

BIF501 Current Grand Quiz Solved By Muhammad Zahid

1) The resolution genome map is the genomic DNA sequence that can be;

Ans: highest, physical

2) One centimorgan is defined as ----- percentage of the total recombination events.

Ans: 1

3) There are ----- domains of life.

Ans: Three

4) Who maintain the gene bank, a nucleotide sequence database-----?

Ans: National Centre for Biotechnology Information (NCBI)

5) How does RNA differ from DNA?

Ans: RNA contain uracil instead of thymine and it is usually single-stranded

6) Which of the following is considered as a start codon?

Ans: AUG

7) Which of the following statement about tandem repetitive DNA are correct?

Ans: Tandem means two repeats next to each other

8) The first published genome was -----.

Ans: *Hemophilus influenza*

9) Consensus score is defined as -----

Ans: Score (s, DNA)

10) Pre-order algorithm is a

Ans: Recursive

11) PAM matrices are based on ----- of protein evolution.

Ans: DayHoff model

12) Which of the following are the properties of dynamic programming problem?

Ans: optimal structure

13) Informatics in health care is known as -----

Ans: health informatics

14) There are ----- possible stop codon, identification of which is straightforward.

Ans: Three

15) The retrieval and search tool of the NCBI is -----.

Ans: Entrez

16) Each record in database is called -----

Ans: File

17) Exonic region contain only ----- of total DNA.

Ans: 2%

18) Which RNA molecule is used to carry genetic information copied from DNA

Ans: mRNA

19) Gel electrophoresis may be used to measure ----- of restriction fragments.

Ans: size

20) Which alignment is useful to detect the highly similar sequences.

Ans: pairwise alignment

21) Nucleic acid contain -----

Ans: Adenine

22) Analyzing or comparing entire genome of species is -----

Ans: Genomics

23) In dynamic programming, the technique of storing the previously calculated values is called-----.

Ans: Memorization

24) How many chromosomes do human have?

Ans: 46

25) You do a BLAST search on a DNA sequence and it identifies it as exon 1 of certain gene. An exon is ---

Ans: A section of eukaryotic gene that is not translated into protein

26) RNAase is a single polypeptide chain of ----- amino acid residues.

Ans: 124

27) Variation between individuals due to single base changes is called-----

Ans: SNPs

28) Bypass is a type of ----- algorithm.

Ans: Branch and bound

29) SWISS PORT is related to -----

Ans: Protein sequence data bank

30) If the query proteome is not available in protein database, then ----- database may be searched.

Ans: EST

31) Three letter code Leu of protein represents -----

Ans: Leucine

32) Production of RNA from DNA is called -----

Ans: Transcription

33) Gene in two organisms that are so similar that they have the same function and evolutionary history are called -----

Ans: Orthology

34) RNA is the genetic material in -----

Ans: In some viruses, prokaryotes and rarely in eukaryotes also

35) Minisatellite is ----- bases long in array of several hundred to thousands kb.

Ans: 15

36) Determining the location of and relative distances between genes on a chromosome is known as -----

Ans: Gene mapping

37) The synthesis of polynucleotide chain of mRNA is catalyzed by the enzyme.

Ans: RNA polymerase

38) Which one is not protein data file?

Ans: PDB (Not Sure)

39) SINES stands for -----

Ans: Short interspersed nuclear elements

40) Gene expression omnibus (GEO) data base has ----- kind of records.

Ans: Four

41) How many reading frames must be considered for a given double-stranded DNA sequence.

Ans: Six

42) Peptide linkage are formed in between -----

Ans: Amino acids

43) Which species have more similar proteome with mammalian proteomes?

Ans: Drosophilla

44) The process of finding relative location of gene on a chromosome is called -----

Ans: Genome mapping

45) What is the full form of BLOSUM?

Ans: BLOcks SUBstitution Matrix

46) Satellite DNA is a tandem array of ----- million bases long.

Ans: 100

47) Protein databases are classified on the bases of -----

Ans: protein structure, sequence and domain

48) If RNA polymerase transcribe DNA with the coding strand (non-template) sequence 5 – GGGCATGCA – 3, what would be the resulting RNA sequence (28)

Ans: 5 – GGGCUAGCA - 3

49) Transcription is the transfer of genetic information from

Ans: DNA to mRNA

50) Protein is extracted from -----

Ans: rRNA

51) The procedure of aligning two sequence by searching for pattern that is in the same order in the -----

Ans: Pairwise alignment

52) RNA is synthesized in

Ans: Nucleus

53) BLAST X program is used for -----

Ans: Translate DNA database

54) Comparison between two genomes is called;

Ans: Comparative genomic

55) Which of the following is untrue about DNA sequencing?

Ans: This does not make use of DNA polymerase

56) How are so many different antibodies from fewer than 300 major genes.

Ans: recombination, deletion and random assortment of DNA segment

57) As the complexity of an organism increases, all the following characteristics merge except -----

Ans: An increase in the number of chromosomes

58) Which is the source of energy for amino acid activation?

Ans: GTP

59) Transpose can move by ----- mechanism(s)

Ans: 2 (by cut and paste)

60) RNA → DNA → RNA → protein is process occurs in;

Ans: Retroviruses

61) Motifs facilitates for binding -----

Ans: Transcription sites

62) Stepwise method for solving problems in computer science is called -----

Ans: algorithm

63) In RNA uracil pairs with -----

Ans: Adenine

64) Which one is an basic step?

Ans: Replication Or Transcription

65) Gene families originating from rare gene duplication events over the evolutionary time are called;

Ans: Paralogs

66) Study of all the person's genes, including interaction of those genes with each other and with person's environment is known as -----

Ans: Genomics

67) Median string problem is one of the ways to find -----

Ans: Motif

68) Name the site where upstream sequence located.

Ans: Prior to start point

69) Database of E. coli is -----

Ans: Ecogene

70) In eukaryotic gene the introns end towards ----

Ans: 5 end as AG

71) An example of homology and similarity tool is -----

Ans: BLAST

72) Long ORF may be gene expected ----- codons before we see a stop codon.

Ans: 64/3 - 21

73) Genomic is referring to the study of genome, where genome refers to the -----

Ans: Entering genes of an organism

74) How many reading frames are applicable in case of translation?

Ans: Three

75) How many steps are involved in genome annotation?

Ans: Three

76) The genetic material of retroviruses such as HIV is -----

Ans: RNA

77) Systick fibrosis gene is found on chromosome number -----

Ans: 7

78) You see your lab partner is starting at a colorful swissport page. He/she is probably trying to -----

Ans: Find out structural and functional information about a protein he/she identified

79) Which form of RNA is required for protein synthesis?

Ans: mRNA

80) Next vertex algorithm provides as an output -----

Ans: Next vertex/Efficient

81) Which of the following is not the objective to perform sequence comparison?

Ans: To study the physical properties of molecule

82) Physical maps are maps of location of identifiable landmarks on a genomic DNA ----- inheritance patterns.

Ans: Regardless of

83) Which of the following is database for protein sequencing?

Ans: EMBL

84) ORF scanning is used to find

Ans: Intergenic sequences

85) Which of the following is nucleotide database?

Ans: SWISS PROT

86) Speciation event results in

Ans: paralogs

87) BLOSUM62 is derived from sequence alignment with ----- identity

Ans: Less than and equal to 62%

88) Which of the following is not property of open reading frame?

Ans: Starts and ends at either end of the mRNA

89) Which statement is more likely explanation for the existence of pseudogenes?

Ans: Mutation events

90) Which statement is not true for transposable elements?

Ans: Move (jump) from one location to another slower than chromosome replicate

91) Which file format is representing the protein data file?

Ans: PDB

92) Which one is not a stop codon?

Ans: UAU

93) Simple motif search algorithm is based on -----

Ans: Branch and bound

94) Next vertex algorithm provides as an output -----

Ans: Efficient

95) The size of the transposable element is -----

Ans: < 1 or 2 kb

96) In eukaryotes, translation is initiated by binding of ribosomes to the -----.

Ans: Poly_A tail

97) We get the best and more occurring residual sequence called;

Ans: Consensus sequence

98) Chimera is used for

Ans: Visualization and editing

99) which of the following is the most frequently use sequence format to present DNA and protein sequence?

Ans: FASTA

100) The direct repeat within the transpose/insertion element has a length of -----

Ans: 1-7bp

101) Waardenburg's syndrome is a genetic disorder in

Ans: Human

102) BLOSUM52 is equal to -----

Ans: PAM 200

103) The DNA chain acting as template for RNA synthesis has the following order of bases, AGCTTCGA.
What will be the order of bases in mRNA?

Ans: UCGAAGCU

104) ----- is integrated search engine which allows users to search and retrieve different data from the NCBI

Ans: Entrez

105) Multiple sequence alignment method is called as ----- alignment method.

Ans: Progressive

106) The role of mRNA in protein synthesis

Ans: It translates genetic code to a specific amino acid

107) The human genome is -----

Ans: All of the DNA and RNA in our cells

108) Which of the following statement is not true for substitution matrices?

Ans: they use system where substitution that are more likely should get a lower score

109) Which of the following terms refers to the relative gene order and orientation of gene on chromosomes between related species?

Ans: Synteny

110) Which of the given statement is incorrect?

Ans: The number of protein sequence that are available insufficient to determine that domain shuffling occurs in evolution

111) Any segment of DNA, able to transpose is known as

Ans: Substitution sequence, insertion sequence, regulatory sequence, promotor sequence

112) Which is the energy rich molecule required for initiation of translation

Ans: GTP

113) DNA sequencing followed by genome annotation are steps of -----

Ans: Structural genomics

114) Which one is the input sequence format in BLAST?

Ans: PIR

115) The amino acid are assemble into polypeptide chain on -----

Ans: Ribosomes

116) During translation, protein is synthesized by

Ans: Ribosomes using the information on mRNA

117) Drosophila proteome is more likely ----- proteome

Ans: Mammalian

118) Which form of structure has been adopted by RNA

Ans: A-form

119) Restriction enzyme break DNA molecule at

Ans: Specific location

120) Genome rearrangement results in change of gene

Ans: Order

121) Motifs are found in

Ans: protein

122) Regulatory motif are generally found in

Ans: promotor region of DNA

123) Exception to the central dogma comes after the discovery of

Ans: Retroviruses

124) Proteomics is the study of

Ans: Entire set of expressed proteins in a cell

125) Literature database are

Ans: PubMed and MEDLINE

126) Drosophila has the core proteome -----the size of that yeast.

Ans: twice