

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, 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 25 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 Pashan algorithm is based on **statistical occurrence** of Amino Acids in known structures.

In 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)**

MCF is used for **proteomics**

XMR 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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