

BIF 401

“Solved past papers for Final term”

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Q. As MS chamber is only be used for ionization then, how can we make possible further fragmentation of protein in it?

ANS: For this sac there will be an addition of fragmentation instrument in MS chamber, which can perform this job nicely.

Q. Name the techniques used for protein fragmentation?

ANS: 1. Electron capture dissociation
2. Electron transfer dissociation
3. Collision induced dissociation

Q. Define PSTs? No option

Ans: peptide sequence tags (PSTs) are actually small amino acid sequence of peptides producing during MS2.

Q. what are three major types of scoring scheme which obtain from protein sequence data base search algorithm?

Ans: 1) MW match score 2) PST match score 3) invitro and in silico match score

Q. Name two types of open formats?

Ans: (1) mzXML (2) MGF

Q. Name some companies that are making mass spectrometer in market?

Ans: Agilent ----- Bruker ----- ABI ----- Micromass ----- Waters ----- Shimadzu

Q. How many types of masses are there? Mention their names.

Ans: 1) Nominal Mass 2) Monoisotopic Mass 3) Average Mass

Q. Differentiate between polar and non polar amino acids?

Ans: Non polar amino acids:

Non polar amino acids are hydrophobic in nature. They are mostly found inside of folded protein. H and C introduce very little dipole movement. e.g Phe, Ala, Leu, Val etc.

Polar amino acids:

These amino acids are polar but are not charged. Prefer to reside or interact to aqueous environment. Mostly found at surface of folded protein. E.g Cys, Gly, Ser, Thr, Tyr etc.

Q. What is meant by “PK” value of an amino acid?

Ans: PK is the value for an amino acid is that PH at which exactly half of amino acids are charged and half are not charged.

Q. what are the key factors participating in protein folding?

Ans: solubility and reactivity are the key factors that are participating in protein folding.

Q. Mention some unique properties of amino acids? No option

Ans: amino acids has unique set of properties such as charge state, polarity and hydrophobicity.

Q. write two methods which we use to obtain 1' structure? No option

Ans: 1. Edman degradation
2. tandem mass spectrometry

Q. briefly describe any three properties of Loops? NO option

Ans: • Loops connect helices and sheets • Loops vary in length and 3-D configurations • Loops are mostly located on the surface of proteins • Loops are more “acceptable” of mutations • Loops are flexible & can adopt multiple conformations • Loops tend to have charged and polar amino acids • Loops are frequently components of active sites

Q. Define angstrom. No options

Ans: Angstrom is a unit of length equal to 10^{-10} m (one tenbillionth of a meter) or 0.1nm .

Q. Name some atomic representation techniques which are helpful in protein structure visualization? No options

Ans: These include CPK, Ribbon and Balls & Stick diagrams.

Q. Name any two Techniques for structure determination. No options

Ans: 1. X-Ray Crystallography
2. Nuclear Magnetic Resonance (NMR) Spectroscopy

Q. What are the other possible structures which beta strands can give rise to?

ANS: 1. Beta Sheet 2. Beta Barrel 3. Beta Sandwiches

Q.. How many types of Domains are there?

ANS: 1). Alpha Domains 2). Beta Domains
3). Alpha/Beta Domains 4). Alpha + Beta Domains
5). Alpha & Beta Multi-Domains 6). Membrane & cell-surface proteins

Q..Name the Algorithms use for Structure Classification? No option

Ans: 1. CATH 2. CSOP 3. FSSP 4. Pclass

Q.What is the abbreviation of I-TASSER?

Ans: Iterative threading assembly refinement (I-TASSER)

Q. How many Strategies are there for Structural Modelling?

Ans: There are three basic Strategies,

1. Homology Modelling
2. Fold Recognition
3. Ab Initio Modelling

Q. How many basic types of Alignments, mention their names ?

Ans: there are two types of alignment,

Global Alignment (Needle Wunsch)

Local Alignment (Smith Waterman)

Q. How many types of Phylogenetic Trees are there?

Ans: There are two types of phylogenetic trees:

- Rooted Trees
- Un rooted Trees

Q. ExPASy stand for ?

Ans: ExPASy is one of the best collection of data and tools for proteomics. It stand for "Expert protein analysis system"

Q. differentiate between bottom up and top down proteomics?

Ans: There are two major types of MS-based proteomics e.g mass spectrometry proteomics,

“Bottom up proteomics deals with peptides”.

“Top down proteomics can handle whole proteins”.

Bottom up proteomics measures the peptide masses produced after protein enzymatic

digestion. And Top down proteomics measures the intact proteins followed by peptides after fragmentation.

Q. how loops are found after the finding of alpha and beta sheets?

Ans: After computing the propensity of alpha helices and beta sheets, we need to settle for loops.

- Let's see how can we find out the loops using Chou Fasman Algorithm.
- For any jth residue in sequence, we calculate $f(\text{Total}) = f(j) f(j+1) f(j+2) f(j+3)$ (tetra peptide).
- If,
- $f(\text{Total}) > 0.000075$.
- The average value for $P(\text{turn}) > 1.00$ in the tetra peptide.
- The averages for the tetra peptide are such $P(\text{a-helix}) < P(\text{turn}) > P(\text{b-sheet})$,
- It is a Turn!

Q. . How protein structure identified?

Ans: If another protein which has a similar sequence also has its structure known, the

structure of an unknown protein can be predicted based on that similar protein. So, it is then possible to identify unknown protein structures by just examining the homologous protein sequences. Good sequence alignment and identity ensures that homology modelling will give accurate results

Thus, Homology modeling is used to predict structures of proteins having high sequence similarity with other proteins with known structures:

Q. What happens when pH is < or > than pK?

Ans: If $\text{pH} < \text{pK}$ for an amino acid the amine side chain gain a proton (H^+) and become a positively charged, hence basic.

If $\text{pH} > \text{pK}$ for an amino acid, the carboxyl side chains loses a proton (H^+) and become negatively charged, hence acidic.

Q. What are the properties and role of amino acids?

Ans: Properties:

Amino acids have several properties such as charge state, polarity and hydrophobicity. Amino acids not only have physical and chemical properties, but also structural properties.

Role:

These structural properties are equally important in giving rise to protein structures. Since some amino acids are hydrophobic, they may be employed in forming a stable core in a protein.

- Also, chemically inactive amino acids reduce chances of destabilizing reactions in core.

Q. Why folding is important?

Ans: Proteins fold spontaneously. Proteins fold to achieve thermodynamic stability. Proteins fold to organize themselves for performing functions in cells.

Q. What is ab initio modelling describe the limitations of this model?

Ans: Ab initio methods have Anfinsen's thermodynamic hypothesis at the center.

- These methods attempt to identify the structure with minimum free energy.

Limitation:

- Computationally expensive
- Suitable for proteins with less than 100 residues

Q. write down the terms of PDB file format.

Ans: HEADER: contain the brief description of the structure, the date and PDB ID code.

TITLE: title of the structure.

SOURCE: identifies which organism the structure came from.

COMPND: brief detail of the structure.

REVDAT: the date of the last revision.

JRNL: one or more literature reference that describe the structure.

KEYWDS: list the set of useful words/phrases that describe the structure.

AUTHOR: the scientist depositing the structure.

REMARKS: detail of the experimental method used to determine the structure are contain in this subsection.

Q. define ionization in terms of proteins?

Ans: ionization of protein means to ionize a protein molecule to make it charged by removing an electron from it. Protein ionization is the first step in MS-based proteomics protocols

- Ionization process involves loading of a proton onto a protein or the removal of a proton from the protein
- Ionization results in an increase or decrease of the protein/peptide mass

Two primary techniques used for ionization of protein,

1. Electrospray ionization (ESI)
2. Matrix - assisted laser desorption/ionization (MALDI)

Q. Briefly describe chou fasman algorithm?

Ans: Chou – Fasman method:

It is a technique for the prediction of secondary structures in proteins i.e. Alpha Helices, Beta Sheets and Turns is Chou – Fasman technique. The method is based on analyses of the relative frequencies of each amino acid in alpha helices, beta sheets, and turns based on known protein structures solved with X-ray crystallography. From these frequencies a set of probability parameters (in our handouts, it is propensity table) were derived

- **For the appearance** of each amino acid in each secondary structure type.
- **To predict the probability** that a given sequence of amino acids would form a helix, a beta strand, or a turn in a protein.

Q. How can alpha helix expressed?

Ans: Chou-fasman algorithm (alpha helix):

- For Alpha Helices, 4 contiguous amino acids are required.
- Their Alpha-Helix propensity should be more than 1.0
- Once this propensity falls below 1.0, Alpha-Helix stops.

Q. Describe scores in silico fragmentation?

Ans: Silico fragmentation scoring:

- Count the matches between in silico and in vitro peaks.
- Give an equivalent score to the candidate protein.
- Weigh each of the aforementioned match by the mass error.
- Accumulate the score

Q. What are hydrophobic amino acids?

Ans: Hydrophobic Amino Acids:

Since H and C introduce very little dipole moments in hydrophobic amino acids, these amino acids are non polar. Hydrophobic amino acids are mostly found at the inside of folded proteins.

Q. Explain summary of alpha helix and beeta sheets?

Ans: Alpha Helices are formed by hydrogen bonding (O-H) between C_i and N_{i+4} atoms in the protein backbone. X-Ray Crystallography of protein shows that Hydrogen atoms of N-Term come together with Oxygen atoms of C-term amino acid at 4th neighboring position to make Hydrogen bonds!

Beta Sheets are an other common secondary structure

- They are constituted by several Beta Strands which come together
- 5 to 10 residues are needed to make a Beta Strand, typically

Q. what is 3D_1D bowie algorithm?

Ans: Proposed by Bowie et al in 1991

- Converts 3D structure into a 1-D string profile for each structure in the fold library
- Align the target sequence to these profiles 3D-1D methods convert structure and environment information into “profiles”
- Score for each amino acid is computed for each profile

Q. public database that commonly used for protein?

Ans: Examples include Uniprot, Swissprot amongst several others.

Write steps of protein sequence identification? OR Enlist protein sequence method.

Ans: Mass spectrometers are used to measure the molecular weight of proteins and peptides.

Following steps involve in protein sequence identification,

1. complex protein
2. separation
3. ionization by mass spectrometry
4. fragmentation MS2
5. mass spectra
6. EST Determination
7. filter protein database
8. in silico fragmentation of candidate protein
9. matching of experimental and insilco peak list
10. post translational modification
11. protein score.

Define Peptide mass finger printing nd shotgun?

Ans: Shotgun proteomics digests the entire protein mix 1st followed by peptide analysis & protein database search

- Peptide mass fingerprinting involves protein separation followed by a single protein's peptide analysis.

Q. Principal of dynamic programming?

“Dynamic programming is an algorithm technique used commonly in sequence analysis”.

Select a nucleotide from RNA sequence

AUGCUGUCAUCG

- List all possible complementary positions for selected nucleotide in the complete sequence

AUGCUGUCAUCG

AUGCUGUCAUCG

AUGCUGUCAUCG

AUGCUGUCAUCG and so on...

DP exhaustively makes all possible nucleotide combinations

- DP then recombines such combinations in a process called “Traceback” to ensure that the highest coupled 2’ structure is reported.

Q. write types of RNA ?

ans: Coding RNAs

- Coding RNAs as is obvious from their name , code for proetein
- **Non-coding RNAs**
- Non-coding RNAs regulate/assist in the process of translation.Q

Other types of RNA are,

1= m RNA

2=t RNA

3= r RNA

4= miRNA

5= si RNA

Q.: Explain different databases and their specificity.

Ans: There are two basic types of data bases,

1. Gene Bank:

It is an online public sequence data base. In Gene Bank we go to online NCBI Gene Bank to find

sequence of DNA and RNA using following Website,

www.ncbi.nlm.nih.gov/genbank

Gene Bank can be research by typing,

1. Sequence name
2. Species
3. ID
4. Locus
5. Author
6. Journal
7. Accession number
8. Name

2.Uniport:

It is also an online public data base. By using Uniport we can find sequence of proteins. If

we want to find a protein sequence we must go an online Website given bellow,

www.uniprot.org

In home page there is a box named “**Swiss Prot**” which contains human curated protein information,

molecular mass, observed and predicted modifications etc.

uniprot can be research by typing.

1. Amino acid 2. Name 3. ID 4. Sequence

Further Data Bases and their specificity is mention bellow,

Taxonomic Database For classification

Genomic Database For Gene level information

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