Virtual University of Pakistan

# (bif401)

# (bioinformatics 1)

# MCQ's for final term

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------- provide mass of intact molecules and its fragments

**MS1 and MS2**

theoratical data is usually ----- as compared to exp. Data,

**larger**

Three scoring schemes can be applied to ------

**score the match at each stage of protein search**

Simply sum the scores up (a linear function)

$$Score = Score_{MW} + Score_{PST} + Score_{Exp <> Thr}$$

In the above scoring method, MW and PST stabs for ____ & _____ respectively

**MS1 & MS2**

_____ are assembled by Ribosomes in cellular cytoplasm

**Proteins**

Amino acids have characteristics like polarity, hydrophobicity, and charge states. these characteristics are governed by

**Elemental composition of an amino acid's side chain (R group)**

Hydrophobic amino acids are non-polar due to

**very little dipole moments between H and C**

Core of amino acids is _____ and surface is _____

**Hydrophobic & hydrophilic**

At pH ____ Five amino acids are charged, 2 negatively and 3 positively

**7**

pK values for an amino acid is the pH at which:

**Exactly half of the chargeable group is charged**

The pK of aspartic and glutamic acids are ___-& ____ respectively.

**3.9 & 4.2**

If pH < pK for an amino acid, the amine side chains____

**Gain proton and hence basic**

If pH > pK for an amino acid, _____ loses a proton and hence acidic

**The carboxyl side chain**

Lysine and arginine have pK ____ &___ respectively.

**10.5 & 12.5**

Glycine residues increase backbone flexibility because :

**They have no R group (only an H)**

_____ reduce the flexibility of polypeptide chains.

**Proline residues**

____ Cement together by making _____ to stabilize 3-D protein structures

**Cysteines, disulfide bonds**

Chemically _____ remain in the core of protein.

**Inactive amino acids**

Backbone is highly polar (hydrophilic) due to polar ___ and ___ in each peptide unit

**-NH & C=O**

A-helices & B-sheets are stabilized by____

**H-bonds**

The very few hydrophobic "patches" on protein surface are involved in:

**Protein-protein interactions**

Alpha Helix is Stabilized by H-bonds between every ____ in backbone

**~ 4th residue**

Proteins fold spontaneously to achieve:

**Thermodynamic stability**

If a protein is ____, then it can lead to a lack of function in the protein

**Misfolded**

Given algorithms and procedures to fold a protein, we can:

**Fold amino acid chains to form 3D proteins**

Each amino acid can fold into____, ____ & ____

**Alpha Helices, Beta Sheets and Loops**

If computations of protein folding take $1/10^{th}$ of a nano-second($10^{-10}$), then to compute all the folding possibilities will take

**$1.6 \times 10^{30}$ years**

All the information required for folding a protein into its native structure is present within the:

**Protein's amino acid sequence**

**(Memorize the table given below)**

**Protein Structures**

**Energies of Various Bonds & Interactions**

| Bond Type | kJ/mol |
|---|---|
| Covalent Bond | 250 |
| Electrostatic | 5 |
| van der Waals | 5 |
| Hydrogen bond | 20 |

Primary sequence can also be referred to as ____

**1' structure**

Protein structures are organized into _____ modular conformations

**1', 2', 3' and 4'**

Edman Degradation & Tandem Mass Spectrometry are methods for obtaining _____

**1' structures**

2' structures are also referred to as

**Secondary structures**

C- Terminus is _____ charged

**Negatively**

N-terminus is _____ charged

**Positively**

2' structures or secondary protein structures are formed as a result of H-Bond formation between _____ in a protein backbone

**N and C termini**

_____ connect helices and sheets

**Loops**

_____ are Secondary structures that are not helices, sheets, or recognizable turns

**Coils**

_____ are also secondary structure which form the first structures after folding of protein's amino acids

**Loops and Coils**

Combinations of Alpha helices, Beta sheets, coils and loops help form _____

**3' structures**

____, ____ & _____ interactions enforce the 3' structure

**Covalent bonds, Hydrogen bonds and hydrophobic**

The stability of all the structures of protein is as:

**4' > 3' > 2' > 1'**

The protein folding into 3D structures leads to:

**Reduction in bond angles**

Peptide bond between two amino acids is _____

**Planar & rigid**

The angle between the 1st, overlapped and the 4th points forms a _____

**Dihedral angle**

_____ can be used to construct the backbone of a protein towards its visualization

**C-Alphas**

The _____ is used to express the size of atoms, molecules and extremely small biological structures, the lengths of chemical bonds, the arrangement of atoms in crystals.

**Angstrom**

Atoms of phosphorus, sulfur, and chlorine are _____ in covalent radius, while a hydrogen atom is _____ respectively.

**~1 Å & 0.25 Å**

Crystallography data gives _____ of atomic coordinates

**Relative positions**

_____ Proteins are used to determine protein structures.

**Crystallized**

(Memorize the below file format of protein data base to attempt additional mcq's in exam, for more, you can read ppt of lecture no. 179)

**HEADER** - Contains a brief description of the structure, the date and the PDB ID code.

**TITLE** - The title of the structure.

**COMPND** - Brief details of the structure.

**SOURCE** - Identifies which organism the structure came from.

**KEYWDS** - Lists a set of useful words/phrases that describe the structure.

**AUTHOR** - The scientists depositing the structure.

**REVDAT** - The date of the last revision.

_____ contains protein structure information

**PDB**

PDB has the coordinates of C-Alphas for over _____ proteins

**50,000**

To view a protein, we need to evaluate the:

**physical location of its atoms**

To trace the backbone of a protein, _____ trace can be used

**CA atoms**

Coordinates of CA atoms can be obtained from the ____

**PDB**

Protein structures are visualized using several online tools. These tools include:

**Rasmol, CHIME, Swiss PDB Viewer and Cn3D.**

CPK stands for:

**Corey-Paulin-Koltun Diagrams**

In CPK diagrams, each atom is represented by a _____

**Solid sphere**

Spheres are equal to atomic _____

**Van der Waal radius**

Ribbon Diagrams represent the protein secondary structures by using:

**Simple cartoon figures**

Balls & Stick (BS) Models have atoms as _____ and intermediate bonds as _____ respectively

**colored balls, sticks**

"Proteins fold for a unique, stable and minimum free kinetic energy structure". The given statement is called:

**Anfinsen's thermodynamic hypothesis**

There is _____ free energy accessible to each atom for further interactions.

**Lesser**

The greater the number of bonds, the more ____ a protein becomes.

**Stable**

The basic idea of thermodynamic stability is to _____ bonding in order to _____ the free energy

**Maximize, minimize**

We can calculate energy of a folded protein based on the _____ of atomic interactions

**number and types**

To determine the number of each type of interaction within a protein, we need to find its _____

**inter-atomic distances**

Based on specific atomic distances in protein, we can guess the _____

**type of atomic interaction**

## Energies of Interactions

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| Force | Strength (kJ/mol) | Distance (nm) |
|---|---|---|
| Van der Waals | 0.4-4.0 | 0.3-0.6 |
| Hydrogen Bonds | 12-30 | 0.3 |
| Ionic Interactions | 20 | 0.25 |
| Hydrophobic Interactions | <40 | varies |

$$Energy_{TOTAL} = Atoms_{VWF} \times Energy_{VWF} + Atoms_{HB} \times Energy_{HB} + Atoms_{IonicInteraction} \times Energy_{IonicInteraction}$$

To determine the structure of protein, we use_____

**X-Ray or NMR**

If two atoms are participating in a covalent bond, their distance is:

**~0.96A**

Incase of hydrogen bond formation between atoms, the inter-atomic distance is :

**~1.97A**

X-Ray data should have a minimum of _____ resolution

**1.97A**

**,"**Helix Formers" are generally _____ amino acids (M, A, L…)

**Hydrophobic**

Alpha Helices are formed by hydrogen bonding (O-H) between _____atoms in the protein backbone

**$C_i$ and $N_{i+4}$**

_____ resides are needed to make a Beta Strand

**5 to 10**

The sub-structures of beta-sheets are:

- **Beta Strand**
- **Beta Sheet**
- **Beta Barrel**
- **Beta Sandwiches**

_____is made of a single beta sheet that twists and coils upon itself.

**Beta-barrel**

Beta Sandwiches are made of two beta sheets which are usually _____so their strands are aligned

**twisted and packed**

Loops are formed by amino acids present in the middle of _____ in a protein backbone

**the Alpha Helices and Beta Sheets**

Variability in _____ allows loops to join Alpha Helices and Beta Sheets in a variety of ways.

**length and conformation**

Loops are mostly comprised of _____ amino acids

**charged and polar**

Hairpin loops are two amino acids long and join _____ Beta strands

**anti-parallel**

Essentially, a secondary structure which is not a helix, sheet or loop, is a _____

**coil**

Coils are apparently_____ regions

**disordered**

_____ are semi-independent functional structures in a protein

**Domains**

Domains have over _____ residues

**~40**

_____interact (H-bonds) more internally than externally

**Locally Compact – Domains**

Domains have a _____ core

**hydrophobic**

various types of domains are:

- **Alpha Domains**
- **Beta Domains**
- **Alpha/Beta Domains**
- **Alpha + Beta Domains**
- **Alpha & Beta Multi-Domains**
- **Membrane & cell-surface proteins**

(must see the structures of these domains in lecture 196)

Domains can be classified into structural classes. Classes can be further classified into

**Architecture and Topologies**

_____ classifies proteins by their structural similarity

**CATH**

FSSP stands for _____ based on the DALI algorithm

**Family of Structurally Similar Proteins**

SCOP stands for:–

**Structural Classification of Proteins**

So for two different proteins, sharing the same domain, we may want to compare:

**only a portion of the overall structure i.e. a domain**

Whole protein structures can be compared by calculating the _____ between their Alpha Carbons positions

**root mean squared difference (RMSD)**

The _____ the RMSD, the similar are the proteins

**Lower**

Full protein structures can be compared and ranked by the overall _____ in positions between their Alpha Carbons

**differences**

_____ tells us about the quality of the matches

**RMSD**

_____ mostly found in Alpha Helices

**Alanine**

The first such algorithm to predict 2' given an amino acid sequence was the:

**Chou-Fasman Algorithm**

we only know _____ 3D protein structures, but 10 times more sequences

**100,000**

For a primary sequence, and a tentative 2' structure, _____ can help us compute the overall propensity

**propensity table**

___ amino acids are needed to start an Alpha Helix and ___ amino acids for Beta Sheet

**4,5**

Loops are small amino acids

**~ 3-4**

Alpha Helices are formed from 4 contiguous amino acids having an Alpha-Helix propensity over _____

**1.0**