BIOSC 1540 - Computational Biology

Quiz 04

Apr 8, 2025

20 points

Please read the following instructions carefully before beginning your assessment.

- **Time limit:** You have 15 minutes to complete and turn in this assessment.
- **Closed note:** You may not use any notes or additional resources during this assessment.
- **No digital devices:** The use of digital devices, including calculators, is not allowed.

I agree to follow the above instructions. I affirm that all work on this assessment will be my own and that I will not give or receive any unauthorized assistance. To have your assessment graded, you must write your name, sign, and provide your student ID below.

KEY _____

Name

KEY _____

Signature

KEY _____

Student ID

Bored area: Draw a scene from your favorite movie, design/name a new animal, or write a micro story from the point of view of your pencil/pen during this quiz.

Problem 1

In a Ramachandran plot, which of the following best explains why certain regions are “forbidden”?
(2 points)

(A) They correspond to bond lengths that are too short.

(B) They would result in steric clashes between atoms.

(C) They require impossible electron configurations.

(D) They only occur in denatured proteins.

Problem 2

What interaction is generally considered the primary driving force for the folding of globular proteins?
(3 points)

(A) Disulfide bonds

(B) Hydrogen bonds

(C) Hydrophobic interactions

(D) Ionic (salt bridge) interactions

Problem 3

In X-ray crystallography, the smallest distance between two points that can be resolved in a protein structure is referred to as the __RESOLUTION__, which is often measured in units of _ANGSTROMS_.
(1 point)

Problem 4

The main source of 3D structures of biomolecules is called the _____PROTEIN DATA BANK_____.
Hint: It does not start with a “Q”.
(3 points)

Problem 5

In the context of binding thermodynamics, which aspect is most likely to be underestimated when relying solely on a single, static structure?
(2 points)

(A) The entropy of the system.

(B) The precise orientation of hydrogen bonds.

(C) The strength of electrostatic interactions.

(D) The direct measurement of binding enthalpy.

Problem 6

In grid-based protein-ligand binding models, if the number of available binding sites (N) increases while the number of ligands (L) remains constant, how does this affect the system's entropy?
(1 point)

(A) The entropy decreases.

(B) The entropy increases.

(C) The entropy remains unchanged.

(D) The entropy first decreases then increases.

Problem 7

Why is it important for the target and template proteins to share a high level of sequence identity?
(2 points)

(A) It leads to consistent secondary structure elements.

(B) It speeds up the energy optimization steps.

(C) It increases the chance that both proteins undergo the same post-translational processing.

(D) It helps generate a more accurate alignment.

Problem 8

Profile-based alignment methods improve the sensitivity of homology detection by:
(1 point)

(A) Use insertions and deletions to emphasize conserved regions.

(B) Speeding up the alignment process at the cost of precision in selecting homologs.

(C) Bypassing the requirement for generating multiple sequence alignments.

(D) Modeling each position in a sequence as a distribution of potential amino acids.

Problem 9

Deep learning approaches, such as AlphaFold, derive critical information on residue-residue contacts from _____**COEVOLUTIONARY DATA/MSA**_____.
(2 points)

Problem 10

Describe two potential reasons why a ligand might have a good docking score (e.g., ΔG of −30 kcal/mol) but not be a successful inhibitor in real-world applications.

(1 point)

Here are a few acceptable answers:

- The ligand may bind tightly to the intended target and to other unintended proteins in the body.
- The target itself may not be directly involved in the disease mechanism.
- The ligand might have great binding affinity *in silico*, but if it cannot reach the target site in the body.
- The ligand targets a cryptic pocket.
- If the target site mutates frequently, resistance could rapidly develop.

Problem 11

Which of the following best describes the role of stochastic algorithms in pose optimization during molecular docking?

(1 point)

(A) They explore the energy landscape by making random modifications to molecular poses and accepting changes based on probability criteria.

(B) They use adaptive energy barriers to guide the sampling of molecular shapes, focusing on maintaining proper transition probabilities.

(C) They group similar molecular shapes by analyzing structural differences to identify key representative conformations.

(D) They apply evolutionary techniques that iteratively select and improve binding poses using scoring functions.

Problem 12

Which statement best describes the role of traditional scoring functions in molecular docking?

(1 point)

(A) They break down binding interactions into local atomic potentials calibrated with experimental and quantum data.

(B) They use machine learning models trained on structural data to predict binding strengths based on geometric and chemical features.

(C) They estimate binding energies using physical forces, statistical data, and solvation effects to rank docking poses.

(D) They assess how well proteins and ligands fit together by combining multiple scoring methods.