

BIO316

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1. Which among the following options is Japanese sibling of GenBank?

EMBL

PIR

ENSEMBL

--->> DDBJ

2. Analysis of nucleic acid composition, secondary structure, transcriptional factors and promoter sites, are components of

Proteomics analysis

Biochemical analysis

Metabolic analysis

--->> Genomic analysis

3. All the following are components of Proteomics analysis except

Determination of amino acid composition

Sequence alignment, phylogenetic analysis

--->> Restriction enzyme cleavage sites

Prediction domains and tertiary structure.

4. The full meaning of ExPASy is

Expressed Protein Analysis System

--->> Expert Protein Analysis System

Export Protein Analysis System

Export Patent Analysis System

5. A Computer-based organization of sequence and structural data of biomolecules is called

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Data

Storagebase

All the options

6. An alignment of a protein sequence to the 3D structure of another protein is called

--->> THREADING

TOPITS

TOPRED

UPGMA

7. The version of BLAST that searches a protein sequence against a protein database is the

BLASTN

--->> BLASTP

BLASTX

BLASTPP

8. In multiple alignment, alignment is scored by one of the following options

Scoring each column of the alignment and adding up the column scores

Scoring a column by its degree of conservedness i.e. more conserved columns, indicate better scoring alignments

Scoring of a column by sum of the scores of all distinct pairs of letters in the column, where a pair of letters is scored via a substitution matrix

--->> All the options

9. A table of matrix representing a visual representation of similarities between two sequences is the

Pairwise Sequence Alignment

Diagonistic analysis

--->> Dotplot Analysis

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10. Three databases, DDBJ, EMBL and GenBank act together in collecting and distributing sequences so that each has copies of all the sequences, thus they act as

tertiary distribution centre for sequences

secondary distribution centre for sequences

--->> primary distribution centre for sequences

All the options

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