

Unit 9 - Week 7

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

Protein structure analysis - IV

Protein structure prediction - I

Protein structure prediction - II

Protein stability - I

Protein stability - II

Demo: Homology Modelling

Quiz : Assignment 7

Quiz : Practice Assignment 7

Bio-Informatics:Algorithms and Applications : Week 7 Feedback Form

Week 8

Week 9

Week 10

Week 11

Week 12

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Assignment 7

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

Due on 2020-03-18, 23:59 IST.

1) Normalized B factor of a residue depends on

1 point

- B-factor of the specific residue
- Mean B-factor
- Deviation of B-factors
- All the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
All the above

2) Disulfide bonds are identified using the distance between the sulphur containing residues

1 point

- Met and Met
- Cys and Cys
- Cys and Met
- All the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
Cys and Cys

3) CASP stands for

1 point

- Critical assessment for secondary structure prediction
- Critical assessment for structure prediction of proteins
- Crucial assessment for structure prediction
- Cumulative assessment for structure prediction of proteins

No, the answer is incorrect.
Score: 0

Accepted Answers:
Critical assessment for structure prediction of proteins

4) The 3D structure models of a protein obtained with homology modelling using a template with 90% sequence homology is similar to

1 point

- High resolution X-ray structures
- Low resolution X- ray structures
- High resolution NMR structures
- Not comparable with experimental structures

No, the answer is incorrect.
Score: 0

Accepted Answers:
Low resolution X- ray structures

5) Which of the following is important for structural alignment?

1 point

- Conserved regions
- Functional annotations
- Active sites or motifs
- All the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
All the above

6) Side chain modelling is generally performed using

1 point

- Available rotamer libraries
- Random search
- Systematic search
- None of the above

No, the answer is incorrect.
Score: 0

Accepted Answers:
Available rotamer libraries

7) The free energy change between folded and unfolded states of a protein is in the range of

1 point

- 0-5 kcal/mol
- 5-20 kcal/mol
- 50-100 kcal/mol
- 100-500 kcal/mol

No, the answer is incorrect.
Score: 0

Accepted Answers:
5-20 kcal/mol

8) Comparing solid, liquid and gas, which medium has the maximum entropy

1 point

- Solid
- Liquid
- Gas
- All the states have the same entropy

No, the answer is incorrect.
Score: 0

Accepted Answers:
Gas

9) Atomic solvation parameters of N+ and O- atoms are

1 point

- Positive and positive
- Positive and negative
- Negative and positive
- Negative and negative

No, the answer is incorrect.
Score: 0

Accepted Answers:
Negative and negative

10) Van der Waals interactions between atoms i and j are defined as (Lennard-Jones potential)

1 point

- $A_{ij}/r_{ij}^{12} - B_{ij}/r_{ij}^6$
- $A_{ij}/r_{ij}^{12} + B_{ij}/r_{ij}^6$
- $-A_{ij}/r_{ij}^{12} + B_{ij}/r_{ij}^6$
- $-A_{ij}/r_{ij}^{12} - B_{ij}/r_{ij}^6$

No, the answer is incorrect.
Score: 0

Accepted Answers:
 $A_{ij}/r_{ij}^{12} - B_{ij}/r_{ij}^6$