

**BIF401 Today Current Final Term Paper Fall 2020**

**28-02-2021**

**Bif401....(9:30 Am)**

- 1) spectrometer (2)
  - 2) salient features of ORF
  - 3) is protein sequence determine difficult?
  - 4) how we have the algorithm of best protein sequence
  - 5) how we can determine the sequence of protein
  - 6) factors affecting the protein folding
  - 7) what happen when protein infolding
  - 8) how can find out the loops when computing the a-helix and b-sheets
- Or mcqs ak, 2 chor K sab midterm K syllabus sy thy
- 9) goal of protein folding
  - 10) Why Chou fasman algorithm is used.

**BIF401 Current Finalterm Papers Fall 2020 | 01-03-2021**

Questions

- 1: shotgun proteomics and fingerprinting?
- 2: How protein sequence are identified?
- 3: what is ab - initio modeling and it's limitations?
- 4: role of Amino acids and goal of Amino acids ?
- 5: Chau fasman for alpha helixes?.
- 6: Define : title, source , compnd ,revdt

**BIF401 Current Finalterm Papers Fall 2020 | 28-02-2021**

Bif401.

Why shotgun method is different from peptide mass spectroscopy.3

Title,CMPND, Source,REVDT .3

Energy function in proteins structure prediction .5

How we can identify proteins sequence .5

Advantage of denatured proteins over folded,role of amino acid,how proteins fold.

What is the goal of folding .5

Difference between DNA and RNA.2

role of amino acid

Fragmentation of protein

how Homology modeling determine unknown sequence of protein

Briefly describe the secondary structure

How chou fasman algorithm help in alpha helix

Advantage or dis advantage of Ab intio algorithm

Or discribe the given below

Role of amino acid

Why folding protein is better than denatured

Fector of protein folding

Gold of protein folding

My today's bif401 ppr

Time# 8:00

12 mcqs from past

1=what is tandem mass spectrometry?

2=what ab initio modeling? Describe its limitations as well?

3=describe following elements

\*Title\*

\*Source\*

\*REVDAT\*

\*COMPND\*

4=What is hydrophobicity of amino acid?

5=how propensity table can help us?

6=describe secondary structure of protein?

7=chou fasman algorithm

8=silico fragment comparison?

9=seven steps of homology modeling?

10=describe

\*advantage of folded protein over denatured protein\*

\*factor that participate in folding protein\*

\*role of amino acid\*

\*goal of folding protein\*

Q#1 Describe the following

1 Advantage of Folded Protein over Denatured Protein?

Factors That Participate In Folding Protein?

Role of Amino Acid?

Folding protein function?

Q#2. Need For Chou Fasman Algorithms?

Q#3 Advantages and Disadvantages Of Ab Initio Modeling?

Q#4 Optimal Energy Function In Protein?

Q#5 Silico Fragments Comparison?

Q#6 How Propensity Table Help Us?

Q#7 Function of Tandem MS?

Q#8 Explain the chou fasman method

Q#9 Tandem Mass spectrometry

Q#10 function of tandem MS

MY BIF401 paper at 2:30

Today bif 401 paper ...

8:00..

Mcqs mostly mid/past papers...

1...difference b/w similarity and identity?with formula?

2..Role of amino acid?

3...Characteristics of amino acids?

4...Ab initio limitations?

5...how protein sequence identified?

6...Summary of Alpha helix by Chou's algorithm?

7...Example about the Chou-Fasman secondary structure of protein?

8...define top down proteomics?

9...difference b/w spectrometry or raw data?

Yeh question yd thy baqi yd nh aa rhy

Top down proteomics

Shotgun proteomic and fingerprinting

How buldges are formed ?

How protein structures are identified ?

Define title ,source, cmpnd , revdat.

How protein sequence are uidentified ?

What is ab initio modelling and its limitations ?

Home message of this

course ?

Advantages of folding of proteins over denature proteins?

Role of amino acids,

Goal of amino acids

Characteristics of amino acids,?

Chaou fasmsn for alpha helecies?

Chaou fasman for secondary structures?

Name 3 hydrophobic amino acids?

Prediction of protein structures ?

Forces involved in protein folding

Techniques for protein structure

Protein ionization

Orf and fasta stands for

Use of sequence data

Importance of phylogenetics

Choufasaman algorithm for beta turns

And for alpha helix

Ab initio and limitation

Protein folding goal ,importance of protein folding and disruptive protein structure,importance of amino acids.

Compnd,title ,source, revdat

Bif401

13/9/2020

Sunday 2:30pm

- What are pseudoknots? (2 marks)
- What is hydrophobicity of amino acids? (2 marks)
- Ab initio modeling and limitations? (3 marks)
- Chou fasman algorithm for alpha helix (5 marks)
- Chou fasman algorithm for beta sheets (3 marks)
- what are the following PDB formats

TITLE, SOURCE, COMPND, REVDAT (5 marks)

- Advantage of folding protein over denatured

Role of amino acids

Goals of folding protein (5 marks)

- Difference b/w fasta35 and fastx35 (3 marks)
- Difference between shotgun proteomics and protein mass fingerprinting (3 or may be 5 marks)
- PAM matrix (5 marks)

MCQs from ppts (zyada asan nahi thay lekin mushkil bhi nahi thay as such)



Today bif401 paper 2:30

Top down proteomics

Shotgun proteomic and fingerprinting

How buldges are formed ?

How protein structures are identified

Define title ,source, cmpnd , revdat

How protein sequence are uidentified

What is ab initio modelling and its limitations ?

Home message of this course ?

Advantages of folding of proteins over denature proteins?

Role of amino acids

Goal of amino acids

Characteristics of amino acids,?

Chaou fasmsn for alpha helecies?

Chaou fasman for secondary structures?

Name 3 hydrophobic amino acids?

Prediction of protein structures ?