

BIF401 CURRENT PAPER MCQS

FOR FINALS

- ❖ Genomics, evolutionary studies and system biology are application of **bioinformatics**
- ❖ Exact matching require which type of nucleotide-**same number of nucleotide**
- ❖ Accurate solution of protein structure is one of the ___ **toughest problems**
- ❖ **Tract back** is overlap matches can start from any position in scoring matrix
- ❖ The matrix hasscores. **Positive and negative**
- ❖ **MASCOT**___can search people mass finger printing and shotgun proteomics data set
- ❖ Spectrometer measures the protein by _____ **Mass/charge**
- ❖ Simulation of the folding process depends _____ **Energy function**
- ❖ Information about **DNA/RNA** is available on gene bank
- ❖ **TDP** is used to measure the molecules weight of intact proteins.
- ❖ Coordinates of **alpha carbon** in the protein backbone can be used for structural visualization.
- ❖ in structure visualization c-alpha atoms are traced to recreate a _____**3D protein structure**
- ❖ in UPGMA distance is calculated btw _____ **two clusters and between two trees**
- ❖ pk value of Aspartic acid **3.9**
- ❖ Largest amino acid **Tryptophan**
- ❖ 2nd STRUCTURE of proteins can be obtained by using_____ **Chou Fasman algorithm**
- ❖ NJ Algorithm strategy is used to predict ___ **RNA 2` structure**
- ❖ The loop of hair pin must be at least ___ in length **2 aminoacids**
- ❖ Fold recognition is also called**threading**
- ❖ Ab initio method in contrast ,base their prediction on **low energy model**.
- ❖ Bioinformatics require.....smart mind, and connected to internet, **both**,
- ❖ Sequence alignment tool is.....**PROSIGHT and MASCOT**
- ❖ MS1,MS2 provide us data identifying unknown.....**Proteins sequence**.
- ❖ **MGF** files develop as an open standard for..... **proteomics data**.

- ❖ **PDB** coordinates alpha carbon in protein back bone can be used for comparison .
- ❖ Alpha carbon atom can be obtained from.....**PDB**
- ❖ in formation of 2nd structure of protein C & N can make.....**Hydrogen bonds**
- ❖ information for protein folding is into its native structure is in..... **protein's amino acid sequence!**
- ❖ Energy **released** during bond formation.
- ❖ hydrogen bonding occur in ...**secondary** ..Protein structure
- ❖ Bond between C and H in alpha helices____**Hydrogen bonding**
- ❖ Amino acid having 3 codons____ **isoleucine**
- ❖ MALDI typically adds a to protein or peptide. **Proton**
- ❖ low quality match gets____**lower score**
- ❖ ____ are sequences of amino acids produced during MS2. **PST (peptide sequence tags)**
- ❖ MS2 data can be used to extract..... **peptide sequence tags.**
- ❖ The alpha helices propensity should be more than____(**1.0**)
- ❖ How many types are of protein sequencing techniques__ (**2**)
- ❖ Blast can find sequences of ____**nucleotides amino acid**
- ❖ If a protein sequence of 26 amino acids is fragmented at 11 amino acid **C11, Z25**
- ❖ To find out unknown sequence of nucleotide we use . **NGS or Mass spectrometry**
- ❖ How many types of peptide May be injected in mass spectrometry chamber.. . **three hundred thousand to four hundred thousand**
- ❖ **.MASCOT** can search peptide mass finger printing and shotgun proteomics dataset.
- ❖ Stabilizing and destabilizing energy give us **quality of 2nd structure** .
- ❖ The Fasman algorithm is based on **statistical occurrence** of Amino Acids in known structures.
- ❖ DP recombinant the nucleotide recombination through process of **Traceback**
- ❖ **MALDI**.....add proton to a protein and a peptide..
- ❖ Positively charged amino acids are..... **3**
- ❖ Aromatic amino acid include **phenylalanine, tyrosine tryptophan**
- ❖ Homology modelling fail to predict **quality structure**

- ❖ How many forces are involved in protein folding. **4**
- ❖ Pairwise alignments tells the similarity between sequence... **by maximizing the matches.**
- ❖ Dot plots employ dot matrix with two sequence plotted represents.....**pairwise alignment and comparison.**
- ❖ Differentiate b/w DNA and RNA sequence..... **RNA has more variety of sequence**
- ❖ Cell molecule are produced after transformation of **DNA to protein**
- ❖ Dot plot cannot deal with..... **Insertion, deletion and gaps.**
- ❖ Exons are may be more **conserved.**
- ❖ In dynamic algorithm we can do comparison of more sequence. **Three**
- ❖ Mass/Charge ratio helps calculate the mass of the **Protein**
- ❖ In scale tree branches lengths are equal to the magnitude of change in the **nodes.**
- ❖ How many types of peptides mix in MS chamber..... **300,000 – 400,000**
- ❖ mRNA is a structure. **Planer**
- ❖ When unpaired bases of 2' structure join to form..... **3' structure**
- ❖ N Jackobson use to pridict **2' structure.**
- ❖ Aromatic amino acid **Tyrosine**
- ❖ Positive charge amino acids..... **Lysine, arginine, histidin**
- ❖ MS begins with the measure of **intact protein**
- ❖ Amount of amino acids in alpha helix.....**(4)**
- ❖ Intact mass of protein can be found by..... **MS1**
- ❖ MSA can be done by..... **CLUSTAL**
- ❖ Which is used as sequence alignment tool..... **PROSIT**
- ❖ MS1 and MS2 help to identify **(PST)**
- ❖ MGF is used for **proteomics**
- ❖ X,Y,Z positions of alpha carbon available online on **(PDB)**
- ❖ Method to determine RNA structure **NMR, X-Ray crystallography**
- ❖ CLUSTLA runs..... **Slow accurate/ fast appropriate**
- ❖ Which give info about precursor protein..... **PSTS**
- ❖ Raw data files format can be converted to **Open format**

- ❖ Which of the following is cartoonic figure..... **Ribbon diagram**
- ❖ In CATH protein recognize according to their..... **structural similarity**
- ❖ Method for obtaining 1' structure..... **(Edman Degradation Tandem Mass Spectrometry).**

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