

My paper of bif 401 at 15 aug 11:00 am

BIF 401 final paper today at 11:00 am

1. the term ExPANSy stands for?(2)
2. differentiate between bottom up proteomics and bottom down proteomics (3)
3. how loops are found after the finding of alpha and beta sheets (5)
4. how proteins sequences identified?(5)
5. explain all (5)
 - * role of amino acids.
 - * how folding of proteins are useful over the denature proteins
 - * why folding is important
 - * what factors are used for folding process
6. why the tertiary structure of RNA is less stable over the secondary structure of RNA (5)
7. what is ab initio modelling describe the limitations of this model (3)
8. write down the following terms of PDB (3)
 - * title
 - * source
 - * COMPND
 - * REVEDAT
9. how we find the secondary structures of proteins by using a model?(3)
10. what happens when pH is less than the pK value (2)
11. define ionization in terms of proteins (2)
12. what you have a home message from this course (3)

BIF401:TODAY 11am

AB initio modeling? limitations

Optimal functions in protein structure?

What happens when $pH < pK$?

Define ionization in protein?

identification of protein?

Chou fasman algorithm?

How can alpha helix expressed?

Explain summary of beta helix?

PDB explain compnd, source, title?

3D_1D bowie algorithm?

Ab initio modeling?

top down and bottom up proteomic?

public database that commonly used?

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Role of amino acid

Folding of protein goal

Chou fasman

Why difficult to determine structure of protein

What is hydrophobicity of amino acids

Bif 401 time 2 30

1 Choufman alpha or beta structure of 2ndry structure

2 system biology and application

3 if pH is less than pK then wt happend

4 deffine followng

Goals of folding

Factors in foling

Charactr of amino acid

5 scores in silico fragmentation

6 what is hydrophobicity of amiini acid

7 what are cgaracteristic of amino acid

Thnko

Mostly paper was repeated.

Bif401

1.Ab initio modelling

2. Chao fasman for alpha helix nd beta turn

3.Principal of dynamic programming.

4.Comparison insilico fragments wala.

5.Protein scoring.

6.Ionizing of protein

7 5 types of RNA and functions.

8Which determines RNA 1 and 2 structure

9. TITLE SOURCE REVDAT

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AB initio modeling?limitatons

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3D_1D bowie algorithm

Chaous algorithm

Enlist protein sequence method

Peptide mass finger printing nd shotgun

Chaous ka ek aur questn tha..

Ab initio modeling.

Chaos limitations.

Long:

Sequence identification protein 5 (topic 124)

How we detect loops in alpha helices and beta sheets. 5

Describe following:

1: Advantage of folded protein over denatured protein

2: role of A.A

3: role of folded protein.

4: protein sequence.

MCQs easy they but MS waly topic se they zda.

mera 80% paper MS spectrometry se aya...

mera ek long question tha protein sequence identification. aur short question mai just enlist krna tha yehi question..

mujhy laga homology modelling wala hai.. 😞, mera wo long aur short dono ghlt 😞, mujhy zra b andaza nhi rha k ye question b MS spectrometry se hai 😞.

[Mohsin Raza](#) bhai... kia mujhy ab in questions mai 1 b numbr nhi mily ga?? mera in 2 questions ki wajh se pura paper khrb hora hai

Bif

Today 11.pm

AB initio modeling

Optimal functions in protein structure

What happened when $pH < pK$

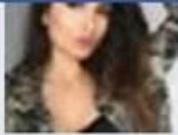
Define ionization in protein

Scoring in protein

Chou fasman algorithm

Kch bhol gae

← Message Details



Noor Butt

34 seconds ago



Forward

Bif 401

Mcqs were easy

Questions are

1. Describe

Blastx, blastn, tblastx, tblastn

2. enlist experimental technique for bioinformaticians.

3. f(total) of tetrapeptide describe and write its formula.

4. Chou Fasman algorithm prediction

5. folding protein k baare m tha kch

6. long m In silico fragment comparison

7. describe following

a. folding protein over denatured protein

b. role of amino acid

c. goal of amino acid

d. ek yaad ni ara protein ka e tha

Ek short ques b yad ni araa

Menu