

Unit 11 - Week 9

Course outline

How does an NPTEL online course work?

Prerequisite Assignment

Week 1

Week 2

Week 3

Week 4

Week 5

Week 6

Week 7

Week 8

Week 9

Protein folding rate I

Protein folding rate II

Protein interactions I

Protein interactions II

Computer aided drug design I

Quiz : Assignment 9

Quiz : Practice Assignment 9

Bio-Informatics:Algorithms and Applications : Week 9 Feedback Form

Week 10

Week 11

Week 12

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Assignment 9

The due date for submitting this assignment has passed. As per our records you have not submitted this assignment.

Due on 2020-04-01, 23:59 IST.

1) Protein folding rates provide the information on 1 point

- 3D structure from sequence
- How fast or slow a protein can unfold
- How fast it assumes its native structure
- All of the above

No, the answer is incorrect. Score: 0

Accepted Answers:
How fast it assumes its native structure

2) What is the approximate time for a typical protein, cytochrome C to fold? 1 point

- 1 hour
- 1 s
- 1 millisecond
- 1 microsecond

No, the answer is incorrect. Score: 0

Accepted Answers:
1 microsecond

3) Usually which type of proteins fold faster? 1 point

- All-alpha
- All-beta
- Alpha+beta
- Alpha/beta

No, the answer is incorrect. Score: 0

Accepted Answers:
All-alpha

4) How contact order and long-range order relate with each other? 1 point

- No relationship
- Negatively correlate
- Positively correlate
- Can't say

No, the answer is incorrect. Score: 0

Accepted Answers:
Positively correlate

5) How to predict protein folding rates from sequence? 1 point

- Predict contacts, LRO and folding rate
- Relate amino acid properties with folding rates
- Relate properties, predicted secondary structure and ASA with folding rates
- All the above

No, the answer is incorrect. Score: 0

Accepted Answers:
All the above

6) Which type of interactions is generally used to identify lead compounds in drug design? 1 point

- Protein-protein
- Protein-nucleic acid
- Protein-ligand
- All the above

No, the answer is incorrect. Score: 0

Accepted Answers:
Protein-ligand

7) Binding site residues refer to 1 point

- Residues at the interface
- Residues, which are interacting between a pair of proteins
- Residues, which are close to each other between a pair of proteins
- All the above

No, the answer is incorrect. Score: 0

Accepted Answers:
All the above

8) If the solvent accessibility of Lys28 in bound and unbound forms is 72.3 Å² then 1 point

- It is at the interface
- It is not at the interface
- Information is not sufficient to define the binding sites
- Neighboring residue information is necessary to define the binding site

No, the answer is incorrect. Score: 0

Accepted Answers:
It is not at the interface

9) Which database contains the binding affinity of protein-protein complexes upon mutation? 1 point

- ProTherm
- ProNIT
- PROXIMATE
- PDBsum

No, the answer is incorrect. Score: 0

Accepted Answers:
PROXIMATE

10) Binding mode provides the information on 1 point

- Cavity in the protein
- Location where a ligand binds
- Geometry of the ligand at the binding site
- All the above

No, the answer is incorrect. Score: 0

Accepted Answers:
Geometry of the ligand at the binding site