

CURRENT SOLVED MCQ (BIF 401)

FOR MID TERM PREPARATION

- 1: Gaps are produced by insertion or deletion.
- 2: Example of energy base Zuker algorithm.
- 3: Two forms of DNA rending sequence.
- 4: Translation involves coding of protein by RNA at ribosome.
- 5: some medicine have side effect on certain patient Frontiers in personalized medicine.
- 6: By comparing sequence we can get similarity, specific difference, relationship, evolutionary insight.
- 7: Non clustering method include Maximum parsimony.
- 8: Destabilizing energy of a nucleotide has (+) value.
- 9: Comparison of protein sequence can be done with... Uniprot
- 10: Function is a property of the RNA structure, which is formed from the RNA sequences.
- 11: Structural information of a molecule obtained by X ray crystallography & Nuclear magnetic resonance.
- 12: Protein have 20 amino acid.
- 13: If sequence are 9 then according formula it will be 9^2 .
- 14: Fast is available online.
- 15: Fasta was developed in 1988.
- 16: Bioinformatics is the interdisciplinary relative new developing field.
- 17: Genbank can be reached by...online website or www.ncbi.nlm.nih.gov/genbank.
- 18: Before starting to match nucleotide or amino acid are need to find the Location of conserved residues.
- 19: some medicine have side effect on certain patient Frontiers in personalized medicine.
- 20: Identity is the number of nucleotide or amino acid which match exactly between two biological sequence.
- 21: Alignment are represented by diagonals in dot matrix.
- 22: Needleman Wunsch algorithm we use for..... Global alignment.

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- 23: **Exons** in protein tend to be more conserved than the **intron**.
- 24: In MSA the distance between 2 sequences is equal to **NO of identical residue/number of aligned residue**.
- 25: All the changes which accrued in our cell **metabolism**
- 26: The loop of the hairpin must be least **4 bases** long
- 28: NJ algorithm is used to produce **Optimal RNA 2' structure**.
- 29: **energy base** algorithm type is Zuker algorithm.
- 30: Types of RNA...present in organism. **(5)**
- 31: The online search is for DNA and RNA is..... **genebank**
- 32: **Rooted** tree is computationally expensive.
- 33: In multiple sequence algorithm **doing so many progressive alignment can be slow**.
- 34: **DNA** dictates the production of cell protein and carbohydrate
- 35: protein have long sequences ...in no?
- 36: **In Exact** partial matching of residue and order with room for variation in both.
- 37: DNA/RNA sequence is available on.... **GENE BANK**
- 38: Martine algorithm predict for structure **2 RNA**.
- 39: In extraction of ORF, 1st step is obtaining the 3 **codons**.
- 40: Example of energy based algorithm **Zukar algorithm**.
- 41: Dynamic programming help us to..... **reduce computational cost**.
- 43: When unpaired bases in 2 region binds is result form **Bulldges**.
- 44: which one of following is not objective based method of phylogenic ... **UPGMA**
- 45: protein sequencing can be done by **Swiss prot & UniProt**.
- 46: Drugs can be better developed after understanding molecular basis of **Disease**
- 47: Online tools are available for **homology modeling**.
- 48: Insertion and deletion in alignment cause..... **gaps**.
- 49: Alligment of insertion and deletion can be performed by **dynamic programming**

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- 50: Exons in proteins tend to be more conserved than **intron.**
- 51: Blast confined sequences from—— **ID,name,spcies**
- 52: ribosomes read RNA and collect amino acid from..... **cell cytosol.**
- 53: **Simulation** can predict diseases progression & outcomes.
- 54: For exact matchingrequired. **Traceback**
- 55: traceback is start from **high score** on couple nucleotide.
- 56: Motif protein chain fold to take **3D structure.**
- 57: Next generation sequencing is used to known about unknown sequences of **nucleotide.**
- 58: RNA fold to form **2 structure.**
- 59: **MFOLD** implement are ungraded version of Zuker.
- 60: Which has less computational cost **Dynamic programming**
- 61: In scoring matrices, we score **with maximum 4 matrix.**
- 62: We compare all length of nucleotides in **Global alignment.**
- 63: we compare smaller fragment **Local** alignments.
- 64: Destabilized RNA molecule have **(+)value.**
- 65: In Zukar algorithm, we need construct **all possible combination.**
- 66: We use **Zukar algorithm** to sum up energy to find lowest matrix.
- 67: Swiss **prot.is** a box in uniprot.
- 68: In comparing RNA structure, we used to select which having **lowest energy.**
- 69: Addition of nucleotide is done by **hydrogen bondi**
- 71: Adman degradationis used for **protein sequencing.**
- 72: Why do we create all possible combination of diagonals in zukar algorithm with overall **lowest energy** is selected.
- 73: We can do repeated sequences alignment by slight modification in **waterman model.**
- 74: Length of hairpin loop is **4 bases.**
- 75: "T" Threonine is an basic element....**true**
- 76: To align sequence what will be necessary firstly..... **to find conserved region.**

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- 77: Sequence of biomolecules can be known by using uniprot or gene bank.
- 78: Defination of Expasy: Expasy provide access to variety of online database and tools.
- 79: Structural information of a molecule can be obtained by X.ray crystallography , nuclear magnetic sequence.
- 80: Compare a protein query sequence against a nucleotide sequence database.....tBlastn
- 81: Protein formation of abnormal folding called Pseudoknots.
- 82: By using uniprot we can find sequence of.....(protein)
- 83: The 5' end of molecule caped with 7 Methyl Guanosine Triphosphate.
- 84: DNA provide blue print for building.
- 85: DNA get modified by mutation, substitution, insertion, deletion.
- 86: UPGMA is used to calculate the distance of each cluster.
- 87: Global alignment used to determin overall conversation.
- 88: if the sequence is multiple there can be several possible alignment.
- 89: can we identify the post translational modifications by Expacy.
- 90: scoring scheme has an extremely crucial role in producing optical alignment.
- 91: why is there need to predict RNA structures to know about its function
- 92: DP recombines the nucleotide recombination through a process of Traceback.
- 93: .how many open reading frame exist for each DNA sequence.6ORFs
- 94: tblastn search translated nucleotide using...Protein query
- 95: Blast can find sequencing from protein or nucleotide database it can find known and unknown sequencing.
- 96: name any two frequently used scoring matrix Blosum and pam.
- 97: From Fasta we can obtain the information on the parent organism, function and evolution history.
- 98: The correct order of progressive alignment for multiple sequencing alignment is Pair wise alignment, Guide tree, branching order in tree.
- 99: CLUSTALW can run in two modes slow/accurate, fast/appropriate.
- 100: Gene bank and UniProt have Large number of sequencing publically.
- 101: In multiple sequencing, we have Global alignment.

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102: Ubiquitin play important role recycling protein.

103: 6 form of DNA ending sequencing.

104: Non-clustering method such as maximum parsimony may be used for making trees.

105: If in Needleman and Smith watermark algorithm along '0' place is in.....relationship. 1st row and 1st column.

107: Faster active alignment by using local alignment and protein nucleotide. pairwise alignment

109: Expasy was develop by Swiss Bioinformatics Institute (SIB)

110: .In phylogenetics tree , ancestor are placed at Root/bottom/ancestor node trees.

111: .In UPQMA two sequence are N_x & N_y .

112: .When unpaired bases in 2 region binds itself form Buldges.

113: Zukers algorithm is use to predict computational and destabilizing energy?

114: In Nussinov Jacob algorithm which turn is added to compare to score for diagonal position set diagonal and lower tri diagonal to zero.

115: Trackback begins from the position in Nussinov Jacobson score matrix. 4th position

VU Medical Zone effort by Amaan Khan