$1 \times 60 = 60$ 



## **BRAINWARE UNIVERSITY**

## Term End Examination 2021 - 22 Programme – Master of Science in Biotechnology Course Name – Genomics & Proteomics Course Code - MBT205 (Semester II)

Time allotted: 1 Hrs.15 Min. Full Marks: 60

[The figure in the margin indicates full marks.]

Group-A (Multiple Choice Type Question) Choose the correct alternative from the following: (1) Genome refers a) Total gene pool of an organism b) Total mRNA of an organism c) Only DNA of a diploid cell d) Only proteins (2) Name the phenomenon which shows the lack of correlation in genome size and genetic complexity. a) Histogram b) Karyogram d) C-value paradox c) Dendrogram (3) The most important tools of genomics are a) Microarray and informatics b) Microarray and BLAST c) BLAST and FASTA d) FASTA and PCR (4) A character or trait is the direct function of a) Gene b) RNA c) Protein d) rRNA (5) Most of the eukaryotic nuclear genome has a) Repetitive DNA b) Unique DNA c) GC island d) Single copy (6) What is the genome size of yeast? a) 12 kb b) 120 kb c) 330 kb d) 1000 kb (7) Human has a genome. b) About 500 kb a) About 100 kb

d) About 3000 kb

b) DNA found at centromere

c) About 1000 kb

(8) What is alphoid DNA? a) Large size DNA

c) Unique DNA sequence	d) Repetitive DNA
(9) Exons are	
a) Non coding regions of genome	b) Coding regions of genome
c) Repetitive regions of genome	d) All of these
(10) Human genome contains about	
a) 10-20k genes	b) 30-40k genes
c) 50-80k genes	d) More than 100k genes
(11) The largest genome is belonging from which	
a) E. coli	b) Homo sapiens
c) T4	d) Carsonella ruddii
(12) DNA sequence is the linear order of	
a) Nucleotides	b) Neucleosides
c) Amino acids	d) Glucose moieties
(13) Maxam-Gilbert used which of the following of	,
a) ddNTP	b) dNTP
c) Base modifiers	d) Base analogues
(14) Chain-termination is a type of	,
a) Sequencing	b) Vector generation
c) Antibiotic production	d) Gene manipulation
(15) Which type of DNA cleavage is done in the M	· -
a) Edge	b) Interstitial
c) Base-specific	d) Gene-specific
(16) The Klenow fragment is basically a	, 1
a) DNA polymerase	b) RNA polymerase
c) Gyrase	d) Nuclease
(17) Prior to get electrophoresed in sequencing get	
a) Separated	b) Denatured
c) Renatured	d) Degraded
(18) NGS is based on the Principles of	a) Degraded
a) Sanger sequencing	b) Maxam-Gilbert sequencing
c) MALDI-TOF	d) ESI-MS
(19) NGS relies on which of the following techniq	,
a) PFG electrophoresis	b) SDS PAGE
c) Capilary electrophoresis	d) Native PAGE
(20) Which one of the following is not belonging to	,
a) Pyrosequencing	b) Ion torrent semiconductor sequencing
c) Illumina techniques of sequencing	d) Dideoxy method of sequencing
(21) Which of the following techniques is used to	, ,
binding region (known as an adapter) which he (i.e. the sequence that is to be sequenced) on	has been conjugated to the target sequence
a) Emulsion PCR	b) Nested PCR
c) Hot-start PCR	d) All of these
(22) Advanced genome annotation includes the stu	udy of
a) Polymorphic DNA markers	b) Gene model structure
c) Transcripts	d) All of these

(23) which of the given is wrongly matched?	
a) Escherichia coli – Bacteria	b) Methanococcus jannaschii – Archaea
c) Synechocystis sp. – Archaea	d) Aquifex aeolicus – Bacteria
(24) Which of the following is incorrect regarding go	ene ontology?
<ul> <li>a) It exists because there is a need to standardize protein functional descriptions</li> </ul>	b) It uses a limited vocabulary to describe molecular functions
<ul> <li>c) Biological processes are not described though</li> </ul>	<ul> <li>d) The cellular components are described using limited vocabulary</li> </ul>
(25) A minimal constitutes genome, which is a a free living cellular organism.	_ set of genes required for maintaining
a) maximum	b) maximal
c) highest number of set of	d) minimal
(26) If you have a sequence, but you are not sure wh you can align it to the genome with	at the gene name or ID in Ensembl is,
a) BLAST	b) BLAT
c) Both of these	d) None of these
(27) BLAST will allow	
a) Lower scoring hits	b) Higher scoring hits
c) Basic scoring hits	d) Only peptide hits
(28) Ensembl is a	
a) Genome browser	b) Protein browser
c) Both of these	d) None of these
(29) Pyrosequencing is based on which of the follow	ving principles?
a) Sanger sequencing	b) Maxam-Gilbert sequencing
c) Ion torrent sequencing	d) Sequencing by synthesis
(30) Which of the following is used for DNA fragme	ents' cluster generation on a microchip?
a) Emulsion PCR	b) Bridge PCR
c) Both of these	d) None of these
(31) Pyrosequencing was developed for the first time	
a) Celera Genomics	b) 454 Life sciences
c) Roche	d) Sanger
(32) The polymer of amino acids are known as	, 3
a) DNA	b) RNA
c) Protein	d) Lipid
(33) If you want to submit a new protein sequence, we platform?	, <del>-</del>
a) NCBI	b) SWISSPROT
c) EMBL	d) DDBJ
(34) How frequent the Ensembl site is updated?	
a) In every one month	b) In every two months
c) In every three months	d) Needs no update
(35) How many configurations of an amino acid are	possible?
a) 1	b) 2
c) 3	d) 4
(36) What do you mean by primary structure of a pro-	,
	b) Its simple linear arrangement of amino acids

	linked with peptide bonds
c) Its an alpha helix	d) Its a beta pleated sheet
(37) Long repeat sequences are difficult to detect wit	h which of the following techniques?
a) Ion torrent sequencing	b) Pyrosequencing
c) SoliD sequencing	d) None of these
(38) Trypsin gold is the most widely used enzyme in bonds after which amino acid(s)?	MS analysis. It digest the peptide
a) R	b) K
c) Both of these	d) None of these
(39) Glutathione is a tripeptide of	
a) ECG	b) DCG
c) ACG	d) BCG
(40) Which of the following is an example of Homol	ogy and similarity tool?
a) BLAST	b) RasMol
c) EMBOSS	d) PROSPECT
(41) Which of the following scientists created the first	st Bioinformatics database?
a) Dayhoff	b) Pearson
c) Richard Durbin	d) Michael.J.Dunn
(42) The first molecular biology server expasy was in	n the year
a) 1992	b) 1993
c) 1994	d) 1995
(43) The identification of drugs through the genomic	study is called .
a) Genomics	b) Pharmacogenomics
c) Pharmacogenetics	d) Cheminformatics
(44) Proteomics refers to the study of	
a) Set of proteins in a specific region of the cell	b) Biomolecules
c) Set of proteins	d) The entire set of expressed proteins in the cell
(45) The computational methodology that tries to fine molecules, a receptor and ligand are called	d the best matching between two
a) Molecular fitting	b) Molecular matching
c) Molecular docking	d) Molecule affinity checking
(46) The stepwise method for solving problems in co	omputer science is called
a) Flowchart	b) Algorithm
c) Procedure	d) Sequential design
(47)involves isolating DNA from multiple	species within an environmental niche.
a) Metagenomics	b) Genomics
c) Proteomics	d) Metabolomics
(48) Genomics can be used in agriculture to:	
a) Generate new hybrid strains	b) Improve disease resistance
c) Improve yield	d) All of these
(49) Which of the following is an example of model	organism?
a) Mangifera indica	b) Arabidopsis thaliana
c) Cocos nucifera	d) Porteresia coarctata
(50) EcoGene is the database of:	

a) E. coli	b) S. cerevisiae
c) Human genome	d) Rat
(51) Model of alpha helix was proposed by	
a) Watson	b) Linus Pauling
c) Krebs	d) Moorey
(52) Which of the following is responsible for speci	ifying the 3D shape of a protein?
a) The peptide bond	b) The amino acid sequence
c) Interaction with other polypeptides	d) Interaction with molecular chaperons
(53) What is the average molecular weight of an am	nino acid residue in a protein?
a) 110	b) 120
c) 130	d) 140
(54) Which of the following statements is true about	t proteins?
a) Proteins are made up of amino acids.	b) Proteins are essential for the development of skin, teeth and bones.
<ul> <li>c) Protein is the only nutrient that can build, repair and maintain body tissues.</li> </ul>	d) All of these
(55) Which of the following statements is correct ab	bout proteins?
a) Proteins are polymers of glucose	b) Proteins are polymers of amino acids
c) Proteins are polymers of peptide bonds	d) Proteins are polymers of disulfide bridges
(56) Which of the following statements is true about	t the complete proteins?
<ul> <li>a) High-protein foods that stabilize body weight</li> </ul>	b) Food that has a balanced amount of fat and protein
c) Foods that provide all the amino acids that the body needs	d) All of these
(57) Which of the following disorders is caused by	the deficiency of proteins?
a) Weight loss	b) Muscle fatigue
c) Loss in muscle strength	d) All of these
(58) Which of the following is not the function of p	roteins?
a) Helps in digesting food	b) Carries genetic information
c) Fights against the invading pathogens	d) Helps in transporting oxygen in the blood
(59) Which of the following statements is true about	at the (primary ) 1° structure of proteins?
a) The helical structure of the protein	b) Subunit structure of the protein
c) Three-dimensional structure of the protein	<ul> <li>d) The sequence of amino acids joined by a peptide bond</li> </ul>
(60) The process of protein synthesis takes place in	which of the following cell organelles?
a) Nucleus	b) Mitochondria
c) Vacuoles	d) Cytoplasm