SYLLABUS FOR THE BATCH FROM YEAR 2025 TO 2026

FOR

Certificate in Bioinformatics

(Credit Based Evaluation and Grading System)

Semester: I-II

EXAMINATIONS: 2025-2026

The Certificate/Diploma Programme Offered:

- **Certificate Course in Bioinformatics (6 Months duration)**

Program Outcomes:

- **Fundamental Knowledge of Computer Applications** – Students will gain an understanding of the bioinformatics tools, enabling them to use these tools effectively and analyze the results effectively.
- **Enhanced Technical Skills** – The program focuses on improving students' technical abilities in sequence alignment, structural bioinformatics, biological data analysis and drug designing.
- **Practical Experience** – Through hands-on assignments and projects, students will develop problem-solving skills by working on real-world scenarios.
- **Career Readiness & Employability** – The program prepares students for research position in institutes and Biotechnology Company.

Name of the Department: Department of Biotechnology

In collaboration with

Directorate of Open & Distance Learning and Online Studies

GURU NANAK DEV UNIVERSITY
AMRITSAR

Certificate/Diploma in Bioinformatics (SEMESTER SYSTEM) under Directorate of Open & Distance Learning, Guru Nanak Dev University, Amritsar

Eligibility:

- +2 in science stream with at least 45% marks in aggregate (40% for SC/ST candidates).
- Any student doing Bachelor in science, Master in science, M.Phil.,M.Tech, Ph.D.

SEMESTER-I

Paper Code	Subject	Marks			Credits
		Internal Assessment	End Term	Total	
ODCIB111T	**Molecular biology**	30	70	100	4
ODCIB112T	**Bio-manufacturing and Synthetic biology**	30	70	100	4
ODCIB113T	**Sequence alignment**	30	70	100	4
ODCIB114T	**Structural bioinformatics**	30	70	100	4
Total Marks & Credits		**120**	**280**	**400**	**16**

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CIB (ODL) (Semester – I)

Molecular Biology ODCIB111T

Time: 03 Hours **Max. Marks: 100 Marks**
Internal Assessment: 30 Marks
End Term: 70 Marks

Instructions for the Paper-Setter/examiner:

1. Question paper shall consist of Four sections.
2. Paper setter shall set Eight questions in all by selecting Two questions of equal marks from each section. However, a question may have sub-parts (not exceeding four subparts) and appropriate allocation of marks should be done for each sub-part.
3. Candidates shall attempt Five questions in all, by at least selecting One question from each section and the 5 th question may be attempted from any of the Four sections.
4. The question paper should be strictly according to the instructions mentioned above. In no case a question should be asked outside the syllabus.

Section-A

DNA Structure and Replication: DNA: Basic introduction; Forms of DNA: A, B, Z & C-value paradox; Watson-Crick DNA Model; DNA Replication Mechanisms.

Section-B

Prokaryotic Gene Expression and Translation: Structure of Prokaryotic Genes; Transcription & Regulation (lac, his, trp); Translation in Prokaryotes.

Section-C

Eukaryotic Transcription and Translation: RNA Polymerases, Promoters, Enhancers, Silencers; Post-transcriptional Modifications; Translation & Genetic Code.

Section-D

Genetic Recombination and Transposons: Prokaryotic and Eukaryotic Recombination; Experiments: Messelson-Weigle, RecA, RecBCD; Transposable Elements: Insertion Elements, Transposons.

Text / Reference Books:

1. Lodish, H. F. (2016). Molecular Cell Biology (8th Ed.). New York: W.H. Freeman.
2. Krebs, J. E., Lewin, B., Kilpatrick, S. T., & Goldstein, E. S. (2014). Lewin's Genes XI.Burlington, MA: Jones & Bartlett Learning.
3. Watson J., Baker T., Bell S., Gann A, Levine M and Loscik R. (2008). Molecular Biology of the Gene. 6th Ed. Pearson Education.

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CIB (ODL) (Semester – I)
Bio-manufacturing and Synthetic biology
ODCIB112T

Time: 03 Hours | **Max. Marks: 100 Marks**
Internal Assessment: 30 Marks
End Term: 70 Marks

Instructions for the Paper-Setter/examiner:

5. Question paper shall consist of Four sections.
6. Paper setter shall set Eight questions in all by selecting Two questions of equal marks from each section. However, a question may have sub-parts (not exceeding four subparts) and appropriate allocation of marks should be done for each sub-part.
7. Candidates shall attempt Five questions in all, by at least selecting One question from each section and the 5 th question may be attempted from any of the Four sections.
8. The question paper should be strictly according to the instructions mentioned above. In no case a question should be asked outside the syllabus.

SECTION-A

Introduction to bio-manufacturing, Growth parameters, specific growth rate, biomass yield. Introduction, structure and function of bioreactors. Aseptic operation and Sterilization of bioreactors.

SECTION-B

Introduction to fermentation processes. Metabolic pathways: Ethanol, lactic acid, acetic acid. Manufacturing of vinegar, beer, wine, beer, whisky, yoghurt, paneer, cheese.

SECTION-C

Introduction to synthetic biology, DNA synthesis and assembly, Tools for genetic engineering; restriction enodnucleases, ligases, polymerases, primers, vectors.

SECTION-D

Genetic Engineering, Metagenomics. Advanced gene editing tools; CRISPER-Cas, TALENs, ZFNs. Need of genetic modifications.

Text / Reference Books:

4. Shuler, M. L., & Kargi, F. (2002). Bioprocess Engineering: Basic Concepts. Upper Saddle River, NJ: Prentice Hall.
5. Stanbury, P. F., & Whitaker, A. (2010). Principles of Fermentation Technology. Oxford: Pergamon Press.
6. Blanch, H. W., & Clark, D. S. (1997). Biochemical Engineering. New York: M. Dekker.
7. El-Mansi, M., and amp; Bryce, C. F. (2007). Fermentation Microbiology and Biotechnology. Boca
8. Raton: CRC/Taylor & Francis.
9. Brown, T.A., Gene Cloning and DNA Analysis: An Introduction. Willey-Blackwell.
10. Nagpal, M.L., Boldura, O-M., Baltă, C and Enany S. Synthetic Biology - New Interdisciplinary Science. IntechOpen.

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CIB (ODL) (Semester – I)

Sequence alignment

ODCIB113T

Time: 03 Hours

Max. Marks: 100 Marks
Internal Assessment: 30 Marks
End Term: 70 Marks

Instructions for the Paper-Setter/examiner:
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2. Paper setter shall set Eight questions in all by selecting Two questions of equal marks from each section. However, a question may have sub-parts (not exceeding four subparts) and appropriate allocation of marks should be done for each sub-part.
3. Candidates shall attempt Five questions in all, by at least selecting One question from each section and the 5 th question may be attempted from any of the Four sections.
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Section-A

Biological datatabases: Types and significance. File formats: GenBank, FASTA, PDB, SMILES, SDF; Searching databases using keywords, sequence and structure. Scoring matrix: significance and types of BLOSUM and PAM

Section-B

Pairwise sequence alignment, Local and global alignment concepts, dot matrix, dynamic programming: Tools and algorithm, NW and SW; Multiple sequence alignment: significance, tools and algorithm, phylogenetic analysis: types of trees, distance based method.

Section-C

Searching databases using sequence, BLAST and FASTA, types of BLAST and their application, PSSM and PSI-BLAST

Motifs and pattern: definitions, databases, tools for searching motifs and pattern. Hidden markov model

Section-D

Genome sequencing, genome assembly and annotation tools, Genome databases, gene and promoter prediction tools; Identification of somatic and germline variations: SNPs and SNVs

Text / Reference Books:

Mount D. W. (2004). Bioinformatics & Genome Analysis. Cold Spring Harbor Laboratory Press.

Baxevais B.F. and Quellette F. (2004). Bioinformatics a Practical Guide to the Analysis of Genes and Proteins. Wiley-Interscience.

CIB (ODL) (Semester – I)
Structural bioinformatics
ODCIB114T

Time: 03 Hours | **Max. Marks: 100 Marks**
Internal Assessment: 30 Marks
End Term: 70 Marks

Instructions for the Paper-Setter/examiner:
1. Question paper shall consist of Four sections.
2. Paper setter shall set Eight questions in all by selecting Two questions of equal marks from each section. However, a question may have sub-parts (not exceeding four subparts) and appropriate allocation of marks should be done for each sub-part.
3. Candidates shall attempt Five questions in all, by at least selecting One question from each section and the 5 th question may be attempted from any of the Four sections.
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Section-A

Amino acid, peptide bond, Protein structure: Primary structure, secondary, tertiary and quaternary; 3D structure determination methods: principles of X-Ray diffraction, NMR and CD Spectroscopy, Mass Spectroscopy and Protein sequencing; Ramachandra Plot

Section-B

Structure databases: PDB, small molecule databases; Classification of three dimensional structure of protein in protein data banks (SCOP, CATH). Structure visualization tools: Rasmol, Chimera. Structure visualization and analysis

Section-C

Protein secondary structure Prediction methods: First, second, third and fourth generation methods: CHOU-FASMAN, GOR, PHD, PSIPRED, SOPM. Concepts, algorithms and their limitations. Benchmarking, CASP, CAFASPs

Section-D

Methods for Prediction Tertiary structures of Proteins: Knowledge-based Structure prediction, Fold recognition, Ab initio methods for structure prediction. Assessement of Protein Structure predictions, Tools for Protein Structure Comparison and alignment

Text / Reference Books:

Mount D. W. (2004). Bioinformatics & Genome Analysis. Cold Spring Harbor Laboratory Press.

Bourhe P. E. and Weissig H. (2003). Structural Bioinformatics (Methods of structural Analysis). Wiley-Liss.

Creightons T.E. (2005). Proteins: Structures and Molecular Properties. WH Freeman Publishers