Bif 401 Final term object and sbjctive.

1. Genomics, evolutionary studies and system biology are application of _____bioinformatics

2. Exact matching require which type of nucleotide-_____same number of nucleotide .

3. Accurate solution of protein structure is one of the _____ toughest problems

4. …is overlap matches can start from any position in scoring matrix_____ Tract back .

5. The matrix has ……scores. _____Positive and negative

6. ___ can search people mass finger printing and shotgun proteomics data set_____ MASCOT

7. Spectrometer measures the protein by _____ Mass/charge

8. Simulation of the folding process depends _____ Energy function

9. Information about …..is available on gene bank_____ DNA/RNA

10.

…is used to measure the molecules weight of intact proteins._____ TDP

11.

Coordinates in the protein backbone can be used for structural visualization._____

_____ of alpha carbon

12.

In structure visualization c-alpha atoms are traced to recreate a ____3D protein structure

13.

In UPGMA distance is calculated btw _____ two clusters and between two trees

14.

Pk value of Aspartic acid _____3.9

15.

Largest amino acid …… _____Tryptophan

16.

2 STRUCTURE of proteins can be obtained by using_____ Chou ndFasman algorithm

17.

NJ Algorithm strategy is used to predict __ _____ RNA 2` structure

18.

The loop of hair pin must be at least _____ in length 2 aminoacids

19.

Fold recognition is also called …….._____threading

20.

Ab initio method in contrast ,base their prediction on _____low energy model.

21.

Bioinformatics require…….smart mind, and connected to internet,___ _____both,

22.

Sequence alignment tool is……_____.PROSIGHT and MASCOT

23.

MS1,MS2 provide us data identifying unknown…….____Proteins sequence.

24.

MGF files develop as an open standard for……. _____proteomics data.

25.

..coordinates alpha carbon in protein back bone can be used for comparison ._____ PDB

26.

Alpha carbon atom can be obtained from……_____PDB

27.

In formation of 2nd structure of protein C & N can make……_____Hydrogen bonds

28.

Information for protein folding is into its native structure is in…….. _____

_____ protein's amino acid sequence

29.

Energy …during bond formation._____ released

30.

Hydrogen bonding occur in …….Protein structure_____ secondary

31.

Bond between C and H in alpha helices_ _____Hydrogen bonding

32.

Amino acid having 3 codons_____ isoleucine

33.

MALDI typically adds a …… to protein or peptide. _____ Proton

34.

Low quality match gets____ _____lower score

35.

____ are sequences of amino acids produced during MS2. _PST (peptide sequence tags)

36.

MS2 data can be used to extract……_____peptide sequence tags.

37.

The alpha helices propensity should be more than_____(1.0)

38.

How many types are of protein sequencing techniques__ _____(2)

39.

Blast can find sequences of _____nucleotides amino acid

40.

If a protein sequence of 26 amino acids is fragmented at 11 amino _____acid C11, Z25

41.

To find out unknown sequence of nucleotide we use . _____NGS or Mass spectrometry

42.

How many types of peptide May be injected in mass spectrometry chamber.. . _____

_____ three hundred thousand to four hundred thousand

43.

…..can search peptide mass finger printing and shotgun proteomics dataset._____ MASCOT

44.

Stabilizing and destabilizing energy give us …….. _____quality of 2nd structure

45.

The Fasman algorithm is based on ..of Amino Acids in known structures._____

_____ _____ statistical occurrence

46.

DP recombinant the nucleotide recombination through process of ……. _____Traceback

47.

…..add proton to a protein and a peptide.._____ MALDI

48.

Positively charged amino acids are….. _____3

49.

Aromatic amino acid include ……. . _____phenylalanine, tyrosine tryptophan

50.

Homology modelling fail to predict ……._____ quality structure

51.

How many forces are involved in protein folding. _____4

52.

Pairwise alignments tells the similarity between sequence… _____

_____ by maximizing the matches.

53.

Dot plots employ dot matrix with two sequence plotted represents……_____

_____ pairwise alignment and comparison.

54.

Differentiate b/w DNA and RNA sequence…….RNA has more variety of sequence

55.

Cell molecule are produced after transformation of ……. _____DNA to protein

56.

Dot plot cannot deal with……. _____Insertion, deletion and gaps.

57.

Exons are may be more ……. _____conserved.

58.

In dynamic algorithm we can do comparison ……. of more sequence. _____Three

59.

Mass/Charge ratio helps calculate the mass of the …. _____Protein

60.

In scale tree branches lengths are equal to the magnitude of change in the …….. ____nodes.

61.

How many types of peptides mix in MS chamber……. _____300,000 – 400,000

62.

mRNA is a …… structure.___ _____Planer

63.

When unpaired bases of 2′ stricture join to form……. _____3′ structure

64.

N Jackobson use to pridict _____2

Nd

′structure

65.

Aromatic amino acid ……. _____Tyrosine

66.

Positive charge amino acids……. _____Lysine, arginine, histidine

67.

MS begins with the measure of …….. _____intact protein

68.

Amount of amino acids in alpha helix…….____(4)

69.

Intact mass of protein can be found by….. _____MS1

70.

MSA can be done by……. _____CLUSTAL

71.

Which is used as sequence alignment tool……. _____PROSIT

72.

MS1 and MS2 help to identify …… _____(PST)

73.

MGF is used for …….. _____proteomics

74.

X,Y,Z positions of alpha carbon available online on …… _____(PDB)

75.

Method to determine RNA structure …….. _____NMR, X-Ray crystallography

76.

CLUSTLA runs…….._____ Slow accurate/ fast appropriate

77.

Which give info about precursor protein……. _____PSTS

78.

Raw data files format can be converted to ……. _____Open format

79.

Which of the following is cartoonic figure……..._____ Ribbon diagram

80.

In CATH protein recognize according to their…….. _____structural similarity

81.

Method for obtaining 1´ structure……_____

_____ (Edman Degradation Tandem Mass Spectrometry)

82.

In dot plot matrix, if one nucleotide with one but not in diagonal fashion called _____Noise

83.

Dot plot employ dot matrix with two sequences…. _____top and left matrix

84.

Match, mismatch and gap penalty is used to compute score from.._____ each position

85.

Functional domain in proteins tend to be more conserved than the_hydrophobic

Core

86.

Trackback in overlap matches, can start from any position.._____ Yes

87.

FASTA the online software can perform genome and proteome similarity search..___ _True

88.

Is thrionine(T) is a hydrophobic amino acid.._____ No

89.

The main difference between fast and approximately and slow and accurate method in

CLUSTULAW is that there is no need to mention is slow and accurate method……_____

_____ _____Window size

90.

What does meant by MS/MS measured of molecular weight of protein.._____

_____ Peptide will be analyzed two times after fragmentation

91.

…reverse the chemical direction of RNA molecules.._____ hairpin

92.

Mass of peptide search in…._____ bottom up proteomics

93.

Amino acid are building block of…_____ protein

94.

Aromatic amino acid include… _____ Phenylalanice, Tyrosine and Tryptophan

95.

Protein are assembled at which organelles in a cell _____ Ribosome

96.

Why do we create all possible combination of diagonals in Zukar.._____

_____ to minimize stacking destabilizing energy

97.

Score is awarded on the basis of closeness B/W.._____theoretical and experimental

98.

Which is not required in protein structure threading…__ structure of entire backbone

99.

Chu fasman used to predict ….structure of protein_ _____Secondary

100. The structure classification of protein is carried out to _____ _____

_____to check hierarchy of classification

101. Multiple sequence alignment can be done through the following alignment

Software…_____CLUSTAL

102. Threading involves.. _____Passing

Nucleotide sequence through each fold in database

103. How many strategies for structural modeling_ _____Three

104. …are sequence for peptide produce during MS2_ --_____ PST

105. Composite scoring scheme are needed to combine scores coming in from _____

____ _____ Multiple criteria

106. ….can make the MS comprise of m/z ratio and intensities of each molecules that is

Measured…_____ Data output

107. …coordinate of alpha carbon is protein backbone can be used for comparison_ _____PDB

108. The(x,y,z) position of alpha carbon atoms can be obtained from.. _____PDB

109. If we are given an amino acid sequence, then we can check the..table. _____ Propensity

110. ….are formed OH between Ci and Ni + 4..____Alpha helices

111. Secondary structure of protein formed by H bond formation between N terminal and C

Terminal portion backbone

112. 1 angstrom is equal to __.. _____0.1

113. Structure is represented by secondary structures fold using simple ____cartoon figures.

114. . How many types of RNA present in a cell……..____5

115. Amino acid have unique structural properties ….._____protein folding

116. Alpha helix are formed by ……._____hydrogen bonding

117. Hydrogen atoms of N-Term may come together with Oxygen atoms

118. Atomic distances tell us about atomic interactions with neighboring _____atoms

119. Fold recognition called ……._____Threading technique

120. In structure visualization alpha helix carbon are traced to form …._3Dprotein structure

121. Which is the largest amino acid ….._____Tryptophan

122. 3D-10 methods convert structure and environment information into "_____profiles"

123. Unique, stable & kinetically accessible minimum free energy_____ Anfinsen's dogma

124. Each component of structure protein has unique and precise role in construction

…_____hydrophobic and hydrophilic

125. Beta Sheets which are stabilized by _____H-bonds!

126. Using the masses reported by Ms1, protein databases can be filtered for _____

_____ candidate protein

127. PST stands ……._____Peptide sequence tags

128. Mass spectrometer is used to measure mass/charge ratio of ionized proteins and

Peptides

129. Mass Spectrometry proteomics identifies as well as determines the protein __sequence

130. The backbone of tyrosine strongly prefers two rotamers

131. Threading technique useful when homology modeling fail to predict___ quality structure

132. Bio informatics is _____new developing field

151-250

1. ----- provide mass of intact molecules and its fragments _____MS1 and MS2

2. Theoratical data is usually ----- as compared to exp. Data, _____ larger

3. Three scoring schemes can be applied to ------_____score the match at each

4. In the above scoring method, MW and PST stabs for ____ & ___ respectively_____MS1 & MS2

5. _____ are assembled by Ribosomes in cellular cytoplasm _____Proteins

6. 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)

7. Hydrophobic amino acids are non-polar due to _____

_____very little dipole moments between H and C

8. Core of amino acids is _____ and surface is _____ Hydrophobic & hydrophilic

9. At pH ____ Five amino acids are charged, 2 negatively and 3 positively _____7

10.

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

_____ Exactly half of the chargeable group is charged

11.

The pK of aspartic and glutamic acids are ___-& ____ respectively. _____3.9 & 4.2

12.

If pH < pK for an amino acid, the amine side chains_____Gain proton and hence basic

13.

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

_____The carboxyl side chain

14.

Lysine and arginine have pK ____ &___ respectively. _____10.5 & 12.5

15.

Glycine residues increase backbone flexibility because :_____-- They have no R

Group_____(only an H)

16.

_____ reduce the flexibility of polypeptide chains. _____Proline residues

17.

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

_____Cysteines, disulfide bonds

18.

Chemically _____ remain in the core of protein._____ _____Inactive amino acids.

19.

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

Unit_____-NH & C=O

20.

A-helices & B-sheets are stabilized by_____ H-bonds

21.

The very few hydrophobic “patches” on protein surface are involved in: _____

_____Protein-protein interactions

22.

Alpha Helix is Stabilized by H-bonds between every ____ in backbone _____~ 4th residue

23.

Proteins fold spontaneously to achieve: _____Thermodynamic stability

24.

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

25.

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

_____Fold amino acid chains to form 3D proteins

26.

Each amino acid can fold into____,__ & ____-Alpha Helices, Beta Sheets and Loops

27.

If computations of protein folding take 1/10th of a nano-second(10 -10), then to compute all the

Folding possibilities will take_____1.6 x 1030 years

28.

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

_____-Protein's amino acid sequence

29.

Primary sequence can also be referred to as ____ _____1' structure

30.

Protein structures are organized into _____ modular conformations_____1', 2', 3' and 4'

31.

Edman Degradation & Tandem Mass Spectrometry are methods for obtaining_1' structures

32.

2’ structures are also referred to as _____---Secondary structures

33.

C- Terminus is _____ charged _____Negatively

34.

N-terminus is _____ charged _____Positively

35.

2’ structures or secondary protein structures are formed as a result of H-Bond formation

Between ___ in a protein backbone _____N and C termini

36.

_____ connect helices and sheets _____Loops

37.

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

38.

____ are also secondary structure which form the first structures after folding of protein’s

Amino acids _____Loops and Coils

39.

Combinations of Alpha helices, Beta sheets, coils and loops help form _____ 3’ structures

40.

___, ____ & _____ interactions enforce the 3’ structure _____Covalent

Bonds, Hydrogen _____bonds and hydrophobic

41.

The stability of all the structures of protein is as: _____4’ > 3’ > 2’ > 1’

42.

The protein folding into 3D structures leads to: _____Reduction in bond angles

43.

Peptide bond between two amino acids is _____ _____Planar & rigid

44.

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

45.

____ can be used to construct the backbone of a protein towards its visualization_____

_____C-Alphas

46.

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

47.

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

Is _____ respectively. _____~1 Å & 0.25 Å

48.

Crystallography data gives _____ of atomic coordinates _____Relative positions

49.

____ Proteins are used to determine protein structures. _____Crystallized

50.

_____ contains protein structure information _____PDB

51.

PDB has the coordinates of C-Alphas for over _____ proteins _____ 50,000

52.

To view a protein, we need to evaluate the: _____physical location of its atoms

53.

To trace the backbone of a protein, _____ trace can be used_____CA atoms

54.

Coordinates of CA atoms can be obtained from the ____ _____PDB

55.

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

_____ Rasmol, CHIME, Swiss PDB Viewer and Cn3D.

56.

CPK stands for: _____Corey-Paulin-Koltun Diagrams

57.

In CPK diagrams, each atom is represented by a _____ _____Solid sphere.

58.

Spheres are equal to atomic _____ Van der Waal radius

59.

Ribbon Diagrams represent the protein secondary structures by using: _____

_____Simple cartoon figures

60.

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

_____colored balls, sticks

61.

“Proteins fold for a unique, stable and minimum free kinetic energy structure”. The given

Statement is called: _____--Anfinsen’s thermodynamic hypothesis

62.

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

63.

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

64.

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

Energy _____Maximize, minimize

65.

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

_____number and types

66.

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

_____ inter-atomic distances

67.

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

_____type of atomic interaction

68.

To determine the structure of protein, we use_____ _____ X-Ray or NMR

69.

If two atoms are participating in a covalent bond, their distance is: _____-~0.96A

70.

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

_____ ~1.97A

71.

X-Ray data should have a minimum of _____ resolution _____1.97A

72.

“Helix Formers” are generally _____ amino acids (M, A, L…) _____Hydrophobic

73.

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

Backbone _____Ci and Ni+4

74.

_____ resides are needed to make a Beta Strand _____5 to 10

75.

_____is made of a single beta sheet that twists and coils upon itself. _____-Beta-barrel

76.

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

Aligned _____twisted and packed

77.

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

_____ _____ the Alpha Helices and Beta Sheets

78.

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

Ways._____length and conformation

79.

Loops are mostly comprised of _____ amino acids _____charged and polar

80.

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

81.

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

82.

Coils are apparently_____ regions _____disordered

83.

_____ are semi-independent functional structures in a protein _____Domains

84.

Domains have over _____ residues _____~40

85.

_____interact (H-bonds) more internally than externally _Locally Compact – Domains

86.

Domains have a _____ core _____-- hydrophobic

87.

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

_____Architecture and Topologies

88.

_____ classifies proteins by their structural similarity _____CATH

89.

FSSP stands for _____ based on the DALI algorithm _____

_____Family of Structurally Similar Proteins

90.

SCOP stands for:– _____Structural Classification of Proteins

91.

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

92.

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

Carbons positions _____root mean squared difference (RMSD)

93.

The _____ the RMSD, the similar are the proteins _____Lower.

94.

Full protein structures can be compared and ranked by the overall _____ in positions

Between their Alpha Carbons_____ _____differences

95.

____ tells us about the quality of the matches _____RMSD

96.

_____ mostly found in Alpha Helices _____Alanine

97.

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

_____Chou-Fasman Algorithm

98.

We only know _____ 3D protein structures, but 10 times more sequences_____ 100,000

99.

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

Propensity___ _____propensity table

100. _ amino acids are needed to start an Alpha Helix and ___ amino acids for Beta Shee_____4,5

101. Loops are small amino acids _____~ 3-4

102. Alpha Helices are formed from 4 contiguous amino acids having an Alpha-Helix propensity

Over _____-__ 1.0

103. Chou Fasman Algorithm helps predict _____Alpha Helices, Beta Sheets and Turns

104. Chou Fasman can be improved to better predict secondary structures by incorporating___

_____ __biochemical factors

105. Structure visualization, classification and prediction are important for: _____ _____

_____ ___Understanding disease and designing drugs for treating them

106. There are_____ salient steps in any Homology Modelling pipeline _____seven

107. The backbone of _____ strongly prefers two rotamers and the real side-chain may fit one of

Them _____Tyrosine

108. _____is a software for homology modelling _____
Modeller

109. A _____ is defined by the way the secondary structure elements of the structure are arranged

Relative to each other in space _____-protein fold

110. Common folds include _____ bundle and the TIM barrel. _____--4-helix

111. There are _____ stable folds in nature _____5,000

112. Fold recognition or Threading is a technique for predicting : _____protein structures

113. Threading involves _____ the amino acid sequence through each fold in the database

_____"passing"

114. Software for automated protein structure &function prediction based on the sequence-tostructure-tofunction. _____Iterative

Threading assembly refinement (I-TASSER) server

115. _____ helps thread amino acid sequences on fold and secondary structure

Databases_____ iTASSER

116. Fold recognition or threading is useful in cases where _____ fails to predict quality

Structures ____ _____homology modeling

117. 3D-1D Bowie Algorithm was Proposed by _____ Bowie et al in 1991

118. 3D-1D Bowie Algorithm Converts____structure into a ____ string profile for each structure in

The fold library _____3D, 1-D

119. 3D-1D Bowie Algorithm Identify amino acids based on: _____protein core, side

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

b) Equality d) all of these

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

) Ionization b) fragmentation c) measure the mass

c) 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

c) ALL

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

a) Having different splitting sites

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

b) Ion d) atom

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

a) Removing b) adding

b) Transfer d) All of these

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

c) 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

b) Peptide sequence tags

c) 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

b) 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

b) Data base protein d) PST protein

Q.19 Experimental peptides also known as ……

a) Data base peptide b) observational peptide

b) Invitro peptide

c) 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

b) 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

b) 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

c) 400,00 – 500,00

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

c) 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

b) 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

c) 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

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

c) 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

b) Lipids d) a and c

Q. 46 …….. residue has no R group.

a) Cystine b) proline c) glycine

c) Adinine

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

a) Increase b) decrease

b) 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

c) Backbone

Q. 50 After polymerization ……. Are formed.

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

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

b) 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

c) 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

b) Tertiary structure d) All

Q. 56 The protein super structure are called ……

a) Primary structure b) secondary structure c) tertiary structure

c) 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

c) None

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

a) Covalent b) hydrogen

b) 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

c) Five points

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

a) Phi b) psi c) both

d) None

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,

b) 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

b) 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

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

b) ~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

c) P – N

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

a) 3 – 4 b) 5 – 10

b) 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

c) 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

b) ~50 residues d) ~60 residues

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

a) Architecture b) Topologies c) both

c) 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.

a) Sequence b) free energy c) structure

c) 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

b) Energy d) All

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

a) Equal b) higher c) lower

c) 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

b) 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

c) Adenine

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

a) Individual propensity b) overall propensity

b) 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, AlphaHelix

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

b) 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

c) Different

Q.102 Chou Fasman Algorithm helps us to predict,

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

b) 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

c) Nucleotides

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

…….. protein sequences

a) Heterogeneous b) homologous

b) 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

b) 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

c) 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

b) Anchor

c) 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

Q.115 In homo logy modeling when protein backbone is ready,then next, ……. Were modelled

And used to bridge gaps.

a) A 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

b) 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

b) 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

c) 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

B) 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 ……..

a) Software b) packets c) profiles

c) Subunits

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

…… residues

a) Cheap – 500 b) expensive – 100

b) 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

b) Breakdown d) bonding

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

a) Chemical b) statistical c) physical

c) All

Q.133 Global optimization finds the most …….

a) Matching sequence b) stable structure

b) Similar pattern d) a and c

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

a) Native

b) Invitro c) insilico

c) Stable

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

a) Easy b) difficult

b) 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

c) 8

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

a) Easy and expensive b) Expensive and complex

b) Cheap and easy

c) 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

Q.142 Maximum Parsimony etc are…… Methods (not included in this course).

a) Clustring b) nonclustering

b) 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

b) Smaller d) mech smaller.

MUHAMMAD IMRAN BIF401 -Bioinformatics I

MCQs&Questions final term Past papers /2019/2020

1. What Are Uses Of Mass Spectrometry? 2

Mass spectrometry (MS) is an analytical technique that ionizes chemical species and sorts the ions

Based on their mass-to-charge ratio. In simpler terms, a mass spectrum measures the masses within a

Sample. Mass spectrometry is used in many different fields and is applied to pure samples as well as

Complex mixtures.

2. Need For Chou Fasman Algorithms? 2

The Chou-Fasman algorithm is simple in principle.The conformational parameters for each amino acid

Were calculated by considering the relative frequency of a given amino acid within a protein, its

Occurrence in a given type of secondary structure, and the fraction of residues occurring in that type of

Structure.

3. Three individual scores Integrative Scoring Scheme? 2

Three individual scores can be obtained including

1. MW Match Score

2. PST Match Score

3. In vitro & In silico Match Score.

4. Write benefits of phylogenetic studies marks • 03

5. **Advantage of Folded Protein over Denatured Protein. 5**

Difference Between Folding Protein and Denature Protein, / What Factors Are Used For

Folding Proceeds?

Protein folding is the physical process by which a protein chain acquires its native 3-dimensional

Structure, a conformation that is usually biologically functional, in an expeditious and reproducible manner.

Denaturation of proteins involves the disruption and possible destruction of both the secondary and

Tertiary structures. Since denaturation reactions are not strong enough to break the peptide bonds, the

Primary structure (sequence of amino acids) remains the same after a denaturation process.

Protein folding is a process by which a polypeptide chain folds to become a biologically active protein in

Its native 3D structure. Protein structure is crucial to its function. Folded proteins are held together by

Various molecular interactions. … The amino acid sequence of a protein determines its 3D structure. The

Forces involved in protein folding include: • Electrostatic interactions, • van der Waals interactions, •

Hydrogen bonds, • Hydrophobic interactions

6. **Score in Silico fragment scoring?.5**

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

7. **How Loops Are Found After The Finding Of Alpha And Beta Sheets?5**

Alpha helices and beta strands are connected by these turns and loops. … Loops and turns generally

Lie on the surfaces of proteins so they often participate in interactions between proteins and other

Molecules. In a loop, there are no regular structures as can be found in helices or beta strands.

8. Tandem mass spectrometry ?

Tandem mass spectrometry (MS-MS) is a related technology in which compounds are separated by

Molecular weight by one mass spectrometer, fragmented as they exit, and identified on the basis of

Their fragments by a second mass spectrometer

9. Advantage and disadvantage of Ab initio method?

Advantages:

Ab Initio methods can fold any target sequence using only physical atomic properties. Predictions are

Mostly accurate and correctly describe the natural folding process. Disadvantages:

Ab initio methods are the very difficult to design (energy function). These methods are slow due to

The huge possibilities.

10. Types of secondary structures of RNA:

1. Single stranded:

3’end may fold on to the 5’ end.

2. Helices:

Double stranded RNA helix of stacked base pairs 3.

Hairpin loop:

The loop of the hairpin must at least four bases long to avoid steric hindrance with base-pairing in the

Stem part of the structure 4. Bulge Loops:

Bulges, are formed when a double-stranded region cannot form base pairs perfectly.

4. Interior loop:

Interior loops are formed by an asymmetric number of unpaired bases on each side of the loop.

5. Junctions or intersections:

Junctions include two or more double-stranded regions converging to form a closed structure. The

Unpaired bases appear as a bulge

11.

How homology modeling is used for knowing the sequence of unknown

Protein sequence?

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:

11. Role of Amino Acid?

Protein plays a crucial role in almost all biological processes and amino acids are the building blocks of it.

A large proportion of our cells, muscles and tissue is made up of amino acids, meaning they carry out

Many important bodily functions, such as giving cells their structure.

12. Write Down The Following Terms Of PDB (3)

Title (Title of the structure)

Source (Identify which organism structure from)

COMPND (Brief detail of the structure)

REVEDAT (The data of last revision

13. What Happend When Ph Is Less Than The Pk Value?

If the pH is higher than the pKa, then the compound will be deprotonated. A further consideration is the

Charge on the compound. Acids are neutral when protonated and negatively charged (ionized) when

Deprotonated. Bases are neutral when deprotonated and positively charged (ionized) when protonated.

14. Chou Fasman Algorithm?

The Chou–Fasman method is an empirical technique for the prediction of secondary structures in proteins,

Originally developed in the 1970s by Peter Y. Chou and Gerald D. Fasman.

15. Function of Tandem MS?

Tandem MS helps in measurement of mass to the fragments as well. This process provides another step in

Further scoring and ranking and Protein identification thus becomes

Easier.

16. Factors That Participate In Folding Protein?

The external factors involved in protein denaturation or disruption of the native state include temperature,

External fields (electric, magnetic), molecular crowding, and even the limitation of space, which can have a

Big influence on the folding of proteins

17. Need For Chou Fasman Algorithms?

The Chou-Fasman algorithm is simple in principle.The conformational parameters for each amino acid

Were calculated by considering the relative frequency of a given amino acid within a protein, its occurrence

In a given type of secondary structure, and the fraction of residues occurring in that type of structure.

18. Optimal Energy Function In Protein?

Results: For a single protein sequence, the probability of success (i.e. the probability that the folded state

Is the lowest energy state) is derived. We then maximize the average probability of success for a set of

Proteins to obtain the optimal potential energy function

19. Silico Fragments Comparison?

Matching experimental fragments with in silico fragments is the final resort in protein search & identification

20. 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.

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.

21. Improvements Of Chou Fasman Algorithm?

The Chou-Fasman algorithm, one of the earliest methods, has been successfully applied to the prediction.

… We improved Chou-Fasman method in three aspects. (a) Replace the nucleation regions with extreme

Values of coefficients calculated by the continuous wavelet transform.

22. What is hydrophobicity of amino acid?

In chemistry, hydrophobicity is the physical property of a molecule that is seemingly repelled from a mass

Of water. In contrast, hydrophiles are attracted to water. Hydrophobic molecules tend to be nonpolar and,

Thus, prefer other neutral molecules and nonpolar solvents.

23. How propensity table can helps us?

24. Seven Steps present in flow chart of homology modeling?

1. Template recognition and initial alignment.
2. Alignment correction.
3. Backbone generation.
4. Loop modeling.

5. Side-chain modeling.

6. Model optimization.

7. Model validation

25. Role of Amino Acid?

Protein plays a crucial role in almost all biological processes and amino acids are the building blocks of it.

A large proportion of our cells, muscles and tissue is made up of amino acids, meaning they carry out

Many important bodily functions, such as giving cells their structure.

26. Role of Global Protein?

Global protein function prediction from protein-protein interaction networks. … The availability of entire

Genome sequences and of high-throughput capabilities to determine gene coexpression patterns has

Shifted the research focus from the study of single proteins or small complexes to that of the entire

Proteome.

27. Acidic and Basic Amino Acid?

There are three amino acids that have basic side chains at neutral pH. These are arginine (Arg), lysine

(Lys), and histidine (His). Their side chains contain nitrogen and resemble ammonia, which is a base. Their

pKa's are high enough that they tend to bind protons, gaining a positive charge in the process.

28. Points of Bottom up Proteomic?

The major alternative workflow used in high-throughput proteomics is called top-down proteomics and does

Not use proteolytic digestion. Essentially, bottom-up proteomics is a means of determining the protein

Make- up of a given sample of cells, tissues, etc. (Internet)

29. Varies RNA Secondary Structure?

Types of RNA Secondary Structures – I

• RNA Complementary bases in primary structure bond together to fold RNA into a secondary structure

Types of RNA Secondary Structures – II

• RNA 1’ sequence (5’ – 3’) can fold onto itself to make 2’ structures.

• Two previous examples of 2’ structures include Helix and Hairpin structures. Types of RNA Secondary

Structures – III

• RNA can be fold to form helices, bulge loops, and interior loops. An other 2’ RNA structure is the Junction

Or Intersection.

31.

Objective Base Method and Clustering Approach?

Clustering Approach UPGMA WPGMA Neighbor Joining Single Linkage Complete Linkage Objective

Based Methods Least Square Distances Maximum Likelihood Maximum Parsimony

32.

Shot Gun and Peptide Mass Finger Printing?

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.

33. **substitution and Indels?**

Substitution at adjacent nucleotides (primarily substitutions at two adjacent nucleotides, but substitutions at

Three adjacent nucleotides have been observed.

Indels, being either insertions, or deletions, can be used as genetic markers in natural populations,

Especially in phylogenetic studies.

34. **Prediction of Protein Structure?**

Protein structure prediction is the inference of the three-dimensional structure of a protein from its amino

Acid sequence—that is, the prediction of its folding and its secondary and tertiary structure from its primary

Structure.

35. **How Can We Predict Amino Acid In Alpha Helix And Beta Sheets?**

Proteins that convert from alpha helix to beta sheet: implications for folding and disease. The sequence of

A protein normally determines which amino acid residues will form alpha helices, and which one beta

Sheets, to an extent that allows secondary structure prediction to be made with a reasonable reliability..

36. **Rooted Un Rooted Tree?**

Rooted Tree:

Each node with descendants represents the inferred most recent common ancestor of the descendants.

The edge lengths in some trees may be interpreted as time estimates.

Rooted trees can show temporal evolutionary direction.

Expensive.

Unrooted:

•

Only the relatedness of the leaf nodes.

Do not require the ancestral root to be known or inferred.

•

Less expensive.

Uses: In bioinformatics, such as

Rooted and unrooted trees can be used to show phylogenetic relationships between sequences..

37. **Molecular biology?**

It is the branch of biology that deals with the structure and function of the macromolecules (e.g. proteins

And nucleic acids) essential to life. Molecular biology is the study of biology at a molecular level.

38. **Protein Fragmentation techniques?**

Electron Capture Dissociation (ECD).

Electron Transfer Dissociation (ETD).

Collision Induced Dissociated (CID).

39. **Protein structure prediction?**

There are three different strategies for structure prediction

1. Homology Modelling

2. Threading/Fold Recognition

3. Ab Initio Modelling

MCQS final term

1) Fasta Was Develop In_____(Ans1988)

2) In Corey Paulin Modal Of The Protein Each Atom Is Represented By____(Solid Sphere)

3) How Many Storages Use For Structural Modling _____(3)

4) Modeler Software Use For Homology Modling Which Use(Phython File Format,Not Confrm)

5) Mass Of The Based Proteomic Begin With Measure Of(Intact Protein Amino Acid)

6) Protein Sequence Obtained From(Uni Port)

7) During The Formation Of The 5 Nucleotide Hydrogen Bond Energy Release(-12kcal/Mol)

8) Which Method Is Not Use For Making Polygenatic???Msa

9) Rna Dont Have Structer???Quatnaryy

10) Large Numbr Of Sequence Availble??Publically

11) Coding Region Of Dna Is???Exon

12) Blast Use For???Unknown And Known Protein

13) Expasy Develop By???Sib

14) Variation In Sequence Develop By???

Insertion,Deletion And

Substituin

15) Bond Form Between C And N Terminas???

Hydrogen Bond

16) X.Y.Z Position Of Protein Are Available By??? Pdb

17) Technique Use To Measure The Mass Of Protein??? Mass Spactrometry

18) Large Amino Acid???

Tryptophan

19) Positive Charge Amino Acid???

Lysine And Arginine

20) Mrna Has???

Single Strand

21) C.Alpha Atom Are Traced To Recreat???

3d Structer Of Protein

22) Bond Form Between Two Atom???

Energy Release

23) Provide Clue Of Precurser Protein Peptide Sequence??Pst

24) Amino Acid Requird For Betasheet???

3-5

25) ……Are Formed By Bonding Betweenci And Ni+4n Protein Backbone??? Alpha Halix 26)

Blasta Stand For???

Basic Local Alignment Search Tool

26) Amino Acid Have Uniwe Trait Which Can Help In??? Protein Folding 28)

Align Comparison Betweendna/Dna Anddna/Protein??? Fasta.

29) Ratio Use To Calculate Mass Of Protein???

M/Q.

30) **Treading Not Requied For???**

Structer Of Entire Backbone.

31) **Needle Man Wounch Man Or Smith Water Man Algorithm Use For???**

Local And Global Alignmnt.

32) **Dianamic Programing Recombinant Nucleotide By???** Traseback.

33) Insertion And Deletion Cause???

Gap.

34) Information Required For Follding Of Amino Acid Is Present In??? Amino Acid.

35) Mgf Use For???

Proteomic.

36) Nj Algorith Use To Pridict The???

2nd Structer Of Rna..

37) Genomics, evolutionary studies and system biology are application of bioinformatics

38) Exact matching require which type of nucleotide-same number of nucleotide

39) Accurate solution of protein structure is one of the ___ toughest problems

40) Tract back is overlap matches can start from any position in scoring matrix

41) The matrix has ……scores. Positive and negative

42) MASCOT___can search people mass finger printing and shotgun proteomics data set

43) Spectrometer measures the protein by _____ Mass/charge

44) Simulation of the folding process depends _____ Energy function

45) Information about DNA/RNA is available on gene bank

46) TDP is used to measure the molecules weight of intact proteins.

47) Coordinates of alpha carbon in the protein backbone can be used for structural visualization.

48) in structure visualization c-alpha atoms are traced to recreate a _____3D protein structure

49) in UPGMA distance is calculated btw _____ two clusters and between two trees

50) pk value of Aspartic acid 3.9

51) Largest amino acid …… Tryptophan

52) 2

Nd STRUCTURE of proteins can be obtained by using_____ Chou Fasman algorithm

53) NJ Algorithm strategy is used to predict __ RNA 2` structure

54) The loop of hair pin must be at least ___ in length 2 aminoacids

55) Fold recognition is also called …….threading

56) Ab initio method in contrast ,base their prediction on low energy model.

57) Bioinformatics require…….smart mind, and connected to internet, both,

58) Sequence alignment tool is…….PROSIGHT and MASCOT

59) MS1,MS2 provide us data identifying unknown…….Proteins sequence.

60) MGF files develop as an open standard for……. Proteomics data.

61) PDB coordinates alpha carbon in protein back bone can be used for comparison .

62) Alpha carbon atom can be obtained from……PDB

63) in formation of 2nd structure of protein C & N can make……Hydrogen bonds

64) information for protein folding is into its native structure is in…….. protein's amino acid sequence!

65) Energy released during bond formation.

66) hydrogen bonding occur in …secondary ..Protein structure

67) Bond between C and H in alpha helices____Hydrogen bonding

68) Amino acid having 3 codons_____ isoleucine

69) MALDI typically adds a …… to protein or peptide. Proton

70) low quality match gets_____lower score

71) ____ are sequences of amino acids produced during MS2. PST (peptide sequence tags)

72) MS2 data can be used to extract…… peptide sequence tags.

73) The alpha helices propensity should be more than____(1.0)

74) How many types are of protein sequencing techniques__ (2)

75) Blast can find sequences of _____nucleotides amino acid

76) If a protein sequence of 26 amino acids is fragmented at 11 amino acid C11, Z25

77) To find out unknown sequence of nucleotide we use . NGS or Mass spectrometry

78) How many types of peptide May be injected in mass spectrometry chamber.. . three hundred

Thousand to four hundred thousand

79) .MASCOT.can search peptide mass finger printing and shotgun proteomics dataset.

80) Stabilizing and destabilizing energy give us …….. quality of 2nd structure .

81) The Fasman algorithm is based on statistical occurrence of Amino Acids in known structures.

82) DP recombinant the nucleotide recombination through process of ……. Traceback

83) 83) MALDI…..add proton to a protein and a peptide..

84)Positively charged amino acids are….. 3

85)Aromatic amino acid include ……. . phenylalanine, tyrosine tryptophan

86)Homology modelling fail to predict …… quality structure

87) How many forces are involved in protein folding.

88)

Pairwise alignments tells the similarity between sequence… by maximizing the matches.

89)

Dot plots employ dot matrix with two sequence plotted represents……pairwise alignment and

Comparison.

90)

Differentiate b/w DNA and RNA sequence…….. RNA has more variety of sequence

91)

Cell molecule are produced after transformation of …… DNA to protein

92)

Dot plot cannot deal with…… Insertion, deletion and gaps.

93)

Exons are may be more …… conserved.

94)

In dynamic algorithm we can do comparison …… of more sequence. Three

95)

Mass/Charge ratio helps calculate the mass of the …. Protein

96)

In scale tree branches lengths are equal to the magnitude of change in the …….. nodes.

97)

How many types of peptides mix in MS chamber…….. 300,000 – 400,000

98)

mRNA is a …… structure. Planer

99)

When unpaired bases of 2´ stricture join to form…….. 3´ structure

100) N Jackobson use to pridict 2´structure.

101) Aromatic amino acid ……. Tyrosine

102) Positive charge amino acids……. Lysine, arginine, histidin

103) MS begins with the measure of …….. intact protein

104) Amount of amino acids in alpha helix…….(4)

105) Intact mass of protein can be found by….. MS1

106) MSA can be done by……. CLUSTAL

107) Which is used as sequence alignment tool……. PROSIT

108) MS1 and MS2 help to identify …… (PST)

109) MGF is used for …….. proteomics

110) X,Y,Z positions of alpha carbon available online on …… (PDB)

111) Method to determine RNA structure …….. NMR, X-Ray crystallography

112) CLUSTLA runs……. Slow accurate/ fast appropriate

113) Which give info about precursor protein……. PSTS

114) Raw data files format can be converted to ……. Open format

115) Which of the following is cartoonic figure…….. Ribbon diagram

116) In CATH protein recognize according to their…….. structural similarity

117) Method for obtaining 1´ structure…… (Edman Degradation Tandem Mass Spectrometry).

118) FASTA achieves alignment by using short lengths of exact matches.

119) Dot plots cannot capture insertions, deletions and gap indications

1. Dot plots employ dot matrix with two sequences plotted on top and left of the matrix

2. In multiple sequencing, we have both

3. CLUSTALW can run in two modes slow/accurate, fast/appropriate.

4. The correct order of progressive alignment for multiple sequencing alignment is Pair wise

Alignment, Guide tree, branching order in tree.

5. Blast can find sequencing from protein or nucleotide database it can find known and unknown

Sequencing.

6. : Next generation sequencing is used to known about unknown sequences of nucleotide.

7. In multiple sequence algorithm doing so many progressive alignment can be slow.

8. : Structural information of a molecule obtained by X ray crystallography & Nuclear magnetic

Resonance.

9. Before starting to mach nucleotide or amino acid are need to find the Location of conserved

Residues.

10.Bioinformatics is an interdisciplinary relative new development of biology, mathematics, computer

Science, chemistry and physics.

11.Fasta online software Can also perform genome and proteome similarity search .true

12.From Fasta we can obtain the information on the parent organism, function and evolution

History.

13.name any two frequently used scoring matrix Blosum and pam.

14.Amino acids are chained together by peptide bonds

15.To find out the unknown sequence of nucleotide and protein we use blast.

16.GenBank and Uniprot, have A large number of sequences are available in publically .

17.Protein databank is a data base

18.In dynamic programming we can do multiple sequence alignment upto 21 sequence .

19.How many types of secondary structure can be formed possible of RNA? 5.

20.RNA structures have the lowest (or close) quantity of free energy.

21.RNA can play role due to its structure . all of above.

22.Rna contains ribose sugar?

23.Thymine is replaced by uracil in rna.

24.RNA molecules readily degrade due to their short shelf life .

25.Each Nucleotide in rna has covalently bonded to the backbone .

26.Gibbs Free Energy" is the free energy of an RNA molecule available for reaction .

27.The structure of rna sampled can be measured by.Atomic Force Microscopy

28.The 3'-end of mRNA has a poly A tail

29.The role of mRNA Carry genetic information from DNA to Ribosomes where proteins are being

Assembled .

30.Messenger rna is only 5-10% of rna content in the cell.

33

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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
. 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
Dihedral Angles always form between .....
a) two points b) three points c) four points d) five points
angles are taken up as a result of folding of protein.

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

.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

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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
According to "Anfinsen's thermodynamic hypothesis" protein folds for making

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molecular weight increases by..... Of proton

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

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

ECD gives out "C" and.....ions,

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

CID gives out "B" and..... ions,

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

PST is abbreviation of…..

a) Protein sequence tags b) protein sequence tools c) Peptide sequence tags d) peptide sequence tools

PST is sequence of peptidesproduced during…..

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

Fragmentation at consecutive sits lead to a mass difference equal to that of a single

…..

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

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

Experimental peptides also known as ……

a) data base peptide b) observational peptide c) invitro peptide d) sample peptide

Errors in peak matching also considered by…….

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

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

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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

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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

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

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

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

by looking up at the bond/energy table, we can compute the …….
a) overall energy b) molecular mass c) atomic mass d) bond sequence

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

"Helix Formers" are generally…….amino acids (M, A, L…)
a) acidic b) basic c) hydrophilic d) hydrophobic

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

resides are needed to make a Beta Strand,typically
a) 3 – 4 b) 5 – 10 c) 6 – 7 d) 5 – 6

Loops are the…… of secondary structure
a) 1st b) 2nd c) d) 4rth

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

are flexible & can adopt multiple conformations.

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

are apparently disordered regions with random structure and random length.
a) coils b) helices c) loops d) beta sheets

are Non-functional Combinations of 2' structures)
a) loops b) coils c) beta sheets d) motifs

Domains are semi-independent functional structures in a protein having over ……..
a) ~30 residues b) ~40 residues c) ~50 residues d) ~60 residues

is one such system in which proteins are organized into classes, architecture, topology & homology.
a) CATH b) FSSP c) LOCK d) DOLI

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

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

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

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

The……the RMSD, the similar are the proteins.
a) Equal b) higher c) lower d) random

RMSD tells us about the quality of the matches
a) matches b) mismatches c) sequence d) bonding

There are over a million protein sequences but only about ……protein structures.
a) 10,000 b) 100,000 c) 10,0000 d) 1,000

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

Product of propensity values is computed for ……..for each 2' structure.
a) individual propensity b) overall propensity c) greatest propensity d) All

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

In chou fasman algorithm Alpha Helices can be finalized if their propensity is

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

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Q. 22 We can't add these three scoring comparison until we divide them by their……

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

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

large scale proteomics is a developed form of

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

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

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

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

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mzData was developed by ……

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

MASCOT is an online …… Search engine,

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

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

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

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

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

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

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

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

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**

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

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

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Q. 46 ……residue has no R group.

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2) In Corey Pauling Modal Of The Protein Each Atom Is Represented By(Solid Sphere)
3) How Many Storages Use For Structural Modling (3)
4) Modeler Software Use For Homology Modling Which Use(Phython Interface) (N... Confrm)
5) Mass Of The Based Proteomic Begin With Measure Of(Intact Protein Amino Acid)
6) Protein Sequence Obtained From(Uni Port)
7) During The Formation Of The 5 Nucleotide Hydrogen Bond Energy Release(-12kcal/Mol)
8) Which Method Is Not Use For Making Polygenatic???Msa
9) Rna Dont Have Structer???Quatnaryy
10) Large Numbr Of Sequence Availble??Publically
11) Coding Region Of Dna Is???Exon
12) Blast Use For???Unknown And Known Protein
13) Expasy Develop By???Sib

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Variation In Sequence Develop By??? Insertion,Deletion And Substituin
Bond Form Between C And N Terminas??? Hydrogen Bond
X.Y.Z Position Of Protein Are Available By???Pdb
Technique Use To Measure The Mass Of Protein???Mass Spactrometry
Large Amino Acid??? Tryptophan
Positive Charge Amino Acid??? Lysine And Arginine
Mrna Has??? Single Strand
C.Alpha Atom Are Traced To Recreat??? 3d Structer Of Protein
Bond Form Between Two Atom??? Energy Release
Provide Clue Of Precurser Protein Peptide Sequence??Pst
Amino Acid Requird For Betasheet??? 3-5
Are Formed By Bonding Betweenci And Ni+4n Protein Backbone??? Alpha Halix
Blasta Stand For??? Basic Local Alignment Search Tool
Amino Acid Have Uniwe Trait Which Can Help In??? Protein Folding
Align Comparison Betweendna/Dna Anddna/Protein??? Fasta.
Ratio Use To Calculate Mass Of Protein??? M/Q.
Treading Not Requied For??? Structer Of Entire Backbone.
Needle Man Wounch Man Or Smith Water Man Algorithm Use For??? Local And Global Alignmnt.

Q.1. In mass electrometer chamber protein is deflected according to its .....
a) charge b)velocity c)charge, mass d) volume

in MS chamber mass/charge ratio can be measured by ..... of protein molecules.
a) volume b) mass c) charge d) speed

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

Tandem MS is used to..... of protein fragments.
a) Ionization b) fragmentation c) measure the mass d) sequence

Fragmentation techniques split the molecules of protein into.....
a) Two part b) three part c) four part d) multiple part

Tandem MS is typically called as,
a) MS b) MS1 c) MS2 d) ALL

Dianamic Programing Recombinant Nucleotide By??? Traseback.
Insertion And Deletion Cause??? Gap.
Information Required For Follding Of Amino Acid Is Present In??? Amino Acid.
Mgf Use For??? Proteomic.
Nj Algorith Use To Pridict The??? 2nd Structer Of Rna..

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

Mass spectrometer use o measure the mass of protein and .....
A) Amino acids b) lipids c) peptides d) DNA

Protien ionization is the.....step in MS based proteomics.
a) first b) second c) third d) fourth

Ionization process involve gaining and removal of .....
a) electron b) proton c) ion d) atom

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molecular weight increases by..... Of proton
a) removing b) adding c) transfer d) All of these

a) Fold recognition b) Swiss Model c) Threading d) a and c
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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
cannot be predicted using threading.
a) invtro protein b) primary protein c) 2ndary protein d) Novel proteins
3D-1D Bowie Algorithm Proposed by Bowie et al in .....
A) 1997 B) 1991 C) 1995 D) 1998
3D-1D Identify amino acids based on .....
a) protein core b) side chain positioning c) solubility d) All
3D-1D methods convert structure and environment information into .....
a) software b) packets c) profiles d) subunits
Ab initio modeling is Computationally..... Suitable for proteins with less than ..... residues
a) cheap – 500 b) expensive – 100 c) cheap – 100 d) expensive - 500
Ab Initio Modelling methods attempt to identify the structure with minimum .....
a) charge ratio b) distance c) molecular weight d) free energy
Energy released during the.....process is computed for predicting structure.
a) Sequencing b) folding c) breakdown d) bonding
Ab initio methods base their predictions on .....models of folding mechanisms
a) Chemical b) statistical c) physical d) all
Global optimization finds the most .....
a) matching sequence b) stable structure c) similar pattern d) a and c
structure not always at the global minimum.
a) Native b) invitro c) insilico d) stable
Ab initio methods are the very ..... to design.
a) easy b) difficult c) suitable d) accessible
In homology modeling first we perform ..... and then .....
a) Loop modeling - Backbone generation b) Backbone generation - Loop modeling
There are .....Steps of Homology Modelling.
A) 5 b) 6 c) 7 d) 8
Ab initio modeling is Computationally ..... And..... process.
a) easy and expensive b) Expensive and complex c) cheap and easy
d) difficult and cheap
Ab initio methods predict protein structures by folding proteins based on each constituent atom's .....
a) volume b) charge c) mass d) all
UPGMA is a ..... method.
a) clustering b) non clustering c) both
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

maximum Parsimony etc are ..... methods (not included in this course).
a) clustring b) nonclustering c) mapping d) visualizing
Online tools: .....
a) mascot b) sequest c) prosight PC d) all
Number of known protein sequences is..... as compared to known proteins structures
a) larger b) much larger c) smaller d) mech smaller