Enrolment No. _____

AHMEDABAD UNIVERSITY

School of Arts and Sciences
Integrated Masters in Life Sciences
2025-2026 WINTER SEMESTER
MID-SEMESTER EXAMINATION
BIO335 Computational Structural Biology

Date: 21-02-2026 Total Marks: 30
Time: 11.00 am – 01.30 pm No. of printed pages: 00

General Instructions:

1. Students must carry their identity card during the examination.
2. No break is allowed during the examination under any circumstances. In case of an emergency, with prior permission of the invigilator and an escort, a break of maximum five minutes is allowed.
3. No unauthorized devices, such as mobile phones, any kind of watches, other gadgets, or any kind of material is allowed on person.
4. Any violation of examination rules and an intent of malpractice will lead to strict disciplinary action, including a possible expulsion from the university.

Course Specific Instructions:

WARNING : *ANSWER TO THE POINT. NO LONG STORIES. I WILL STOP READING AFTER TWO SENTENCES STRICTLY AND WILL DEDUCT MARKS FOR LONG ANSWERS. USE extra sheets, to think, for ideas, to do calculations to for any rough work. In the answer sheet I would like to see your refined, well-articulated thoughts – precise to the point.*

Answer in no more than 50 words (strictly). Marks indicated as below. Total 30 marks.

1. What are the PRECISE differences in stabilization of secondary, tertiary and quaternary structures? (**5 marks**)

2. A simple protein folding experiment, using recombinant protein, was being conducted in aqueous medium, where the protein is known to take the usual path towards folding into a compact globular structure. The experiment was repeated many times and validated via biochemical experiments before arriving at a conclusion that the protein was indeed active like the native protein purified from biological material. This implies is well folded. By mistake, in one of the experiments, the experimenter added a hydrophobic solution (in 1:5 ratio, i.e. 1 part hydrophobic per 5 parts of hydrophilic solution) while repeating the same experiment. How will the protein fold in this case ? (**8 marks**)

3. We have studied the Ramachandran map that is based on torsion angles phi and psi. If you **did not** invoke the concept of torsion angles, how would you present a map that captures the essence of the Ramachandran map, i.e. the ability to distinguish one secondary structure from the other. (Hint: think of an alternative to the Ramachandran map, if you only had the bond angles, bond lengths, other stereochemical parameters and the connections that form the poly peptide chain). (**5 marks**).

4. Draw a dipeptide on your answer sheet and indicate the torsion angles phi, psi and omega. (**5 marks**).

5. Make a model of a dipeptide with the atom kit being provided to you – a combination of phi and psi values are given in a chit (please pick one) and use these to build your model. Keep omega = 180. Take a video of your model and upload in the link provided to you by the TA. Also deposit the model to him with your name and roll number. Draw the dipeptide on your answer sheet and indicate the torsion angles. (**7 marks**)