BIF 401 MCQ

(For final term)

FROM LECTURE NO: 126 - 250

Q.1. In mass electrometer chamber protein is deflected according to its ……

a) charge b)velocity c)charge, mass d) volume

Q.2 in MS chamber mass/charge ratio can be measured by …… of protein molecules.

a) volume b) mass c) charge d) speed

Q.3 while scoring protein mass score is awarded on the base of ……. b/w experimental and theoretical mass.

a) Distance b) closeness c) equality d) all of these

Q.4 Tandem MS is used to …… of protein fragments.

a) Ionization b) fragmentation c) measure the mass d) sequence

Q.5 Fragmentation techniques split the molecules of protein into……..

a) Two part b) three part c) four part d) multiple part

Q.6 Tandem MS is typically called as,

a) MS b) MS1 c) MS2 d) ALL

Q.7 Each fragmentation technique differ in their work on bases of ,

a) Having different splitting sites

b) Having different time duration

c) Having different mass detection

d) all of these

Q.8 Mass spectrometer use o measure the mass of protein and ……

A) Amino acids b) lipids c) peptides d) DNA

Q.9 Protien ionization is the …… step in MS based proteomics.

a) first b) second c) third d) fourth

Q.10 Ionization process involve gaining and removal of …….

a) electron b) proton c) ion d) atom

Q.11 molecular weight increases by ……. Of proton

a) removing b) adding c) transfer d) All of these

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Q.12 We can score each protein hit in away that the better match gets a ……

a) higher score b) lower score c) equal score d) opposite score

Q.13 ECD gives out "C" and …….. ions,

a) B b) Y c) Z d) A

Q.14 CID gives out "B" and …….. ions,

a) Y b) Z c) B d) C

Q.15 PST is abbreviation of…..

a) Protein sequence tags b) protein sequence tools

c) Peptide sequence tags d) peptide sequence tools

Q.16 PST is sequence of peptidesproduced during…..

a) MS b) MS1 c) MS2 d) ALL

Q.17 Fragmentation at consecutive sits lead to a mass difference equal to that of a single …..

a) peptide b) amino acid c) protein d) DNA

Q.18 The data base protein which have matching PSTs to invitro protein are known as ……

a) Sample protein b) candidate protein c) data base protein d) PST protein

Q.19 Experimental peptides also known as ……

a) data base peptide b) observational peptide

c) invitro peptide d) sample peptide

Q.20 Errors in peak matching also considered by…….

a) Sequence b) fragmentation c) ionization d) scoring scheme

Q.21 Which one is the right sequence of steps to create a composite protein search engine.

a) PST – MW – In silico comparison b) MW – PST – In silico comparison

c) In silico comparison – MW – PST c) MW – in silico comparison – PST

Q. 22 We can´t add these three scoring comparison until we divide them by their……

a) length b) error c) numbers d) distance

Q.23 Typtic peptides may reach upto an order of …….

a) 200,000 – 30,000 b) 30,00 – 40,00 c) 300,000 – 400,000 d) 400,00 – 500,00

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Q.24 large scale proteomics is a developed form of

a) mass spectrometry b) BUP technique c) TDP technique d) uniprot technique

Q.25 Mass spectrometry use to measure ……. Ratio of ionized protein or peptide.

a) mass/distance b) charge/distance c) mass/charge d) distance/charge

Q.26 Raw file in a format are often found in ……. That we have to change in an open format so as to make it readable.

a) Theoretical form b) decimal form c) percentile form d) binary form

Q.27 mzData was developed by ……

a) mzML b) HUPO-PSI c) RAW format d) MGF

Q.28 MASCOT is an online ……. Search engine,

a) Bottom up proteomic b) top down proteomic c) both d) none

Q.29 …….. is a simple human readable format for MS/MS developed by Matrix Science.

a) MASCO b) ABI c) MGF d) RAW format

Q.30 theoretical vs experimental fragments comparison helps us as the …….. Stage for short listing candidate protein list.

a) 1st b) 2nd c) 3rd d) 4rth

Q.31 To ensure that all fragments of precursor molecules are also charged, we can use,

a) ESI b) RAW c) BOT d) NONE

Q.32 Monoisotopic mass is the mass of ……..

a) single isotope b) average isotope c) least abundant isotope d) most abundant isotope

Q. 33 Proteins are assembled by ..... in cellular cytoplasm

a.golgi apparatus b.mitochndria **c.ribosomes** d.nucleaus

Q. 34.Each protein is synthesized by polymerization of .....

a.peptide bond **b.aminoacids** c.nucleotide sequance d.all

Q.35.The characteristics are governed by the elemental composition of an amino acid's .....

a.alpha carbon b.H group **c. R group** d.amino group

Q.36 Since ....and ..... introduce very little dipole moments in hydrophobic amino acids, these amino acids are non polar

a.H &C b.H & Y c.Y & H d.A & Z

Q. 37 Mostly ..... aminoacids found at the surface of folded proteins

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a.polar b.nonpolar c.acidic d.basic

Q.38. At pH=7, five amino acids are charged, ... negatively and ..... positively

a.3 & 2 b.3 & 3 **c.2 & 3** d.2 & 2

Q. 39.The charge state depends on the acceptance or donation of ..... from the R group side chains

a.electron **b.proton** c.neutron d.both a & b

Q. 40. Amino acids have property such as .....

a.charge state b.polarity c.hydrophobicity **d.all**

Q. 41 Tendem MS helps to measure the moleculer weight of ……

a) isotops b) precursor protein c) ionized fragments d) invitro protien

Q. 42.If pH >pK for aminoacids carboxyle side losses the proton and bocome negative which is

.....

a.basic b.neutral c.less acidic **d.acidic**

Q. 43. ..... are key factors participating in protein folding

a.solublity b.reactivity **c.both** d.none

Q. 44.The charge state depends on the acceptance or donation of ..... from the R group side chains

a.electron **b.proton** c.neutron d.both a & b

Q. 45. Amno acid with the side chain containing organic acids are soluble in …….

a) ethanol b) water c) lipids d) a and c

Q. 46 …….. residue has no R group.

a) cystine b) proline c) glycine d) adinine

Q. 47 proline residue …… the flexibility of polypeptide chain.

a) increase b) decrease c) stabilize d) no effect

Q. 48 A peptide unit has a backbone of polar NH and C=O which is highly……..

a) hydrophilic b) hydrophobic c) neutral d) acidic

Q.49 Functional group of protein always attach to its hydrophobic ……..

a) surface b) coat region c) core region d) backbone

Q. 50 After polymerization ……. are formed.

a) 3D structure b) alpha helix c) beta sheets d) All of these

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Q. 51 The force involve in protein folding ……

a) electrostatic interactions b) van der waals interactions c) hydrogen bonding d)all

Q. 52 ……folded form of protein is thermodynamically more stable than others.

a) Combined b) native c) partially d) a and b

Q. 53 3´ structural can combine with other polypeptide units to form …….

a) secondary structure b) tertiary structure c) quaternary structure d) all

Q. 54 There is a ……. variety of protein structure exist.

a) rare b) restrict c) limited d) huge

Q. 55 Folded sub structures are called …….

a) primary structure b) secondary structure c) tertiary structure d) All

Q. 56 The protein super structure are called ……

a) primary structure b) secondary structure c) tertiary structure d) All

Q. 57 Lysine and tryptophan have respectively …….. 1-letter codes.

a) L – T b) S – F c) K – W d) N - A

Q. 58 C- terminus is …… charge.

a) negatively b) positively c) neutral d) none

Q. 59 ……. bonds are the reason of 2' structure formation.

a) covalent b) hydrogen c) ionic d) All

Q. 60 Loops and Coils are very important 2' structures in that they form ……. of proteins.

a) active site b) inactive site c) acidic site d) basic site

Q. 61 …….. Enforce the 3' structure.

a) Covalent bonds b) Hydrogen bonds c) hydrophobic interaction d) all

Q. 62 Proteins with ……. chain can form 4' structures.

a) single b) double c) linear d) multiple

Q.62 Dihedral Angles always form between ……

a) two points b) three points c) four points d) five points

Q.63 ……. angles are taken up as a result of folding of protein.

a) phi b) psi c) both d) none

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Q .64 …… can be used to construct the backbone of a protein towards its visualization.

a) N b) C c) C Beta d) C Alpha

Q. 65 Atoms of phosphorus,sulfur, and chlorine are …… in covalent radius.

a) ~1 Å b) ~2 Å c) ~3 Å d) ~4 Å

Q. 66 The angstrom is used to express ……

a) small biological structures b) lengths of chemical bonds,
c) arrangement of atoms in crystals. d) All

Q. 67 Distances between C-Alphas are measured in the unit "Angstrom" by the process of ……..

a) adman degradation b) X Ray crystallography c) Blossom matrix d) PAM Matrix

Q. 68 1 A resolution is better than ……..

a) 9 A b) 8 A c) 7A d) 10 A

Q. 67 PDB contains protein …… information

a) structure b) size c) distance d) function

Q. 68 PyMOL and Cn3D is a python-script based tool for visualizing the ……..

a) protein size b) protein structure c) amino acids size d) a and b

Q.69 BS Models have atoms as colored balls and intermediate bonds as ……..

a) straw b) spindle c) stick d) small line

Q. 70 In CPK diagrams, each atom is represented by a ……..

a) dot sign b) Solid Ball c) doted circle d) solid sphere

Q.71 According to "Anfinsen's thermodynamic hypothesis" protein folds for making a ……..

a) stable structure b) structure having minimum free energy c) structure having maximum free energy d) a and b

Q.72 Hence, the basic idea of thermodynamic stability is to …….. bonding in order to …… the free energy.

a) minimizing, maximizing b) maximizing, minimizing c) maximizing, stable

d) b and c

Q.73 **To determine the number of each type of interaction within a protein, we need to find its ……**

a) type of amino acid b) types of bonds c) inter-atomic distances d) atomic mass

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Q.74 By looking up at the bond/energy table, we can compute the …….

a) overall energy b) molecular mass c) atomic mass d) bond sequence

Q.75 If two atoms are participating in a covalent bond, their distance is ……

a) ~0.95 A b) ~0.96A c) ~0.97 A d) ~0.98 A

Q.76 "Helix Formers" are generally…….. amino acids (M, A, L…)

a) acidic b) basic c) hydrophilic d) hydrophobic

Q.78 Alpha Helices are formed by hydrogen bonding (O-H)between …… and ……. atoms in the protein backbone

a) C – H b) H – N c) C – N d) P - N

Q.79 …… resides are needed to make a Beta Strand,typically

a) 3 – 4 b) 5 – 10 c) 6 – 7 d) 5 – 6

Q.80 Loops are the …… of secondary structure

a) 1st b) 2nd c) 3rd d) 4rth

Q.81 what is made by a single beta sheet when it twists and coils upon itself.

a) Beta Barrel b) beta sandwich c) loops d) coils

Q.82 ……. are flexible & can adopt multiple conformations.

a) coils b) helices c) loops d) All

Q.83 …… are apparently disordered regions with random structure and random length.

a) coils b) helices c) loops d) beta sheets

Q.84 …… are Non-functional Combinations of 2' structures)

a) loops b) coils c) beta sheets d) motifs

Q.85 Domains are semi-independent functional structures in a protein having over ……..

a) ~30 residues b) ~40 residues c) ~50 residues d) ~60 residues

Q. 86 The structural classes of Domains can be further classified into ……

a) Architecture b) Topologies c) both d) none

Q. 87 Architecture also called ……..

a) domain b) motifs c) coil d) fold

Q.88 …….. is one such system in which proteins are organized into classes, architecture, topology & homology.

a) CATH b) FSSP c) LOCK d) DOLI

Q.89 By comparing …….. can help us evaluate if the proteins do similar function.

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a) sequence b) free energy c) structure d) All

Q.90 For comparing the complete or partial protein structures, the position of ……. can be used.

a) N terminal b) C terminal c) Alpha Carbon d) functional group

Q.91 Whole protein structures can be compared by calculating the ……..difference b/w their Alpha Carbons positions.

a) distance b) root mean squared c) energy d) All

Q.92 The ……. the RMSD, the similar are the proteins.

a) Equal b) higher c) lower d) random

Q.93 RMSD tells us about the quality of the matches

a) matches b) mismatches c) sequence d) bonding

Q.94 There are over a million protein sequences but only about …….. protein structures.

a) 10,000 b) 100,000 c) 10,0000 d) 1,000

Q.95 if we have several …… in the sequence, then we can anticipate that a helix may be formed by them.

a) Proline b) Thiamin c) Alanines d) Adenine

Q.96 Product of propensity values is computed for ……. for each 2' structure.

a) individual propensity b) overall propensity c) greatest propensity d) All

Q.97 For Alpha Helices ….. contiguous amino acids are required.

a) 6 b) 5 c) 8 d) 4

Q. 98 Alpha-Helix propensity should be more than ……. Once this propensity falls, Alpha-Helix stops.

a) 1.0 b) 1.5 c) 2.0 d) 2.5

Q. 99 …… amino acids are needed to start an Alpha Helix and ……. amino acids for Beta Sheet.

a) 3 , 4 b) 4 , 5 c) 5 , 6 d) 4 , 6

Q. 100 Regions where overlapping alpha-helices and betasheets occur are declared helices.

a) loops b) coil c) helix d) helices

Q.101 In chou fasman algorithm Alpha Helices can be finalized if their propensity is ……. to the propensity for Beta Sheets.

a) equal b) less c) higher d) different

Q.102 Chou Fasman Algorithm helps us to predict,

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a) Alpha Helices b) Beta Sheets c) Turns d) All

Q.103 Beta sheets can be predicted from …… amino acid sequences

a) primary b) secondary c) tertiary d) quaternary

Q.104Chou Fasman Algorithm is based on statistical occurrence of ……. in known structures.

a) protein b) Amino Acids c) nucleotide d) a and b

Q. 105 Functional evaluation of proteins can be performed by……

a) Structure visualization b) , classification c) prediction d) All

Q.106 Functional evaluation of proteins is important for understanding …….

a) disease b) designing drugs c) treatment d) ALL

Q.107 X-Ray Crystallography and NMR Spectroscopy are used to find the structures of ……..

a) DNA b) Amino acid c) proteins d) nucleotides

Q.108it is then possible to identify unknown protein structures by just examining the …….. protein sequences

a) heterogeneous b) homologous c) multiple d) binary

Q.109In homology modelling, proteins with similar …….. are considered.

a) 1' sequences b) 2' sequences c) 3' sequences d) 4' sequences

Q.110Homology modelling is used to predict structures of proteins having high sequence similarity with other proteins with ……..!

a) known structures b) unknown sequence c) similar sequence d) a and c

Q111 Protein structure can be predicted by…… methods:

a). Homology Modelling b). Threading/Fold Recognition
c). Ab Initio Modelling d). All

Q.112 in homo logy modeling,Definition of Template (……..) & Target (……)

a) known – unknown b) unknown - known c) known – similar d) unknown - similar

Q.113 One way to handle loops is to take some residues before and after the insertion as …….. residues.

a) sample b) predicted c) anchor d) similar

Q.114 The backbone of tyrosine strongly prefers ……. rotamers & the real side-chain may fit one of them.

a) 1 b)2 c)3 d)4

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Q.115 In homo logy modeling when protein backbone is ready,then next, ……. were modelled and used to bridge gaps.

a) α helices b) β sheets c) coils d) loops

Q.116 Loop modeling is ……step of Homology modeling.

a) 2nd b) 3rd c) 4th d) 5th

Q.117 Homology Modelling …….. study conformational changes.

a) can b) cannot c) may be d) some times can

Q.188 We can overcome the limitations of homology modeling by ……..

a) Threading b) Bowie Algorithm c) Ab Initio modeling d) a and c

Q.119 Q……. is a software for homology modelling.

a) Homolog b) Modeller c) iTASSER d) a and b

Q.120 There are …….. stable folds of protein in nature.

a) 30,000 b) 4,000 c) 40,000 d) 5,000

Q.121 Several tools are available to perform homology modelling in a programmatic or automated way such as…..

a) Swiss Model b) Robetta c) 3D Jigsaw d)all

Q.122 Fold recognition is also called …….

a) scoring sequencing c) Threading d) modeling

Q.123 Homology modelling fails to predict quality structures ……. is a technique for predicting these structures.

a) Fold recognition b) Swiss Model c) Threading d) a and c

Q.124 Threading Scoring typically involves using a …….. function based on energy of a molecule

a) Z-Score b) C-score c) A-score d) Y-score

Q.125 …… cannot be predicted using threading.

a) invtro protein b) primary protein c) 2ndary protein d) Novel proteins

Q.126 3D-1D Bowie Algorithm Proposed by Bowie et al in ……

A) 1997 B) 1991 C) 1995 D) 1998

Q.127 3D-1D Identify amino acids based on ……..

a) protein core b) side chain positioning c) solubility d) All

Q.128 3D-1D methods convert structure and environment information into ……..

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a) software b) packets c) profiles d) subunits

Q.129 Ab initio modeling is Computationally ……. Suitable for proteins with less than …… residues

a) cheap – 500 b) expensive – 100 c) cheap – 100 d) expensive - 500

Q.130 Ab Initio Modelling methods attempt to identify the structure with minimum …….

a) charge ratio b) distance c) molecular weight d) free energy

Q.131 Energy released during the …….. process is computed for predicting structure.

a) Sequencing b) folding c) breakdown d) bonding

Q.132 Ab initio methods base their predictions on ……. models of folding mechanisms

a) Chemical b) statistical c) physical d) all

Q.133 Global optimization finds the most …….

a) matching sequence b) stable structure c) similar pattern d) a and c

Q.134 ……structure not always at the global minimum.

a) Native b) invitro c) insilico d) stable

Q.135 Ab initio methods are the very …….. to design.

a) easy b) difficult c) suitable d) accessible

Q.136 In homology modeling first we perform ……. and then ……..

a) Loop modeling - Backbone generation b) Backbone generation - Loop modeling

Q.137 There are ……. Steps of Homology Modelling.

A) 5 b) 6 c) 7 d) 8

Q.138 Ab initio modeling is Computationally ……. And …… process.

a) easy and expensive b) Expensive and complex c) cheap and easy
d) difficult and cheap

Q.139 Ab initio methods predict protein structures by folding proteins based on each constituent atom's ……..

a) volume b) charge c) mass d) all

Q.140 UPGMA is a …… method.

a) clustering b) non clustering c) both

Q.141 Homology modelling is performed in cases of …… identity and alignment score • For the "Twilight zone", other strategies are employed

a) high b) low c) equal d) overall

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Q.142 Maximum Parsimony etc are……. methods (not included in this course).
a) clustring b) nonclustering c) mapping d) visualizing

Q.143 Online tools: ……..
a) mascot b) sequest c) prosight PC d) all

Q.144 Number of known protein sequences is …….. as compared to known proteins structures
a) larger b) much larger c) smaller d) mech smaller

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