

BBCS-185

ASSIGNMENT BOOKLET

**Bachelor's Degree Programme
B.Sc. Hons in Biochemistry (BSCBCH)**

BIOINFORMATICS

Valid from January, 2026 to December, 2026



**School of Sciences
Indira Gandhi National Open University
Maidan Garhi
New Delhi-110068.**

Dear Student,

Please read the section on assignments in the Programme Guide for Core Courses that we sent you after your enrolment. A weightage of 30 per cent, as you are aware, has been earmarked for continuous evaluation, **which would consist of one tutor-marked assignment** for this course. The total marks of all the parts are 100, of which 35% are needed to pass it.

Instructions for Formatting Your Assignments

Before attempting the assignment please read the following instructions carefully:

- 1) On top of the first page of your answer sheet, please write the details exactly in the following format:

ROLL NO.:

NAME:

ADDRESS:

.....

.....

COURSE CODE:

COURSE TITLE:

ASSIGNMENT NO.:

STUDY CENTRE: **DATE:**

PLEASE FOLLOW THE ABOVE FORMAT STRICTLY TO FACILITATE EVALUATION AND TO AVOID DELAY.

- 2) Use only foolscap size writing paper (but not of very thin variety) for writing your answers.
- 3) Leave 4 cm margin on the left, top and bottom of your answer sheet.
- 4) Your answers should be precise.
- 5) The assignment answer sheets are to be submitted to your Study Centre as per the schedule made by the study centre. **Answer sheets received after the due date shall not be accepted.**

We strongly suggest that you retain a copy of your answer sheets.

- 6) This assignment is **valid from January 2026 to December, 2026** and submit it as per the instructions given in the Programme Guide.
- 7) **You cannot fill the exam form for this course** till you have submitted this assignment.

We wish you good luck.

**ASSIGNMENT
BIOINFORMATICS**

**Course Code: BBCS-185
Assignment Code: BBCS-185/TMA/2026
Maximum Marks: 100**

Answer all the questions given below.

1. Explain the scope of bioinformatics and describe its role in genomics, proteomics, and systems biology. 10 M
2. Classify biological databases into primary, secondary, and composite databases with suitable examples. 10 M
3. Define similarity, identity, and homology in sequence analysis and explain their significance in sequence alignment. 10 M
4. Describe the principles of pairwise and multiple sequence alignment and differentiate between global and local alignment. 10 M
5. Explain the structure and importance of amino acid substitution matrices such as PAM and BLOSUM in sequence analysis. 10M
6. Describe how bioinformatics tools and databases are used in computer-aided drug design, highlighting structure-based and ligand-based approaches. 10M
7. Explain the steps involved in retrieving a gene or protein sequence from NCBI and analyzing it using BLAST. 10M
8. Discuss the use of metabolic pathway databases such as KEGG and MetaCyc in understanding cellular metabolism and disease pathways. 10M
9. Explain how multiple sequence alignment using CLUSTALW can be applied to study evolutionary relationships among proteins. 10M
10. Describe the practical workflow for downloading a protein structure from the PDB and visualizing it using PyMol, including the role of molecular file formats. 10M