

# National Testing Agency

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## FUNDAMENTALS OF BIOINFORMATICS

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## FUNDAMENTALS OF BIOINFORMATICS-1

<b>Section Id :</b>	603489250
<b>Section Number :</b>	1
<b>Section type :</b>	Online
<b>Mandatory or Optional :</b>	Mandatory

<b>Number of Questions :</b>	100
<b>Number of Questions to be attempted :</b>	100
<b>Section Marks :</b>	100
<b>Enable Mark as Answered Mark for Review and Clear Response :</b>	Yes
<b>Sub-Section Number :</b>	1
<b>Sub-Section Id :</b>	603489479
<b>Question Shuffling Allowed :</b>	Yes

**Question Number : 1 Question Id : 60348912966 Question Type : MCQ Option Shuffling : No Is**

**Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

SWISS PROT is related to

1. Portable data
2. Swiss Bank data
3. Sequence data bank
4. Sequence structure data bank

**Options :**

60348949159. 1

60348949160. 2

60348949161. 3

60348949162. 4

**Question Number : 2 Question Id : 60348912967 Question Type : MCQ Option Shuffling : No Is**

**Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

CLUSTALW is

1. Multiple sequence alignment tool
2. Protein secondary structure predicting tool
3. Data retrieval tool
4. Nucleic acid sequencing tool

**Options :**

60348949163. 1

60348949164. 2

60348949165. 3

60348949166. 4

**Question Number : 3 Question Id : 60348912968 Question Type : MCQ Option Shuffling : No Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The first genome sequenced was that of

1. *Saccharomyces cerevisiae*
2. *Escherichia coli*
3. *Arabidopsis thaliana*
4. Bacteriophage MS2

**Options :**

60348949167. 1

60348949168. 2

60348949169. 3

60348949170. 4

**Question Number : 4 Question Id : 60348912969 Question Type : MCQ Option Shuffling : No Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

MOODLE is an example of

1. CMS
2. LCMS
3. LMS
4. Programming Language

**Options :**

60348949171. 1

60348949172. 2

60348949173. 3

60348949174. 4

**Question Number : 5 Question Id : 60348912970 Question Type : MCQ Option Shuffling : No Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which combination of the following statements regarding ICT is true?

P: ICT is an acronym stands for Indian Classical Technology

Q: Converging technologies that exemplify ICT include the merging of audio-visual, telephone and computer networks through a common cabling system

1. P only
2. Q only
3. Both P and Q
4. Neither P and Q

**Options :**

60348949175. 1

60348949176. 2

60348949177. 3

60348949178. 4

**Question Number : 6 Question Id : 60348912971 Question Type : MCQ Option Shuffling : No Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

MOOC stands for

1. Media Online Open Course
2. Massive Online Open Course
3. Massive Open Online Course
4. Massachusetts Open Online Course

**Options :**

60348949179. 1

60348949180. 2

60348949181. 3

60348949182. 4

**Question Number : 7 Question Id : 60348912972 Question Type : MCQ Option Shuffling : No Is**

**Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which energy molecule is required to start translation?

1. ATP
2. GTP
3. CTP
4. AMP

**Options :**

60348949183. 1

60348949184. 2

60348949185. 3

60348949186. 4

**Question Number : 8 Question Id : 60348912973 Question Type : MCQ Option Shuffling : No Is**

**Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is true regarding transcription and translation?

1. During transcription, an mRNA molecular is created from DNA molecule
2. Translation takes place in the nucleus, while transcription takes place in the cytoplasm
3. Transcription and Translation are coupled in Eukaryotes
4. During translation amino acids are synthesized using DNA sequences

**Options :**

60348949187. 1

60348949188. 2

60348949189. 3

60348949190. 4

**Question Number : 9 Question Id : 60348912974 Question Type : MCQ Option Shuffling : No Is**

**Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

In Prokaryotes, the first amino acid in the polypeptide chain is

1. Methionine
2. N-formyl methionine
3. N-methyl methionine
4. All of these

**Options :**

60348949191. 1

60348949192. 2

60348949193. 3

60348949194. 4

**Question Number : 10 Question Id : 60348912975 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

GenBank, the nucleotide sequence database is maintained by

1. Brookhaven Laboratory
2. DNA database of Japan (DDBJ)
3. European Molecular Biology Laboratory (EMBL)
4. National Centre for Biotechnology Information (NCBI)

**Options :**

60348949195. 1

60348949196. 2

60348949197. 3

60348949198. 4

**Question Number : 11 Question Id : 60348912976 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Submission to GenBank are made using

1. BankIt and Sequin
2. BankIt and BankIn
3. Sequin and BankIn
4. Entrez

**Options :**

60348949199. 1

60348949200. 2

60348949201. 3

60348949202. 4

**Question Number : 12 Question Id : 60348912977 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

All are genome sequencing strategies except

1. Edman degradation method
2. Shot gun library
3. Whole genome shot gun sequencing
4. Directed gene sequencing

**Options :**

60348949203. 1

60348949204. 2

60348949205. 3

60348949206. 4

**Question Number : 13 Question Id : 60348912978 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Sequence similarity can be quantified using \_\_\_\_\_ homology is a \_\_\_\_\_ statement.

1. Percentages, quantitative
2. Percentages, qualitative
3. Ratios, qualitative
4. Ratios, quantitative

**Options :**

60348949207. 1

60348949208. 2

60348949209. 3

60348949210. 4

**Question Number : 14 Question Id : 60348912979 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Two sequences are said to be homologous if

1. They have diverged from a common ancestor
2. Their alignments share 30% identity or more
3. They belong to the same fold family
4. They have converged to share similar functional properties.

**Options :**

60348949211. 1

60348949212. 2

60348949213. 3

60348949214. 4

**Question Number : 15 Question Id : 60348912980 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**



In a protein sequence alignment, \_\_\_\_\_ refers to the percentage of matches of the same amino acid residues between two aligned sequences

1. Sequence identity
2. Sequence homology
3. Sequence similarity
4. Sequence non-homology

**Options :**

60348949215. 1

60348949216. 2

60348949217. 3

60348949218. 4

**Question Number : 16 Question Id : 60348912981 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Cysteine is a very infrequently substituted residue during evolution. Why?

1. Substitution abolishes the enzymatic activity
2. Substitution destabilizes the protein
3. Both the options are correct
4. Both the options are wrong

**Options :**

60348949219. 1

60348949220. 2

60348949221. 3

60348949222. 4

**Question Number : 17 Question Id : 60348912982 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

PAM stands for

1. Point Accepted Mutation
2. Position Accepted Mutation
3. Positive Accepted Mutation
4. Probability Accepted Mutation

**Options :**

60348949223. 1

60348949224. 2

60348949225. 3

60348949226. 4

**Question Number : 18 Question Id : 60348912983 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following does not describe local alignment?

1. A local alignment aligns a substring of the query sequence to a substring of the target sequence
2. A local alignment is defined by maximizing the alignment score, so that deleting a column from either end would reduce the score, and adding further columns at either end would also reduce the score
3. Local alignments have terminal gaps
4. The substrings to be examined may be all of one or both sequences; if all of both are included then the local alignment is also global

**Options :**

60348949227. 1

60348949228. 2

60348949229. 3

60348949230. 4

**Question Number : 19 Question Id : 60348912984 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The three sections of the GenBank file are

1. Header, Identifier, Features
2. Header, Features, Sequence entry
3. Identifier, Features, Sequence
4. Locus, Sequence, Features

**Options :**

60348949231. 1

60348949232. 2

60348949233. 3

60348949234. 4

**Question Number : 20 Question Id : 60348912985 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is not correct about BLAST?

1. The BLAST web server has been designed in such a way as to simplify the task of program selection
2. The programs are organized based on the type of query sequences
3. The programs are organized based on the type of nucleotide sequences, or nucleotide sequence to be translated
4. BLAST is not based on heuristic searching methods

**Options :**

60348949235. 1

60348949236. 2

60348949237. 3

60348949238. 4

**Question Number : 21 Question Id : 60348912986 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The variant of BLAST that uses nucleotide sequences, which are translated in all six frames, to search against a nucleotide sequence database that has all the sequences translated in six frames is.....

1. BLASTX
2. TBLASTX
3. TBLASTN
4. BLASTN

**Options :**

60348949239. 1
60348949240. 2
60348949241. 3
60348949242. 4

**Question Number : 22 Question Id : 60348912987 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is an incorrect statement?

1. In a phylogram, the branch lengths represent the amount of evolutionary divergence
2. Trees like cladogram are said to be scaled
3. The scaled trees have the advantage of showing both the evolutionary relationships and information about the relative divergence time of the branches
4. In a cladogram, the external taxa line up neatly in a row or column

**Options :**

60348949243. 1
60348949244. 2
60348949245. 3
60348949246. 4

**Question Number : 23 Question Id : 60348912988 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is true regarding the algorithms UPGMA, NJ, Fitch–Margoliash and minimum evolution?

1. UPGMA and Fitch-Margoliash are clustering type algorithms
2. UPGMA and NJ are clustering type algorithms
3. Fitch-Margoliash and minimum evolution are clustering type algorithms
4. NJ and minimum evolution are clustering type algorithms

**Options :**

60348949247. 1

60348949248. 2

60348949249. 3

60348949250. 4

**Question Number : 24 Question Id : 60348912989 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is NOT CORRECT about NJ method?

1. This method begins with a completely unresolved star tree by joining all taxa onto a single node
2. The taxa with the shortest corrected distance will be joined first as a node
3. It creates a rooted tree
4. The tree construction process is called star decomposition

**Options :**

60348949251. 1

60348949252. 2

60348949253. 3

60348949254. 4

**Question Number : 25 Question Id : 60348912990 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The sequence of steps in homology modelling is

1. Template selection, building model framework, alignment of target and template, adding loops and side chains, model optimization, model evaluation
2. Template selection, alignment of target and template, building model framework, adding loops and side chains, model optimization, model evaluation
3. Template selection, alignment of target and template, adding loops and side chains, building model framework, model optimization, model evaluation
4. Template selection, building model framework, adding loops and side chains, alignment of target and template, model optimization, model evaluation

**Options :**

60348949255. 1

60348949256. 2

60348949257. 3

60348949258. 4

**Question Number : 26 Question Id : 60348912991 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is a web server that models loops using the database search approach?

1. PETRA
2. CODA
3. FREAD
4. All of these

**Options :**

60348949259. 1

60348949260. 2

60348949261. 3

60348949262. 4

**Question Number : 27 Question Id : 60348912992 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is NOT CORRECT regarding MODELLER, the web server for homology modelling?

1. The user provides a predetermined sequence alignment of the template and the target
2. The program models the backbone using a homology-derived restrain method
3. Conserved residues are given low restraints and less conserved residues, including loops residues are given high constraints
4. The entire model is optimized by energy minimization and molecular dynamics procedures

**Options :**

60348949263. 1

60348949264. 2

60348949265. 3

60348949266. 4

**Question Number : 28 Question Id : 60348912993 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is a natural drug?

1. Digoxin
2. Amphetamines
3. Methaqualone
4. Heroin

**Options :**

60348949267. 1

60348949268. 2

60348949269. 3

60348949270. 4

**Question Number : 29 Question Id : 60348912994 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The process of deriving a pharmacophore model from multiple active compounds is often termed as

1. Pharmacophore mapping
2. Pharmacophore fingerprinting
3. Both the options
4. None of these

**Options :**

60348949271. 1

60348949272. 2

60348949273. 3

60348949274. 4

**Question Number : 30 Question Id : 60348912995 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

If you have a known structure of target and known ligand, what method you will follow to perform a structure based drug design?

1. De novo design
2. QSAR
3. Molecular Docking
4. Pharmacophore mapping

**Options :**

60348949275. 1

60348949276. 2

60348949277. 3

60348949278. 4

**Question Number : 31 Question Id : 60348912996 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**



When DNA is electrophoresed in a gel, DNAs that are small (20 base pairs or less) will

1. Remain stationary
2. Move through the gel more quickly than DNAs that are 100 bp long
3. Be found near the top of the gel after the DNA has been electrophoresed
4. Move through the gel more slowly than DNAs that are 100 bp long

**Options :**

60348949279. 1

60348949280. 2

60348949281. 3

60348949282. 4

**Question Number : 32 Question Id : 60348912997 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Dideoxy nucleoside triphosphate

1. has an oxygen at the 2' carbon
2. will terminate DNA synthesis when incorporated into a growing DNA strand
3. has an oxygen at the 3' carbon
4. can form a sugar phosphate bond with a new nucleoside triphosphate during DNA synthesis

**Options :**

60348949283. 1

60348949284. 2

60348949285. 3

60348949286. 4

**Question Number : 33 Question Id : 60348912998 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Once the sequences are obtained from your Next Generation Sequencing experiment what is the first thing you should do?

1. Perform a bioinformatics analysis of your data
2. Check your data using a different method
3. Publish your results
4. Further investigate the sequences of interest

**Options :**

60348949287. 1

60348949288. 2

60348949289. 3

60348949290. 4

**Question Number : 34 Question Id : 60348912999 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Choose the incorrect statement out of the following :

1. Only L amino acids are found in the biological system
2. Glycine is optical inactive
3. Tyrosine is a modified amino acid
4. Seleno cysteine is 21st amino acid

**Options :**

60348949291. 1

60348949292. 2

60348949293. 3

60348949294. 4

**Question Number : 35 Question Id : 60348913000 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

A dipeptide has

1. 2 Amino acids and 1 peptide bond
2. 2 Amino acids and 2 peptide bond
3. 2 Amino acids and 3 peptide bond
4. 2 Amino acids and 4 peptide bond

**Options :**

60348949295. 1

60348949296. 2

60348949297. 3

60348949298. 4

**Question Number : 36 Question Id : 60348913001 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The most common secondary structure is

1.  $\alpha$  helix
2.  $\beta$  sheet
3.  $\beta$  pleated sheet parallel
4.  $\beta$  pleated sheet antiparallel

**Options :**

60348949299. 1

60348949300. 2

60348949301. 3

60348949302. 4

**Question Number : 37 Question Id : 60348913002 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following residues is likely to be found in a turn of a protein?

1. Alanine
2. Glutamate
3. leucine
4. glycine

**Options :**

60348949303. 1

60348949304. 2

60348949305. 3

60348949306. 4

**Question Number : 38 Question Id : 60348913003 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following methods of secondary structure prediction takes into account the influence of neighbouring residues in the propensity for a secondary structure explicitly?

1. Chou-Fasman
2. GOR
3. HMM
4. Artificial Neural Network

**Options :**

60348949307. 1

60348949308. 2

60348949309. 3

60348949310. 4

**Question Number : 39 Question Id : 60348913004 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Co-immunoprecipitation is an example of \_\_\_\_\_ kind of interaction?

1. Stable
2. Weak
3. Moderately
4. Very weak

**Options :**

60348949311. 1

60348949312. 2

60348949313. 3

60348949314. 4

**Question Number : 40 Question Id : 60348913005 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The collaborating host Institutes of UniProt are

1. European Bioinformatics Institute (EMBL-EBI)
2. SIB Swiss Institute of Bioinformatics (SIB)
3. Protein Information Resource (PIR)
4. All of these

**Options :**

60348949315. 1

60348949316. 2

60348949317. 3

60348949318. 4

**Question Number : 41 Question Id : 60348913006 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following regarding the basic mechanism of gene expression is correct?

1. DNA → tRNA → protein
2. DNA → mRNA → protein
3. RNA → DNA → mRNA → protein
4. DNA → protein

**Options :**

60348949319. 1

60348949320. 2

60348949321. 3

60348949322. 4

**Question Number : 42 Question Id : 60348913007 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The commonly used databases for structural data are

1. NCBI, PDB
2. NCBI, GenBank
3. PDB, EMDB
4. GenBank, EMDB

**Options :**

60348949323. 1

60348949324. 2

60348949325. 3

60348949326. 4

**Question Number : 43 Question Id : 60348913008 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following methods is used in testing millions of samples against a protein target ?

1. Similarity search
2. Docking
3. High-throughput Screening
4. Molecular Modeling

**Options :**

60348949327. 1

60348949328. 2

60348949329. 3

60348949330. 4

**Question Number : 44 Question Id : 60348913009 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following are examples for Open access online resources related to life sciences?

1. PubMed
2. PLoS
3. Biomed Central
4. All of these

**Options :**

60348949331. 1

60348949332. 2

60348949333. 3

60348949334. 4

**Question Number : 45 Question Id : 60348913010 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

PubMed is a free search engine accessing primarily the ----- database of references and abstracts on life sciences and biomedical topics

1. PDB
2. MeSH
3. NLM
4. MEDLINE

**Options :**

60348949335. 1
60348949336. 2
60348949337. 3
60348949338. 4

**Question Number : 46 Question Id : 60348913011 Question Type : MCQ Option Shuffling : No**  
**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The information retrieval tool of NCBI GenBank is

1. Entrez
2. STAG
3. SeqIn
4. Text search

**Options :**

60348949339. 1
60348949340. 2
60348949341. 3
60348949342. 4

**Question Number : 47 Question Id : 60348913012 Question Type : MCQ Option Shuffling : No**  
**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**



Unauthorized use of the language and thoughts of another author and the representation of them as one's own original work

1. Plagiarism
2. Copyright
3. Imitation
4. Topography

**Options :**

- 60348949343. 1
- 60348949344. 2
- 60348949345. 3
- 60348949346. 4

**Question Number : 48 Question Id : 60348913013 Question Type : MCQ Option Shuffling : No Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following are non-coding RNAs (ncRNAs) ?

1. tRNA, rRNA
2. tRNA, snoRNA
3. snoRNA, snRNAs
4. All of these

**Options :**

- 60348949347. 1
- 60348949348. 2
- 60348949349. 3
- 60348949350. 4

**Question Number : 49 Question Id : 60348913014 Question Type : MCQ Option Shuffling : No Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

All of the exons within a genome is called

1. Transcriptome
2. Exome
3. Coding fragments
4. All of these

**Options :**

60348949351. 1

60348949352. 2

60348949353. 3

60348949354. 4

**Question Number : 50 Question Id : 60348913015 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Small cDNA sequence that represents a unique segment of an active gene is called

1. SNPs
2. SnRNAs
3. ESTs
4. Contigs

**Options :**

60348949355. 1

60348949356. 2

60348949357. 3

60348949358. 4

**Question Number : 51 Question Id : 60348913016 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

In isoelectric focusing, proteins are separated on the basis of their

1. Relative content of positively charged residue only
2. Relative content of negatively charged residue only
3. Size
4. Relative content of positively and negatively charged residue

**Options :**

60348949359. 1

60348949360. 2

60348949361. 3

60348949362. 4

**Question Number : 52 Question Id : 60348913017 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which is the single international database for the processing and distribution of 3D biological macromolecular structure data ?

1. SWISS PROT
2. CATH
3. DALI
4. PDB

**Options :**

60348949363. 1

60348949364. 2

60348949365. 3

60348949366. 4

**Question Number : 53 Question Id : 60348913018 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is not a gene expression database?

1. Genbank
2. Flyview
3. SeedGenes
4. Body Map

**Options :**

60348949367. 1

60348949368. 2

60348949369. 3

60348949370. 4

**Question Number : 54 Question Id : 60348913019 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is false in case of the database Pfam and its algorithm?

1. Each motif or domain is represented by an HMM profile generated from the seed alignment of a number of conserved homologous proteins
2. Since the probability scoring mechanism is more complex in HMM than in a profile-based approach the use of HMM yields further increases in sensitivity of the database matches
3. Pfam-B only contains sequence families not covered in Pfam
4. The functional annotation of motifs in Pfam-A is often related to that in UNIPROT

**Options :**

60348949371. 1

60348949372. 2

60348949373. 3

60348949374. 4

**Question Number : 55 Question Id : 60348913020 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The PRINTS database consists of protein finger prints that define families in the \_\_\_\_\_ databases

1. SwissProt/TrEMBL
2. SwissProt/EMBL
3. PIR/TrEMBL
4. PIR/EMBL

**Options :**

60348949375. 1

60348949376. 2

60348949377. 3

60348949378. 4

**Question Number : 56 Question Id : 60348913021 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Each DNA or protein sequence database entry has much information, including

1. an assigned accession number(s)
2. source organism
3. name of locus
4. reference number type (s)

**Options :**

60348949379. 1

60348949380. 2

60348949381. 3

60348949382. 4

**Question Number : 57 Question Id : 60348913022 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

According to standard amino acid code letters which of the given pair is not right?

1. K- lysine
2. Y- tyrosine
3. Q- glutamine
4. R- serine

**Options :**

60348949383. 1

60348949384. 2

60348949385. 3

60348949386. 4

**Question Number : 58 Question Id : 60348913023 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following defines best a sequence logo?

1. Representation of nucleotides in different colours
2. The logo used for sequence consortiums
3. A graphical representation of consensus sequence
4. Conserved region in protein sequence

**Options :**

60348949387. 1

60348949388. 2

60348949389. 3

60348949390. 4

**Question Number : 59 Question Id : 60348913024 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following takes the advantage of the profile searching techniques?

1. BLSTN
2. BLASTP
3. PSI-BLAST
4. BLASTX

**Options :**

60348949391. 1

60348949392. 2

60348949393. 3

60348949394. 4

**Question Number : 60 Question Id : 60348913025 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following does not describe BLOSUM matrices?

1. It stands for BLOcks SUBstitution Matrix
2. It was developed by Henikoff and Henikoff
3. The year it was developed was 1992
4. These matrices are logarithmic identity values

**Options :**

60348949395. 1

60348949396. 2

60348949397. 3

60348949398. 4

**Question Number : 61 Question Id : 60348913026 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is NOT CORRECT regarding BLAST and FASTA?

1. FASTA is faster than BLAST
2. FASTA is the most accurate
3. BLAST has limited choices of databases
4. FASTA is more sensitive for DNA-DNA comparisons

**Options :**

60348949399. 1

60348949400. 2

60348949401. 3

60348949402. 4

**Question Number : 62 Question Id : 60348913027 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The procedure of aligning many sequences simultaneously is called

1. Multiple Sequence Alignmnet
2. Pair wise alignment
3. Global Alignment
4. Local Alignment

**Options :**

60348949403. 1

60348949404. 2

60348949405. 3

60348949406. 4

**Question Number : 63 Question Id : 60348913028 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**



ClustalW is a more recent version of Clustal with W standing for

1. Weakening
2. Winding
3. Weighting
4. Wiping

**Options :**

60348949407. 1

60348949408. 2

60348949409. 3

60348949410. 4

**Question Number : 64 Question Id : 60348913029 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following statement is correct regarding E value ?

1. The lower the E-value, the less likely the database match is a result of random chance and therefore the more significant the match is
2. The E-value provides information about the likelihood that a given sequence match is not based on chance
3. If E is between 0.01 and 10, the match is considered significant and a high homology
4. The E value is independent of size of database

**Options :**

60348949411. 1

60348949412. 2

60348949413. 3

60348949414. 4

**Question Number : 65 Question Id : 60348913030 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The 3D structure of a protein can NOT be determined using which of the following methods

1. Electron microscopy
2. Nuclear Magnetic Resonance spectroscopy
3. Light microscopy
4. X-ray crystallography

**Options :**

60348949415. 1

60348949416. 2

60348949417. 3

60348949418. 4

**Question Number : 66 Question Id : 60348913031 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Peptide bond is formed as a result of a/an \_\_\_\_\_ reaction between two amino acids

1. Dehydration
2. Hydrolysis
3. Oxidation
4. Reduction

**Options :**

60348949419. 1

60348949420. 2

60348949421. 3

60348949422. 4

**Question Number : 67 Question Id : 60348913032 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Who maintains PDB?

1. NCBI
2. RCSB
3. PIR
4. Swiss-PROT

**Options :**

60348949423. 1

60348949424. 2

60348949425. 3

60348949426. 4

**Question Number : 68 Question Id : 60348913033 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

PHYML is a web-based \_\_\_\_\_ program using the \_\_\_\_\_

1. Phylogenetic, GA (Genetic Algorithm)
2. Sequence based alignment, GA (Genetic Algorithm)
3. Phylogenetic, dynamic programming
4. Sequence based alignment, dynamic programming

**Options :**

60348949427. 1

60348949428. 2

60348949429. 3

60348949430. 4

**Question Number : 69 Question Id : 60348913034 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

MEGA stands for

1. Multiple Evolutionary Genetics Analysis
2. Molecular Evolutionary Genomic Analysis
3. Molecular Evolutionary Genetics Analysis
4. Multiple Evolutionary Genomic Analysis

**Options :**

60348949431. 1

60348949432. 2

60348949433. 3

60348949434. 4

**Question Number : 70 Question Id : 60348913035 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is incorrect regarding the terminologies of phylogenetics?

1. The branching pattern in a tree is called tree topology
2. When all branches bifurcate on a phylogenetic tree, it is referred to as dichotomy
3. In case of dichotomy, each ancestor divides and gives rise to multiple descendants
4. An unrooted phylogenetic tree does not assume knowledge of a common ancestor

**Options :**

60348949435. 1

60348949436. 2

60348949437. 3

60348949438. 4

**Question Number : 71 Question Id : 60348913036 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is false regarding PAUP?

1. It is a Macintosh program with a very user-friendly graphical interface
2. To complete an analysis the user is not required to move between different subprograms while keeping modifying names of the intermediate output files
3. PAUP can perform parsimony programs only
4. It is expanded as Phylogenetic Analysis Using Parsimony

**Options :**

60348949439. 1

60348949440. 2

60348949441. 3

60348949442. 4

**Question Number : 72 Question Id : 60348913037 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is incorrect regarding the side chain refinement in homology modeling?

1. Once main chain atoms are built, the positions of the side chains that are not modelled must be determined
2. The easy way to achieve this is by searching every possible conformations at every torsion angle of the side chain to select the one that has the lowest interaction energy with neighbouring atoms
3. Side chain prediction programs uses the concept of rotamers, which are favoured side chain torsion angles extracted from known protein crystal structures
4. Modelling side chain geometry is very important in evaluating protein-ligand interactions at active sites

**Options :**

60348949443. 1

60348949444. 2

60348949445. 3

60348949446. 4

**Question Number : 73 Question Id : 60348913038 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

CATH is an example of

1. Homology modelling tool
2. Protein visualization tool
3. Protein structure classification tool
4. All of these

**Options :**

60348949447. 1

60348949448. 2

60348949449. 3

60348949450. 4

**Question Number : 74 Question Id : 60348913039 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following are protein structure visualization tools?

1. Rasmol and Molscript
2. Rasmol and DALI
3. DALI and VAST
4. VAST and SCOP

**Options :**

60348949451. 1

60348949452. 2

60348949453. 3

60348949454. 4

**Question Number : 75 Question Id : 60348913040 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following is incorrect about Multiple Structure Alignment?

1. The alignment strategy is different than the Clustal sequence alignment using a progressive approach
2. All structures are first compared in a pairwise fashion
3. A distance matrix is developed based on structure similarity scores such as RMSD
4. The aligned structures create a median structure that allows other structures to be progressively added for comparison based on the hierarchy described in the guide tree

**Options :**

60348949455. 1

60348949456. 2

60348949457. 3

60348949458. 4

**Question Number : 76 Question Id : 60348913041 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

What is meant by docking?

1. The process by which two different structures are compared by molecular modelling
2. The process by which a lead compound is simplified by removing excess functional groups
3. The process by which drugs are fitted into their target binding sites using molecular modelling
4. The process by which a pharmacophore is identified

**Options :**

60348949459. 1

60348949460. 2

60348949461. 3

60348949462. 4

**Question Number : 77 Question Id : 60348913042 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which one of the following is a genetic algorithm for docking flexible ligands into protein binding sites?

1. FlexX
2. GOLD
3. Flex and GOLD
4. None of these

**Options :**

60348949463. 1

60348949464. 2

60348949465. 3

60348949466. 4

**Question Number : 78 Question Id : 60348913043 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The identification of drugs through the genomic study is called

1. Genomics
2. Pharmacogenomics
3. Pharmacogenetics
4. Cheminformatics

**Options :**

60348949467. 1

60348949468. 2

60348949469. 3

60348949470. 4

**Question Number : 79 Question Id : 60348913044 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**



A pose is a ?

1. spatial arrangement of particular atom
2. orientation of a particular conformation of a ligand
3. binding mode with some interesting characteristics
4. all of these

**Options :**

60348949471. 1

60348949472. 2

60348949473. 3

60348949474. 4

**Question Number : 80 Question Id : 60348913045 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

If you have a unknown structure of target and known ligand, what approach you will follow to perform a drug design?

1. Structure based drug design
2. Ligand based drug design
3. Structure based and ligand based drug design
4. None of these

**Options :**

60348949475. 1

60348949476. 2

60348949477. 3

60348949478. 4

**Question Number : 81 Question Id : 60348913046 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The important approaches for pharmacophore generation include

1. structure based and ligand based
2. structure based and interaction based
3. ligand based and polarity based
4. All of these

**Options :**

60348949479. 1

60348949480. 2

60348949481. 3

60348949482. 4

**Question Number : 82 Question Id : 60348913047 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

How many sequencing reactions are performed in a manual Sanger sequencing?

1. Five
2. Three
3. Two
4. Four

**Options :**

60348949483. 1

60348949484. 2

60348949485. 3

60348949486. 4

**Question Number : 83 Question Id : 60348913048 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The DNA sequence obtained by both the manual and automatic sequencing corresponds to the

1. Template DNA strand
2. Complementary DNA strand
3. Messenger RNA
4. tRNA

**Options :**

60348949487. 1

60348949488. 2

60348949489. 3

60348949490. 4

**Question Number : 84 Question Id : 60348913049 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The basic methodological steps of NGS include:

1. Template preparation, emulsion PCR, sequencing, data analysis
2. Template preparation, sequencing and imaging, data analysis
3. Template amplification, sequencing and imaging, data analysis
4. Template preparation, sequencing and imaging, alignment to a reference genome

**Options :**

60348949491. 1

60348949492. 2

60348949493. 3

60348949494. 4

**Question Number : 85 Question Id : 60348913050 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

When did the HGP begin?

1. 1988
2. 1989
3. 1990
4. 1991

**Options :**

60348949495. 1

60348949496. 2

60348949497. 3

60348949498. 4

**Question Number : 86 Question Id : 60348913051 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which is the sequencing method used for HGP?

1. Sanger
2. Shotgun
3. Pyrosequencing
4. Solexa

**Options :**

60348949499. 1

60348949500. 2

60348949501. 3

60348949502. 4

**Question Number : 87 Question Id : 60348913052 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Choose a nano peptide out of the following

1. Oxytocin
2. Vasopressin
3. Bradykinin
4. All of these

**Options :**

60348949503. 1

60348949504. 2

60348949505. 3

60348949506. 4

**Question Number : 88 Question Id : 60348913053 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which out of the following is a peptide antibiotic?

1. Erythromycin
2. Gramicidin
3. Ciprofloxacin
4. Tetracycline

**Options :**

60348949507. 1

60348949508. 2

60348949509. 3

60348949510. 4

**Question Number : 89 Question Id : 60348913054 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The secondary structure is primarily maintained by

1. Van der waals force
2. Hydrogen bond
3. Ionic bond
4. Hydrophobic bond

**Options :**

60348949511. 1

60348949512. 2

60348949513. 3

60348949514. 4

**Question Number : 90 Question Id : 60348913055 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which of the following amino acid is a alpha helix terminator?

1. Cysteine
2. Alanine
3. Proline
4. Isoleucine

**Options :**

60348949515. 1

60348949516. 2

60348949517. 3

60348949518. 4

**Question Number : 91 Question Id : 60348913056 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

In scurvy, which amino acid that is normally part of collagen is not synthesized?

1. Hydroxy Tryptophan
2. Hydroxy Tyrosine
3. Hydroxy Alanine
4. HydroxyProline

**Options :**

60348949519. 1

60348949520. 2

60348949521. 3

60348949522. 4

**Question Number : 92 Question Id : 60348913057 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Which out of the following is not a haemoprotein?

1. Catalase
2. Myeloperoxidase
3. Glutathione peroxidase
4. Aconitase

**Options :**

60348949523. 1

60348949524. 2

60348949525. 3

60348949526. 4

**Question Number : 93 Question Id : 60348913058 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

The 3D structure of protein can be determined by

1. X ray crystallography
2. NMR
3. X ray crystallography and NMR
4. Spectrophotometry

**Options :**

60348949527. 1

60348949528. 2

60348949529. 3

60348949530. 4

**Question Number : 94 Question Id : 60348913059 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

One of the parameters for calculating binding energy is

1. Centrifugation
2. Immunoprecipitation
3. Hydrogen bonding
4. Membrane filtering

**Options :**

60348949531. 1

60348949532. 2

60348949533. 3

60348949534. 4

**Question Number : 95 Question Id : 60348913060 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**



TBST is

1. A mixture of phosphate buffer and Tween 20
2. A mixture of Tris-Buffered Saline and Tween 20
3. A mixture of Tris-Buffered Saline and Trinitro toluene
4. A mixture of DMSO and Tris-Buffered Saline

**Options :**

60348949535. 1

60348949536. 2

60348949537. 3

60348949538. 4

**Question Number : 96 Question Id : 60348913061 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

ORF finder identifies all ..... using the standard or alternative genetic codes?

1. RNA
2. Intron
3. Exon
4. ORF

**Options :**

60348949539. 1

60348949540. 2

60348949541. 3

60348949542. 4

**Question Number : 97 Question Id : 60348913062 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

A typical protein-coding gene in humans might be divided into a dozen ....., each less than two hundred base pairs in length

1. RNA
2. Chromosome
3. Intron
4. Exon

**Options :**

60348949543. 1

60348949544. 2

60348949545. 3

60348949546. 4

**Question Number : 98 Question Id : 60348913063 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

Gene discovery in eukaryotic organisms is more difficult than in prokaryotic genomes, due to their\_\_\_\_\_

1. Low gene density
2. High gene density
3. Complexity of genes
4. All of these

**Options :**

60348949547. 1

60348949548. 2

60348949549. 3

60348949550. 4

**Question Number : 99 Question Id : 60348913064 Question Type : MCQ Option Shuffling : No**

**Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

A major challenge in computational gene prediction is therefore to design \_\_\_\_\_ that are able to deal with different types of information from heterogeneous sources?

1. Simple sequence repeats
2. Good statistical models
3. Expression of genes
4. Quantity of genes

**Options :**

60348949551. 1

60348949552. 2

60348949553. 3

60348949554. 4

**Question Number : 100 Question Id : 60348913065 Question Type : MCQ Option Shuffling : No  
Is Question Mandatory : No**

**Correct Marks : 1 Wrong Marks : 0**

A high degree of similarity to a known \_\_\_\_\_ or protein product is strong evidence that a region of a target genome is a protein-coding gene

1. hnRNA
2. tRNA
3. rRNA
4. mRNA

**Options :**

60348949555. 1

60348949556. 2

60348949557. 3

60348949558. 4