solvent to be used as the mobile phase.

The molecules which are present in the sample are pumped through a specialized column containing such micro porous packaging material i.e gel.

The molecules that are above a certain size are totally removed from the pores, while the molecules of small size enters the interior of the pores partly or wholly.
The flow of mobile phase hence will cause molecules to pass through the column which are large in size , without penetrating the gel matrix, whereas the molecules which are smaller in size will be retarded according to their penetration of the gel.
The principle of gel chromatography is very simple. A column of gel particles or porous glass granules is in equilibrium with a suitable solvent for the molecules to be separated. Large molecules will pass through the interstitial spaces, while all the molecules smaller in size will be distributed between the solvent inside and outside the molecular sieve and then they will pass through the column at a lower rate. (17)

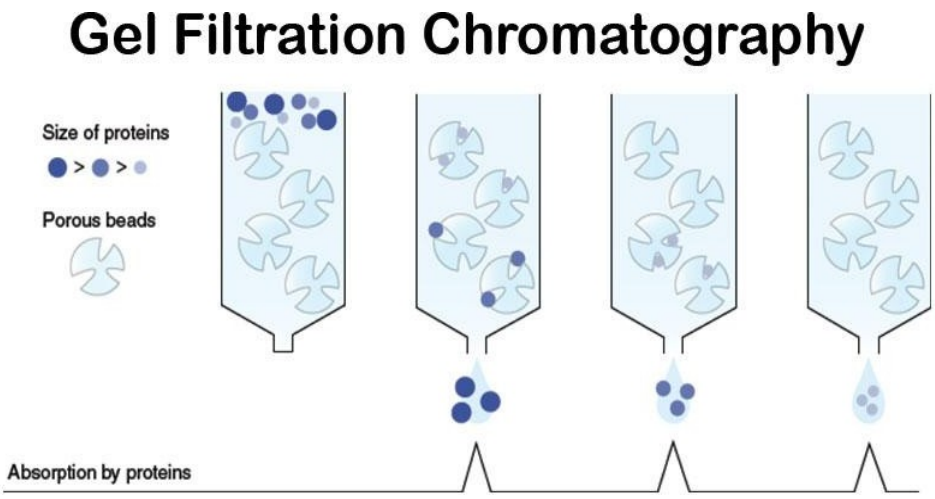

Fig 8: Gel filteration chromatography (separation on the basis of molecular weight)(17)

Stationary phase
It is composed of semi-permeable membrane and a porous polymer gel beads with a defined range of pore sizes.
It had following properties:

- Chemicallyinert
- Mechanicallystable
- With ideal and homogeneous porous structure (wide pore size give lowresolution).
- A uniform particle and poresize.

The Mobile Phase
It is composed of a liquid which is used to dissolve the bio-molecules for making the mobile phase permitting high detection response and wet the packing surface.

Columns

- Analytical column- 7.5–8mm diameters.

- Preparativecolumns-22–25mm
- Usual column lengths-25, 30, 50, and 60cm.
- Narrow-bore columns- 2–3mm diameter have beenintroduce

Types of resins used:

Sephadex

Sephadex is a cross-linked dextran gel which is used for the gel filtration. It has manufactured in a bead form and has used for the gel filtration columns. By varying the degree of cross-linking, the fractionation properties of the gel can be altered. These highly specialized gel filtration and chromatographic media are composed of macroscopic beads synthetically derived from the polysaccharide dextran. (18)

Sephadex is used to separate molecules on the basis of their molecular weight.

It is a quick alternative to do de –salting requires a low dilution factor.

Sephadex G-75 was used in the purification of phytase : Sephadex **-75** is suitable for the buffer exchange and for the cleanup of large biomolecules greater than 80000 molecular weight.

Sephadex **Gel type**	**Globular protein** **(**molecular weight)
SephadEx G -10	<=700
Sephadex G -15	<=1500
SephadEx G -25	1000-5000
SephadEx G -50	1500-30,000
SephadEx G -75	3000-80,000
SephadEx G -100	4000-150,000
SephadEx G -150	5000-300,000
SephadEx G -200	5000-600,000

Sephacryl

Sephacryl High Resolution size exclusion chromatography resins allow fast and reproducible purification of proteins, polysaccharides, and other macromolecules by size exclusion chromatography at laboratory and industrial scale.(19)

It is used in the chromatography separation biomolecules.

Sephacryl **Gel type**	**Globular protein** **(**molecular weight)
SephacrylG-100	1000-100,000 Da
SephacrylG-200	5-250 kDa
SephacrylG-300	10-1500 kDa
SephacrylG-400	20-8000000 kDa
SephacrylG-500	40000-20000000 Da

Properties of resin:

Tolerance for detergents, chaotropic agents, formamide etc.
Tolerance for water –miscible organic solvents.
Operating pressure
Flow rate
Size exclusion limit**.**

Procedure :

1) Firstly, a gel beads column is set up for the gel filterationchromatography.
2) The packed bed is equilibrated with abuffer.
3) At this point, a test solution is eluted through thecolumn.
4) The particle in the test will go into or diffuse out of the porous gelnetwork.
5) The particles that have less molecular weight will stay longer inside the column and the molecules with larger molecular weight will be passed out easily through thecolumn.
6) In this way, the elution of molecules of different size and shape happens at differentstretches. The components eluted can beidentified.

Applications : proteins fractionation
Purification
Determination of molecular weight
Separation of sugar, proteins, peptides, rubbers and others on their basis of size
Can determine the quaternary structure of purified protein.

Advantages : short analysis time
Well definedseparation
Narrow bands and good sensitivity
There is no sampleloss.
Small amount of mobile phaserequired
The flow rate can beset.

Troubleshoot:

SITUATION	CAUSE	REMEDY
Molecular weight or shape is not as expected	Protein has changed during storage.	prepare fresh sample.
	Ionic interaction between protein and matrix.	maintain ionic strength of buffersabove 0.05M (preferably include 0.5MNaCl)
	Precipitation of protein in	if possible clean the column, exchange or

	the column filter or at the top of the bed.	clean the filter or use a new column.
More sample is recovered than expected	Protein co-eluting with other substances	Optimize conditions to improve resolution. Check buffer conditions used for assay before and after the run. Check selection of medium.
Air bubble in the bed	Column packed or stored at cool temperature and then warmed up	Remove small bubbles by passing degassed buffer through the column. Take special care if buffers are used after storage in a fridge or cold-room. Do not allow column to warm up due to sunshine or heating system.
	Buffers not properly degassed	Buffers must be degassed properly.
Cracks in the bed	Large air leak in column	Check all concentrations for leaks. Repeat the column if possible.
Peak of interest is poorly resolved from other major peakes	Sample volume is too high	Decrease sample volume and apply.
	Incorrect medium	Check the selectivity curve, adsorption effects, consider effect of denaturants or detergents if possible.
	Uneven temperature	Use column with a water jacket

Affinity chromatography

It is a type of liquid chromatography used for the separation and purification of sample components.
It utilizes the reversible biological interaction or molecular recognition called affinity which refers to the attracting forced exerted in different degrees between atoms which cause them to remain in combination.(18)
Example: Enzyme with and inhibitor, antigen with an antibody etc.

Principle: The stationary phase in the affinity chromatography consists of a support medium, on which the substrate is covalently bound.
As the unrefined mixture of the substances is let to pass through the chromatography column, substances with binding site for the immobilized substrate bind to the stationary phase, while all other substances is eluted in the void volume of the column.

Once the other substances are removed, the bound target molecules can be removed by methods such as including a competing ligand in the mobile phase or changing the pH, ionic strength or polarity conditions.(19)

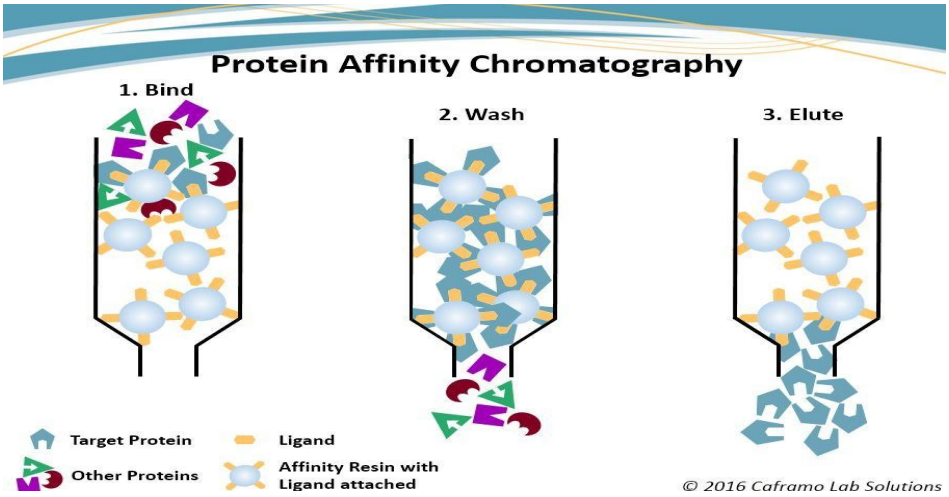

Fig 9: Affinity chromatography(19)

Procedure :

1).The column is loaded with the solid support such as agarose, cellulose etc.
2).Selected the ligand
3).Between the ligand and solid support, attach the spacer arm.
4).Mixture of substances is poured into the elution column.
5).Allowed it to run at a controlled rate.
6).Recovered the target substance by changing conditions to favor elution of the bound molecules**.**

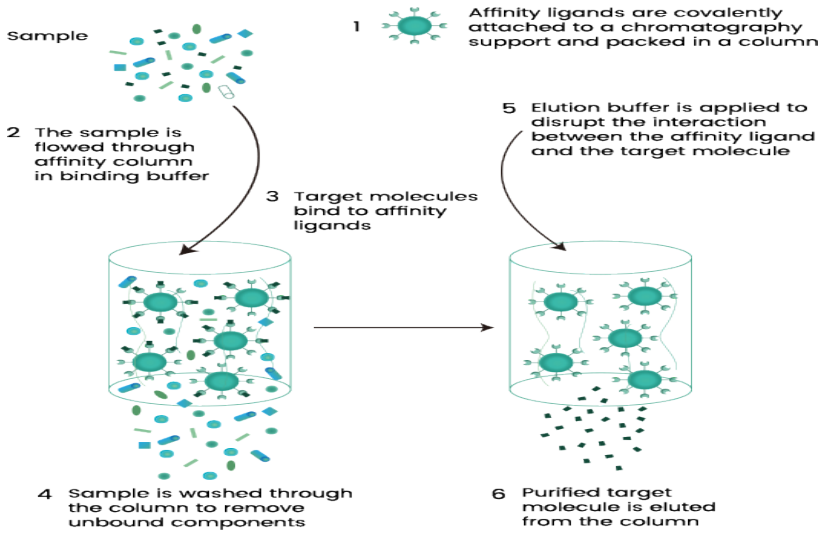

Fig 10: Steps of affinity chromatography(20)

	Crosslinked 4% beaded agarose	Crosslinked 6% beaded agarose	Superflow agarose (highly crosslinked)	Ultralink biosupport (acrylamide-azlactone polymer)
Bead size range	45 to 165 micrometer	45 to 165 micrometer	45 to 165 micrometer	50 to 80 micrometer
Exclusion limit	20,000 kDa	4000 kDa	6000 kDa	2000 kDa
pH	3-11	3-11	2-12	1-13
Coupling capacity	Medium	Medium	Medium	High

Applications:

Mixture of compounds can be seperated
Impurities can be removed or in purification process.
In enzyme assays
Detection of substrates
In in vitro antigen-antibody reaction
It is a sample purification technique, used for biological molecules such as proteins.

Advantages:

High specificity
Target molecules can be obtained in a highly pure stat
Purification is done in single step.
The matrix can be reused rapidly.
The matrix is a solid, can be easily washed and dried.

Troubleshoots : (23)

SITUATION	CAUSE	REMEDY
Distorted bands as sample passes down the bed	Column poorly packed	Suspension too thick too thin. Bed packed at a temperature different from run. Bed insufficiently packed Column packed at a too high presure
Protein does not bind or elute as expected	Sample has not been filtered properly	clean the column, filter the sample and repeat.
	Column is overloaded with	decrease the sample load.

	the sample	
	Proteins or lipids have precipitated on the column	Clean and regenerate the column or use a new column Decrease the sample load.
Reduced or poor flow through the column	Blocked column filter	If possible, replace the filter or use new column. Always filter the sample and buffer before use.
	Precipitated protein	Clean the column using recommended methods or use a new column.
	Bed compressed	If possible repack the column or use new column

Refrences :

1. https://en.wikipedia.org/wiki/Phytase#:~:text=A%20phytase%20(myo-inositol%20hexakisphosphate,releases%20a%20usable%20form%20of

2. https://www.dsm.com/anh/en/feedtalks/phytase-and-myo-inositol.html

3. Lei, X.G., Porres, J.M. Phytase enzymology, applications, and biotechnology. *Biotechnology Letters* **25,** 1787–1794 (2003).https://doi.org/10.1023/A:1026224101580

4. https://www.sciencedirect.com/science/article/abs/pii/S0924224418305752

5. Herrmann, K., Ruff, A. J., Infanzón, B., Schwaneberg, U.; Engineered phytases for emerging biotechnological applications beyond animal feeding; Appl Microbiol Biotechno, 2019. DOI:10.1007/s00253-019-09962-1

6. Lei X.G., Porres J.M., Mullaney E.J., Brinch-Pedersen H. (2007) Phytase: Source, Structure and Application. In: Polaina J., MacCabe A.P. (eds) Industrial Enzymes. Springer, Dordrechthttps://doi.org/10.1007/1-4020-5377-0_29

7. Young-OkKig.,‡Hyung-KwounKim*.,Kyung-SookBae†.,Ju-HyunYu‡Tae-KwangOh*.,Purificationandpropertiesofathermostablephytasefrom*Bacillus*sp.DS11https://doi.org/10.1016/S0141-0229(97)00096-3

8. Georgiev, Danail., Dobrev, Georgi., Shilev, Stefan., 2018 Purification and properties ofa phytase from Candida melibiosica2491

9. Ralf Greiner, Lucineia Gomes da Silva, Sonia Couri Braz J Microbiol. (2009). Purification and characterization of an extracellular phytase from *Aspergillus niger* . Braz J Microbiol.https://doi.org/10.1016/S0960-8524(02)00145-1

10. https://www.thermofisher.com/in/en/home/life-science/protein-biology/protein-assays-analysis/protein-assays/bradford-assays.html

11. Georgiev, D., G. Dobrev, and S. Shilev. "Purification and Properties of a Phytase from Candida Melibiosica 2491". *Emirates Journal of Food and Agriculture*, Vol. 30, no. 11, Dec. 2018, pp. 927-34,doi:https://doi.org/10.9755/ejfa.2018.

12. Demir, Y., Dikbaş, N. & Beydemir, Ş. Purification and Biochemical Characterization of Phytase Enzyme from *Lactobacillus coryniformis* (*MH121153*). *Mol Biotechnol* **60,** 783–790 (2018).https://doi.org/10.1007/s12033-018-0116-1

13. https://www.google.com/url?sa=t&rct=j&q=&esrc=s&source=web&cd=&ved=2ahUKEwiPr733v7DqAhVv73MBHTDmDocQFjAUegQIBRAB&url=https%3A%2F%2Fen.wikipedia.org%2Fwiki%2FIon_chromatography&usg=AOvVaw1CGTDc3c9yoDk9wHrExNK3

14. https://microbenotes.com/ion-exchange-chromatography/

15. https://www.intechopen.com/books/column-chromatography/ion-exchange-chromatography-and-its-applications

16. https://www.sigmaaldrich.com/technical-documents/protocols/biology/ion-exchange-chromatography/troubleshooting.html

17. https://microbenotes.com/gel-filtration-chromatography/

18. Protein Purification by Affinity Chromatography;https://www.sinobiological.com/resource/protein-review/protein-purification-by-ac

19. https://en.wikipedia.org/wiki/Sephadex

20. https://en.wikipedia.org/wiki/Size-exclusion_chromatography

21. https://en.wikipedia.org/wiki/Affinity_chromatography

22. https://microbenotes.com/affinity-chromatography/

23. https://www.sigmaaldrich.com/technical-documents/protocols/biology/affinity-chromatography/troubleshooting.html



GENOTYPING OF SINGLE NUCLEOTIDE POLYMORPHISMBY APPLYING PCR-RFLP METHOD

SUMMER INTERNSHIP REPORT 2020

AMANJOT SINGH MALHOTRA

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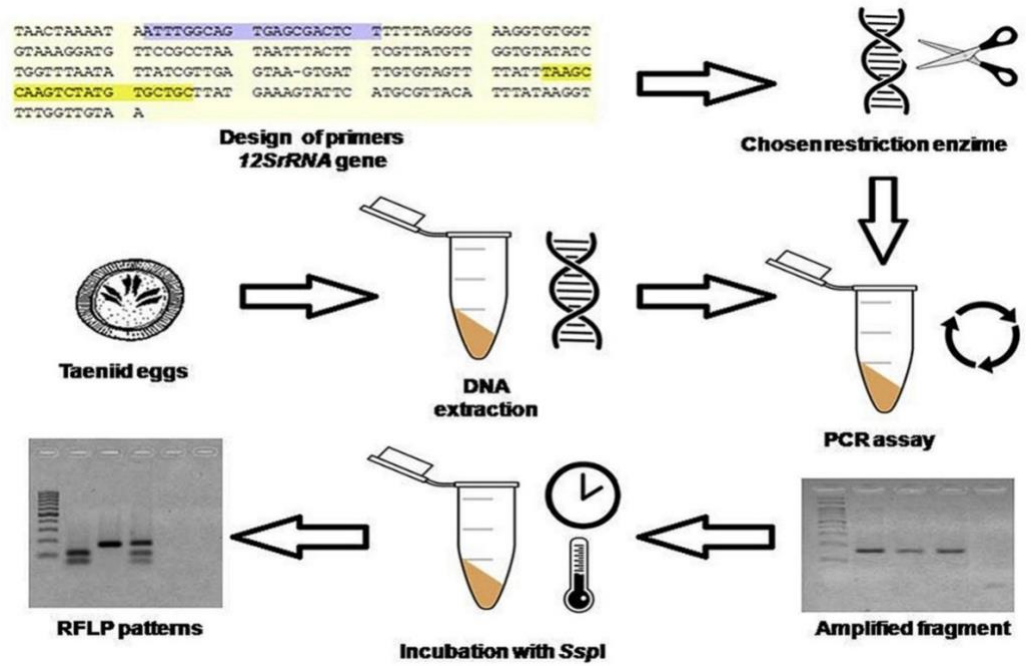
INDEX

SNO	DESCRIPTION	PAGE NO.
1	ABSTRACT	4
2	INTRODUCTION	5
3	EXPERIMENTAL DESIGN	7
4	PROCEDURE	10
5	RESULTS AND CONCLUSIONS	15
6	REFERENCES	16

ABSTRACT

The accurate analysis of DNA sequence variation in not only humans and animals but also other organisms has played a significant role in expanding our knowledge about genetic variety and diversity in a number of different biological areas. The search for an understanding of the causes of genetic variants and mutations has resulted in the development of a simple laboratory technique, known as the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method, for the detection of single nucleotide polymorphisms (SNPs). PCR-RFLP allows rapid detection of point mutations after the genomic sequences are amplified by PCR. The mutation is discriminated by digestion with specific restriction endonucleases and is identified by gel electrophoresis after staining with ethidium bromide. This convenient and simple method is inexpensive and accurate for SNP genotyping and especially useful in small basic research studies of complex genetic diseases. The whole protocol takes only a day to carry out.



INTRODUCTION

Single nucleotide polymorphisms

- Frequently called SNPs (pronounced “snips”), are the most common type of genetic variation among people. Each SNP represents a difference in a single DNA building block, called a nucleotide. For example, a SNP may replace the nucleotide cytosine (C) with the nucleotide thymine (T) in a certain stretch of DNA.
- SNPs occur normally throughout a person’s DNA. They occur almost once in every 1,000 nucleotides on average, which means there are roughly 4 to 5 million SNPs in a person's genome. These variations may be unique or occur in many individuals; scientists have found more than 100 million SNPs in populations around the world. Most commonly, these variations are found in the DNA between genes. They can act as biological markers, helping scientists locate genes that are associated with disease. When SNPs occur within a gene or in a regulatory region near a gene, they may play a more direct role in disease by affecting the gene’s function.
- Most SNPs have no effect on health or development. Some of these genetic differences, however, have proven to be very important in the study of human health. Researchers have found SNPs that may help predict an individual’s response to certain drugs, susceptibility to environmental factors such as toxins, and risk of developing particular diseases. SNPs can also be used to track the inheritance of disease genes within families. Future studies will work to identify SNPs associated with complex diseases such as heart disease, diabetes, and cancer.

SNP genotyping

SNP genotyping is the measurement of genetic variations of single nucleotide polymorphisms (SNPs) between members of a species. It is a form of genotyping, which is the measurement of more general genetic variation. SNPs are one of the most common types of genetic variation. A SNP is a single base pair mutation at a specific locus, usually consisting of two alleles (where the rare allele frequency is > 1%). SNPs are found to be involved in the etiology of many human diseases and are becoming of particular interest in pharmacogenetics. Because SNPs are conserved during evolution, they have been proposed as markers for use in quantitative trait loci (QTL) analysis and in association studies in place of microsatellites. SNPs can also provide a genetic fingerprint for use in identity testing.The increase of interest in SNPs has been reflected by the furious development of a diverse range of SNP genotyping methods.

Genotyping single nucleotide polymorphisms applying pcr rflp method

- **The application and refinement of the PCR method** since its invention in the **1980s**has dramatically progressed molecular genetic research. This simple and sensitive enzymatic technique for the amplification of DNA fragments has been used for various purposes, but especially for the detection of nucleic acid polymorphisms to find biological meaning in genetic variation and molecular divergence in living organisms. The majority of polymorphisms in the human genome are single nucleotide polymorphisms (SNPs) that account for more than 90% of sequence variation and are utilized as an important tool for the study of the structure and history of our genome.

- There are more than **27 million SNPs in the human genome** that have been recorded and stored in the SNPs database (http://www.ncbi.nlm.nih.gov/SNP). This immense amount of data provides valuable information for SNP-based studies, identification of candidate genes involved with complex genetic diseases, pharmacogenetic analysis, drug development, population genetics, evolutionary studies and forensic investigations.

- Over the past twenty years, many different methods have been developed for **SNP genotyping** by PCR, including hybridization16, allele-specific PCR, primer extension, oligonucleotide ligation, direct DNA sequencing and endonuclease cleavage after amplification of the subjected genomic region by PCR. Recent technologies for SNP genotyping (Taq Man method, Invader method, MALDI-TOF method, GeneChips) have the potential for high-throughput, but they require the purchase of expensive equipment. Often, however, the throughput needs for SNP detection may be relatively low as this will depend mostly on the aim of the study.One inexpensive, simple and convenient method for SNP genotyping is PCR-RFLP and its utility in molecular genetic studies has been demonstrated in a wide range of fields.

- **PCR-RFLP is based on endonuclease digestion of PCR-amplified DNA**. The specific restriction endonuclease recognizes and cleaves the DNA in the region of the point mutation of the PCR products. The SNP type is easily identified by using gel electrophoresis to confirm and separate the sizes of the smaller DNA fragments generated by the endonuclease digestion.
- **The PCR-RFLP is a simple, sensitive and reliable method** and requires minimal investment in instrumentation. The limitations of this protocol are in the cases such that the sequences of target SNPs are not suitable for commercial restriction enzymes, and inversely, that the sequences have too many recognition sites for a single restriction enzyme. This method is available for genotyping not only a SNP, but also insertion/deletion polymorphisms and multiple mutations such as Human Leukocyte Antigen (HLA) alleles, which consist of multiple assemblies of SNPs. The ABO blood group polymorphism was the first molecular polymorphism to have been observed and analyzed in humans. This antigenic variation for red blood cells is due to a few DNA single-base substitutions that produce the A, B, and O alleles that can be identified as the ABO genotypes by the PCR-RFLP method.

Experimental Design

Choice of Restriction Enzymes and design of PCR Primers for PCR-RFLP

- PCR-RFLP always starts with the need to design an optimum primer pair and to find the restriction enzymes that will identify the SNPs in the PCR-amplified product.
- To obtain high quality results, it is important to design specific amplification primers and select an appropriate restriction enzyme from the REBASE Restriction Enzyme Database(http://rebase.neb.com).
- To assist with this potentially difficult and tedious step, several comprehensive and automated search tools have been provided by web interfaces that are available at orhttp://bioinfo.bsd.uchicago.edu/SNP_cutter.html .These programs are capable of designing primers for either natural PCR-RFLP or mismatch PCR-RFLP, depending on the sequence data of the targeted genomic region; natural PCR-RFLP can be used if discriminative restriction sites are found at the SNP site, otherwise, additional mismatched bases are introduced to adjacent sites in order to provide artificial restriction sites (known as mismatch PCR-RFLP); even if the target SNP has no cleavage site for available restriction enzymes, it is possible to use the mismatch PCR-RFLP method.
- This method uses a primer containing an artificial restriction site (an additional mismatched base) adjacent to the SNP site. PCR primer sets should be designed to amplify a given DNA region but not to amplify an orthologous non-specific region or a paralogous (duplicated) region. Of course, it is alternatively possible to manually find an appropriate restriction enzyme and to design the corresponding primers using either commercial software (e.g. Genetyx, Genetyx Co, Japan; DNASIS Pro, Hitachi Software Engineering Co. Ltd., Japan) or free software (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). To find the appropriate restriction sites and amplification primers for producing PCR products, a comprehensive software tool has been created for PCR-RFLP assay design.

Template preparation for PCR-RFLP

- Template DNA isolation methods for PCR-RFLP vary considerably in the starting material (e.g., fresh or frozen animal tissues and cells, blood, body fluids, buccal swab, paraffin-embedded tissue, formalin-fixed tissue, insects, yeasts or bacteria). The most commonly used method for genomic DNA preparation is based on phenol extraction and ethanol precipitation41.
- Alternatively, many DNA preparation kits are now commercially available and can be useful to obtain high quality and quantity template DNA. The purity of template DNA is determined by

calculating the ratio of absorbance at 260 nm to absorbance at 280 nm. An A260/A280 ratio of 1.7-1.9 means pure template DNA and is better suited for PCR procedure.

- **Procedure for DNA extraction:**

1- To 300ul of blood sample, RBC lyses buffer (three times the volume of blood sample taken) is added, shaken at room temperature until the RBCs are completely lysed.
2- Centrifuge at 13,000 rpm for 1 minute to obtain creamish white WBC pellet.
3- The supernatant is discarded and the WBC pellet is suspended in 300 ul TE buffer (pH 8.0), using a vortexing machine. Thereafter, 20 ul of 10% SDS solution is added and the mixture is incubated at 56 degree for 30 minutes on dry bath.
4- To the above solution 150 ul of 7.5M ammonium acetate is added, centrifuged at 13,000rpm, at RT, for 15 minutes.
5- The clear supernatant is transferred to a fresh sterile micro-centrifuge tube. To this chilled absolute ethyl alcohol is added (twice the vol of clear supernatant) (mixed gently).
6- The genomic DNA precipitates to be centrifuged at 13,000 rpm for 10 min. The latter should be subsequently washed in 150 ul of 70% ethanol and air dried at RT for 10-15 minutes.
7- 100 ul of TE buffer (pH 7.3), incubated at 65 degree Celsius for 10 minutes. The dissolved DNA was finally stored at 20 degree C till further use.

CONTROLS

- Prepare at least one positive control for amplifying each of the alleles and one negative control with no DNA. Amplification for a positive control and a negative control is performed in parallel with sample in a different tube. Each gel should also include the controls for checking enzyme function.
- When we use single enzyme for single sample or multiple samples, we need to prepare internal control DNA which has a restriction site with each enzyme to check the activity of each enzyme or slip of enzyme addition to a reaction tube. Meanwhile, using multiple enzymes for single sample or multiple samples, it is best to prepare same numbers of different internal control DNA as numbers of enzyme. Each internal control DNA is consisted of an appropriate length PCR products from plasmid DNA which has a restriction site by each enzyme.

MATERIALS REAGENTS

1. 10xPCR buffer
2. Taq Polymerase (use hot-start PCR depending on PCR specificity)
3. dNTP Mixture (dATP, dCTP, dGTP, dTTP)
4. PCR primers (forward and reverse: 20 µM in TE buffer)
5. Sterile water (autoclaved)
6. Template DNA

NOTE : 10ng to 50ng of good quality of template DNA, extracted from various samples as described in the Experimental Design can be used for PCR-RFLP.

7. Restriction Enzymes

NOTE : Enzyme activity drops quickly if restriction enzymes are not kept at -20 °C. They should be kept on ice during handling and never be left on ice after use.

8. Restriction Digestion Buffer
9. Agarose

NOTE: Usually discriminates DNA fragments less than 1,000bp. Within a given range of differently sized DNA fragments, the smaller DNA less than 1,000 bp are best separated in TBE buffer.

10. Tris base
11. Boric acid
12. 10% (wt/vol) AP (ammonium persulfate) prepared freshly each time.
13. Acrylamide

Caution: Acrylamide is highly neurotoxic and readily absorbed through the skin. Mask and gloves should be worn when handling this chemical. *N,N'-Methylene bisacrylamide

Caution: Bisacrylamide is highly neurotoxic and readily absorbed through the skin. Mask and gloves should be worn when handling this chemical.

14. TEMED (N,N,N',N'-tetramethylethylenediamine) stored at 4 ºC.
15. Ethidium bromide (0.5 µg/ml) Stock solution is prepared as 10 mg/ml in water and stocked in light-resistant bottle at room temperature.

Caution: Ethidium bromide is a mutagen with potential carcinogenicity; should wear gloves and take care in handling, storage, and disposal.

16. Bromophenol Blue
17. Xylene cyanol FF
18. Glycerol
19. An optimal DNA size marker used in analysis for PCR products.

EQUIPMENTS REQUIRED

1. PCR tubes, 96-well multiwell plates
2. PCR Thermal Cycler
3. Pipettors and autoclaved tips (filter tips are better for avoiding cross-contamination)
4. Horizontal minigel electrophoresis apparatus
5. Vertical polyacrylamide gel electrophoresis
6. Dry block heater REAGENT SETUP
7. TE buffer, pH8.0 (Tris/EDTA): 10mM Tris-Cl, 1mM EDTA
8. 10 x Stock solution electrophoresis buffer (TBE), 1 liter: 108 g Tris base, 55 g Boric acid, 40 ml 0.5M EDTA, pH8.0 CRITICAL: Store at room temperature and remake if major residues appear in solution.
9. Gel-loading dye: 0.25% Bromophenol Blue ,0.25% Xylene cyanol FF, 50% glycerol , 1mM EDTA (pH8.0).
10. Acrylamide-bisacrylamide stock solution (29:1): prepared as an unpolymerized 30% solution (wt/vol) in H2O as a stock solution, as follows: 29g Acrylamide, 1g N,N'-Methylenbisacrylamide, water to 100 ml.

NOTE: Stock solution is protected from light and stored in the refrigerator.

11. Caution: Acrylamide and bisacrylamide are highly neurotoxic and readily absorbed through the skin. Mask and gloves should be worn when handling these chemicals.
12. Polyacrylamide gels: the stock acrylamide-bis solution is mixed with water and 10 x TBE to yield the appropriate percentage, volume, and buffer concentration (1 x) (e.g. for 100 ml of 12% polyacrylamide gel; 40ml of 30 %acrylamide-bis solution + 10 ml of 10 x TBE + 49 ml of water + 1 ml of 10% AP). This solution is gently deaerated by swirling to make a well polymerized gel. Then, 60 µl of TEMED is added. After mixing well for a moment, pour polyacrylamide gel solution into the glass plate of the electorphoresis apparatus.

PROCEDURE

PCR-amplification of DNA samples - TIMING 1.5 - 2.5 h

1. PCR reactions can be set up to amplify a single DNA sample for digestion with a single restriction enzyme (see option A), or to amplify more than one DNA sample for digestion with multiple restriction enzymes (option B):

A. PCR set up to amplify a single DNA sample for digestion with a single restriction enzyme.

i) To PCR-amplify a single DNA sample, set up a 20µl reaction mixture in a 0.2 ml micro amplification tube, as follows:

component	volume (µl)	final concentration
10 x PCR buffer ($Mg2^+$)	2.0	1 xPCR buffer
dNTP mix (each 2.5 mM)	1.6	0.2mM of each dNTP
Primer (forward) (100pmol/µl)	0.2	1µM forward primer
Primer (reverse) (100pmol/µl)	0.2	1µM reverse primer
Taq polymerase (5U/µl)	0.2	1 unit Taq polymerase
Sample DNA (10-50 ng/µl)	1.0	10-50 ng
DNase-free water	14.8	
total	20.0	

B. PCR set up to amplify more than one DNA sample for digestion with multiple restriction enzymes.

i) To PCR-amplify more than one DNA sample, prepare a master reaction mixture in a 1.5ml tube, as follows, adding the template DNA individually to PCR tubes in advance**:**

component	n=10* volume (µl)
10 x PCR buffer ($Mg2^+$)	22.0
dNTP mix (each 2.5 mM)	17.6
Primer (forward) (100pmol/µl)	2.2
Primer (reverse) (100pmol/µl)	2.2
Taq polymerase (5U/µl)	2.2
Sample DNA (10-50 ng/µl)	11.0
DNase-free water	162.8
total	220.0

dispense DNA sample in advance

*: add extra 10% more samples, finally make up 11 samples

NOTE: Calculate the total volume of the master reaction mixture as the volume required for one DNA sample multiplied by the number of DNA samples plus an extra 10 % to account for loss of liquid during pipetting steps.
NOTE: If the PCR products are to be digested by more than one restriction enzyme, increase the total volume proportional to the number of enzymes that will be used.

2. Perform PCR-amplification of template DNA using an automated thermal cycler, with a standard amplification program, as follows, and stop PCR reactions by chilling at 4°C:

	Standard PCR		Hot start PCR	
Initial activating step	5 min	95°C	15min	95°C
3-step cycling				
Deanaturation	0.5-1 min	95°C	0.5-1 min	95°C
Annealing	0.5-1 min	55-65 °C		50-70 °C
Extension	1 min	72°C		72°C
Number of cycles	25-30		30-40	
Final extension	5 min	72°C	10min	72°C

Initial activating step 5 min 95°C 15min 95°C 3-step cycling Deanaturation 0.5-1 min 95°C 0.5-1 min 95°C Annealing 0.5-1 min 55-65 °C 50-70 °C Extension 1 min 72°C 72°C Number of cycles Final extension 5 min 72°C 10min 72°C Standard PCR Hot start PCR 25-30 30-40
NOTE: The program is generally designed according to manufacturer's instructions of Taq polymerase and primers used in PCR. Temperatures and cycling times are optimized for individual templates and primer pairs.

Analysis of PCR Products by Gel Electrophoresis • TIMING 0.5 - 1 h

3. To separate and determine the PCR product sizes, the PCR yield and nonspecific background, load 6 µl (5 µl of each PCR reaction product plus 1µl of gel-loading dye) onto a 2% (w/v) agarose gel. Load an optimal DNA size marker (e.g. 100 bp ladder, pBR322-HaeIII, φx174-Hae III, or φx174-Hinf I) in a separate lane that is parallel with the samples on the gel.
4. Run the gel for appropriate times at constant voltage.
NOTE: Running time depends on the expected size of the amplified product and concentration of agarose gel. Usually electrophoresis is performed 20 min at 100 V in 2 % agarose when the size of PCR fragment is ranging from 100 to 500 bp.
5. Stain the gel with ethidium bromide at 0.5 µg/ml for 10 minutes.
NOTE: Alternatively, Ethidium bromide may be included in the gel and running buffer at 0.5 µg/ml.
6. Visualize PCR products using a UV-transilluminator and record the results by photography. Check whether the amplified product with the expected size is observed on the gel by comparing with an optimal DNA size marker. Amplicons of the correct size is preferable to be greater than 25 ng per band for use in the next digestion step. (An approximate mass of PCR products is figured comparably from

the intensity of the bands with the size marker used, e.g. 100 bp ladder NEB; N3231L)
TROUBLESHOOTING CAUTION: Safety glasses and preferably a face mask should be worn around UV light sources.

Restriction Enzyme Digestion of PCR products • TIMING 2 - 3 h

7.The general method for digestion of PCR-amplified DNA is the addition of a restriction enzyme directly to a reaction tube containing an aliquot of the PCR product. Restriction enzyme digests can be set up to digest PCR products with a single enzyme (option A) or to digest PCR products with multiple enzymes (option B):

A. Restriction enzyme digest set up to digest PCR products with a single restriction enzyme.

i) Prepare a master-mix solution to digest a number of PCR products with a selected restriction enzyme, as follows; each sample is reacted in a total of 10 µl of mixture containing 5-10 units of enzyme, 1x restriction digestion buffer and 6 µl of PCR product:

	n=1	n=50*
	µl	µl
10 x enzyme buffer	1.0	55.0
restriction enzyme (10U /ml)	0.5	27.5
internal control DNA$ (20ng/ml)	0.5	27.5
DNase-free water	2.0	110.0
total	4.0	220.0

n: sample number
*: add extra 10% more samples, finally make up 55 samples
$: purified PCR products after amplification of plasmid DNA which has a cleavage site with subjected restriction enzyme.

ii) Transfer 5 µl of PCR products to a PCR tube or a 96-well multiwell plate.
iii) Dispense 5µl of digestion master-mix to each well containing the PCR product.

B. Restriction enzyme digest set up to digest PCR products with multiple restriction enzymes.

i) Prepare a master-mix solution to digest PCR products with multiple restriction enzymes (e.g. typing HLA alleles; Figure 1), as follows:

	n=1	n=10*
	µl	µl
10 x enzyme buffer	1.0	11.0
PCR product	6.0	66.0
DNase-free water	2.0	22.0
total	9.0	99.0

n: number of enzyme for analysis
*: add extra 10% more samples, finally make up 11 samples

NOTE:A 10 µl volume of mastermix should be made for each restriction enzyme and sample combination. For example, if 9 restriction enzymes are employed to determine HLA alleles, then we would prepare a tenfold quantity of reaction mixture based on the total volume (10 µl), for each sample

ii) Transfer 9 µl of the master-mix containing the PCR product to a new PCR tube or a 96-well multiwell plate.

NOTE: The volume of the master-mix may vary according to an activity of restriction enzyme; units/µl). One unit of restriction enzyme will completely digest 1 µg of substrate DNA in a 50 µl reaction in 60 minutes by definition. Enzyme activity is usually dictated in the statement of commercially available restriction enzymes.

iii) Add 1 µl of restriction enzyme (5-10 units/µl) to the master-mix and mix the reaction solution gently.

NOTE: An important factor to achieve complete digestion with a restriction enzyme is gentle mixing (pipetting the reaction mixture up and down or tapping the reaction tube gently).

NOTE: Enzymes should be stored at -20°C. While in use, enzymes should be carefully maintained on ice.

8. Incubate reaction mixture (restriction enzyme and PCR product) on a PCR Thermal Cycler or a Dry block heater at the optimal temperature (depending on restriction enzyme) for appropriate times (2 hrs to overnight).

NOTE: Generally 1 U of restriction enzyme digests 1 µg of DNA in 1 hour. If an excess of enzyme is added to the reaction, the length of incubation time may be decreased to save time. Conversely, a longer incubation time might be expected to conserve on the amount of an expensive enzyme by using fewer units for the reaction.

Analysis of PCR-RFLP products by Gel Electrophoresis• TIMING 1 - 1.5 h

9. Load 6 µl (5 µl of each sample plus 1µl of gel-loading dye) of the amplified DNAs digested by restriction enzymes (from step 8) onto either a 6%-12% polyacrylamide gel or a 4% agarose (NuSieve 3:1) gel. Also load an optimal DNA size marker (e.g. 100 bp ladder, pBR322-HaeIII, φx174-Hae III, or φx174-Hinf I) in a separate lane and in parallel with samples on the gel.

NOTE: Gel choice depends on user's choice. Polyacrylamide gel is less expensive than agarose gel, however requires more time and is more complicated to make up.

10. Run the gel for appropriate times at constant voltage. Running conditions depend on the respective gel. When electrophoresis is performed in horizontal minigel electrophoresis, experimental conditions are 1 hr at 100 V for 12% polyacrylamide gel and 45 minutes at 100 V for 4% agarose gel.

11. Stain the gel with ethidium bromide at 0.5 µg/ml for 10 minutes.

12. Visualize products using a UV-transilluminator and a record the results by photography. Check the cleaved fragments or undigested PCR product on the gel by comparing with an optimal DNA size marker.

TIMING

- Preparation DNA samples: 1- 24 h (depend on DNA extraction methods and samples)
- PCR amplification of DNA samples (steps1-2): 1.5-2.5 h Analysis of PCR products by gel electrophoresis (steps 3-6): 0.5-1 h
- Restriction enzyme digestion of PCR products (steps7-8): 2 - 3 h Analysis of PCR-RFLP products by gel electrophoresis (steps 9-12): 1-1.5 h

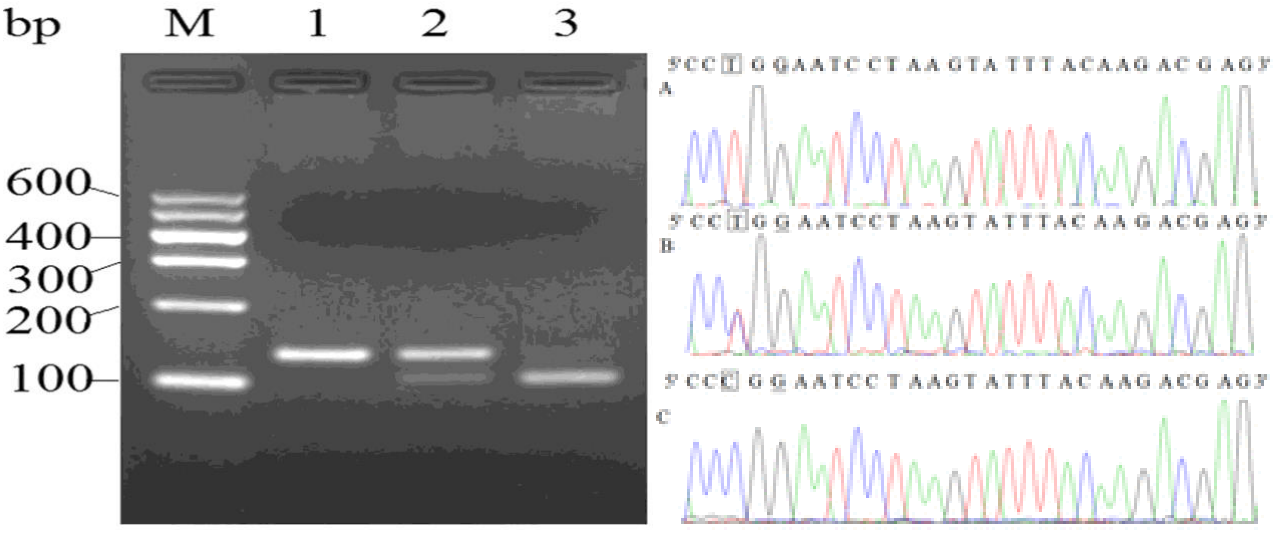
Troubleshooting PROBLEMS

If RFLP fragments are not observed as expected, then the unexpected outcome might be due to many different reasons, such as e.g.
(1) the digestion of PCR products is inefficient,
(2) the efficiency of the restriction enzyme reaction is poor or inactive,
(3) some restriction enzymes are inhibited by methylation, 42 of nucleotides within their recognition sequences,
(4) star activity of some restriction enzymes, which cleave similar but not identical sequences at other sites besides those containing the defined recognition site. This altered or relaxed specificity is termed “star” activity. The star activity is induced under certain extreme conditions (including high endonuclease concentrations, high glycerol concentrations, low ionic strength, and high pH, and so on).

Problems	Possible Causes	Solutions
Step 6 Presence of extra amplification products	Incorrect thermal cycling program was used.	Repeat amplification and ensure the cycling program. Change annealing temperature. Change extension temperature. Change cycling numbers.
	Amplification mixture was not optimized.	Ensure that primer concentration is optimized. Decrease volume of the template DNA. Change Mg^{2+} concentration.
	Template DNA or Work area was contaminated.	Eliminate all sources of contamination.
Step 6 Absence of PCR products	Taq polymerase was not added to the amplification mix.	Repeat amplification paying attention to the addition and mixing of Taq with the amplification mix.
	Taq polymerase was inactivated.	Use new Taq or another Taq from different company.
	Amplification mixture was not optimized.	Check whether all reagents were optimal, especially template DNA concentration was optimal.
	Thermal cycler failure	Check the cycler run history and ensure workings of the thermal cycler.
Step 12 Unexpected fragments	Digestion was incomplete	Use new enzyme or another enzyme from different company. Increase volume of enzyme. Dilute PCR product. Perform digestion with longer incubation time. Check reaction temperature. remove PCR additives such as DMSO or glycerol.
	PCR products were contaminated	Purify PCR products with the DNA extraction kit.

ANTICIPATED RESULTS AND CONCLUSION

- PCR-RFLP method has been used since 1988 , and it has been was shown to be a rapid and sensitive method for the detection of gene polymorphism.
- PCR-RFLP allows rapid detection of point mutations after the genomic sequences are amplified by PCR. The mutation is discriminated by digestion with specific restriction endonucleases and is identified by gel electrophoresis after staining with ethidium bromide (EtBr). This convenient and simple method is inexpensive and accurate for SNP genotyping and especially useful in small basic research studies of complex genetic diseases.
- IT is a relatively simple and inexpensive method of genotyping mainly single nucleotide polymorphisms (SNPs). This method enables not only the discrimination of homozygous and heterozygous samples at the target point mutation, but also the genotyping of multiple mutations such as Human Leukocyte Antigen (HLA) alleles. This method is especially convenient to confirm nucleotide sequences at particular sites of interest without complex typing methods such as hybridization, nucleotide sequencing DNA chips etc.



REFERENCES

1. irk BW, Feinsod M, Favis R, Kliman RM and Barany F (2002) Single nucleotide polymorohism seeking long term association with complex disease. Nucleic Acids Res 30:3295-3311.
2. Haliassos A, Chomel JC, Tesson L, Baudis M, Kruh J, Kaplan JC and Kitzis A (1989) Modification of enzymatically amplified DNA for the detection of point mutations. Nucleic Acids Res 17:3606.
3. Mullis, K.B. & Faloona, F.A. Specific synthesis of DNA in vitro via a polymerase-catalyzed chain reaction. Methods Enzymol. 155, 335-350 (1987).
4. 4. Collins, F.S., Brooks, L.D. & Chakravarti A. A DNA polymorphism discovery resource for research on human genetic variation. Genome Res. 8, 1229-1231, (1998).

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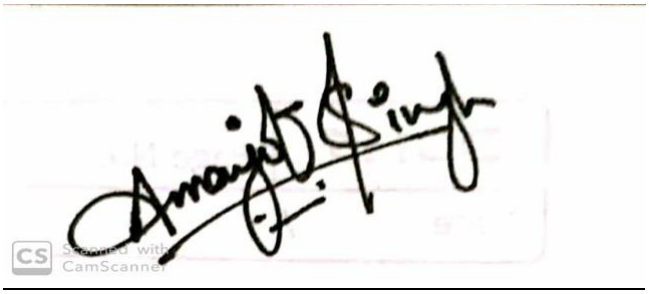


SIGNATURE OF TEACHER : DR. HARISH CHANGOTRA

A project report submitted in partial fulfillment of the requirement for the degree of Bachelor of Technology

In

DEPARTMENT OF BIOTECHNOLOGY AND BIOINFORMATICS BY

RISHAB ROY

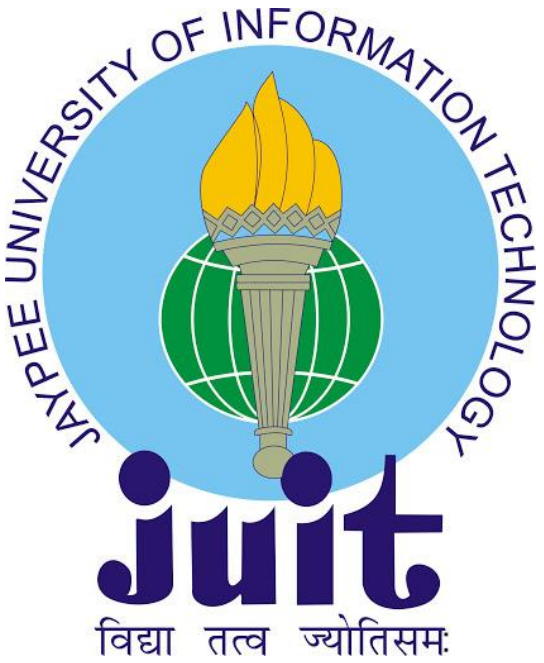
171832

Under the supervision of

Dr. Sudhir Syal

Professor and Head department of biotechnology and bioinformatics

to



JAYPEE UNIVERSITY OF INFORMATION AND TECHNOLOGY, WAKNAGHAT, SOLAN – 173234, HIMACHAL PRADESH

CANDIDATES DECLARATION

I hereby declare that the work presented in this report entitled "**STUDY ON ATCC (AMERICAN TYPE CULTURE COLLECTION)**" in the partial fulfilment of the requirement for the degree of Bachelor of technology in biotechnology department is an original record carried under the guidance of Dr. Sudhir Syal.

Rishab Roy

(171832)

This is to certify that the above statement made by the candidate is true to the best of my knowledge.

NAME OF THE SUPERVISER:

Dr. Sudhir Syal

Professor and Head department of biotechnology and bioinformatics

ACKNOWLEDGEMENT

I would like to express my special thanks of gratitude to my teacher and mentor **Dr. Sudhir Syal** who gave me the golden opportunity to do this project on the topic**,** which also helped me in doing a lot of research and I came to know about so many new things. I am really thankful to him.

AMERICAN TYPE CULTURE COLLECTION :

ATCC is a global biological material resource and standards organisation. Its main aim is the authentication , production , procreation , development and distribution of standard references microorganisms , cell lines , etc.

ATCC was established in 1925 when a committee of scientists recognised a need for central collection of microorganisms.

ATCC headquarters and bioproduction facilities are located in Manassous , Virginia , national capital and the US national institute of health.

POTENTIAL CUSTOMERS / CUSTOMER DATABASE :

- ATCC products and services are used both nationally and internationally by researchers in academic and government , as well as private industry.
- Over 80% of ATCC's customers comes from academia and industry
- 42% from universities and colleges.
- 41% from private industries.
- Government customers comprise nearly 6% of organisations total.
- Three quarters of ATCC's customers are from the US , while the remaining 25% are the international customers.
- ATCC maintains authorised distributors in Europe , Japan , Australia , New Zealand , South Korea , Singapore and makes other shipments directly from the Virginia facilities.
- Among the industries represented ATCC's customer base are the pharmaceuticals , biotechnology , agriculture and diagnostics , as well as food , beverages and make up industries.

ATCC's EXTENSIVE COLLECTION :

- ATCC's collection includes a wide range of biological material for research including cell lines , molecular genomes , tools , organisms and bio products.
- There are more than 3400 continuous cell lines available by species , tissue/disease type at signalling pathways.
- Tumour cell and molecular panels for cancer research annotated with gene mutation and molecular profiles.
- Ethnic and gender diverse induces pluripotential stem cell collection derived from normal disease.
- Over 11000 bacterial strains useful in industries applications using development.
- More than 3000 human and animal viruses.
- Fungi and yeast representing over 7600 species.

- Over 500 microbial caterers recommended as quality control reduce strains.

ATCC's EDUCATIONAL REQUIREMENTS :

- Biologists : bachelors degree in a science related field and 2.5 years at relevant experience
- Senior biologist : bachelor's degree in science plus 4-8 years at relevant experience . Experience working with virus at cell culture.
- Customer Service Responsible : minimum of high school , 1-4 years customer service experience.
- Reposting Technician : high school diploma or GED ,1-4 years experience with data entry , shipping and sample management.
- License Associate : bachelor's degree in a biological science or business intellectual property law. Min 3-5 years work experience in licensing technology.

Working of ATCC:

Beginning with an ATCC Bacterial Strain

ATCC bacterial strains are dispatched solidified on dry ice in plastic cryopreservation vials, as lyophilized societies in glass ampoules or serum vials, or as live societies on agar inclines or in stock medium. Endless supply of solidified societies, promptly resuscitate societies by defrosting and in this manner moving societies to a suitable development medium. In the event that this is absurd, store solidified vials in fluid nitrogen fume (beneath - 130°C). On the other hand, the solidified material can be put away between - 70°C and - 80°C for brief periods (1 to 5 days); be that as it may, practicality will decrease at temperatures above - 130°C. Freeze-dried societies can be put away securely at 4°C or lower. Upon receipt, rehydrate or weaken societies utilizing the proper medium and brooding conditions indicated on the item sheet. Live societies ought to be moved to a fitting development medium upon receipt and hatched under the conditions determined on the item sheet.

Item Sheet

ATCC bacterial strains are transported with an item sheet that contains point by point data on the inception and extension of materials, just as perfect development and engendering conditions. This item sheet, just as extra data, can be found on the ATCC site or can be mentioned from the ATCC Technical Service Department.

Classification Changes

Changes in scientific classification or further investigation of bacterial strains may prompt an adjustment in terminology. These progressions are shown on item sheets and can be discovered online on the item page. Additional data on bacterial

classification changes can be found on the List of Prokaryotic Names with Standing in Nomenclature (LPSN).

Arrangement of Medium

Ahead of time, set up the proper medium and extra reagents fundamental for bacterial strain restoration and development. Guarantee that the correct hatching conditions are prepared. Data for the plan and readiness of the media and hatching conditions for these items is accessible on the ATCC site.

Opening Glass Ampoules

All societies ought to be considered conceivably perilous and ought to be opened by people prepared in microbiological strategies working in offices with regulation necessities suitable for the biosafety level of the way of life. ATCC suggests that the taking care of or opening of glass ampoules be acted in a natural security bureau. In the event that this is beyond the realm of imagination, wear defensive attire, gloves, a face shield or wellbeing goggles, and hold the vial away from your body. Guarantee that every single void vial are cleaned before removal.

Beginning with an ATCC Bacterial Strain

Opening Double-Vial Preparations

1. Warmth the tip of the external vial in a fire.

2. Include a couple of drops of water on the hot tip to split the glass.

3. Strike the finish of the vial with a document or pencil to expel the tip.

4. Expel the protection and inward vial with sterile forceps. Tenderly raise the cotton plug.

Opening Single-Vial Preparations

1. To recuperate the cell suspension from the glass ampoule, score the neck of the ampoule with a little, sterile document.

2. Clean the outside of the ampoule with newly arranged 70% ethanol or plunge it into a measuring utencil of newly arranged 70% ethanol.

3. Wrap the ampoule inside a few folds of a sterile towel or cloth to dry leftover ethanol.

4. Working in a laminar stream hood, hold the vial upstanding and snap open the vial. Guarantee that your bandage doesn't turn out to be excessively wet with

ethanol, or liquor could be sucked into the way of life when the vacuum is broken. Rehydrate the material right away.

Starting Frozen Cultures

1. Set up a sterile test tube that contains the suggested mechanism for bacterial development as recorded in the provided item sheet. Guarantee that the medium contains every single fundamental reagent and is equilibrated for temperature and pH.

2. Defrost the example vial by means of delicate unsettling in a water shower that is set to the typical development temperature of that strain. Defrosting will be fast; around 2 minutes or until all ice gems have dissolved.

3. Expel the vial from the water shower and clean the external surface utilizing 70% ethanol. Follow severe aseptic conditions in a laminar stream hood for every further control.

4. Unscrew the head of the vial and move the whole substance to a sterile test tube containing the fitting development medium. Extra test cylinders can be immunized by moving 0.5 mL of the essential culture to extra auxiliary societies.

5. Brood societies under the proper temperature and environmental conditions as suggested on the item sheet.

6. Look at societies after the suggested brooding time frame. The hatching period will shift among strains and is recorded on the item sheet

Kind OF CULTURE PRESERVATION DONE

- >buffers and strains

- > Cryopreservation

- > Media

Web based ORDERING STEPS

1. Make profile

2. Set up client account

3. Submit a request

4. Track your requests

It offers open and private-part associations in accomplishing redid answers for overseeing natural materials.

For the board a few focuses are to be followed: -

- >Authentication and portrayal considers

- >Storage and cryopreservation

- >Data the executives, request satisfaction and dissemination

- >Intellectual property the executives

- >Regulatory and legitimate consistence

- >cold chain the executives

- >off-site biorepository the executives

NAMING OF FUNGI

Every species has two names a nonexclusive or family and a particular name eg:Amanita muscaria.

1) Genus name is initiate with a capital letter and explicit one is followed in lower case.

2) Species name is either underlined or stress and is trailed by the reference of that individual who have first portrayed the specific species variation.

3) Then various sort are gathered into families with individuals having same highlights eg: as referenced above Amanita muscaria and Amanita australis are of same family for example Amanitaceae.(family name consistently end with - aceae)

4) Groups of family are at that point accumulated into orders with more extensive resemblance which all end with - lagers. In this manner Amanitaceae have a place with the requests Agaricales alongside the Agaricaceae(common palatable mushroom Agaricus campestris has a place)

5) Orders are then assembled into subclasses or class, which end with either mycetidae or mycetes for the last mentioned.

6) Evolutionary tree delivers this structure.

WORKING OF MTCC CHANDIGARH , INDIA IN COMPARISON WITH ATCC :

The Microbial Type Culture Collection and Gene Bank (MTCC), a national office built up in 1986 is supported together by the Department of Biotechnology (DBT) and the Council of Scientific and Industrial Research (CSIR), Government of India. The MTCC, housed at the Institute of Microbial Technology (IMTECH), Chandigarh, has set up itself as a recognized culture assortment place for microbial assets in India. It is an offshoot individual from the World Federation for Culture Collections (WFCC) and is enrolled with the World Data Center for Microorganisms (WDCM).The fundamental targets of this national office are to go about as a vault, to gracefully genuine microbial societies and to offer related types of assistance to the researchers working in research organizations, colleges and enterprises.

The MTCC was perceived by the World Intellectual Property Organization (WIPO), Geneva, Switzerland.

MTCC causes you in portrayal of your microorganisms

Store - Store your strains in Patent Deposit, Safe Deposit or Public Deposit

MTCC researchers are effectively associated with research exercises identified with microbial decent variety, scientific classification and natural biotechnology. Around 100 novel taxa (genera and types) of microscopic organisms, actinomycetes and yeasts have been portrayed by the MTCC researchers. Having distributed around 100 exploration papers during the most recent decade, MTCC has now settled itself as a main place in microbial scientific categorization and assorted variety contemplates.

Examination foundations, scholarly associations, pharmaceutical, biotech and food ventures engaged with microbiological and biotechnological research consistently approach MTCC not just for microbial societies and other microbiology-related administrations, yet additionally for the execution of exploration ventures.

OVERVIEW OF THE REPORT :

By this report the things we learnt are as follows :

- What is ATCC ? – About ATCC , it's working , ordering techniques , culture preservations etc.
- Types of culture preservation done
- Online ordering methods , and other ordering techniques
- Management of ATCC
- 3400 continuous cell lines
- Over 18000 bacterial strains
- 3000 human and animal viruses
- 7600 species of fungi and yeast
- 1000 genomic and synthetic nucleic acids
- Over 500 microbial cultures
- Educational requirements
- Working at ATCC , staff
- Fungal preservation
- Comparison of ATCC with MTCC ,Chandigarh

Summer Training Report

on

Vaccination

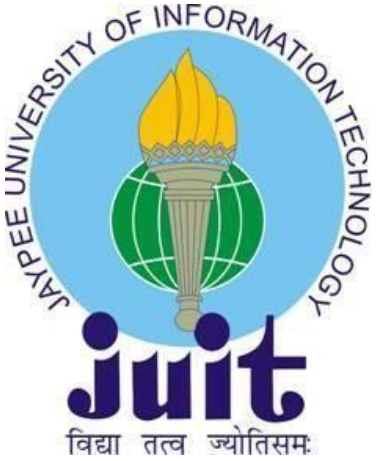
Submitted in partial fulfillment of the requirement for the degree of Bachelor of Technology

By

Manvhi Rastogi (171834)

Under the supervision of

Dr. Rahul Shrivastava



Department of Biotechnology and Bioinformatics
Jaypee University of Information Technology Waknaghat, Solan- 173234, Himachal Pradesh

Declaration

I hereby declare that the work presented in this report entitled **"Vaccination"** in partial fulfillment of the requirements for the award of the degree of **Bachelor of Technology** in **Biotechnology** submitted in the Department of Biotechnology & Bioinformatics, Jaypee University of Information Technology, Waknaghat is an authentic record of our own work carried out over a period from May 2020 to June 2020 under the supervision of **Dr. Rahul Shrivastava.**

The work done embodied in the report has not been appeased for the award of any other degree or diploma.



Manvhi Rastogi
171834

This is to certify that the above affirmation made by the candidates is true to the best of my knowledge.



Dr. Rahul Shrivastava
Associate Professor
Department of Biotechnology & Bioinformatics
Jaypee University of Information Technology
Wakhnaghat, Distt-Solan, H.P. - 173234
Date – 3rd July 2020

Table of contents

1. Introduction
2. Routes of Administration
3. Immunological Mechanisms of Vaccination
4. Vaccine Delivery System
5. Phases of Vaccine Development and Commercialization
6. Diseases and its Vaccines
7. Scheduled vaccines for a child by WHO
8. Reference Manager
9. Endnote
10. References

1. INTRODUCTION

Vaccines are the biological entities prepared by humans for acquiring active immunity against various diseases. This is the era of vaccine development and our knowledge has made it possible to develop against many infectious diseases in the world. These vaccines are generally made from weakened or killed form of microbes or toxins or surface proteins. Now with new advancements other forms like DNA, RNA etc. are also being used. Vaccines are developed on two features either prophylactic that is preventing the disease or therapeutic that is healing the disease. With its development we have been successful in eradicating smallpox and also controlled polio, measles, tetanus and many more. Basically if we take a look in its mechanism, both natural infection and vaccines induces an immune response in the body. Some strategies which are being used in its development are-

1. Weakening the virus: Weakened virus is unable to reproduce so as to cause disease but enough to induce memory B cells. It is not given to people with compromised immunity like those suffering from cancer or AIDS. These live attenuated vaccines are produced by growing the organisms in abnormal culture conditions so that they lose their ability to grow well in human body. Example - BCG vaccine, Sabin(polio), MMR etc.

2. Inactivated virus: In this, the virus is completely killed and it can be give to low immunized people. Absence of live virus or bacteria makes it possible to protect severly weakened immune system as well. Many doses (booster doses) are required as they do not always give strong and long lasting response. Adjuvants are the substances used in this case The killing is done either by heating or by chemical processes. Some examples are flu, rabies, polio.

3. Using the parts of virus: These types of vaccines contains purified antigen rather than the whole organism. Proteins, polysaccharides, peptides can be used. It can be administered to people with weak immunity. Examples are Hib, HPV, Whooping cough.

4. Using parts of bacteria: There are toxins produced by bacteria. These toxins can be used in making vaccines which are inactivated by chemicals. Exotoxins produced are firstly inactivated by formaldehyde which results in toxoid. Example- diphtheria, tetanus.

5. DNA vaccines and recombinant vaccines are the upcoming and new strategies in the field of vaccine development. The virus or bacteria for which we need to make vaccineis taken and its

DNA is taken out. It is then inserted to other cells where the active substance is produced. This substance is purified and used as an active ingredient in vaccine. [1]

2. ROUTES OF ADMINISTRATION

There are various routes of administration of vaccines and its knowledge is of utmost importance.

1. Oral route: Administered by mouth.

2. Subcutaneous route: When the vaccine is administered beneath the skin basically into the fatty connective tissues.

3. Intramuscular route: Injecting the vaccine in muscular tissues.

4. Intradermal: When vaccine injected in the layers of skin.

5. Intranasal: Vaccine administered into the nose.

Rotavirus and OPV are taken by oral means. Hepatitis B, IPV, Hib, PCV-7, DTaP are taken by intramuscular route. Subcutaneous route is followed by vaccines like measles and yellow fever. BCG is administered intradermally.

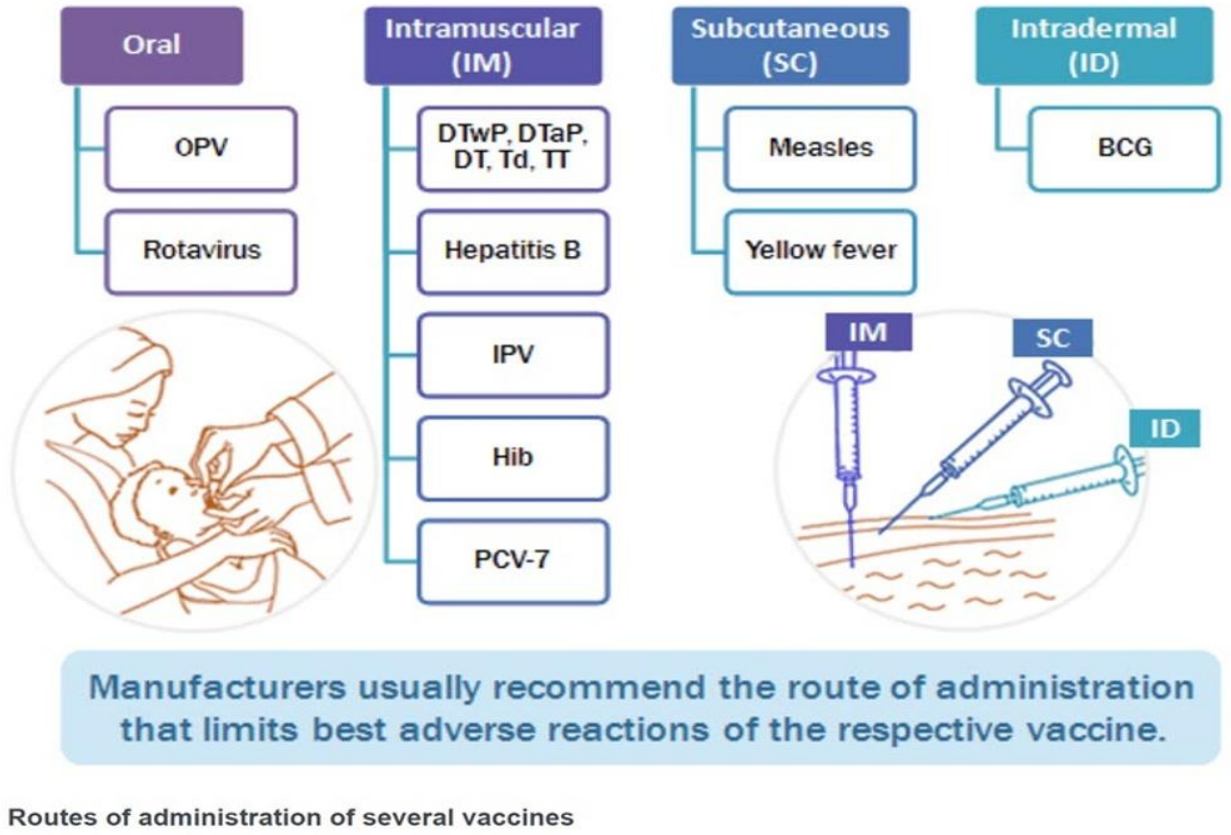


Figure 1: Examples of various routes of administration

(https://vaccine-safety-training.org/route-of-administration.html)

3. IMMUNOGICAL MECHANISMS OF VACCINATION

One of the most essential task is to understand the proper immunological mechanisms which vaccines induce protective immunity. Artificial active acquired immunity prevails when vaccine administration is done inside the body. It can be B cell or T cell mediated. B cells are antibody mediated. T cells are of two types Th cells which stimulate direct activity of B cells while Tc cells release chemicals and destroy infected cells. Antigens are the non self-molecules which binds to the B or T cell receptor in conjunction with MHC molecule. Antibodies produced by the B cells eliminates antigen from the system, neutralize toxins and prevent the viral replication.

Over the period of time we have seen that our immune system has evolved its responses against many pathogens. Like the T helper cell has many different types Th1, Th2, Th17 which provides protection against pathogens. Follicular helper T cells helps in differentiating B cells and generate memory cells by the production of Interleukin 21. CD8+ T cells (cytotoxic T lymphocytes) are also there which release enzymes like perforin, granzyme thereby creating pores to kill the cells directly. Peptides presented by MHC class 1 is recognized by them. It is important immune defense against intracellular pathogens and release of cytokines is one of the primary steps. CD4+ T cells (T helper cells) are a part of adaptive immune system and its functions include activation of B cells to produce antibodies, macrophages to destroy microbes and to activate cytotoxic T cells. Also, there are pattern recognition receptors (PRR) in our body which recognizes PAMPs (Pathogen associated molecular patterns) and also the vaccine determinants and induces innate immune system. [2]

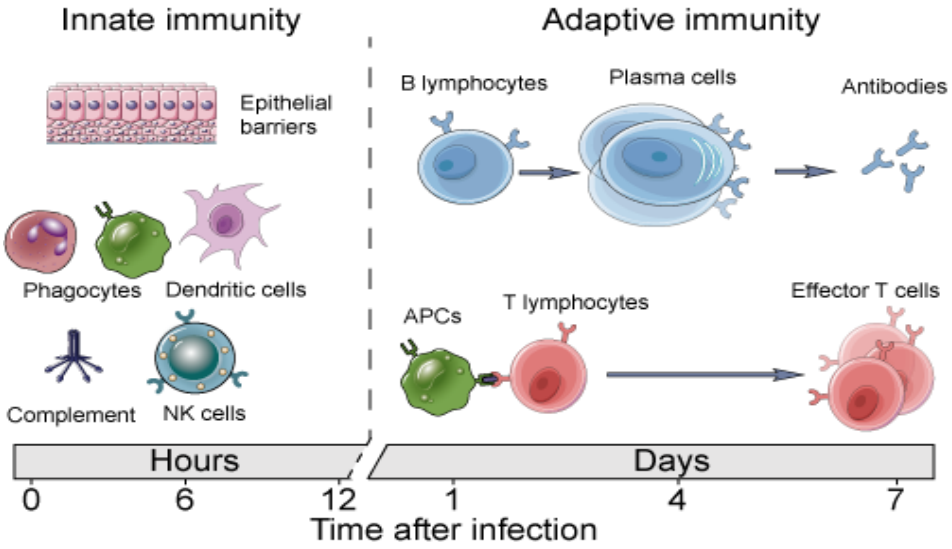


Figure 2: Different cells and mechanisms of innate and adaptive immunity and time taken (https://www.creative-diagnostics.com/innate-and-adaptive-immunity.htm)

Some vaccines like live attenuated ones are against the invariant pathogens and there has been many studies in case of PRRs like toll like receptors (TLR) etc. Then there are some pathogens which mutate rapidly like HIV and hence there are more challenges. There are subunit vaccines, toxoid vaccines, conjugate vaccines which usually have adjuvants. Novel subunit vaccines

consists of some individual immunogenic parts of pathogen which needs to be recognized. Vaccine delivery system like adjuvants are also required. The adjuvants have important function and used in many types of vaccines. It enhances the immunogenity and works as helper in stimulation of immune responses. They also work as delivery system. We need the delivery system so that we no longer have to use booster doses.

1. Lipopeptide adjuvants - Toll like receptors (TLR2) detects lipoteichoic acid, peptidoglycan, bacterial lipoproteins. These adjuvants have good potential to produce immunogenic vaccines via mucosal routes. Elicitation of both antibody mediated immunity and cell cytotoxic immunity takes place when using this adjuvant. The problem with this is that conjugation with recombinant proteins can complicate the situation as proteins might denature in organic solvents. This can be overcome by using PEG (polyethyleneglycol).

2. Lipopolysaccharide based adjuvants - They are the cell wall component of gram negative bacteria and have potential in activation of humoral and cellular responses. Antigen specific antibody and CTL immunity is stimulated by these adjuvants. But these are also toxic in nature because of which we need to use alternatives in case of trials in human. Mimics of LPS like monophosphoryl lipid a (MPLA) can be an alternative.

3. Flagellin based adjuvants - Flagellin is a subunit protein which also plays a role in stimulating and promoting CTL and mixed Th1/Th2 response. It is a carrier protein which activates T cells and is associated with TLR 5. These adjuvants are potent as mucosal adjuvants and has the ability to trigger responses at low doses. Flagellin adjuvanted influenza vaccine s an example.

4. There are some DNA and RNA products which are derived from pathogens only and can be useful in promoting immune responses. Viral double stranded RNA is associated with TLR 3 while single stranded RNA with TLR 7 and 8.[3]

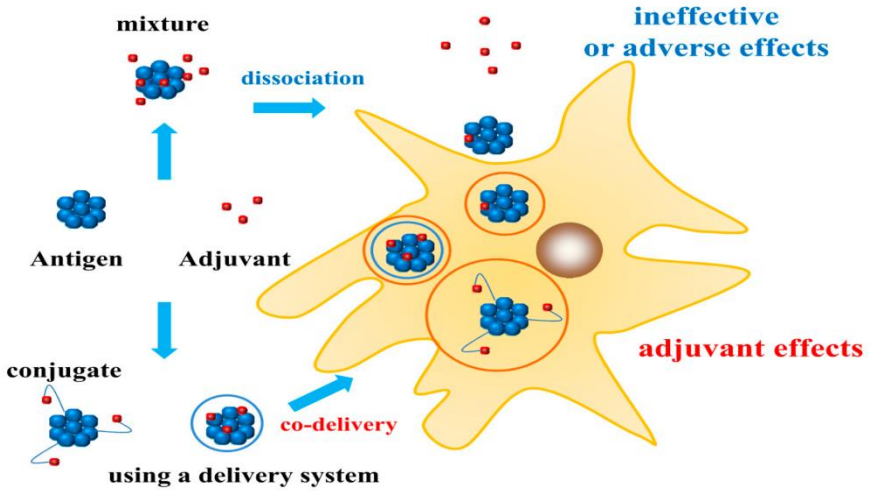


Figure 3: Interactions between antigens and adjuvants and its effects [3]

4. VACCINE DELIVERY SYSTEM

1. Solid particulates - Antigen is entrapped in microsphere and lipospheres and when taken up by M cells they generate immunity. These microparticles are less than 10µm in diameter and enter the gut associated lymphoid tissue (GALT) within 1 hr of oral administration. Combination of large and small particles are also used which mimic of prime and booster.

2. Liposomal Delivery system - It constitutes of liposome and derivatives of lipoplexes. These are hollow spherical of phospholipid layer and antigens like virus, proteins, glycoproteins, carbohydrates are coated on it. They are particulate in nature and has ability to bind with cell surface lipid receptor. Also, polymerized liposomes are there on which targeting molecules are coated and enhances the stability in gastrointestinal tract.

3. Virosomes - These are spherical unilamellar lipid membrane vesicles embedded with viral membrane proteins but they are devoid of genetic material. Its membrane fuses with target cells and deliver the contents which elicit immune response. Afterwards it degrades. The antigens present on the surface of virosomes are presented by MHC 2 and induce humoral responses while the antigens present inside is presented by MHC 1 and induce strong CTL response.

4. Emulsion Delivery System - This is the heterogeneous liquid system that is water in oil, oil in water, multiple emulsions. Basically antigen in dissolved in water and then emulsified in oil in presence of emulsifier. Factors for efficiency depends on viscosity of oil phase, oil to water phase ratio, emulsion droplet size.

5. Micellar Delivery System - They are self-aggregated clusters of amphiphilic surfactant molecules and the antigen is entrapped within for proper delivery. Oral delivery is also possible.

6. Edible vaccines - Few of its characteristics are inexpensive, oral, avoid contamination, improved stability of heat labile vaccine components and mucosal/systemic immune response. Some examples of plant derived vaccinogens are tobacco and lettuce derived hepatitis B, tobacco and potato derived bacterial diarrhoea etc.

7. DNA delivery systems - Tattooing to the skin cells, gene gun, electroporation are some of the methods included in this. Jet injectors are used for needle free delivery. In this pressurized gases force the aerosolized drug solution through the skin, directly into muscles. Array of microstructured projections coated with vaccines called as microneedles are used.

8. Melt in mouth strips are also used usually for children. Immunogen is present on the strip which melts in child's mouth.[4]

5. PHASES OF VACCINE DEVELOPMENT AND COMMERCIALIZATION

For the complete development of vaccines and their commercialization, it has to pass through various phases-

1. Preclinical trials - In this phase extensive research is done in medical centers, universities or biotechnology companies. It takes around 5-10 years. Various iterative testing and safety data is collected. After the success of this phase, scientists get approvals for testing in humans.

2. Clinical Trial Authorization - For getting authorization we need to file with the Medicine and Health care products Regulatory agency.

3. Phase 1 - The vaccine is tested in small number of healthy adults to check its safety. Dose given in small quantity. Adjuvants, preservatives, stabilizers are used in it when testing humans. Generally 1-2 years of time is required. Any side effects must be noted.

4. Phase 2 - Proper dose of vaccine is given to establish manufacturing consistency. Vaccine's safety is studied in an extensive manner. Usually it takes 2 years or more for the completion of phase 2 trial.

5. Phase 3 - It is the final stage of development before company requests product licensing. 3-4 years is the average time taken in this phase. It enrolls in 100 or more people. This is a placebo controlled vaccine trial in which randomization is the key. Each patient is studied carefully and in case of severe side effects the trials are stopped immediately.

6. Phase 4 - It is the post marketing surveillance and monitoring when the licensing is done and distribution has started. It is mainly studied to check the performance of vaccine in real life scenarios and to know the long term risk and benefits.

7. After post license monitoring, license amendment is done if required.[5]

Gaining approval from the Food and drug administration (FDA) and getting the license is one of the longest step in the whole process. After FDA license doctors get involved and recommends many things like safety, doses, which group of population will benefit and many more.

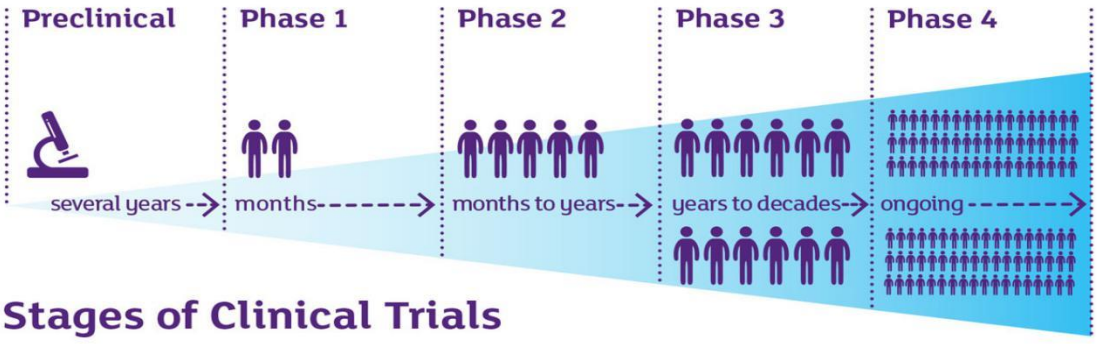


Figure 4 : Phases for the vaccine development and commercialization

(https://www.cancer.nsw.gov.au/data-research/clinical-trials/how-do-clinical-trials-progress)

6. DISEASES AND ITS VACCINES

Some diseases for which vaccines are developed and few of its characteristics are mentioned below-

1. Polio - It is caused by polio virus. It lives in throat and mucosal layer of intestine and spreads through food, water, feces of infected person, droplets from sneezing or cough. It affects spinal cord and can cause paresthesia, paralysis. Inactivated polio vaccine and oral polio vaccine are commonly used for its prevention. IPV should not be used if a person has severe allergy or sickness.

2. Tetanus - *Clostridium tetani* produce toxins that cause painful muscle contractions. It causes lock jaw that is neck and jaw muscles are locked. It is non communicable and found in soil, dust, manure, rusting iron. DTaP is the most common vaccine for tetanus, diphtheria and pertussis in children. Tdap for preteens and Td for adults also used.

3. Diphtheria - *Corneybacterium diphtheria* causes thick covering in back of the throat-difficulty breathing, heart failure, paralysis, death. It attacks the lining of respiratory system and release toxins. This toxin destroy healthy tissues. Complications like blocking airway, damage heart muscle and nerves, paralysis may prevail. Doses of DTaP can be given to children. Booster doses also given.

4. Mumps - It is virus infecting, highly contagious and infects salivary glands. Complications like inflammation of testicles, ovary, pancreas, brain, meningitis can be seen. MMR (measles, mumps, rubella) or MMRV (V stands for varicella) are the vaccines commonly used.

5. Measles - Virus infecting and especially contagious to children. Symptoms include fever, cough, red eyes, white spots inside mouth, measle rash, diarrhea, pneumonia etc. MMR and MMRV are the two vaccines used.

6. Pertussis - It is called whooping cough. *Bordtella pertussis* is the pathogen responsible and it is highly contagious communicable respiratory disease. The bacteria attach to cilia that line part of upper respiratory system and the toxins are released which damage the cilia and swells the airways. Initially the symptoms include runny nose, fever, cough, apnea but at later stages it

cause paroxymes with whoop sound, vomiting. So, for this vaccines like DTap and Tdap are used.

7. Pnuemococcal disease - Streptococcus pneumoniae causes range of infections like ear and sinus infection, pneumonia, bacteremia (bloodstream infection), lungs infection. Pneumococcal meningitis, pneumococcal bacteremia, sepsis, lung infections cause severe symptoms. For its prevention various vaccines were developed and used like PCV 13/prevnar 13 which is a conjugate vaccine containing 13 types of bacteria. PPSV 23/pneumovaz 23 is a polysaccharide vaccine.

8. Hepatitis B - Hepatitis B virus attacks liver and is transmitted with blood, semen, body fluid. It can be of acute type which have symptoms like fever, nausea, loss of appetite, joint pain, jaundice while in chronic liver cancer may happen which might lead to death. Its prevention is done using single antigen vaccines like ENGERIX-B, HEPLISAV-B and combination vaccines like PEDIRIX (Hepatitis-B, diphtheria, tetanus, pertussis and IPV), TWINRIX (combined hepatitis A and B).

9. Rotavirus - It is contagious for children and cause severe diarrhea and dehydration. In that case patient needs to be hospitalized. It can cause death as well. Its vaccine is the first vaccine to be given to an infant. First three doses vary from 2,4 and 6 months respectively.

10. Dengue - It has four serotypes and close relation between the strains E1, E2, E3, E4 might be an issue. If the body generates cross reactive antibody upon infection by one strain there by causing more problems in the body. So, an assembly of four in one virus particle was done and after vaccine production in yeast, a 4 in 1 shot was ready. A dengue tetravalent vaccine was developed which was illustrated by ICGEB, New Delhi. [6]

There are many other vaccines which has been developed and used by us currently and research has been going on for various diseases like HIV, influenza, SARS-Cov. With new advancements and more investments in health care research and development we can tackle with all these contagious diseases. Many biotechnology and pharmaceutical companies like Glaxosmithkline (gsk), Merck, Novartis, Indian Immunologicals limited etc. are working towards it.



Figure 5: Various biotech and pharma companies working in vaccine development

7. SCHEDULED VACCINES FOR A CHILD BY WHO[7]

Antigen	**Age of 1st dose**	**Doses in primary series**	**Interval b/w 1st and 2nd dose**	**Interval b/w 2nd and 3rd dose**	**Interval b/w 3rd and 4th dose**	**Booster Dose**
Recommendations for all children						
BCG	As soon as possible after birth	1				
Hepatitis B	As soon as possible (before 24h)	4	4 weeks min with DTPCV 1	4 weeks min with DTPCV 1	4 weeks min with DTPCV 1	
Polio bOPV + IPV	6 weeks	4	4 weeks min with DTPCV 2	4 weeks min with DTPCV 3		
IPV/OPV sequential	8 weeks	1-2 IPV 2 bOPV	4-8 weeks	4-8 weeks	4-8 weeks	
IPV	8 weeks	3	4-8	4-8 weeks		

				weeks			
DTP containing vaccine		6 weeks	3	4-8 weeks (min)	4-8 weeks (min)		3 boosters 12-23 months (DTP) 4-7 years(Td/DT) 9-15 years(Td)
Haemophilus influenzae type b	Option 1	6 weeks (min) 59 months (max)	3	4 weeks (min) with DTPCV2	4 weeks (min) with DTPCV2		
	Option 2	6 weeks (min) 59 months (max)	2-3	8 weeks if only 2 doses 4 weeks if 3 doses	4 weeks if 3 doses		Atleast 6 months after last dose
Pneumococcal (Conjugate)		6 weeks (min)	2	8 weeks(min)			9-18 months
Rotavirus		6 week with DTP1	2-3	4 weeks with DTPCV2	For 3 dose- 4 week with DTPCV3		

Measles	9-12 months	2	4 weeks			
Rubella	9-12 months with measle containing vaccine	1				
HPV	As soon as possible from 9 years(females)	2	6 months			

Recommendations for children residing in certain regions

Japanese Encephalitis	Inactivated vero cell derived	6 months	2 generally	4 weeks			
	Live attenuated	8 months	1				
	Live recombinant	9 months	1				

Yellow Fever	9-12 months	1					

Recommendations for children in some high risk population

Typhoid	TCV(typbar)	>6 months	1				
	Vi PS	2 years	1				Every 3 years
	Ty21a	Capsules 5 years	3-4	1 day	1 day	1 day	Every 3-7 years
Cholera (Dukoral)		2 years	3(2-5 yrs) 2(>6 years)	Max 7 days min 6 weeks	Max 7 days min 6 weeks		Every 6 months Every 2 years
Meningococcal	MenA conjugate	9-18 months	1				
	MenC conjugate	2-11 months	2	8 weeks			After 1 year
	Quadrivalent	9-23 months	2	12 weeks			
Hepatitis A		1 year	Atleast 1				
Rabies		As required	2	7 days			
Dengue		9 years	3	6	6		

			months	months		

Recommendations for children receiving vaccinations from immunization organization with certain characteristics

Mumps	12-18 months	2	1 month to school entry			
Seasonal influenza	6 months	2(<9years) 1(>9 years)	4 weeks		Revaccinate anually	
Varicella	12-18 months	1-2	4 weeks-3months			

8. REFERENCE MANAGER

It is a reference management software package which are particularly designed for scholars and authors. It is used for in-document citations, organizing reference libraries and also helpful in case of reformatting references for manuscript resubmission and revisions. Authors use them in building local libraries that they organize, sort and reference while writing. Researchers need to handle large amount of data from various publications and also searching large library databases, reading the research, making notes etc. can be a very hectic and messy process. Reference Manager gives bibliographic solutions and searching online databases, organizing references, getting your bibliography as you proceed writing makes it easier for academicians a lot.

The first reference manager software was developed by Earnest Beutler and Earl Beutler in 1982 through their company, Research Information System. At that time it was a very simple tool only

used for organizing the references. Now the software has become much more sophisticated adding so many useful tools. Some of the advantages are-

1. Inserting references – Software inserts coded citation information that refers back to locally saved libraries of authors. We can set the specifications and depending on it the formatting differences can automatically be adjusted.

2. Creating Bibliographies – When we draft a paper, only after its completion citations are inserted. Usually the large bibliography is kept in a separate file and there can be a lot of fuss while using notes and placeholders. Reference managers can manage the order in which citations will be added which will also reduce our drafting time.

3. Changing the reference system for resubmission – When the authors have to prepare the manuscripts of various journals, there are different requirements and reorganization of papers and reformatting of references and bibliography are required. Sequential numbering, alphabetical numbering, author's date can be the systems and changing them from one another can be time consuming. This software can easily help the authors and significantly reduce the time for the same.

4. Culling resources automatically from online databases – One of the most valuable features is that it can take up citations automatically from the internet search engines.

Few of the reference management programs are RefWorks, Zotero, EndNote, Mendeley and Citationsy. Overall, research managers have been integral part of research and has helped in overcoming the fragmented academic life.

9. ENDNOTE

End Note is a reference manager software and one of the best reference manager used worldwide. It is great and generally preferred when people wants to collaborate on a research paper as it lets you share with upto 14 people all over the world thereby making collaborations

easier. It manages bibliographies and references when writing papers, essays and articles. Other than the usual references there are many other types like interviews, podcasts, conference papers and press releases included. It lets you add citations to Microsoft PowerPoint slides and this is basically more beneficial when presentation need to be in a group. Endnote has a huge catalogue of format options and over 6000 reference styles. This attribute make it beneficial for researchers of any discipline.

As a researcher it gets tedious to complete a lot of tasks, publishing your research, coordinating with all the collaborators in the department and the world. So, endnote is a very useful tool in reducing the tedious work of manually collecting and curating research materials, formatting bibliographies and coordinating with other colleagues.

Some of the characteristics of Endnote are-

1. Searching numerous online resources for references and PDF.

2. Find full text for the references.

3. Read, review, annotate and search PDF.

4. Create rules to automatically organize references as you work.

5. Build the bibliographies using latest reference types.

6. Ensure bibliographic accuracy with refreshed journal and referencing styles.

7. Share the library or a portion of it with collaborators and track the teammate's activities on shared libraries.

8. Keep the data accurate by automatic reference and link updating.

9. Access the research on your desktop, online or any other platforms.

10. REFERENCES

1. Vartak, Abhishek, and Steven J. Sucheck. "Recent advances in subunit vaccine carriers." *Vaccines* 4, no. 2 (2016): 12.

2. Pulendran, Bali, and Rafi Ahmed. "Immunological mechanisms of vaccination." *Nature immunology* 12, no. 6 (2011): 509.

3. Wang, Zhi-Biao, and Jing Xu. "Better Adjuvants for Better Vaccines: Progress in Adjuvant Delivery Systems, Modifications, and Adjuvant–Antigen Codelivery." *Vaccines* 8, no. 1 (2020): 128.

4. CH Saroja, PK Lakshmi, Shyamala Bhaskaran. Received: 10-01-11, Revised: 14-02-11, Accepted: 21-02-11. DOI: 10.4103/2230-973X.82384

5. Sanford, Jay P., Nalini M. Philipose, and Violaine S. Mitchell, eds. *The children's vaccine initiative: Achieving the vision*. National Academies Press, 1993.

6. https://www.who.int/immunization/diseases/en/vaccines

7. https://www.who.int/immunization/policy/immunization_tables/en/

INTERNSHIP REPORT

Topic: ANIMAL CELL CULTURE TECHNIQUES

Guide: Dr Udaybanu



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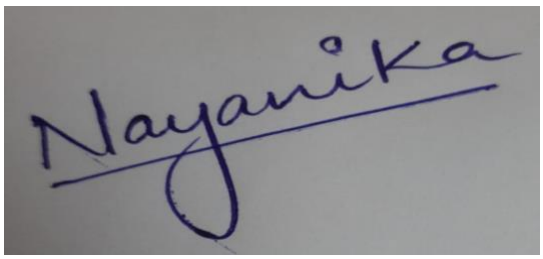


Cell culture refers to the process by which cells are grown in a controlled artificial environment. Cells can be maintained in vitro outside of their original body by this process which is quite simple compared to organ and tissue culture.

In a cell culture technique, cells are removed from an animal or a plant and grown subsequently in a favorable environment. For animal cell culture the cells are taken from the organ of an experimental animal. The cells may be removed directly or by mechanical or enzymatic action. The cells can also be obtained by previously made cell line or cell strain. Examples of cells used to culture are fibroblast, lymphocytes, cells from cardiac and skeletal tissues, cells from liver, breast, skin, and kidney and different types of tumor cells.

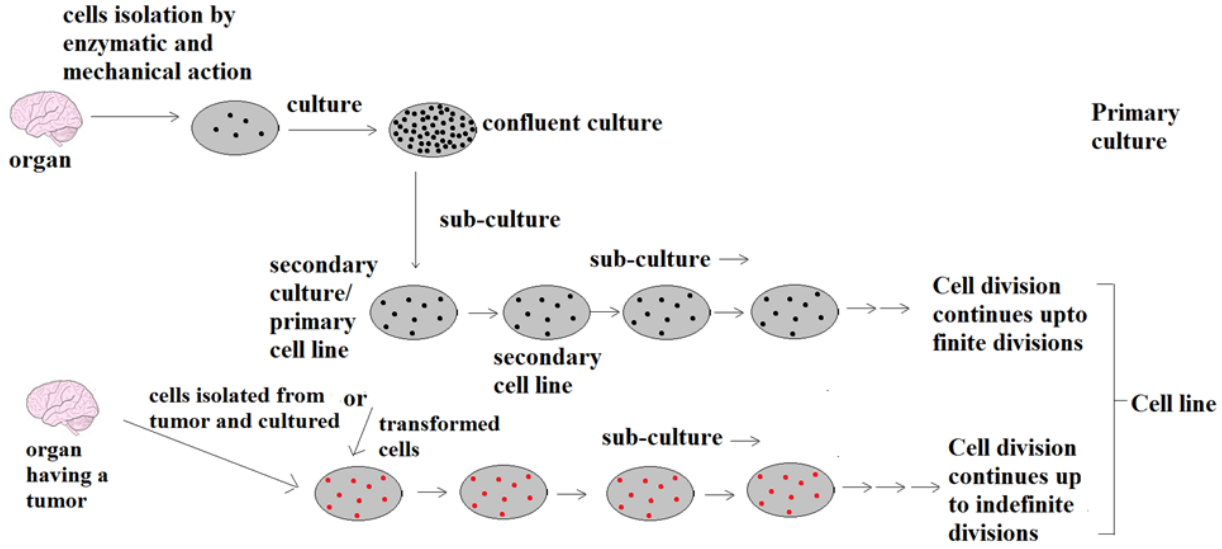


fig: animal cell culture

Requirements for Animal Cell Culture:

a. Sterile Work Area:

Where possible, a separate room should be made available for clean cell culture work. This room should be free of “through traffic” and, if possible, equipped with an air flow cabinet which supplies filtered air around the work surface.

A HEPA (High Efficiency Particle Air Filter) filtered air supply is desirable but not always affordable. Primary animal tissue and micro-organisms must not be cultured in or near the cell culture laboratory and the laboratory must be specifically designated for clean cell culture work.

b. Incubation Facilities:

In addition to an airflow cabinet and benching which can be easily cleaned, the cell culture laboratory will need to be furnished with an incubator or hot room to maintain the cells at 30-40°C. The incubation temperature will depend on the type of cells being cultivated. Insect cells will grow best at around 30°C while mammalian cells require a temperature of 37°C.

c. Refrigerators and Freezer:

Both items are very important for storage of liquid media at 4°C and for enzymes (e.g., trypsin) and some media components (e.g., glutamine and serum) at -20°C. A refrigerator or cold room is required to store medium and buffers.

A freezer will be needed for keeping pre aliquot stocks of serum, nutrients and antibiotics. Reagents may be stored at a temperature of -20°C but if cells are to be preserved it may be necessary to provide liquid nitrogen or a -70°C freezer.

d. Microscopes:

A simple inverted microscope is essential so that cultures can be examined in flasks and dishes. It is vital to be able to recognize morphological changes in cultures since these may be the first indication of deterioration of a culture.

A very simple light microscope with x 100 magnification will suffice for routine cell counts in a haemocytometer, although a microscope of much better quality will be required for chromosome analysis or autoradiography work.

e. Tissue Culture Ware:

A variety of tissue culture plastic-ware is available, the most common being specially treated polystyrene. Although all tissue culture plastic-ware should support cell growth adequately, it is essential when using a new supplier or type of dish to ensure that cultures grow happily in it.

The tests to ensure this, such as growth curves and time of reaching a confluent monolayer, are similar, to those used to ensure that serum batches are satisfactory. Cells can be maintained in Petri dishes or flasks (25 cm^2 or 75 cm^2) which have the added advantage that the flasks can be gassed and then sealed so that a CO_2 incubator need not be used. This is particularly useful if incubators fail. Tissue culture ware is always chosen to match the procedure.

f. Washing Up and Sterilizing Facilities:

Availability of a wide range of plastic tissue culture reduces the amount of necessary washing up. However, glassware such as pipettes should be soaked in a suitable detergent, then passed through a stringent washing procedure with thorough soaking in distilled water prior to drying and sterilizing.

Pipettes are often plugged with non-absorbent cotton wool before putting into containers for sterilizing. Glassware, such as pipettes, conical flasks, beakers (covered with aluminum foil) are sterilized in a hot air oven at 160°C for one hour.

All other equipment, such as automatic pipette tips and bottles (lids loosely attached) are autoclaved at 121°C for 20 min. Sterilizing indicators such as sterile test strip are necessary for each sterilizing batch to ensure that the machine is operating effectively. Autoclave bags are available for loose items. Aluminum foil also makes good packaging material.

g. Liquid Nitrogen Deep Freezer:

Invariably for continuous and finite cell lines, samples of cultures will need to be frozen down for storage. It is important to maintain continuity in cells to prevent genetic drift and to guard against loss of the cell line through contamination and other disasters.

The procedure for freezing cells is general for all cells in culture. They should be frozen in exponential phase of growth with a suitable preservative, usually dimethylsulfoxide (DMSO). The cells are frozen slowly at 1°C/min to -50°C and then kept either at -196°C immersed in liquid N_2 (in sealed glass ampoules) or above the liquid surface in the gas phase (screw top ampoules). Deterioration of frozen cells has been observed at -70°C, therefore, -196°C (liquid N_2) seems to be necessary.

To achieve slow freezing rates a programmable freezer or an adjustable neck plug or freezing tray for use in a narrow-necked liquid nitrogen freezer can be used. Alternatively, ampoules may be frozen in a polystyrene box with 1" thick walls. This will insulate the ampoules to slow the freezing process to 1°C/min in a -70°C freezer.

h. Water Still or Reverse Osmosis Apparatus:

A double distilled or reverse osmosis water supply is essential for preparation of media, and rinsing glassware. The pH of the double distilled water should be regularly checked as in some cases this can vary. Variations in the quality of water used may account for variation in results.

Therefore, water from one source should be used. Water is sterilized by autoclaving at 121°C for 20 min. The distilled water must be glass distilled and stored in glass if it is to be used for the preparation of media. Storage in plastic may result in leaching of toxic substances from the plastic into the water.

i. Filter Sterilization:

Media that cannot be autoclaved must be sterilized through a 0.22 mm pore size membrane filter. These are obtainable in various designs to allow a wide range of volumes to be filtered (e.g., Millipore, Gelman).

They can be purchased as sterile, disposable filters, or they may be sterilized by autoclaving in suitable filter holders. Culture media, enzymes, hormones, cofactors and bicarbonate buffers are examples of non-autoclavable substances.

j. Other Requirements:

(a) Temperature:

In most of the mammalian cell cultures, the temperature is maintained at 37°C in the incubators as the body temperature of Homo sapiens is 37°C.

(b) Culture Media:

The culture media is prepared in such a way that it provides:

a. The optimum conditions of factors like pH, osmotic pressure, etc.

b. It should contain chemical constituents which the cells or tissues are incapable of synthesizing.

Generally the media is the mixture of in- Organic salts and other nutrients capable of sustaining cells in culture such as amino acids, fatty acids, sugars, ions, trace elements,vitamins, cofactors, and ions. Glucose is added as energy source—its concentration varies depending on the requirement.

Table 13.2: A variety of equipments used in animal cell culture

Essential equipment	Beneficial equipment	Useful additional equipment
Incubator	Laminar Flow Hood	Low-Temperature Freezer
Sterilizer	Cell Counter	Glassware Washing Machine
Microscope	Vacuum Pump	Closed-Circuit TV
Washing-up Equipment	CO_2 Incubator	Colony Counter
Sterilizing & Drying Oven	Preparation & Quality Control	Cell sizing
Water Purification	Upright Microscope	Time-Lapse
Centrifuge	Temperature Recorder	Cinemicrography
Cell Freezing	Bulk culture	Controlled-Rate Cooler
	Pipette Aids &	Centrifugal Elutriator
	Automatic Pipetting	Fluorescence-Activated Cell Sorter

Types of animal cell culture

Based on the number of cell division, cell culture can be classified as primary cell culture and cell lines.

Cell lines can undergo finite or infinite cell divisions.

A. Primary cell culture

This is the cell culture obtained straight from the cells of a host tissue. The cells dissociated from the parental tissue are grown on a suitable container and the culture thus obtained is called primary cell culture. Such culture comprises mostly heterogeneous cells and most of the cells divide only for a limited time. However, these cells are much similar to their parents.

When cells are surgically removed from an organism and placed into a suitable culture environment, they will attach, divide and grow. This is called a Primary Culture. There are two basic methods for doing this.

First, for Explant Cultures, small pieces of tissue are attached to a glass or treated in a plastic culture vessel and bathed in culture medium. After a few days, individual cells will move from the tissue explant onto the culture vessel surface or substrate where they will begin to divide and grow.

The second, more widely used method, speeds up this process by adding digesting (proteolytic) enzymes, such as trypsin or collagenase, to the tissue fragments to dissolve the cement holding the cells together. This creates a suspension of single cells that are then placed into culture vessels containing culture medium and allowed to grow and divide. This method is called Enzymatic Dissociation.

Depending on their origin, primary cells grow either as an adherent monolayer or in a suspension.

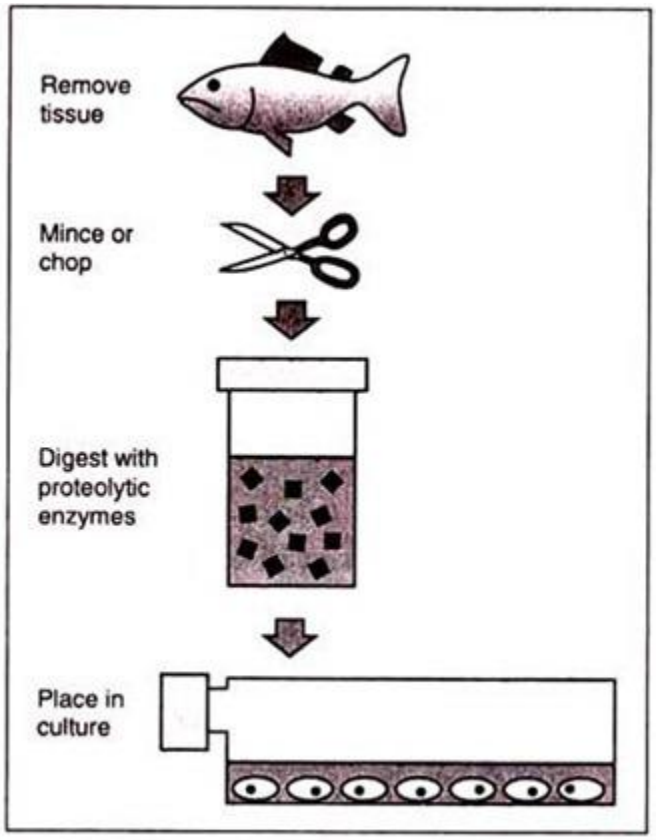


Fig. 13.2: The basic steps of Primary cell culture

i. Adherent cells

These cells are anchorage dependent and propagate as a monolayer. These cells need to be attached to a solid or semi-solid substrate for proliferation. These adhere to the culture vessel with the use of an

extracellular matrix which is generally derived from tissues of organs that are immobile and embedded in a network of connective tissue. Fibroblasts and epithelial cells are of such types.

When the bottom of the culture vessel is covered with a continuous layer of cells, usually one cell in thickness, these are known as monolayer cultures. Majority of continuous cell lines grow as monolayers. As being single layers, such cells can be transferred directly to a cover slip to examine under microscope.

ii. Suspension cells

Suspension cells do not attach to the surface of the culture vessels. These cells are also called anchorage independent or non-adherent cells which can be grown floating in the culture medium. Hematopoietic stem cells (derived from blood, spleen and bone marrow) and tumor cells can be grown in suspension. These cells grow much faster which do not require the frequent replacement of the medium and can be easily maintained. These are of homogeneous types and enzyme treatment is not required for the dissociation of cells; similarly these cultures have short lag period.

Confluent culture and the necessity of sub-culture

After the cells are isolated from the tissue and proliferated under the appropriate conditions, they occupy all of the available substrate i.e. reach confluence. For a few days, it can become too crowded for their container and this can be detrimental to their growth, generally leading to cell death if left for a long time. The cells thus have to be subculture i.e. a portion of cells is transferred to a new vessel with fresh growth medium which provides more space and nutrients for the continual growth of both portions of cells. Hence subculture keeps cells healthy and in a growing state.

A passage number refers specifically to how many times a cell line has been sub-cultured. In contrast with the population doubling level in that the specific number of cells involved is not relevant. It simply gives a general indication of how old the cells may be for various assays.

B. Secondary cell culture and cell line

When a primary culture is sub-cultured, it is known as secondary culture or cell line or sub-clone. The process involves removing the growth media and disassociating the adhered cells (usually enzymatically).

Sub-culturing of primary cells to different divisions leads to the generation of cell lines. During the passage, cells with the highest growth capacity predominate, resulting in a degree of genotypic and phenotypic uniformity in the population. However, as they are sub-cultured serially, they become different from the original cell.

On the basis of the life span of culture, the cell lines are categorized into two types:

I. Finite cell lines

The cell lines which go through a limited number of cell division having a limited life span are known as finite cell lines. The cells passage several times and then lose their ability to proliferate, which is a genetically determined event known as **senescence**. Cell lines derived from primary cultures of normal cells are finite cell lines.

II. Continuous cell lines

When a finite cell line undergoes transformation and acquires the ability to divide indefinitely, it becomes a continuous cell line. Such transformation/mutation can occur spontaneously or can be chemically or virally induced or from the establishment of cell cultures from malignant tissue. Cell cultures prepared in this way can be sub-cultured and grown indefinitely as permanent cell lines and are immortal.

These cells are less adherent, fast growing, less fastidious in their nutritional requirements, able to grow up to higher cell density and different in phenotypes from the original tissue. Such cells grow more in suspension. They also have a tendency to grow on top of each other in multilayers on culture-vessel surfaces.

Common cell lines

Human cell lines:

1. MCF-7 (breast cancer)
2. HL 60 (Leukemia)
3. HeLa (Human cervical cancer cells)

Primates cell lines: Vero (African green monkey kidney epithelial cells)

Cell strain

Lineage of cells originated from the primary culture is called strain. These are either derived from a primary culture or a cell line by the positive selection or cloning of cells having specific properties or characteristics. A cell strain often acquires additional genetic changes subsequent to the initiation of the parent line.

Types of Cells:

Cultured cells are usually described based on their morphology (shape and appearance) or their functional characteristics.

There are three basic morphologies:

1. Epithelial:

Like: cells that are attached to a substrate and appear flattened and polygonal in shape.

2. Lymphoblast-Like:

Cells that do not attach normally to a substrate but remain in suspension with a spherical shape.

3. Fibroblast-Like:

Cells that are attached to a substrate and appear elongated and bipolar, frequently forming swirls in heavy cultures. It is important to remember that the culture conditions play an important role in determining shape and that many cell cultures are capable of exhibiting multiple morphologies.

Using cell fusion techniques, it is also possible to obtain hybrid cells by fusing cells from two different parents. These may exhibit characteristics of either parent or both parents. This technique was used in 1975 to create cells capable of producing custom tailored monoclonal antibodies.

These hybrid cells (called Hybridomas) are formed by fusing two different but related cells. The first is a spleen-derived lymphocyte that is capable of producing the desired antibody. The second is a rapidly dividing myeloma cell (a type of cancer cell) that has the machinery for making antibodies but is not programmed to produce any antibody.

The resulting hybridomas can produce large quantities of the desired antibody. These antibodies, called Monoclonal Antibodies due to their purity, have many important clinical, diagnostic, and industrial applications with a yearly value of well over a billion dollars.

Methods

Growth Requirements

The culture media used for cell cultures are generally quite complex, and culture condition widely varies for each cell type. However, media generally include amino acids, vitamins, salts (maintain osmotic pressure), glucose, a bicarbonate buffer system (maintains a pH between 7.2 and 7.4), growth factors, hormones, O_2 and CO_2. To obtain best growth, addition of a small amount of blood serum is usually necessary, and several antibiotics, like penicillin and streptomycin are added to prevent bacterial contamination.

Temperature varies on the type of host cell. Most mammalian cells are maintained at 37°C for optimal growth, while cells derived from cold-blooded animals tolerate a wider temperature range (i.e. 15°C to 26°C). Actively growing cells of log phage should be used which divide rapidly during culture.

Process to obtain primary cell culture

Primary cell cultures are prepared from fresh tissues. Pieces of tissues from the organ are removed aseptically; which are usually minced with a sharp sterile razor and dissociated by proteolytic enzymes (such as trypsin) that break apart the intercellular cement. The obtained cell suspension is then washed

with a physiological buffer (to remove the proteolytic enzymes used). The cell suspension is spread out on the bottom of a flat surface, such as a bottle or a Petri dish. This thin layer of cells adhering to the glass or plastic dish is overlaid with a suitable culture medium and is incubated at a suitable temperature.

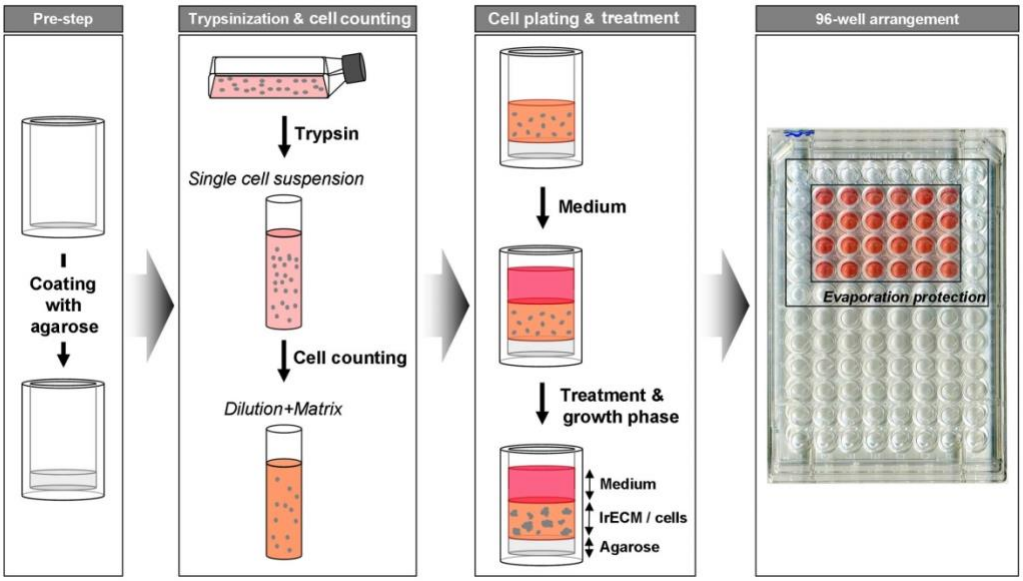
Aseptic techniques

Bacterial infections, like Mycoplasma and fungal infections, commonly occur in cell culture creating a problem to identify and eliminate. Thus, all cell culture work is done in a sterile environment with proper aseptic techniques. Work should be done in laminar flow with the constant unidirectional flow of HEPA filtered air over the work area. All the material, solutions and the whole atmosphere should be of contamination-free.

Cryopreservation

If a surplus of cells is available from sub-culturing, they should be treated with the appropriate protective agent (e.g., DMSO or glycerol) and stored at temperatures below –130°C until they are needed. This stores cell stocks and prevents original cell from being lost due to unexpected equipment failure or biological contaminations. It also prevents finite cells from reaching senescense and minimizes risks of changes in long term cultures.

When thawing the cells, the frozen tube of cells is warmed quickly in warm water, rinsed with medium and serum and then added into culture containers once suspended in the appropriate media.



Procedures of the following techniques were learnt:

Trypsinising cells

• To change the media in a 7d flask begin by placing the appropriate media in a warm water bath at 37°C.This should take about 5 to 10 mins

• Prepare the biosafety cabinet being sure to remember all aspect of proper sterile technique.

• Take out the T75 flask from the incubator and place it inside the hood.

• Take out a bottle of sterile PBS and spray it with isopropyl alcohol before placing it inside the hood.

• You will also need 3 10 mil pipettes, a 15 mil conical tube, a 1000 micro litre pipettor , a bottle of warm media and tube of trypsin.

• Spray all items and place inside the hood

• Aspirate the media in the flask using a 10 mil pipette and discard into the waste beaker.

• Change the pipette so that you are using a clean pipette to rinse the flask with PBS.

• Aspirate 10 mils of the PBS and put it in the flask.

• Make sure the tips are always sterile.

• After letting the PBS sit in the flask for a minute or two swirl it around to make sure the entire flask is covered. Then aspirate the PBS and discard it into the waste beaker.

• Take the 1000 micrometer pipette and adjust it to the desired volume of 1000 microlitres.

• Carefully aspirate 1000 microlitres of trypsin and put it into the flask.

• Swirl the trypsin to completely cover the flaks by rocking the flask.

• After all of the cells have been covered with trypsin , remove the trypsin from the flask and discard in the waste beaker.

• Place the flask inside the incubator for 5 mins

• After 5 mins take out the flask. Add 10 ml of media to the flask, spraying the inside surface of the flask to disperse the cells.

• Pipette the media up and down and continue to spray the surface of the flask a few times to ensure that all cells have been dispersed.

• The media should turn cloudy.

• Aspirate all 10 ml of the media containing the dispersed cells and place it in a 15ml conical tube.

• From this point you can pass into these cells into another flask, count the cells using a hemocytometer, seeding experiment or cryogenically freeze them down for future use.

Aseptic Techniques

- Successful cell culture depends heavily on keeping the cells free from microorganism contamination. This can be accomplished with proper knowledge of sterile environments working slowly and deliberately and following all of the guidelines for sterile technique always wear basic personal protective equipment or PPE when working in the laboratory .
- Talk to the safety team at your Institute for your required PPE.
- Remember to review the MSDS information before working with any media or reagents.
- Wear closed toed shoes and clothes that cover your legs .
- Washing your hands before handling cells or performing culture work removes bacteria and microscopic dead skin particles .Dead skin cells can be a potential source of contamination
- 70% ethanol wash kills microorganisms that could contaminate the cultures
- Cleanliness is one of the most important parts of sterile technique. Always clean the hood before and after use. Spray alcohol should not be used in any area where a flame is being used due to the fire hazard.
- Remember to clean each item placed in the hood with ethanol. You may choose to spray the item before placing it in the hood or immediately after. You clean the item and place it into the cell culture hood put it in the correct position enter the hood with your hands in a forward motion try not to sweep across the front and disrupt the airflow.
- Proper setup of the cell culture hood includes not overcrowding the work surface, not only does this increase the risk of contamination through accidental touching but it also interrupts the airflow through the chamber which will not maintain the sterile field .For the same reason it is important to keep the front sash in the lower position when working.
- The basic idea is to keep your media and reagents sterile by only touching them with sterile objects.Using sterile media reagents and supplies is a big step in keeping your cultures free from contamination notice.
- How the cell culture hood is set up to make the following actions easier. The pipette aid is on the right side so you can easily control the pipetting in your right hand .Reagents are in the center back so you can easily open the bottles and pipette from them
- It is very important to have the setup in this manner so you're not crossing your hands or supplies over top of sterile items
- When opening the pipette package be sure the pipette does not touch anything non sterile. Grasp the pipette high on the neck insert the pipette into the pipette aid turn the desired measurement marks toward you and then discard the wrapper .Discard any pipette you accidentally contaminate.
- Opening your media reagents and supplies in the cell culture hood opening these items outside the sterile field will result contamination.

- When holding the cap it is important not to touch the inside edge or you could contaminate it. Replace the cap as soon as possible if you must set the cap down in order to free your hand set it down with the interior surface facing down .
- When pipetting try not to touch the pipette to anything non sterile particularly the outside of containers or contamination could result.
- each pipette should be used one time and discarded or washed if using glass pipettes
- Reusing pipettes by dipping directly into another media bottle or by leaving it standing in a media bottle increases your chances of spreading contamination.
- Gently mix the contents after supplementation.
- Labeling the bottle after supplementation is a good laboratory practice
- Sometimes you'll need to transfer large volumes of liquid from one container to another the best way to transfer is always to use a sterile pipette but with practice it is possible to aseptically pour you should pour quickly and deliberately using the front corner of the bottle to channel the liquid and improve the speed and accuracy of your pour. Any spills should be wiped with ethanol immediately.
- Wipe down the work surface with ethanol again and straighten up the hood before you leave.

Culture preparation and Plating

- These HEK two nine three cells were cultured in a tissue culture flask and maintained between 10 and 90 percent confluency in a humidified 37 degrees Centigrade ten percent CO2 incubator, the researcher confirms the correct density of cells using microscopy.
- Cell culture medium is removed from the cells.
- Then cells are washed one time with PBS.
- 4075 flask 2 milliliters of Tripoli trips and solution are added to detach cells from the plate.
- The cells are incubated with the trypsin solution for two minutes.
- After incubation, the researcher verifies under a microscope that the cells are detached and that all clumps are dispersed.
- Tripsinization is stopped by adding 10 milliliters of Assay medium to 4075 flask .cells in the assay medium are dispersed by pipetting up and down.
- The cell suspension is transferred to a conical tube.
- A hemocytometer is used to quantify. The number of cells in solution cells is counted in order to determine their concentration for subsequent assays.
- The cells are pelleted at 500G for five minutes at 18 degrees Centigrade.
- After centrifugation the supernatant is removed.
- The cells are re-suspended in Assay medium to achieve a final concentration of 1 million cells per milliliter.
- The cells are then pipetted into a 96-well plate.

- Cell-free assay medium was pipetted at 100 microliters / well around the perimeter of the plate as a background control.
- 90 ml of cell suspension were added to the remaining wells ,10 ml of DMSO solution were added to half of the wells as an unstimulated control. And 10 ml of forskolin solution were added to stimulate the cells in the remaining Wells.
- The plate was then incubated for 4 hours at 37 degrees centigrade and 10% CO2
- After incubation the researcher will add assay reagents to the plate and determine stimulated cell activity.

PASSAGING CELLS

- The growth of cells in culture follows a standard pattern a leg after seeding is followed by a period of exponential growth called The Log phase cells should be passage when they cover the plate or the cell density exceeds the capacity of the medium. maintaining log phase growth will maximize the number of healthy cells for your experiment .before retrieving your flasks from the incubator sterilize the hood and have all required supplies at hand.

- Examine your culture carefully for signs of contamination or deterioration handle the cells with care during transport.

- For adherent cells remove the spent medium from the flask using a sterile pipette.

- Rinse the cells with a balanced salt solution such as DPPS .make sure to use a salt solution without calcium and magnesium as these May inhibit your cell dissociation reagent.

- After rinsing the cells remove the salt solution .each time you aspirate liquid off the cells place the next Solution on quickly.

- Add your cell dissociation reagent to remove cells from the plate use just enough solution to cover the cell sheet consider using a gentle dissociation reagent such as triple Express to avoid damaging your cells during dissociation.

- Make sure that the solution completely covers the cells you may want to tap gently on the plate to help the cells detach.
- Use a microscope to confirm the cells have released from the flask.

- They will start to appear round as they release from the substrate and will move or slide with a flask is tilted .complete dissociation is necessary. Do not leave the dissociation reagent on too long, especially if you're using a reagent other than triple.

- You may choose to manually break up lingering clumps by repeatedly pipetting warmed medium over them .A single cell suspension is important to achieve an accurate cell count. If you are using trypsin, the collection medium will need serum or you'll need to use a trypsin inhibitor to inactivate the trypsin.If you're using triple inactivation is achieved by dilution alone. No Serum is needed.

- Transfer the cells to a conical tube and centrifuge to remove any residual dissociation reagent the speed and time of centrifugation will vary based on your cell type .after centrifugation You should have a well-formed pellet.

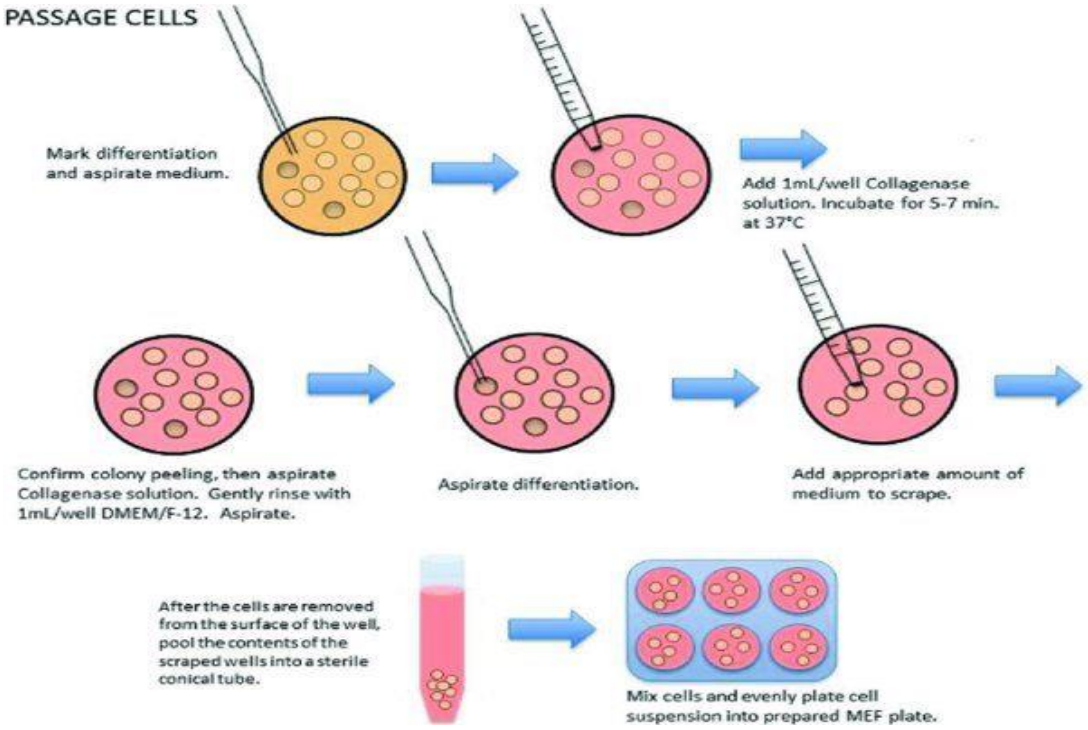
- Remove the medium from the centrifuge tube with a pipette and discard the medium into a waste container. Try not to disturb the pellet .Resuspend the palette with warm complete growth medium.

- Gentle pipetting will disperse the cells to ensure a homogeneous solution of single cells .remove a small sample for cell Counting.

- Trypan blue is used when counting cells to indicate the ratio of live to dead cells. The stain turns dead cells blue, but healthy cells with an intact membrane will remain white or colorless.

    - Using the microscope count the total number of cells and the number of dead or blue cells.Based on your cell count determine how much additional fresh medium to add for optimal seeding density add the required medium mix the cells gently and pipette the solution into fresh flasks.
    - Cap the vented caps on your flask tightly. If the Caps are not vented cap Loosely this keeps contamination out while allowing adequate gas exchange.
    - Use a north-south-east-west motion to evenly distribute the cells and transport the flasks to the incubator.
    - When passageing suspension cells, you'll begin by removing a small sample from the cell culture flask for counting. You'll follow the same counting procedure for adherent cells using trypan blue and either a hemocytometer or the Countess automated cell counter .based on your cell count add additional fresh medium to the flasks stay within the minimum and maximum volumes. This is important to maintain optimal air exchange and shaking flow. You may need to split the culture into multiple flasks.
    - Cap the flasks appropriately depending upon whether they are vented or not and return them to the incubator.

    - Every three weeks gently spin the cells remove the medium and replace with completely new medium. This eliminates cell debris and metabolic waste.



COUNTING CELLS

- A hemocytometer is a device that is used for counting cells. It's a modified microscope slide containing two identical Wells or Chambers into which a small volume of cell suspension is pipetted.
- Remove 100 microliters of our cell suspension and placed it in a microcentrifuge tube.

- Dilute the suspension by adding 100 microliters of trypan blue.

- Trypan blue is a Dye that helps distinguish between living and dead cells the dye passes through the membranes of dead cells. So they will appear blue under a microscope living cells exclude and will appear mostly clear.

- Load both Chambers by pipetting the suspension under the cover slip. Now place the hemocytometer under the microscope.

- Each chamber is divided into a grid pattern consisting of nine large squares. Each square has the same dimensions and contains 10 to the negative fourth power milliliters of suspension the rules for counting cells sometimes differ from Lab to lab in our lab. We count cells in the four large Corner squares and the Center Square.
- Count the cells in the first square. About the cells that are touching the outside boundaries of the square ,count the cells that touch the top and left boundaries and we ignore the cells that touch the right and bottom boundaries nine ten.

- We need to Count the number of both living and dead cells.

- Remember the dead cells will appear blue occasionally, you will see artifacts objects or debris that appear blurry and don't have a well-defined shape.

- Sometimes cells will appear as clumps or small groups. It may be difficult to determine exactly how many cells are in a group the method of counting clumps of cells differs from Lab to lab. So be sure to follow the procedure in your lab.

  To calculate the dilution factor:

- The dilution equals the final volume divided by the volume of cells.

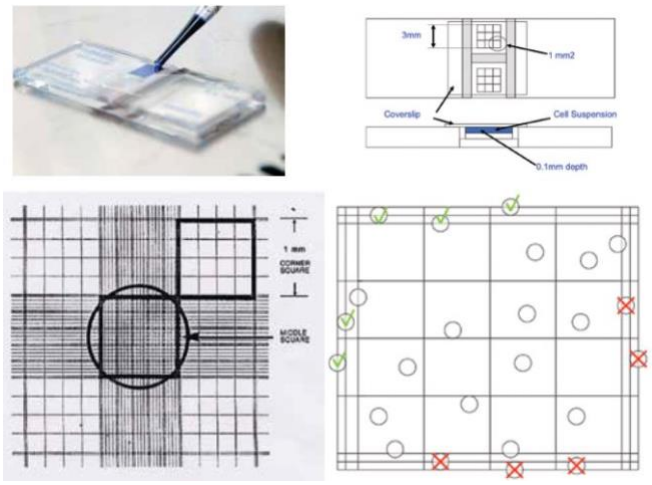


Fig: Counting cells using a hemocytometer and trypan blue. Viable cells contain intact cell membranes and do not uptake trypan blue, appearing bright/clear in the hemocytometer. Dead cells have damaged cell membranes and uptake trypan blue, appearing blue in the hemocytometer. Cell viability can be estimated by taking the ratio of live/dead cells.

PREVENTING CONTAMINATION

- Preventing contamination is an everyday task in cell culture. Avoiding contamination is much easier than dealing with it.

- One of the major sources of germ transfer is you the person working in the cell culture lab wearing personal protective equipment and applying constant aseptic techniques protects, not only yourself but also the cells you are working with After disinfection, let your hands dry before you start working.

- Make sure you have everything you need in the biological safety cabinet, but avoid an overcrowded workspace as the laminar air flow may be disturbed.

- Everything that is placed in the biosafety cabinet.

- The water bath represents a constant risk of germ transfer be sure that it is cleaned on a regular basis and add bacteria sites and fungicides to the water. Thoroughly disinfect every vessel you warm in the water bath only open sterile packages inside the cabinet work with one cell type at a time and disinfect the work surface in between seal packages with remaining product properly

- Before removing them from the cabinet in short easy access to all items in the cabinet and keep a clear workspace in the center of the cabinet. it Avoid leaving the incubator door open for long periods an additional glass door, not only allows monitoring the inside without disturbing the chamber environment. It also minimizes the risk of contaminants entering the incubator. New cells are a potential danger to the existing sell stocks keeps them in a designated incubator until proved absence of contaminants.

- When working with flasks caps can be held in the hand during petting but this requires practice and routine. Sometimes it is necessary to place the cap to one side. If the cap is placed inside down sterile SE cannot be absolutely guaranteed.

- If the cap is placed inside up Airborne particles or droplets can enter the cap by placing it onto its side. It is not in contact with the air flow or with the work surface.

- During all petting steps. Make sure the tip of the pipette does not touch areas that are not sterile the optimized geometry of the app and or flask not only reduces the risk of touching the neck with the pipette. It also provides improved access to the whole growth area.

- Unintentional removal of the lid presents a constant danger during transport and handling outside the cabinet.

- Eppendorf cell culture dishes have a corrugated handling ring that reduces this risk and also makes it easy to transport dishes Instax. Eppendorf cell culture plates have a lid. With support tabs, which minimize contact with the work surface if the lid is placed to one side. Thus the risk of germ transfer is reduced to a minimum. All eppendorf cell culture plates have a high contrast alphanumeric labeling for fast and easy. Well identification.

FREEZING CELLS

- A properly maintained Frozen sell stock is an important part of cell culture. It gives the opportunity to go back to early passage cells or Thalmor cells is needed in preparation for freezing. Be sure to label each vial with cell type passage number and date using a permanent marker.

- You will need pre-chilled freezing medium and Mr. Frosty container filled with isopropanol.
- The general freezing method is the same for suspension and adherent cells except that adherent cells need to be removed from the culture plates before starting the freezing procedure first. The conditioned media is aspirated off and discarded.
- The attached cells are washed with PBS.
- Then triple is added to dissociate the culture and detach the cells from the flask.
- If needed the flask can be tapped to dislodge and break up cell clumps cells from multiple plates should be collected into one or two 15 milliliter centrifuge tubes add medium to the cells.
- Mix gently and transfer to a centrifuge tube.
- No inactivation is necessary when using triple take a small sample for cell Counting.
- Make sure your tubes are balanced in the centrifuge.
- Spin down the cells to form a pellet while the cells are spinning count the sample for total cell number and percent viability.
- The Countess automated cell counter can be used for a fast and accurate reading make sure the percent viability is greater than 90% only healthy cells should be frozen.
- Optimal cell concentration for freezing varies by cell type also calculates the volume of freezing medium. You'll need based on the number of cells and concentration for each file.
- Once the centrifuge completely stops remove the tubes.
- Return to the hood and clean with ethanol remove and discard the medium paying close attention not to disturb the cell pellet.
- Resuspend the pellet in the correct volume of cold freezing medium for optimal cell density for freezing triturate the cells for a single cell suspension.
- Transfer approximately 1 milliliter of cell solution into each cryo vile.

- If you have a large volume resuspends the cells frequently. So they're homogeneous use the mr. Frosty container or similar device to ensure the cell solution decreases in temperature by one degree Celsius each minute slow regulated freezing minimizes cell damage.

- After freezing overnight at minus 80 degrees Celsius, the cells are frozen and ready for permanent storage in the liquid nitrogen tank always wear the appropriate protective equipment and handle liquid nitrogen carefully do not attempt to handle liquid nitrogen until you read and fully understand the potential hazards their consequences and the related safety precautions when transferring cryo vials. Don't let the cells solution begin thawing you risk decreasing selves.

- Ability freezing is a very stressful process for the cells make sure every step is performed quickly and carefully under optimal conditions of temperature medium formulation and freezing density.

Thawing of cells

- Always wear basic PPE and review the MSDS for safety information. DMSO and cell culture freezing medium is toxic.
- Thawing cells is a very stressful process for them to endure to aid your cell survival perform each step quickly and under optimal conditions such as temperature, medium formulation and seeding density.Clean and set up the cell culture hood before you remove the cells from liquid nitrogen storage.

- You will need 10 milliliters of pre-warmed medium and a cell culture flask.

    This protocol is the same for cells thawed into a suspension flask, but the flask used will be different.

- Be careful working with liquid nitrogen ,ask the safety team at your Institute. If you're unsure what your PPE requirements are or how to safely work with liquid nitrogen .working quickly so that no cells thaw while they're out of the liquid nitrogen storage tank pull the vial of cells you need and place in a cup of dry ice to keep them cold in transit to the water bath.

- The vial of cells should be thawed in a 37 degrees Celsius water bath quickly. Be careful not to submerge the vile as this increases the risk for contamination .remove the vial from the water bath when a small chunk of ice remains inside the ice chunk will melt as you move it to the cell culture hood. wipe the vial with ethanol before placing it in the hood working quickly use a small pipette to transfer the contents of the vial to a 15 milliliter centrifuge tube.

- Very carefully add 10 milliliters pre-warmed cell culture medium to the tube. Start to drop by drop then gradually increase your rate in order to avoid osmotic shock.

- Spinning the cells in the centrifuge allows removal of the freezing medium that contains DMSO the speed and time may vary based on the cell type. Some cell lines are too delicate to spin. So this step could be skipped in certain cases .follow the instruction of your laboratory manager if your cells are very delicate.

- Discard the medium by pouring pipetting or using a vacuum. Be careful not to disturb the cell pellet.

- Resuspend cells and appropriate volume usually 10 milliliters of complete pre-warmed medium.

- Medium volume, flask size and number of flasks plated will depend on the cell number Frozen in the vial and the optimal seeding density for the cells. Sometimes a viable cell count is required in order to determine the number of flasks and media volume to be used.

- With a north-south East-West rocking motion to ensure even distribution of the cells and solution .usually cells are checked a few hours later or the next day for good adhesion if adherent and proper morphology.

Subculture

Once you've established your primary cell culture, you might want to subculture or passage your cells.

- You should always refer to the product manual for your specific cell type.Gather all your materials in the hood and set up your instruments .Prepare the basal media and supplements for your particular cells by following the product instructions that are available online and label and date all medium bottles.

- Check your cells under the microscope to see that the confluency is about 80% and that there are mitotic cells present.

- Remove all the culture media from the flask and add nine mL of trypsin EDTA solution.

- Rock the flask to cover the entire surface. Immediately remove all nine mL of trypsin EDTA solution and add 3 mL of fresh troops in EDTA solution. incubate the flask at room temperature until the cells have become completely round which should take 1 to 20 minutes depending on the cell types and use of a coding Matrix. refer to the product manual for incubation times for your cell type a quick inspection under the microscope to confirm dissociation is highly recommended.

- Remaining adherent cells can be dislodged from the surface of the flask by wrapping the flask very gently.

- It is important to not over trypsinise your cells .Following Detachment add 9 ml of tripsyin neutralizer to the flask transfer the cells to a 50 ml conical tube.

- Pipette another nine ml of trypsin neutralizer solution over the flask surface to remove any remaining cells add this solution to the 50 ml conical tube.

- Centrifuge the cells at a 180G for seven minutes. It is very important not to apply excessive G-Force.

- Observe the cell pellet and then carefully remove the supernatant from the tube without disturbing the cell pellet.

- Resuspend the cell pellet in 12 ml supplement medium or an appropriate volume depending on your application gently pipettes the cells up and down with a 10 mL pipette to mix well.

- Determine the concentration of cells in the suspension and then dilute the cells and supplemented medium and Seed new culture vessels at the appropriate density and return them to the incubator.

- You've now successfully subculture primary cells and are ready for any experiments you would like to run.

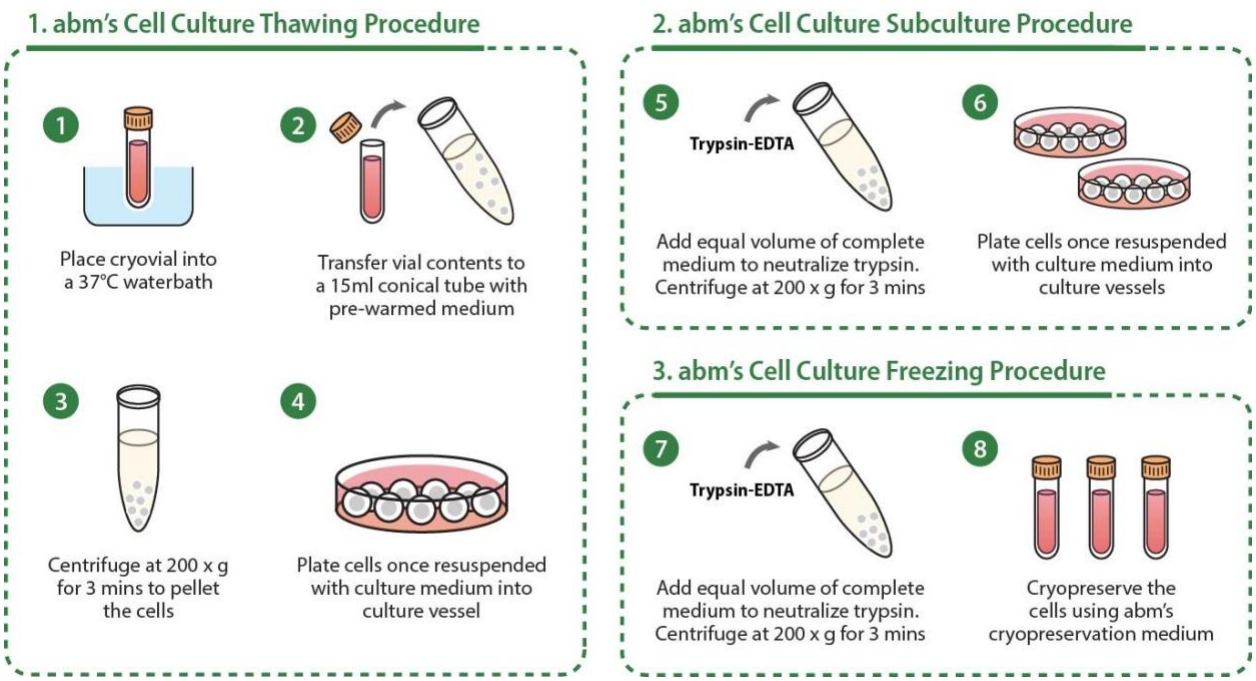


Fig:Thawing, subculturing and freezing prcedures at a glance: Thawing, subculturing and freezing must be done as quickly as possible as excess time outside of their preferred media can result in cell damage.

Applications of Animal Cell Culture:

A. Model Systems:

Cell cultures provide a good model system for studying;

a. Basic cell biology and biochemistry.

b. The interactions between disease-causing agents and cells.

c. The effects of drugs on cells.

d. The process and triggers for aging.

f. Nutritional studies.

B. Toxicity Testing:

Cultured cells are widely used alone or in conjunction with animal tests to study the effects of new drugs, cosmetics and chemicals on survival and growth in a wide variety of cell types. Especially important are liver and kidney derived cell cultures.

C. Cancer Research:

Since both normal cells and cancer cells can be grown in culture, the basic differences between them can be closely studied. In addition, it is possible, by the use of chemicals, viruses and radiation, to convert normal cultured cells to cancer causing cells.

Thus, the mechanisms that cause the change can be studied. Cultured cancer cells also serve as a test system to determine suitable drugs and methods for selectively destroying types of cancer.

D. Virology:

One of the earliest and major uses of cell culture is the replication of viruses in cell cultures (in place of animals) for use in vaccine production. Cell cultures are also widely used in the clinical detection and isolation of viruses, as well as basic research into how they grow and infect organisms.

E. Cell-Based Manufacturing:

While cultured cells can be used to produce many important products, three areas are generating the most interest.

The first is the large-scale production of viruses for use in vaccine production. These include vaccines for polio, rabies, chicken pox, hepatitis B and measles.

The second is the large-scale production of cells that have been genetically engineered to produce proteins that have medicinal or commercial value. These include monoclonal antibodies, insulin, hormones, etc. The third is the use of cells as replacement tissues and organs. Artificial skin for use in treating burns and ulcers is the first commercially available product.

However, testing is underway on artificial organs such as pancreas, liver and kidney. A potential supply of replacement cells and tissues may come out of work currently being done with both embryonic and adult stem cells.

These are cells that have the potential to differentiate into a variety of different cell types. It is hoped that learning how to control the development of these cells may offer new treatment approaches for a wide variety of medical conditions.

F. Genetic Counselling:

Amniocentesis, a diagnostic technique that enables doctors to remove and culture fetal cells from pregnant women, has given doctors an important tool for the early diagnosis of fetal disorders. These cells can then be examined for abnormalities in their chromosomes and genes using karyotyping, chromosome painting and other molecular techniques.

G. Genetic Engineering:

The ability to transfect or reprogram cultured cells with new genetic material (DNA and genes) has provided a major tool to molecular biologists wishing to study the cellular effects of the expression of these genes (new proteins).

These techniques can also be used to produce these new proteins in large quantity in cultured cells for further study. Insect cells are widely used as miniature cells factories to express substantial quantities of proteins that they manufacture after being infected with genetically engineered baculoviruses.

H. Drug Screening and Development:

Cell-based assays have become increasingly important for the pharmaceutical industry, not just for cytotoxicity testing but also for high throughput screening of compounds that may have potential use as drugs. Originally, these cell culture tests were done in 96 well plates, but increasing use is now being made of 384 and 1536 well plates.

I. Gene Therapy:

In modern molecular biology, Gene Therapy is an experimental technique that involves insertion of cloned/altered genes into cells using r-DNA technology to replace defective genes causing genetic abnormalities or to prevent potential disorders.

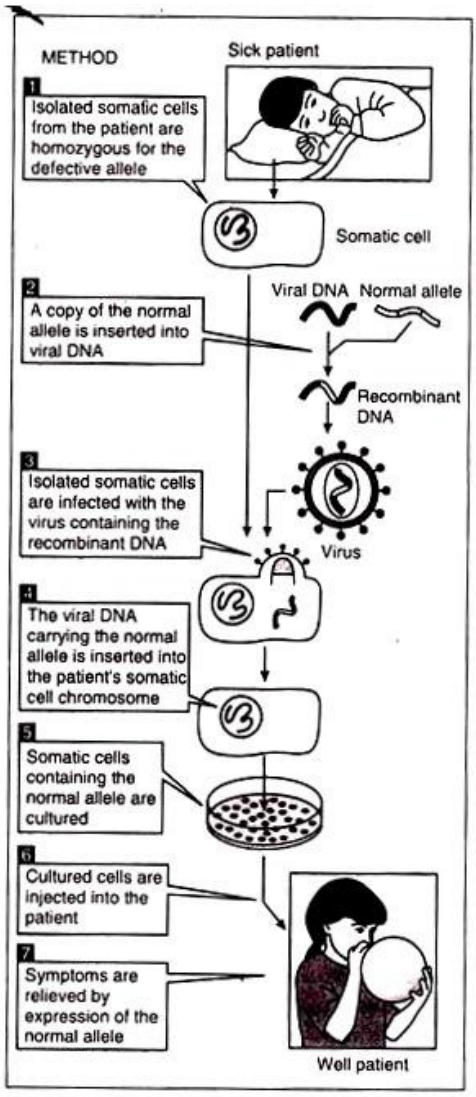


Fig. 13.5: The Principle behind Gene Therapy

Followings are the purpose of Gene Therapy:

a. Swapping harmful mutant alleles with functional ones by selective reverse mutation.

b. Deactivating improperly functioning mutated gene.

c. Inserting a new gene into the body to help battle a disease.

d. Interchanging non-functional gene with normal gene through homologous recombination.

REFERENCES:

1. https://www.biotechnologynotes.com/animals/animal-cell-culture-history-types-and-applications/671

2. https://microbeonline.com/animal-cell-culture-introduction-types-methods-applications/
3. Yao, Tatsuma, and Yuta Asayama. "Animal-cell culture media: History, characteristics, and current issues." Reproductive medicine and biology 16.2 (2017): 99-117.
4. Nema, Rajeev, and Sarita Khare. "An animal cell culture: Advance technology for modern research." (2012).
5. https://www.youtube.com/watch?v=7hEUmLz1Ew0
6. https://www.youtube.com/watch?v=nr1tV_LuqJk
7. https://www.youtube.com/watch?v=CMRKKl9XSDU
8. https://www.youtube.com/watch?v=6vchql21tEE
9. https://www.youtube.com/watch?v=pP0xERLUhyc
10. https://www.youtube.com/watch?v=P4dTbKVDIZ4
11. https://www.youtube.com/watch?v=tCNtKrxlZPs
12. https://www.youtube.com/watch?v=4HxqQOHifkU
13. https://www.youtube.com/watch?v=k2PMEET4Smo

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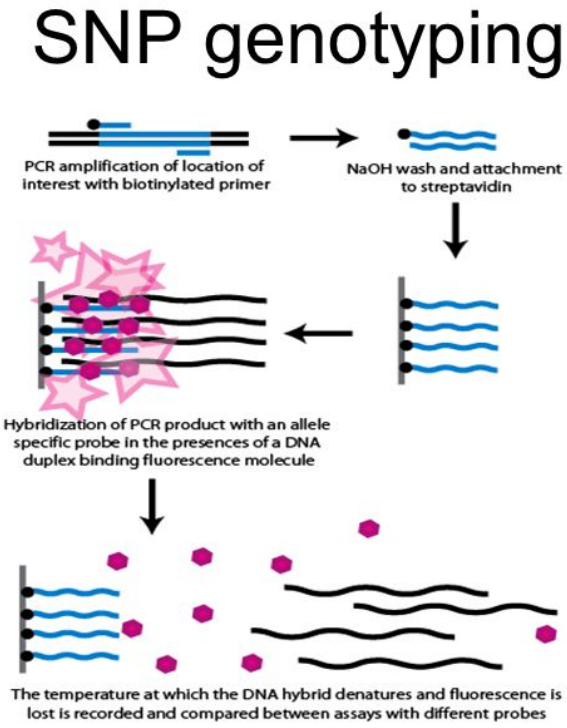
Topic: Genotyping single nucleotide polymorphisms applying ARFLP-PCR method

INTRODUCTION

Single nucleotide polymorphisms, frequently called SNPs (pronounced “snips”), are the most common type of genetic variation among people. Each SNP represents a difference in a single DNA architecture block, called a nucleotide. For example, a SNP may alter the nucleotide cytosine (C) with the nucleotide thymine (T) in a certain stretch of DNA.

SNPs occur commonly throughout a person’s DNA. They occur about already in every 1,000 nucleotides on average, which means there are almost 4 to 5 million SNPs in a person's genome. These variations may be unique or occur in many individuals.

Most SNPs accept no effect on health or development. Some of these genetic differences, however, have proven to be actual important in the study of human health. Researchers have found SNPs that may help predict an individual’s response to certain drugs, susceptibility to ecology factors such as toxins, and accident of developing accurate diseases. SNPs can also be used to track the inheritance of disease genes within families. Future studies will assignment to analyze SNPs associated with circuitous diseases such as heart disease, diabetes, and cancer.



PCR-ARFLP is similar to PCR-RFLP, the only difference is that, in this process the mutagenic primers are used to create a restriction enzyme site and amplify the desired DNA segment.

Restriction analysis of polymerase chain reaction (PCR) products is one of the earliest techniques used for analyzing amplification products. This approach is applicable for distinguishing alleles in which the polymorphic residue results in the creation or removal of a restriction enzyme site. Unfortunately, many polymorphisms are not associated with restriction enzyme site change and thus are not amenable to this analysis. However, by using site-directed mutagenesis using primers with mismatches near the 3' ends, it is possible to create an artificial restriction fragment length polymorphism (A-RFLP) for almost all naturally occurring DNA polymorphisms.

In Artificial RFLP, a restriction site to study the SNP is created using a mutagenic primer. Primer mutagenesis is done near the 3' end of DNA sequence so that the new primer at 3'end could encompass mutation in the created restriction enzyme site. Such that, the sequence containing SNP could only be digested if it is recognized by restriction enzyme. The whole process contains following steps,

1. Designing of Mutagenic primer with 3' end mismatch,
2. Optimization of PCR reaction.

3. PCR Amplification of the desired region of the genome followed by agarose gel electrophoresis to check whether the desired region is amplified or not.
4. Restriction digestion using a specific restriction endonuclease enzyme.
5. Gel electrophoresis of digested products to check the results of restriction digestion reaction and the genotypes.

MATERIALS AND METHODS

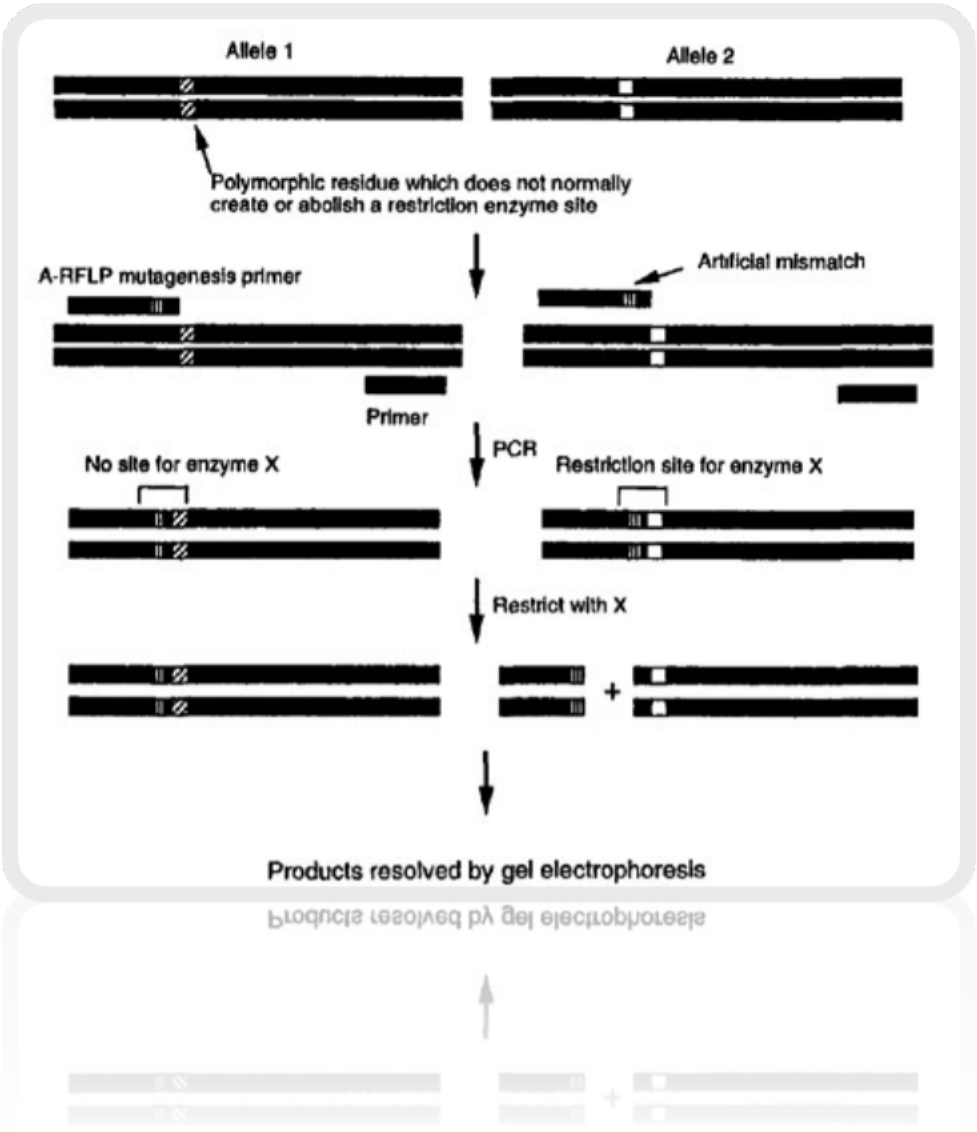
A- DNA Isolation using Inorganic method

1- To 300ul of blood sample, RBC lyses buffer (three times the volume of blood sample taken) is added, shaken at room temperature until the RBCs are completely lysed.
2- Centrifuge at 13,000 rpm for 1 minute to obtain creamish white WBC pellet.
3- The supernatant is discarded and the WBC pellet is suspended in 300 ul TE buffer (pH 8.0), using a vortexing machine. Thereafter, 20 ul of 10% SDS solution is added and the mixture is incubated at 56 degree for 30 minutes on dry bath.
4- To the above solution 150 ul of 7.5M ammonium acetate is added, centrifuged at 13,000rpm, at RT, for 15 minutes.
5- The clear supernatant is transferred to a fresh sterile micro-centrifuge tube. To this chilled absolute ethyl alcohol is added (twice the vol of clear supernatant) (mixed gently).
6- The genomic DNA precipitates to be centrifuged at 13,000 rpm for 10 min. The latter should be subsequently washed in 150 ul of 70% ethanol and air dried at RT for 10-15 minutes.

100 ul of TE buffer (pH 7.3), incubated at 65 degree Celsius for 10 minutes. The dissolved DNA was finally stored at 20 degree C till further use.

B- ARFLP-PCR

Methodology:



RESULT

Single-nucleotide polymorphisms play an important role in the susceptibility of many diseases, evolutionary studies, and genetic mapping. The rs4958843 in IRGM promoter is associated with

tuberculosis and Crohn's disease. As this SNP is not present in any of the restriction sites, PCR -RFLP is not possible. Therefore, there has been developed an artificial-RFLP method to genotype this SNP.

Results of sequencing and A-RFLP were concordant. The developed method was applied to genotype this polymorphism in 100 samples from healthy individuals. The allelic frequencies of SNP rs4958843 were C (0.16) and T (0.84), while corresponding genotypic distribution was CC (2), CT (29), and TT (69).

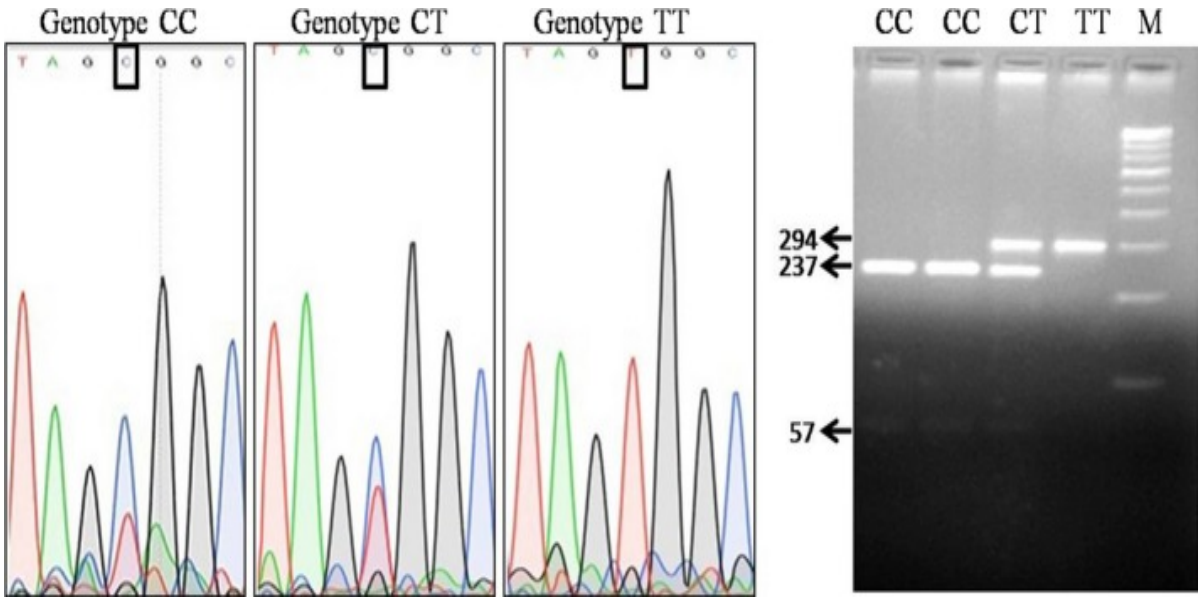


Figure 1

Representative chromatogram of control samples sequenced for rs4958843 showing genotypes (CC, CT, and TT) along with representative agarose gel electrophoresis, arrows indicate the DNA fragments (294, 237, and 57bp) obtained after restriction digestion with NheI enzyme. M in the gel indicates DNA marker and genotype of the sample is shown on the top

CONCLUSION

The newly developed method is simple, easy, and cost-effective which could be used to genotype IRGM polymorphism -1161 C/T (rs4958843) in various populations in the replication studies and has its applicability in the clinical settings. The developed method was applied for genotyping samples from healthy individuals from North India. For the first time, there

shown a report analysing the frequency of this polymorphism from this region.

Supervisor Signature: 

IMMOBLISATION OF ENZYMES, ECONOMICAL AND COMMERCIAL USES, AND THEIR METHODS AND CHARACTERIZATION TECHNIQUES

Report submitted by :

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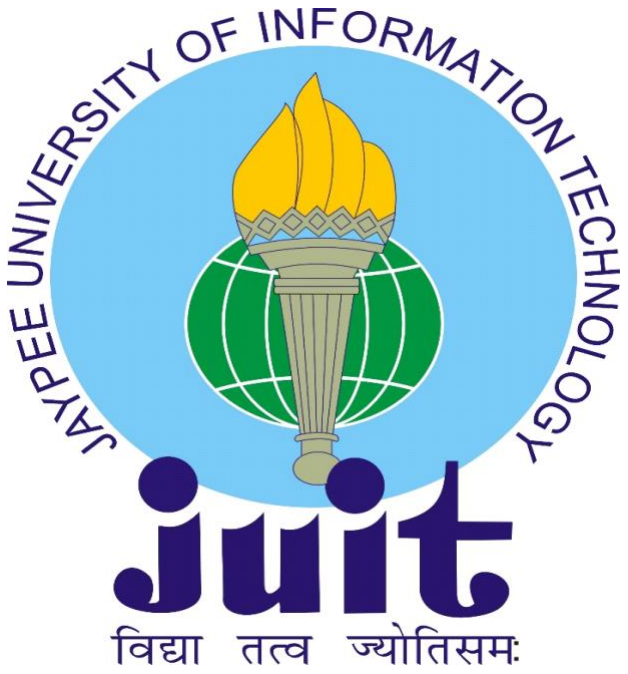
171840

Under the supervision of :

Dr. Ashok Kumar Nadda



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INTRODUCTION

Immobilization is defined as the imprisonment of cell or enzyme in a distinct support or matrix. The support or matrix on which the enzymes are immobilized allows the exchange of medium containing substrate or effector or inhibitoe molecules. The practice of immobilization of cells is very old and the first immobilized enzyme was animo acylase of Aspergillus oryzae for the rpoduction of L-animo acids in Japan.

It can be done by various techniques like adsorption, adhesion, covalent binding, cross-linking, encapsulation and inclusion. Every technique has it’s own advantages and disadvantages and are thus used for different operations.

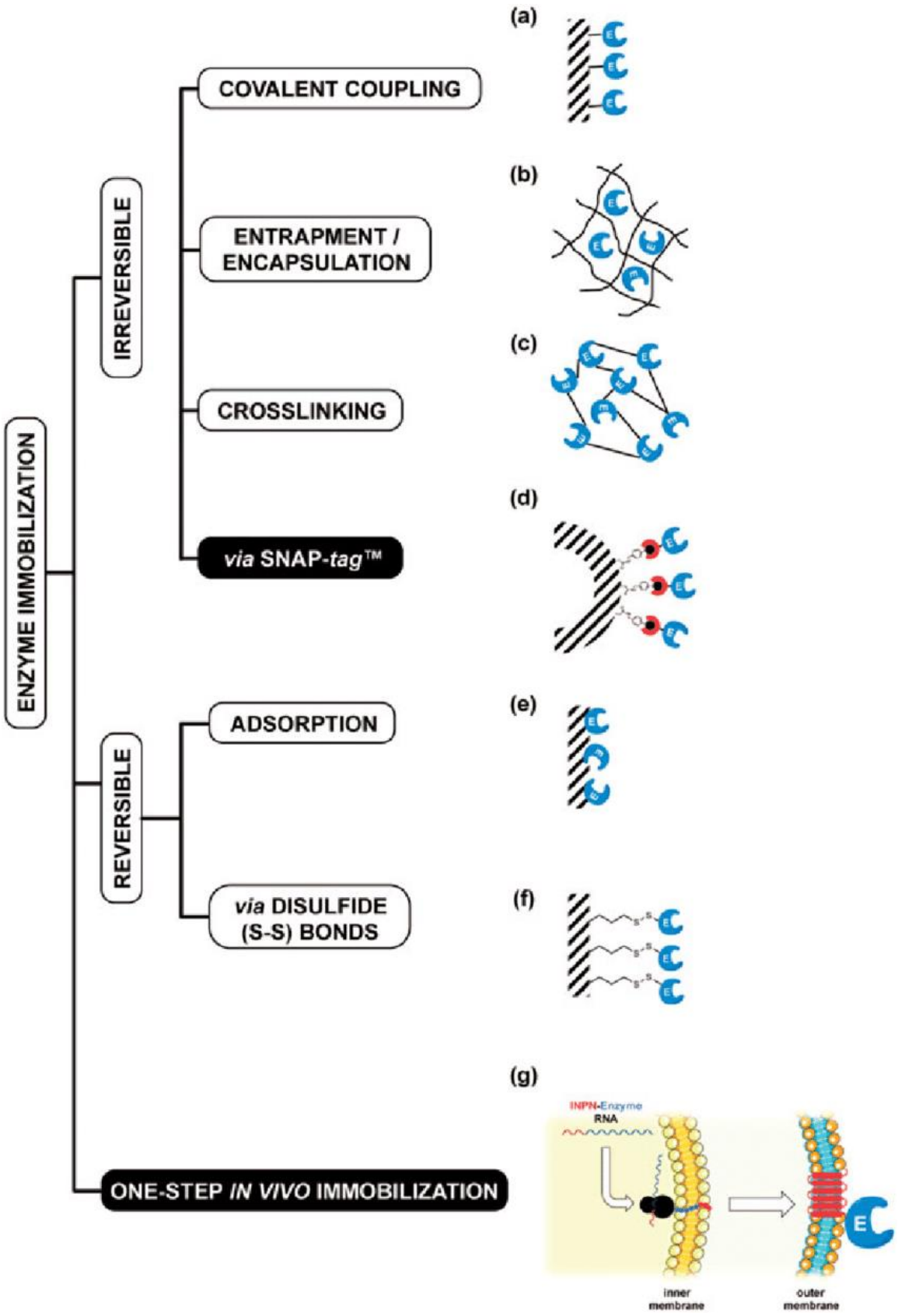
ENZYME IMMOBILIZATION
IRREVERSIBLE
COVALENT COUPLING
ENTRAPMENT / ENCAPSULATION
CROSSLINKING
via SNAP-tag™
REVERSIBLE
ADSORPTION
via DISULFIDE (S-S) BONDS
ONE-STEP IN VIVO IMMOBILIZATION
(a)
(b)
(c)
(d)
(e)
(f)
(g)
INPN-Enzyme
RNA
inner membrane
outer membrane

Figure : This figure represents enzyme immobilisation techniques.

Methods of immobilization of an enzyme

There are various ways by which one can immobilize an enzyme:

- Affinity-tag binding: Enzymes may be immobilized to a surface, e.g. in a porous material, using non-covalent or covalent Protein tags. This technology has been established for protein purification purposes. This technique is the generally applicable, and can be performed without prior enzyme purification with a pure preparation as the result. Porous glass and derivatives thereof are used, where the porous surface can be adapted in terms of hydrophobicity to suit the enzyme in question.[4]
- Adsorption on glass, alginate beads or matrix: Enzyme is attached to the outside of an inert material. In general, this method is the slowest among those listed here. As adsorption is not a chemical reaction, the active site of the immobilized enzyme may be blocked by the matrix or bead, greatly reducing the activity of the enzyme.
- Entrapment: The enzyme is trapped in insoluble beads or microspheres, such as calcium alginate beads. However, these insoluble substances hinder the arrival of the substrate, and the exit of products.
- Cross-linkage: Enzyme molecules are covalently bonded to each other to create a matrix consisting of almost only enzyme. The reaction ensures that the binding site does not cover the enzyme's active site, the activity of the enzyme is only affected by immobility. However, the inflexibility of the covalent bonds precludes the self-healing properties exhibited by chemoadsorbed self-assembled monolayers. Use of a spacer molecule like poly(ethylene glycol) helps reduce the steric hindrance by the substrate in this case.

- Covalent bond: The enzyme is bound covalentely to an insoluble support (such as silica gel or macroporous polymer beads with epoxide groups). This approach provides the strongest enzyme/support interaction, and so the lowest protein leakage during catalysis.

Why is enzyme immobilization important?

Immobilized enzymes are very important for commercial uses as they possess many benefits to the expenses and processes of the reaction of which include: ... Stability: Immobilized enzymes typically have greater thermal and operational stability than the soluble form of the enzyme.

Parameters to consider while immobilising enzymes:

- The support material provides high internal surface area and maximizes the specific activity of the enzymes.
- Interactions between the support surface and the enzymes is also critical.

Random versus Site-directed Enzyme Immobilization

Numerous enzymes of biotechnological importance have been immobilized on various supports (inorganic, organic, composite and nanomaterials) via random multipoint attachment. However, immobilization via random chemical modification results in a heterogeneous protein population where more than one side chains (amino, carboxyl, thiol etc) present in proteins are linked with the support with potential reduction in activity due to restriction of substrate access to the active site.

In contrast, in site-directed enzyme immobilization, the support can be linked to a single specific amino acid (generally N- or C-termini) in a protein molecule away from the active-site. This way maximal enzyme activity is retained due to the free access of the substrate to the active-site. These

strategies are mainly chemical but may additionally require genetic and enzymatic methods to generate functional groups (that are absent in protein) on the support and enzyme.

The choice of SDCM method depends on many factors, such as the type of enzyme (less stable psychrophilic, or more stable thermophilic homologue), pH stability of enzyme, the availability of N- or C-termini to the reagent, non-interference of the enzyme terminus with the enzyme activity, type of catalytic amino acid residue, the availability, price and the ease of preparation of reagents. For example, the generation of complementary clickable functionalities (alkyne and azide) on the support and enzyme is one of the most convenient way for immobilizing enzymes via site-directed chemical modification.

Advantages of immobilized enzymes:

i. Increased functional efficiency of enzyme
ii. Enhanced reproducibility of the process they are undertaking
iii. Reuse of enzyme
iv. Continuous use of enzyme
v. Less labour input in the processes
vi. Saving in capital cost and investment of the process
vii. Minimum reaction time
viii. Less chance of contamination in products
ix. More stability of products
x. Stable supply of products in the market
xi. Improved process control
xii. High enzyme substrate ratio

Disadvantages of enzyme immobilization:

i. Even though there are many advantages of immobilized enzymes, there are some disadvantages also.

ii. High cost for the isolation, purification and recovery of active enzyme (most important disadvantage)

iii. Industrial applications are limited and only very few industries are using immobilized enzymes or immobilized whole cells.(4). Catalytic properties of some enzymes are reduced or completely lost after their immobilization on support or carrier.

iv. Some enzymes become unstable after immobilization.

v. Enzymes are inactivated by the heat generated in the system

Applications of enzyme immobilization:

(1). Industrial production: Industrial production of antibiotics, beverages, amino acids etc. uses immobilized enzymes or whole cells.

(2). Biomedical applications: Immobilized enzymes are widely used in the diagnosis and treatment of many diseases. Immobilized enzymes can be used to overcome inborn metabolic disorders by the supply of immobilized enzymes. Immobilization techniques are effectively used in drug delivery systems especially to oncogenic sites.

(3). Food industry: Enzymes like pectinases and cellulases immobilized on suitable carriers are successfully used in the production of jams, jellies and syrups from fruits and vegetables.

(4). Research: A Research activity extensively uses many enzymes. The use of immobilized enzyme allow researcher to increase the efficiency of different enzymes such as Horse Radish Peroxidase (HRP) in blotting experiments and different Proteases for cell or organelle lysis.

(5). Production of bio-diesel from vegetable oils.

(6). Waste water management: treatment of sewage and industrial effluents.

(7). Textile industry: scouring, bio-polishing and desizing of fabrics.

(8). Detergent industry: immobilization of lipase enzyme for effective dirt removal from cloths.

Supports or Matrix used in immobilization technology:

The matrix or support immobilizes the enzyme by holding it permanently or temporarily for a brief period of time. There are a wide variety of matrixes or carriers or supports available for immobilization. The matrix used should be cheap and easily available. Their reaction with the components of the medium or with the enzyme should be minimum as possible. The matrixes or supports for immobilization of enzymes or whole cells are grouped into three major categories

(1). Natural polymers:

(a). Alginate: A natural polymer derived from the cell wall of some algae. Calcium or magnesium alginate is the most commonly used matrix. They are inert and have good water holding capacity.

(b). Chitosan and chitin: They are structural polysaccharides occurring naturally in the cell wall of fungi and the exoskeleton of Arthropods. The various functional groups in enzymes can bind to the – OH group of chitin and can form covalent bonds.

(c). Collagen: It is the protenaceous support with good porosity and water holding capacity. The side chains of the amino acids in the collagen and that of enzyme can form covalent bonds to permanently hold the enzyme to the support.

(d). Carrageenan: It is a sulfated polysaccharide obtained from some red algae. Their good gelling properties together with its high protein holding capacity makes it good support for immobilizing enzymes.

(e). Gelatin: Gelatin is the partially hydrolyzed collagen with good water holding capacity.

(f). Cellulose: Most abundant polymer of nature and it is the cheapest support available as carrier of enzymes. The hydroxyl group of the monomer units (glucose) can form covalent bonds with that of the amino acids of enzyme.

(g). Starch: A natural polymer of amylose and amylo-pectin. It has good water holding capacity.

(h). Pectin: It is a structural polysaccharide of plants found in their primary cell wall and they also acts as the inter-cellular cementing material in plant tissues. Pectin is a gelling agent with good water holding capacity.

(2). Synthetic polymers:

They are ion exchange resins or polymers and are insoluble supports with porous surface. Their porous surface can trap and hold the enzymes or whole cells. Example: Diethylaminoethyl cellulose (DEAE cellulose), Polyvinyl chloride (PVC), UV activated Polyethylene glycol (PEG)

(3). Inorganic materials:

(a). Zeolites: They are microporous, aluminosilicate minerals with good adsorbing properties and extensively used for immobilizing enzymes and whole cells.

(b). Ceramics: They are nonmetallic solids consisting of metal and nonmetal atoms held in ionic and covalent bonds. The composition and bonding pattern varies with different types.

(c). Diatomaceous earth: They are silicious sedimentary rocks formed by fossilized accumulations of the cell wall of diatoms. Celite is the trade name of diatomaceous earth. It is a good adsorbent and are resistant to high pH and temperature.

(d). Silica:

(e). Glass:

(f). Activated carbon

(g). Charcoal

Immobilization efficiency: Immobilization efficiency is the protein binding capacity of a particular matrix/support that you are using. The percent of the total protein bound onto the matrix indicate its immobilization efficiency.

Immobilization yield: Immobilization yield represents the total enzyme we use for immobilization vs the enzyme we finally receive in the carrier.

BET analysis : BET analysis tries to explain the physical adsorption of gas molecules on a solid surface and it can used to calculate the specific surface area of materials. It explains about multilayer adsorption and utilizes gases which do not react chemically with the surface material, Nitrogen is commonly employed gaseous adsorbate.

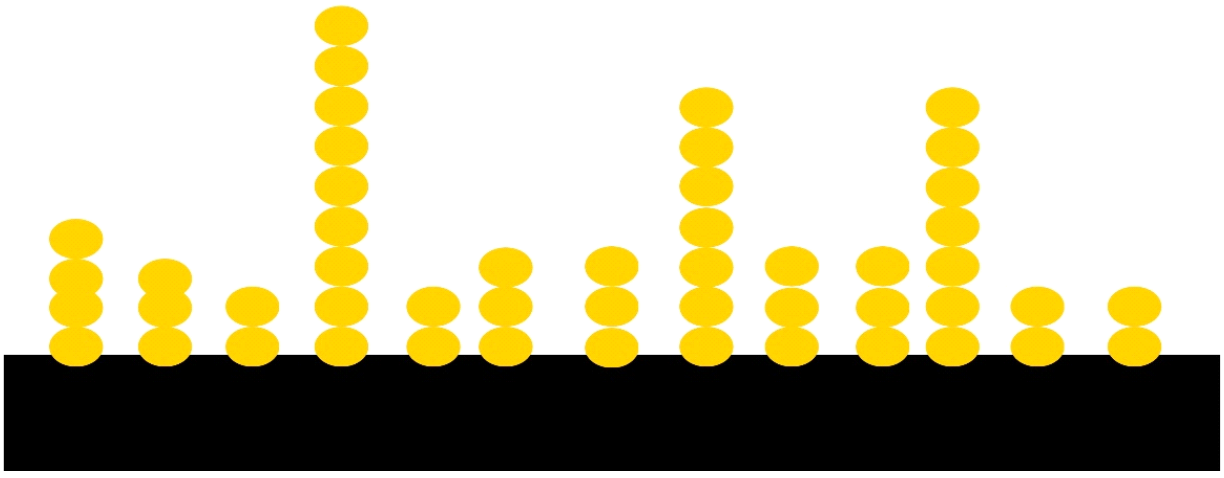

Figure: This figure represents BET analysis technique

- The gaseous molecules start to get adsorbed in the surface infinitely
- The molecules of gas interacts only with adjacent layers
- The enthalpy of the adsorption for the first layer is constant and will always be greater than the second layer

Working of BET:

The samples are degased in a vacuum at high temperatures, the samples are placed in the glass cells and then are analysed by the BET machine then, the cells are placed into heating mantles and lastly connected to the output port. After that the liquid nitrogen is employed which is used to cool the cells or the samples and by doing that , a low temperature is maintained . This ensures adsorption to occur. The nitrogen gas is injected into the sample,on the other hand Helium gad used to run as a blank as helium does not adsorb onto the particles

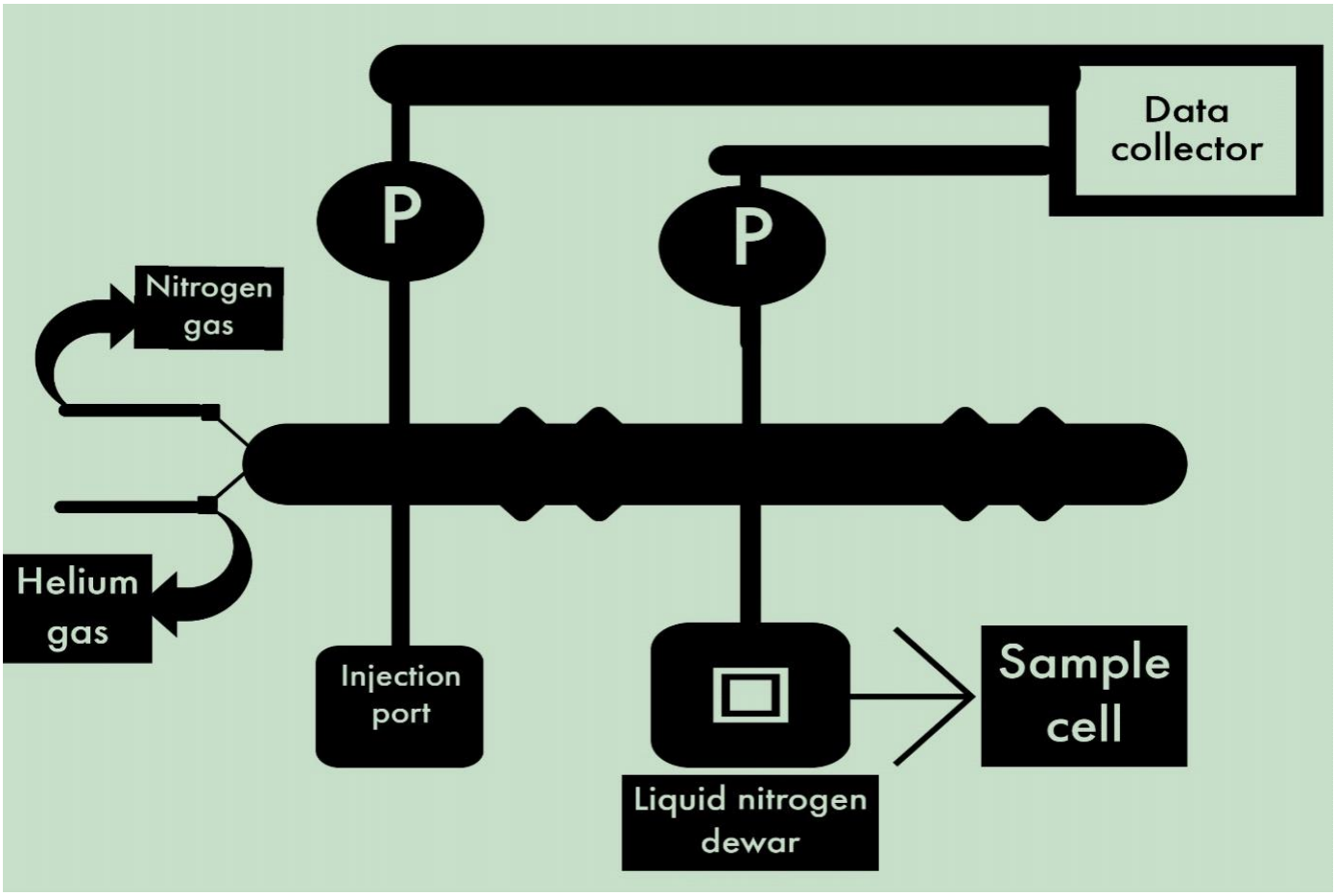

Figure : This figure represents the instrumentation model of BET

Multi-point Bet : At relative pressures higher than 0.5, there is the onset of capillary condensation, and at relative pressures that are too low, only monolayer formation is occurring. When the BET equation is plotted, the graph should be of linear with a positive slope. If such a graph is not obtained, then the BET method was insufficient in obtaining the surface area.

The BET procedure has a few drawbacks when contrasted with NMR, which can likewise be utilized to quantify the surface region of nanoparticles. Wager estimations must be utilized to decide the surface territory of dry powders. This method requires a ton of time for the adsorption of gas particles to happen. A great deal of manual readiness is required.

ELECTROCHEMICAL IMMOBILISATION OF ENZYMES

The utilization of a compound related to an amperometric cathode gives an adaptable technique for the advancement of a wide scope of biosensors. The methodology joins the particularity of the protein for its normal substrate with the focal points of electrochemical identification. Various cathodes of this sort are accessible. These can work in one of three different ways: the terminal can basically distinguish an item (or reactant) in the common enzymatic response, a homogeneous go between might be utilized , or the protein may respond at the terminal itself . For various applications especially for in vivo investigations, it is beneficial to have the option to make little terminals. A promising way to deal with this issue is to utilize an electrochemical strategy for the immobilization of the compound. This has the potential preferences that the measure of compound immobilized is promptly controlled, that its spatial conveyance is very much characterized, that multilayer structures can be created, and that the technique is anything but difficult to complete. Lowe et al., had portrayed work on the immobilization of glucose oxidase in electrochem-ically developed films of polypyrrole.

References

- Sirisha, V. L., Ankita Jain, and Amita Jain. "Enzyme immobilization: an overview on methods, support material, and applications of immobilized enzymes." In *Advances in food and nutrition research*, vol. 79, pp. 179-211. Academic Press, 2016.
- Bolivar, Juan M., Ingrid Eisl, and Bernd Nidetzky. "Advanced characterization of immobilized enzymes as heterogeneous biocatalysts." *Catalysis today* 259 (2016): 66-80.
- Hwang, Nina, and Andrew R. Barron. "BET surface area analysis of nanoparticles." *The Connexions project* (2011): 1-11.
- Lohcharoenkal, Warangkana, Liying Wang, Yi Charlie Chen, and Yon Rojanasakul. "Protein nanoparticles as drug delivery carriers for cancer therapy." *BioMed research international* 2014 (2014).
- Sharifi, Majid, Mohammad Javad Sohrabi, Sara Haji Hosseinali, Anwarul Hasan, Pegah Hashemi Kani, Amir Jouya Talaei, Abdulkarim Yasin Karim et al. "Enzyme

immobilization onto the nanomaterials: application in enzyme stability and prodrug-activated cancer therapy." *International Journal of Biological Macromolecules* 143 (2020): 665-676

- Ren, Yuhong, Jose G. Rivera, Lihong He, Harsha Kulkarni, Dong-Keun Lee, and Phillip B. Messersmith. "Facile, high efficiency immobilization of lipase enzyme on magnetic iron oxide nanoparticles via a biomimetic coating." *BMC biotechnology* 11, no. 1 (2011): 63.
- Li, Chunfang, Shuhui Jiang, Xinying Zhao, and Hao Liang. "Co-immobilization of enzymes and magnetic nanoparticles by metal-nucleotide hydrogelnanofibers for improving stability and recycling." *Molecules* 22, no. 1 (2017): 179.
- Sheldon, R. A. "Cross-linked enzyme aggregates (CLEA® s): stable and recyclable biocatalysts." *Biochemical Society Transactions* 35, no. 6 (2007): 1583-1587.
- Kumar, Ashok, In-Won Kim, Sanjay KS Patel, and Jung-Kul Lee. "Synthesis of protein-inorganic nanohybrids with improved catalytic properties using Co 3 (PO 4) 2." *Indian journal of microbiology* 58, no. 1 (2018): 100-104.
- Freag, May S., and Ahmed O. Elzoghby. "Protein-inorganic nanohybrids: a potential symbiosis in tissue engineering." *Current Drug Targets* 19, no. 16 (2018): 1897-1904.
- Bartlett PN, Whitaker RG. Electrochemical immobilisation of enzymes: Part I. Theory. Journal of electroanalytical chemistry and interfacial electrochemistry. 1987 Jun 10;224(1-2):27-35.
- NC. Foulds and C.R. Lowe, J. Chem. Sot., Faraday Trans. 1, 82 (1986) 1259.
- https://www.easybiologyclass.com/enzyme-cell-immobilization-techniques/
- https://www.youtube.com/watch?v=oVJ2LJxO6tU HYPERLINK "https://www.youtube.com/watch?v=oVJ2LJxO6tU&t=1027s"& HYPERLINK "https://www.youtube.com/watch?v=oVJ2LJxO6tU&t=1027s"t=1027s
- https://www.youtube.com/watch?v=-dh8goOimPk
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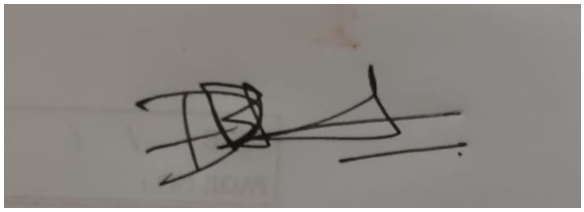
- https://www.youtube.com/watch?v=xmLW5NdRodU

Student's sign



Teacher's sign

