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 tendem 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 helps 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#1Describe the following

1Advantage 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#3Advantages and Disadvantages Of Ab Initio Modeling?

Q#4Optimal Energy Function In Protein?

Q#5Silico Fragments Comparison?

Q#6How Propensity Table Help Us?

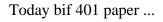
Q#7Function of Tandem MS?

Q#8Explain the chou fasman method

Q#9 Tendom Mass spectrometry

Q#10 function of tendom MS

MY BIF401 paper at 2:30

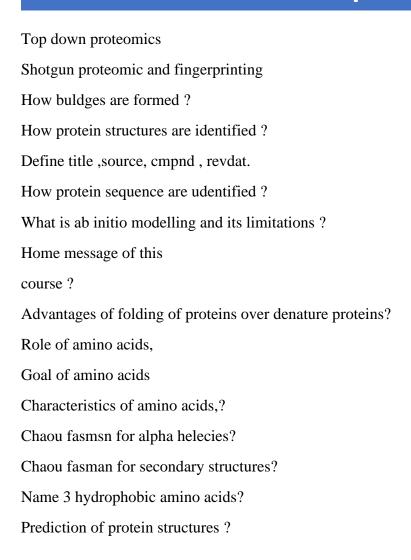


8:00..

Mcqs mostly mid/past papers...

- 1...differnce b/w similarty and identity?with formula?
- 2..Role of amino acid?
- 3...Charctersitc of amino acids?
- 4...Ab initio limitations?
- 5...how protein sequnce identified?
- 6...Summary of Alpha helix by chou's algorithum?
- 7...Example about the the chous fasman secondary structre of protein?
- 8...define top down pretomics?
- 9...difffernce b/w spectrometry or raw data?

Yeh question yd thy baqi yd nh aa rhy



Forces involved in protein folding

Techniques for protein structure

Protein ionization

Orf and fasta stands for

Use of sequence data

Importance of phylogemetics

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 psudoknots? (2 marks)
- What is hydrophobicity of amino acids? (2 marks)
- Ab initio modeling and limitaions? (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 udentified

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?