SHARDA UNIVERSITY
Beyond Boundaries

NAAC A+ ACCREDITED

SHARDA SCHOOL OF
BIO SCIENCE &
TECHNOLOGY

COURSE

Omics Technologies in Life Sciences (NVF2005)

VALUE ADDED
COURSE BROCHURE-30 HRS
2025-26

ABOUT THE UNIVERSITY

Sharda University is a leading Educational institution based out of Greater Noida, Delhi NCR. A venture of the renowned Sharda Group of Institutions (SGI), The University has established itself as a high quality education provider with prime focus on holistic learning and imbibing competitive abilities in students.

The University is approved by UGC and prides itself in being the only multi-discipline campus in the NCR, spread over 63 acres and equipped with world class facilities.

Sharda University promises to become one of the India's leading universities with an acknowledged reputation for excellence in research and teaching. With its outstanding faculty, world class teaching standards, and innovative academic programs, Sharda intends to set a new benchmark in the Indian education system.

Sharda School of Bioscience and Technology (SSBT) boasts of providing exposure in molecular biology, genetic engineering, bioinformatics, biochemistry, plant biotechnology, microbiology, zoology, animal biotechnology & environmental biotechnology

ABOUT SCHOOL

Sharda School of Bioscience and Technology (SSBT) The Sharda School of Bio-Science and Technology is one of the most dynamic and vibrant School for Life Sciences and Biological Engineering in the Delhi-NCR, Greater Noida India. The school is providing excellent and quality educational opportunities in are areas of Moleuclar Biology, Biochemistry, Immunology, Microbiology, Virology, Cancer Biology, Plant Molecular Biology, Agriculture Biotechnology, Animal Biotechnology etc by training the student community for Entrepreneurship development, Research and technical skills for the student community in particular for those coming from the diverse cultural and socio-economic background of the nation. SSBT offers innovative postgraduate and PhD programmes that inculcate personal and professional enrichment leading to the formation of vivacious and enthusiaistic student community.

ABOUT THE COURSE

This course provides a comprehensive introduction to the principles and practices of genomics and proteomics, with a strong emphasis on bioinformatics tools and databases. The course also covers advanced topics in protein structure prediction and validation, equipping students with the skills to analyze molecular data for applications in biotechnology, molecular biology, and biomedical research and thus employability in the same sector.

Course Schedule

Week	Content	Duration (Hrs)
1	Introduction to Nucleic acid databases – NCBI/DDBJ/ ICGI.	2
2	Retrieval of Nucleotide sequence – NUCLEOTIDE and GENE databases – Flat file/FASTA/Graphical formats	2
3	Uploading the sequences into NCBI – Sequin and BankIt tools.	2
4	Accessing Expasy-Swiss Prot databases.	2
5	Retrieval of protein sequence from UniProtKb – File formats.	2
6	Protein sequence characterization – PROT PARAM.	2
7	BLAST analysis of nucleic acid and protein sequences.	2
8	Protein pair wise alignment – EBI EMBOSS tool.	2
9	Multiple alignment of nucleic acids and proteins – CLUSTALX.	2
10	Trimming of multiple aligned sequences – DAMBE	2
11	Conversion of file formats for Phylogenetic analysis	2
12	Construction of Phylogenetic trees through Maximum Likelihood/ Maximum Parsimony/ Neighbour Joining methods – PHYLIP and MEGA.	2
13	Retrieval of protein structures from PDB database, Molecular visualization of proteins.	2
14	Secondary structure prediction of unknown proteins – GOR, PSIPRED.	2
15	Tertiary structure prediction of proteins – SWISS MODEL server. Validation of protein structures.	2
Total		30 hrs

Resource Persons

Prof. (Dr.) Satyawada Rama Rao

Prof. Satyawada Rama Rao has been a Professor in the Department of Biotechnology and Bioinformatics, North-Eastern Hill University, Shillong, Meghalaya. He obtained his Ph.D. (1990) from University of Jodhpur, Jodhpur, India. He served twice as Head of the Department of Biotechnology and Bioinformatics and Director, Human Resource Development Centre at the same University. His research interest includes Cellular and Molecular Cytogenetics, Biodiversity and Phylogenetics. He has published many scientific research and review articles in international peer-reviewed journals and refereed in many high-impact journals. In addition, he successfully executed nine research projects funded by DBT, DST, UGC, ICAR as PI,Co-PI and Project Co-Ordinator. He is a fellow of Association of Biotechnology and Pharmacy and has visited different countries including China under INSA-Academic Exchange Program, New Delhi.

Dr. Ashwini Kumar

Dr Ashwini Kumar is presently working as an Assistant Professor in the Department of Life Sciences, Sharda School of Basic Sciences and Research, Sharda University, Greater Noida, Uttar Pradesh. Previously, he has served as an Assistant Professor in the Biotechnology and Bioinformatics Area at NIIT University, Neemrana (Rajasthan), Department of Biotechnology at IMS Engineering College, Ghaziabad, and as a Lecturer in the Department of Biotechnology, National Institute of Technology, Raipur, Chhattisgarh. The central component of Dr Kumar's research has been biomaterial science, more specifically, in the field of novel drug delivery systems. The target applications of his research are formulating non-invasive and minimally invasive drug delivery approaches for better results both in terms of pharmaceutics and patient compliance. His interest also lies in the field of tissue engineering and diabetes. He has authored 23 journal articles in national and international journals, 9 book chapters, and a book. He also holds a patent on his work from PhD.

School:		**SSBT** **Batch: 2023-2026**	
Program:		**UG** **Current Academic Year: 2025-26**	
Branch:			
1	Course Code	**NVF2005**	
2	Course Title	**Omics Technologies in Life Sciences**	
3	Credits	**0**	
4	Contact Hours	**30**	
	Course Type	**Value Added Course**	
5	Course Objective	The course aims to introduce undergraduate students to the foundational and applied aspects of genomics and proteomics, with a strong emphasis on the use of bioinformatics tools and databases. Through hands-on exposure to widely used platforms such as NCBI, UniProtKB, BLAST, MEGA, and SWISS-MODEL, the course prepares students for research and industry roles in biotechnology, molecular biology, and biomedical sciences.	
6	Course Outcomes	On successful completion of the course, students will be able to: CO1: Understand and utilize nucleotide sequence databases such as NCBI, DDBJ, and ICGI for the retrieval and submission of nucleic acid sequences using tools like Sequin and BankIt. CO2: Access and analyze protein sequence data from databases like Swiss-Prot and UniProtKB, including sequence characterization using computational tools such as PROT PARAM. CO3: Perform pairwise and multiple sequence alignments of nucleotide and protein sequences using tools such as BLAST, EMBOSS, and CLUSTALX for comparative analysis. CO4: Conduct phylogenetic analysis by trimming aligned sequences, converting file formats, and constructing phylogenetic trees using methods like Maximum Likelihood, Maximum Parsimony, and Neighbor Joining with software such as MEGA and PHYLIP. CO5: Retrieve, visualize, and interpret protein structures using the PDB database and molecular visualization tools to understand structural features. CO6: Integrate knowledge of nucleotide and protein sequence management, alignment techniques, phylogenetic analysis, and protein structure prediction to interpret biological data and solve complex problems in genomics and proteomics using a range of bioinformatics tools and databases.	
7	Course Description	This course provides a comprehensive introduction to the principles and practices of genomics and proteomics, with a strong emphasis on bioinformatics tools and databases. The course also covers advanced topics in protein structure prediction and validation, equipping students with the skills to analyze molecular data for applications in biotechnology, molecular biology, and biomedical research and thus employability in the same sector.	
8	Outline syllabus		CO Mapping
	Unit 1	**Nucleotide sequence Management**	
	A	Introduction to Nucleic acid databases - NCBI/DDBJ/ ICGI.	CO1, CO6
	B	Retrieval of Nucleotide sequence – NUCLEOTIDE and GENE databases – Flat file/FASTA/Graphical formats	CO1, CO6
	C	Uploading the sequences into NCBI – Sequin and BankIt tools.	CO1, CO6
	Unit 2	**Protein sequence Management**	
	A	Accessing Expasy-Swiss Prot databases.	CO2, CO6

	B	Retrieval of protein sequence from UniProtKb – File formats.	CO2, CO6
	C	Protein sequence characterization – PROT PARAM.	CO2, CO6
	Unit 3	**Pair wise and multiple alignments**	
	A	BLAST analysis of nucleic acid and protein sequences.	CO3, CO6
	B	Protein pair wise alignment – EBI EMBOSS tool.	CO3, CO6
	C	Multiple alignment of nucleic acids and proteins – CLUSTALX.	CO3, CO6
	Unit 4	**Phylogenetic analysis:**	
	A	Trimming of multiple aligned sequences – DAMBE	CO4, CO6
	B	Conversion of file formats for Phylogenetic analysis	CO4, CO6
	C	Construction of Phylogenetic trees through Maximum Likelihood/ Maximum Parsimony/ Neighbour Joining methods – PHYLIP and MEGA.	CO4, CO6
	Unit 5	**Protein structure management**	
	A	Retrieval of protein structures from PDB database, Molecular visualization of proteins.	CO5, CO6
	B	Secondary structure prediction of unknown proteins – GOR, PSIPRED.	CO5, CO6
	C	Tertiary structure prediction of proteins – SWISS MODEL server. Validation of protein structures.	CO5, CO6
	Mode of examination	Quiz/Viva	