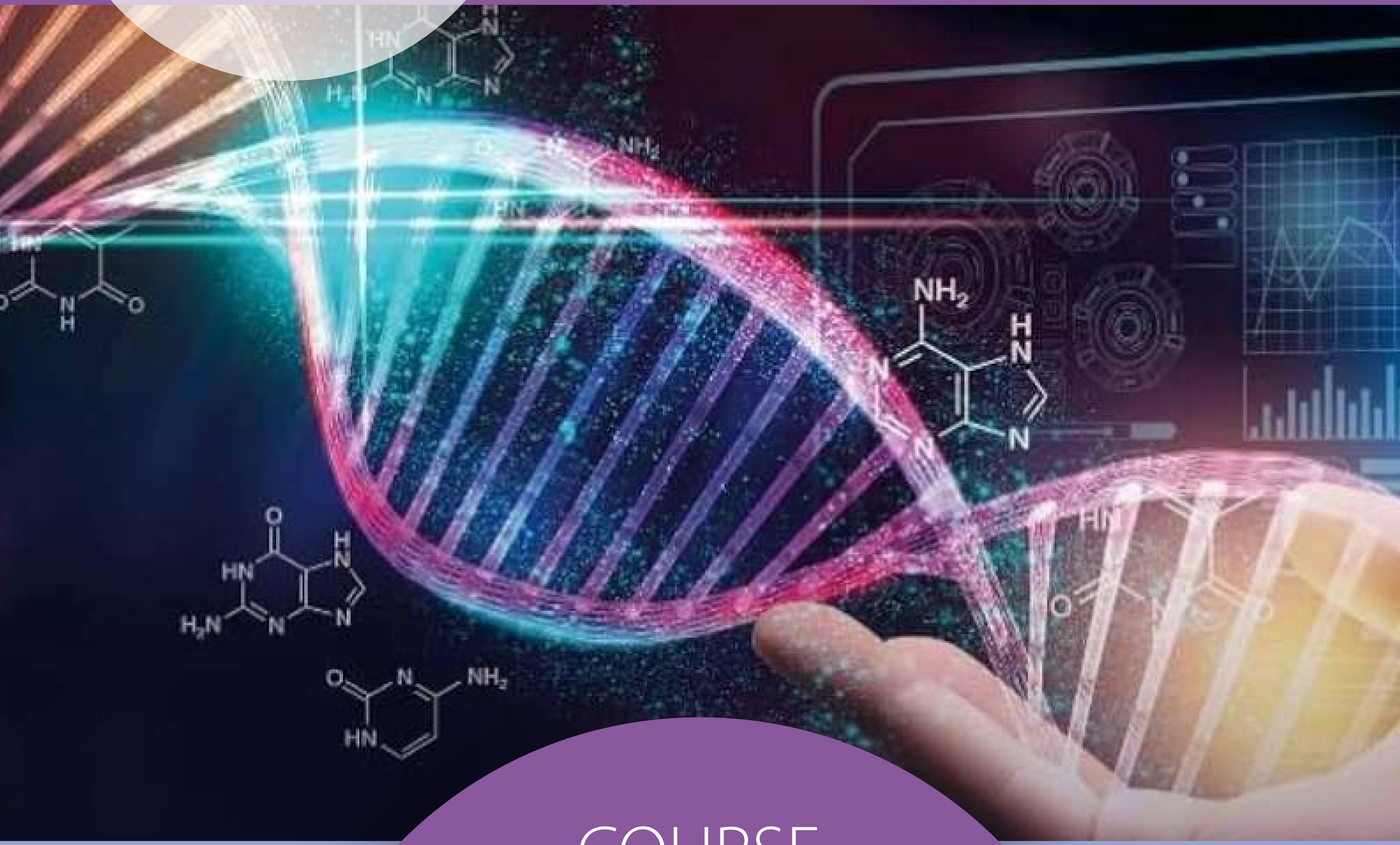
SHARDA
UNIVERSITY
Beyond Boundaries

NAAC
A+
ACCREDITED

SHARDA SCHOOL OF BIO-SCIENCE & TECHNOLOGY



COURSE

OMICS TECHNOLOGIES IN LIFE SCIENCES

(NVF2005)

VALUE ADDED
COURSE BROCHURE-30 HRS
2026-27

SHARDA 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 THE SCHOOL

The Sharda School of Bio-Science and Technology is one of the most dynamic and vibrant School for Life Scinces 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.

VISION OF SCHOOL

To become a global centre for higher learning in pursuit of academic excellence, innovation, and entrepreneurship in various disciplines of Bioscience and Technology Biosciences aim to create innovative solutions in various agriculture, Medical and industrial frontiers. Establish progressive growth in national and international scientific scenario.

MISSION OF SCHOOL

M1: To adapt and update students with rapidly changing technologies through self-improvement with continuous learning and professional ethics.

M2: To enable students for community-collaborative learning processes beyond classrooms in various disciplines of biotechnology.

M3: To conduct cutting-edge multi-disciplinary research in plant, animal, medical, industrial, microbial, and environmental biotechnology.

M4: To motivate and train students for industrial practices, higher studies, lifelong learning skills, and entrepreneurship

ABOUT DEPARTMENT

Life sciences are study of composition, structure and function of living forms and their interaction with environment. The scope of life sciences is wide and is one of the most promising areas of research. Life sciences enhance our understanding of nature of life, and provide new insights to diverse areas in biology such as disease pathogenesis, diagnosis, prevention and cure. The acquired knowledge in Life sciences also helps us to combat various environmental issues, finding out ways of sustainable management, and biodiversity conservation, to name a few. Department of Life sciences offers undergraduate and or postgraduate courses in various disciplines such as Biotechnology, Microbiology, Food Science and Technology, Botany and Zoology.

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 PERSON

Dr. Swati Garg

Dr. Swati Gargs scientific expertise spans molecular parasitology, host–pathogen interactions, and drug discovery, with a primary focus on malaria and other neglected tropical diseases. Her research explores host-directed therapeutic strategies, parasite invasion mechanisms, and molecular targets for antimalarial intervention. She has contributed extensively to understanding the molecular basis of Plasmodium infection and resistance, leading to publications in reputed international journals. Integrating molecular biology, immunology, and translational research, Dr. Gargs studies aim to develop innovative therapeutic and diagnostic approaches to combat parasitic diseases effectively.

Abhinav Nair

Mr. Abhinav Nair is working as an assistant professor at Sharda University, Greater Noida, Uttar Pradesh, India. He has done his M.Sc. in Biochemistry from Amity University Haryana, India. He has done his B.Sc. from Simon Fraser University, Canada. He has 2 publications and 1 design patent. He has 3.5 years of research experience.

MODULE

School: SSBT	**Batch: 2024-2029**
Program: UG	Current Academic Year: 2026-27
Branch:	
1. Course Code	**NVF2005**
2. Course Title	**Omics Technologies in Life Sciences**
3. Credits	0
4. Contact Hours	**(30 Hours)**
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.	CO3/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	Quizzes & Viva	