

BIF401- Bioinformatics I

BIF401 MCQS... Ppts 126 to 140

Q1. Once a protein is ionized, it can be deflected by a..... in proportion to its mass.

1. Electric 2. mechanical 3. **Magnetic** 4. Electrochemical

2. Proteins can then be measured for their..... in a Spectrometer(MS)

1. **Mass** 2. Weight 3. Intensity 4. Height

3. ratio helps calculate the mass of the protein.

1. Mass/height 2. Mass/weight 3. **Mass/charge** 4. Mass/Average

Ans: **3.mass/charge**

4. "Mass-select" can help select a specific.... For further analysis.

1. MS1 2. MS2 3. MS3 4. MS4

Ans: **MS1.**

5. MS1 spectra the intact protein masses for all proteins in a protein complex.

1. Analyze 2. identify 3. Manage 4. Reports.

4.Reports

6. Using the masses reported by MS1, protein databases can be filtered for candidate..... matches (or hits). 1. Amino-acids 2. lipids 3. proteins 4. molecules

3.Proteins

7. The masses of all molecules converted to.....

1..... **1+mass** 2..... 2+mass 3..... 3+mass 4.... 4+ mass

1.. 1+mass

8. Once we have filtered away..... charged peaks, we retain only those peaks with charge 1

1... single 2.... double 3... tripple 4..... **multiple**

4... multiple

9.: A Protein Sequence Obtained from Database "....."

1..... ABCD 2..... **MQLF** 3..... WDLC 4..... EFGH.

ANS: **2.MQLF**

10. $MScore = 1 / (\sqrt{(M_{Exp} - M_T)^2})$ is a formula of

1....Sequence Analysis 2....Scoring Scheme 3....both

11. Score is awarded on the basis of the Between experimental and theoretical mass.

1....Difference 2....Closeness 3....Relativity 4.none

12. Protein fragmentation techniques are

1.....1 2.....2 3.....3 4.....4

13. Each fragmentation technique results in a specific type of

1. Fragment 2....parts 3...points 4.All of above

14. we can award..... on the basis of the similarity of experimental and theoretical mass

1....Sequence 2....Analysis 3.....Score 4.... None

15. Steps in the MS² and MSⁿ are.....

1...1 2....2 3.....3 4....4

16. Tandem MS helps in of mass to the fragments as well!

1...Length 2....weight 3....Measurement

17. Peptide Sequence Tags (PST) are sequences of..... produced during MS²

1.... Peptides 2...proteins 3...lipids.

18. Peptide sequence tags can be extracted from.... List.

1..rooted 2...peak 3...unrooted 4...ladder

19. PSTs provide..... of the precursor protein/peptides sequence.

1...clues 2....sequence 3...parts 4...All of above

20. The proteins in the database, we find out which..... exist in which proteins

1....MQLF 2....PSTs 3....both 4...None

21. The protein reporting the most PSTs is more.... To be the precursor protein.

1...weak 2....strong 3....profitable 4....probable

22. We extracted PSTs and searched the entire.... For those protein who report these PSTs

1...database 2....steps 3...sequences

23 Is the root mean square error

1...RMSE 2....MQLF 3...ABCD 4....RFLP.

24. Fragmentation techniques determine product ions e.g..... -> c/z and -> b/y ions etc.

1...ECD and CID. 2....RFLP and PQLF 3....MQ...FP

25. For obtaining all possible theoretical fragments in a protein, we need to compute the.... of each fragment individually

1...MQLP 2...MWs² 3...RFLP 4....ALL

26. Scoring scheme should also consider the....in peak matching

1...errors 2...peaks 3....points

27. Integrating MW, PST and and insilico comparison algorithms in a..... can help create a composite protein search engine

1...worksheet 2...workflow 3....work database 4. work comparison.

28. The ability of a scoring scheme to better isolate.... Positives from.... Positives is important!

1..false. form false 2...false from true 3...correct/wrong 4....wrong/true

29. Tryptic peptides may reach up to an order of–400,000.

1...300,00 2. 200,000 3. 100,000 4. 600,000

30. In whole proteome samples, protein count may be over

1...50,000 2...40,000 3. 30,000 4....10,000

31. One way forward would be to transfer to the MS chamber in a step-by-step manner

1... peptides 2....proteins 3....parts.

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1.. Mass spectrometer is used to measure mass/charge ratio of..... proteins and peptides.

1...Charged 2...uncharged 3....ionized

2. Data output from the MS comprises of m/z..... and intensities of each molecule that is measured.

1...Quantity 2....ratio 3....Amount

3. Molecular Mass of Tuolene is

1...92 2.....93 3.....94

4. formats exist which come implemented as software with hardware.

1....Extensive 2....Proprietry 3...Readable

5.software standards exist for interoperability etc.

1...Open 2.....closed 3....strong 4.....weak

6. RAW file is a format in which an instrument outputs data in Form.

1...Binary 2....Digital 3....Decimal

7. Multiple RAW file formats are prevailing in the.....

1....School 2....college 3.....university 4....industry

8. WE can convert proprietary formats into Formats

1...OPEN 2....closed 3....both 4....None

9. MGF –.....

1...Multiple generic format 2....Mount generic format 3....Mascot generic format

10. MGF is a simple.....-readable format for MS/MS data developed by Matrix Science

1...Internet 2....Man 3....Human

11. MGF file format was developed as an..... standard for proteomics data.

1. Open 2....closed 3....both 4....none

12. Before using an MGF file, it is useful to check its.....

1.....product 2.....property 3.....version 4.... All of above

13.file formats are specific to each instrument and each vendor has its own unique file format.

1...RAW 2....MGF 3....RFLP 4...MQLF

14. Once an instrument is upgraded, datafrom the instrument is also changed

. 1....Inbox 2....output 3...files 4....formats.

15. Proprietary RAW formats are binary formats which are..... to read and parse

1....Easy 2....difficult 3....complex 4....probable

16. If we have the software from the maker of the MS then we can read the RAW..... as well.

1...data formats 2....data files 3.....data information 4....All

17.was developed by HUPO-PSI

1....mzData 2....mzxml 3....both 4....none

18. mzXML was developed at the Institute for Systems.....

1....Computers 2....zoology 3.....informatics 4....biology

19. Each open format has its own unique

1...advantages 2....disadvantages 3.....files 4....rules

20. Matrix Science developed an online Bottom Up Proteomics Search Engine called

1....mzXML 2....MGF 3.....Mzdata 4....MASCOT

21. Mascot is the most widely used online search tool for..... data

1....peptides 2....proteomics 3....proteins

22. MASCOT does not cater for top..... proteomics data

1...up 2...bottom 3...left 4...right.

BIF401 FROM PPT 146 to 165ppts.

Kelleher et al have developed an online Top Down Proteomics Search Engine Called as.....

1...MASCOT 2...mzDATA 3...mzXML 4...PROSITE PTM

2. ProSightPTM searches top down proteomics data and reports the precursor.....

1...Protein 2...peptides 3...molecules

3. ProSight PTM is the state of the art in top..... proteomics search.

1...Up 2...bottom 3...left 4...right

4. Using ProSight PTM, post-translational modifications can be accurately.....

1...Examined 2...Ignored 3...identified

5.is the study of protein sequence and structure.

1...Proteomics 2...transcriptomics 3...both

6. Natural elements occur in.... Isotopes.

1...Single 2...Double 3...triple 4...multiple

7. Isotopes differ in their.....

1...Masses 2...Average 3...weight 4...distance

8. The abundance of each isotopic variant is.....

1...Complex 2...unique 3...Abundant 4...Simple

9. Types of Masses are.....

1...1 2...2 3...3 4...4

10. MS1 data reports the..... distribution of intact molecule's mass.

1...Isotopic 2...monoisotopic 3...diisotopic 4...none

11. The step in protein identification using mass spectrometry involves intact protein/peptide mass measurement.

1...first 2...second 3...third 4...fourth

12. The 2nd step in mass spectrometry involves.....the protein!

1...Fragment 2...Saperation 3...ionization 4...grinding

13. A protein or peptide backbone may be fragmented any where along the peptide.....

1...sidechain 2...bottom up 3...bottom down 4...backbone

14. Formation of two fragments i.e.term fragment andTerm fragment

1...A/B 2...N/C 3...M/G 4...D/C

15. If the fragments of protein are 100 and 100 are attached at their backbone then the total number of fragments are.....

1...100 2... 200 3...300 4...400

16. ESI induces..... charges on the intact molecule.

1...single 2...double 3...triple 4...multiple

17. Since ESI induces multiple charges on the precursor molecule, there is a good chance that upon precursors fragmentation, each fragment will have a portion of the....

1...Protons 2...neutrons 3...particles 4...charges

18. Tandem MS helps measure molecular..... of ionized fragments

1...mass 2...weights 3...Average

19. Peptide sequence tags help deriveabout the sequence of precursor proteins/peptides.

1...Clues 2...tags 3...symbols

20. The short peptide sequences help us in shortlisting candidate proteins from the

1...files 2...Database 3...dataset 4...NCBI

21.or Tandem MS was performed after fragmentation of intact proteins

1...MS1 2...MS2 3...MS3 4...MS4

22. Candidate proteins can be further shortlisted by the....

1...PSTs 2...MQFL 3...LSMF 4...LNTs

23. Theoretical vs experimental fragments comparison helps as the stage for shortlisting candidate protein list will help you arrive at a small number of proteins

1...1st 2...2nd 3...3rd 4...4th

24. MAFSAEDVLKE is a....Sequence

1...Lipid 2...Amino acid 3...protein

25.scoring schemes can be applied to score the match at each stage of protein search can be integrated to arrive at an over all candidate protein score!

1...1 2...2 3... 3 4...4

26.
$$\left[\text{Score} \right]^{\wedge} = (\text{Score } MW) / EMW + \sum_{(i=0)}^m (\text{Score } PST) / RMSEPST + \sum_{(i=0)}^n (\text{Score } Exp \langle Thr \rangle) / (EEXP \langle Thr \rangle)$$
 Is a....scheme?

1...Basic 2...comprehensive 3...complex

27. A comprehensive scoring scheme can combine....the scores.

1...Several 2...few 3... **full** 4...none

28.take properties from the constituent amino acids.

1...proteins 2...lipids 3...carbohydrates.

29. There are....different amino acids.

1...17 2...18 3...19 **4...20**

30. Hydrophobic Amino Acids are....

1...polar **2...non-polar** 3...charged 4...un-charged.

31. Polar Amino Acids have....charge

1...1 2...2 3...few **4...no**

32. At pH=7,.... amino acids are charged.

1...5 2...4 3...3 4...2

33. The charge state of Amino acids depends on the acceptance or donation of from the R group side chains.

1...electrons 2...Acids **3...protons**

34. pK values for an amino acid is the At which exactly half of the chargeable group is charged. 1...Pka 2...pkb 3...constant **4...PH**

36. If pH pK for an amino acid, the amine side chains gain a proton (H⁺) and become positively charged, hence basic.

1...< 2...> 3...= 4.../

37. Elemental composition plays a very important role in determining of amino acids.

1...Structure **2...properties** 3...sequence 4...All

38. Solubility and reactivity are key factors participating in protein.....

1...folding 2...sequence 3...structure

39. Glycine residues increase backbone flexibility because they have nogroup.

1...H **2...R** 3...C 4...NONE

40. Cysteines cement together by making disulfide bonds to stabilize.....protein structures.

1...1-D 2...2-D **3...3-D** 4...4-D

41. some amino acids are hydrophobic, they may be employed in forming a stable.... in a protein.

1...core 2...bundle 3...packing

42. Packing/ burying of side chains into interior is a key driving force in protein folding.

1...hydrophilic **2...hydrophobic** 3...both

43. Hydrophobic core formed by packedstructural elements provides compact, stable core

1...primary 2...secondary 3...tertiary

44. After polymerization of amino acids, chains are formed.

1...linear 2...branched 3...simple 4...complex

45. The folded protein molecule should have the.....possible energy !.

1...highest 2...lowest 3...both

46. Proteins fold to organize themselves for performing functions in

1....orans 2...tissues 3...cells

And 47. Understanding protein folding helps design suitable....

1...Medicines 2...poisons 3...Drugs

48. To study anomalies in structures and to discover newer structural forms, computational Are used. 1...Algorithms 2...tools 3...methods

49. Let's assume that each amino acid can fold into.... Different conformations.

1...1 2...2 3...3 4...4

50. "Levinthal's Paradox" is aestimation of protein

1...time 2...structure 3...folding

51. The forces involved in protein folding are....

1..1 2...2 3...3 4...4

Bif401 mcqs from 166 to 185 ppts

required for folding a protein into its native structure is present within the protein's amino acid sequence! 1.....Instruction 2....information 3....inflow

2. Several..... act together to fold the protein structure.

1...Forces 2....Magnetic resonance 3....interactions

3. Protein structures are very yet they form spontaneously.

1...Simple 2....complex 3....strong 4....weak

4. Interestingly, each protein mega structure gets built out of only a fewstructures!

1...Mega 2....mini 3...Sub 4...Major

5.Alphabet Amino acid tags can be put together linearly to represent a protein sequence.

1...Single 2....double 3....triple

6. Primary sequence can also be referred to as Structure.

1.....1' 2.....2' 3....3' 4.....4'

7. Folded sub structures are called protein structures.

1...primary 2...secondary 3...tertiary 4...Quaternary

8. Secondary structures are also referred to asstructures.

1....1' 2....2' 3....3' 4....4'

9. 2' sub-structures are packed together to form.....structures.

1....Simple 2....complex 3....super

10. Tertiary structures are also referred to as...structures.

1....1' 2...2' 3....3'

11. 3' structures represent the complete protein structure.

1...monomeric 2....dimeric 3....metameric

12. 3' structures can combine with other polypeptide units to form a..... structure

1...primary 2....secondary 3...tertiary 4....quaternary

13. 1' structures are essentially the.....sequence of the proteins.

1....proteins 2....Amino acids 3...peptides

14... Methods for obtaining 1' structures are

1...1 2....2 3.....3 4....4

15. 1' structure lays the foundation forstructures.

1....1' 2....2' 3....3' 4....4'

16. The primary or 1' structure of a protein determines its Properties.

1...Acidic 2....Basic 3...Both 4....None

17. C and N termini can therefore make..... Bonds.

1...Electrostatic 2....chemical 3....Hydrogen

18. Hydrogen Bonds are the reason of.....structure formation.

1....1' 2....2' 3....3' 4....4'

19. Loops vary in..... and 3-D configurations.

1...Mass 2...Size 3....weight 4....length

20. Loops are mostly located on the.... Of proteins.

1....Side chain 2....backbone 3...surface

21. Loops are flexible and can adopt....conformations.

1...Single 2....double 3....triple 4...Multiple

22. Loops are frequently components of..... Sites.

1...Active 2...weak 3...charged 4...un-charged.

23. Covalent bonds in 3' structures are in the form of.....bridges.

1...Monosulphide 2...disulphide 3...trisulphide

24. 4' structures or quaternary structures are formed by different..... chains that make up the protein. 1...Proteins 2...proteome 3...Peptide

25. Proteins with multiple chains can form....structures.

1...1' 2...2' 3...3' 4...4'

26.involving C'-N-C α -C'.

1...phi 2...psi 3...alpha 4...beta

27.Alphas can be used to construct the backbone of a protein towards its visualization.

1...A 2...B 3...C

28. 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.

1...Sigma 2...Angstrom 3...phi 4...Psi

29. 1 angstrom is a unit of length equal to 10⁻¹⁰ m (one ten-billionth of a meter) or

1...0.1nm 2...0.2nm 3...0.3nm 4...0.4nm

30. The data is obtained from by the atoms in a protein structure.

1...distances 2...rays 3...diffractions

31. PDB has the coordinates of C-Alphas for over..... Proteins.

1...10,000 2...20,000 3...50,000 4...80,000

32. Proteins have Carbon and..... in their backbone.

1...Hydrogen 2...nitrogen 3...oxygen

33. To trace the backbone of a protein, atoms trace can be used.

1...CA 2...CB 3...CC 4...CD

34. Rasmol and.....are basic tools for visualizing proteins.

1..CHIME 2...MQLF 3...RSFR

35. Swiss Viewer offers several features such as protein surface view, alignment of several proteins & modelling secondary structures.

1...PDF PGB 3...PDB 4...PDL

36. In CPK diagrams, each atom is represented by a.... Sphere.

1...Liquid 2...solid 3...Gas

37. BS stands for

1...Balls and stick 2...bowl and soul 3...Bin and smooth

38. Anfinsen's thermodynamic hypothesis: Proteins fold for a unique, stable and minimum kinetic energy structure.

1...more 2...free 3...less

39. The greater the number of these bonds, the more.... A protein becomes.

1...stronger 2...stable 3...weaker

40. Hence, the basic idea of thermodynamic stability is to maximize bonding in order to the free energy.

1...Minimize 2...maximize 3...none

Bif401 mcqs from ppts 186 to 205

Experimental methods exist for structure of protein determination are.....

1..1 2....2 3....3 4....4

2. X ray crystallography performed by

1....Rosalin franklin 2....William smith 3....Newton

3. Atomic can help us classify interaction types e.g. hydrogen bonds, electrostatic & polar.

1....Differences 2....Distances 3.... Versions 4....Explosions

4. If two atoms are participating in a covalent bond, their distance is ~.....

1....0.93 2....0.94 3....0.95 4....0.96

5. In case of hydrogen bond formation between atoms, the inter-atomic distance is ~.....

1....1.97 2....1.96 3....1.95 4....1.94

7. X-Ray Crystallography data shows that Hydrogen atoms of N-Term may come together with Oxygen atoms of C-term amino acid at..... neighboring position.

1....1st 2....2nd 3....3rd 4....4th

8. ,“Helix Formers” are generally Amino acids (M, A, L...).

1....Hydrophobic 2....Hydrophilic 3...Both

9. Beta sheets are constituted by several..... Strands which come together.

1....Alpha 2....beta 3....Gamma

10. Residues are needed to make a Beta Strand, typically.

a. 5...10 b. . 6...10 c. 7...10 d. . 8...10

11. Bonds to make in Beta Strands

1...Nitrogen 2...carbon 3...oxygen 4...hydrogen

12. Beta Sheets are an other secondary structure that can be formed as a result of hydrogen bonding..... the protein back bone.

1...in 2...up 3...between 4...down

13. Beta Sheets Properties are....

1...1 2...2 3...3 4...4

14. Beta Barrel is made of a Beta sheet that twists and coils upon itself.

1...Single 2...double 3...Tripple 4...Multiple

15. Beta Sandwiches are made of....beta sheets which are usually twisted and packed so their strands are aligned.

1...1 2...2 3...3 4...4

16. Alpha Helices and Beta Sheets are...structures formed as a result of hydrogen bonding in between protein backbone atoms.

1...primary 2...Secondary 3...Tertiary

17. Loops are variable in length and... conformations.

1-D 2-D 3-D 4-D

18. Loops are formed by present in the middle of the Alpha Helices and Beta Sheets in a protein backbone.

1...Amino acids 2...peptide bonds 3...proteins

19. Loops frequently participate as components of....sites.

1...Active 2...Basic 3...Chaeged 4...uncharged

20. Hairpin loops are....amino acids long and join anti-parallel Beta strands.

1...1 2...2 3...3 4...4

21. Coils are unstructured andloops. Like or unlike?

Ans: unlike

22. Essentially, a secondary structure which is not a helix, sheet or loop is a!

1...structure 2...multiple. 3. loop 4... coil

23. Coils are apparently Regions.

1...ordered 2...disordered 3...charged 4...uncharged

24. are semi-independent functional structures in a protein.

1...Domains 2....Motifs 3....loops

25. Domains haveresidues.

1....10 2...20 3...30 4.....40

26. Locally Compact – Domains interact (H-bonds)....internally than externally.

1...More 2...less

27. we classify proteins by their.....

1...Loops 2...Domains 3....Coils 4...Super coils

28. In homology Pairwise sequence similarity >.....

1...10% 2...20% 3....30%

29. CATH also considers..... organization of the structural components in proteins.

1...internal 2...external

30. CATH is one such system in which..... are organized into classes, architecture, topology and homology.

1...Amino acids 2...proteins 3...peptides

31. Proteins are considered as....bodies.

1....soft 2...hard 3....rigid

32. PDB coordinates of Carbons in the protein back bone can be used for comparison.

1...Alpha 2...Beta 3...Gamma

33. The lower the RMSD, the....are the proteins.

1...Similar 2...stronger 3...weaker

34. Depending on the RMSD, proteins, their motifs and domains can be selectively.....

1...Matched 2....compared

35. RMSD tells us about the of the matches.

1...Advantage 2...Quality 3....Disadvantage

36. Proteins fold spontaneously or with the help of.....or chaperones.

1...units 2....Enzymes 3...Sub-units

37. A deterministic solution of protein folding is a major unsolved problem in biology!

1....Simple 2....system 3...Molecular

38. By looking at the structures in PDB, we know that.... Mostly found in Alpha Helices.

1....Alanine 2....Valine 3...Leucine

1...> 2...< 3...=

13. The average value for P(turn) > in the tetrapeptide.

1...1 2....2 3....3 4...4

14. The averages for the tetrapeptide are such P(a-helix) < P(turn) > P(b-sheet), it is a.....

1...Turn 2....Loop 3...coil

15. The Chou Fasman algorithm is based on occurrence of Amino Acids in known structures.

1...Numerical 2....Statistical

16. Chou Fasman Algorithm helps predict such as Alpha Helices, Beta Sheets and Turns.

1...primary 2...Secondary 3....Tertiary

17. Beta sheets can be predicted from.... amino acid sequences.

1...Primary 2...Secondary 3..Tertiary

18. Secondary structure propensity values of alpha helix, beta sheet and turns should be recalculated with the latest data sets.

1...peptides 2...proteins 3...proteomes.

19. Consider variable coil and loop sizes besides the from ... peptide turns.

1...mono 2....Beta 3....tri 4....Tetra

20.structure of proteins is the sequence of proteins and can be obtained by mass spectrometry.

1...1' 2...2' 3....3' 4...4'

21.structures formed by proteins are the helices, beta sheets, loops and coils.

1...1' 2....2' 3....3' 4...4'

22. structure of proteins is the combination of 2' structures such that the overall protein structure is formed.

1...1' 2....2' 3....3' 4...4'

23.protein structure is formed when two or more proteins complex together.

1....1' 2....2' 3....3' 4....4'

24. Protein sequence gives rise to its

1...Amino acids 2...peptides 3...Structure

25. it is then possible to identify unknown protein structures by just examining the.....protein sequences.

1...Heterologus 2....homologus

26. In homology modelling, proteins with similar....sequences are considered.

1...1' 2...2' 3...3' 4...4'

27. Good sequence alignment and identity ensures that homology modelling will give.....results.

1...Accurate 2....Good 3...Wrong

28. Homology modelling is used to predict structures of proteins having similarity with other proteins with known structures!.

1....High 2...Low

29.Strategies for structure prediction are

1....1' 2...2' 3....3'

30. Steps for homology modelling are

1....1' 2....2' 3....3'

31. Uses a residue exchange scoring matrix.

Residues that are easily exchanged (e.g. Ile to Leu) get a better score than residues that have different properties (for example Glu to Trp).

Function specific conserved residues get the best score (e.g. Cys to Cys).

1...FASTA 2....BLAST UNIPROT 4...GENEBANK

32. Examine the template structure to check which residues are in the hence less likely to change than the residues at the outside.

1...Loop 2...coil 3....core

33. can be helpful to find these places in Homology Modelling.

1...CLUSTAW 2...MSA

34. Gaps have to be shifted around until they are as....as possible.

1...Small 2....Large 3....Big

35. One way to handle loops is to take some residues before and after the insertion as “...” Residues and search the PDB for loops with the same anchor-residues.

The best loop is simply copied in the model.

1...Charged 2....Uncharged 3....Anchor

36. The backbone of strongly prefers two rotamers and the real side-chain may fit one of them!

1...Tryptophan 2....Tyrosine

37. The model with the lowest energy might still be folded completely

1....True 2....Wrong

MCQS from 226 to 240:-

1. Modeller is a for homology modelling.
1....Tool 2....System **3....Software**
2. Homology modelling helps predict.....structures by using prior structural information.
1....Proteins 2....Peptides 3....Proteomes
3. Several tools are available to perform homology modelling in a programmatic or Way!
1....Non-Automated **2....Automated** 3...Sequenced
4. A protein fold is defined by the way the.....structure elements of the structure are arranged relative to each other in space. 1....Primary **2....Secondary** 3...Tertiary
5. Common folds include..... bundle and the TIM barrel.
1....1-helix 2...2-helix 3....3-helix **4....4-helix**
6. stable folds in nature.
1....1000 2...2000 3...3000 4....4000 **5.....5000**
7. Fold recognition is also called
1...Model 2...Tools 3...Threading
8. Employed when homology modelling cannot predict.... Structures.
1...Quality 2....Quantity
9. In the process of “Threading”, we mount an.... Sequence on to the backbone of template structures in a folds library. **1...Amino Acid**
2....Protein 3....Peptides
10. Threading involves “.....” the amino acid sequence through each fold in the database.
1...Pushing **2....Passing** 3....Entering
11. Scoring typically involves using aScore function based on energy of a molecule.
1....A 2.....B c....Y **4....Z**
12. I-TASSER first generates atomic models from multiple threading alignments and iterative structural assembly simulations.
1....1D 2....2D **3....3D** 4....4D
- 13.....helps thread amino acid sequences on fold and secondary structure databases.
1...MSA 2....CLUSTAW **3....iTASSER**
14. Threading helps predict secondary structures of proteins towards structure prediction.

- 1....Primary 2....Secondary **3....Tertiary**
15. For the “Twilight Zone” with....alignment quality and identity, threading is useful.
1....High **2....Low**
16. Fewer than Of
Novel proteins the predicted first hits are true remote homologues.
1....10% 2....20% **3....30%**
17. Bowie Algorithm Proposed by Bowie et al in
1....1991 2...1992 3...1993 4....1994(imp mcq)
18. 3D-1D methods convert structure and environment information into “.....”
1....Protienenes 2....Peptides **3...Profiles**
19. Ab initio methods have Anfinsen’s thermodynamic hypothesis at the....
1...Side **2....Middle** 2....Bottom 4....Down
20. Ab initio Suitable for proteins with less than....residues. **1...100**
2...200 3...300 4...400
21. Ab initio methods rely on computing the of folded proteins.
1,,,Energies 2....Quality 3....Quantity
22. Ab initio methods, in contrast, base their predictions on..... models for these mechanisms.
1,,,Physical 2,,,Chemical 3...Biological
23. Stabilization is measured by released during the folding process.
1,,,Heat **2....Energy** 3....Temperature
24.optimization finds the most stable structure. 1....Local
2....Global
25. Strategies for structure modelling are
1...1’ 2....2’ **3....3’**

Bif401 Mcqs from ppt 240....250

1. Strategies for structural modelling are
1...1" 2....2" **3....3"**
2. Solve the computational problem of finding the....minimum.
1..Global. 2...local
3. Ab Initio strategies can help model the
1....Sequence **2....Structures**
4. MSA stands for.....

- 1...Mutant sequence alignment
 2...Missed sequence alignment
3...Multiple sequence Alignment
5. GenBank is for....
1...DNA 2....RNA 3...PROTEINS
6. UniProt is for
 1....DNA 2...RNA **3...PROTEINS**
7. Online Portals are
 1...1' 2....2' **3....3**
8. The rate of evolution in species is.....
 1....Same **2....Different**
9. is a clustering method.
 1...MSA **2...UPGMA** 3...UNIPROT
10. Techniques of protein sequencing are
 1....1' **2....2'** 3....3'
11. Energy is released as a result of..... coupling.
 1...Proteins 2....Peptides **3...Nucleotides**
12. Folded RNA is more stable in terms of
 1...Heat **2...Energy** 3....Temprature
13. Techniques for determining protein structures are
 1....1' 2....2' **3....3'**
14. Number of known protein sequences is much As compared to known proteins structures.
1...Larger 2....Smaller
15. Bioinformatics as anarea.
 1...Logical 2....community **3...interdisciplinary**