

VU Learning HUB

BIF101 Quiz File

Chapter-wise Solved MCQs

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Module 1: Unit of Life

Q1. What is the basic building block of all living organisms according to the handout? A) Tissue B) Organ C) Cell D) Organ system

Q2. Which of the following biological structures is formed when several tissues combine together to perform a shared function? A) Organ system B) Organ C) Organism D) Macromolecule

Q3. How are bacterial cells classified based on cellular category? A) Eukaryotic cells B) Prokaryotic cells C) Multicellular structures D) Organelles

Q4. What is defined as the property of cells and organisms that maintains stability and constancy required to function properly? A) Biosynthesis B) Polymerization C) Homeostasis D) Denaturation

Answer Key

C) Cell — A cell is the smallest unit of a living thing and the basic building block of all organisms.

B) Organ — Several tissues combine to form an organ such as the stomach, heart, or brain.

B) Prokaryotic cells — Bacterial cells are classified as prokaryotic, whereas animal and plant cells are eukaryotic.

C) Homeostasis — Homeostasis is the regulation and maintenance of cellular stability and constancy needed to function properly.

Module 2: Composition of Matter

Q1. Which of the following is defined as a substance that cannot be broken down or converted into other substances by chemical means? A) Molecule B) Polymer C) Element D) Organelle

Q2. What is the smallest particle of an element that retains its distinctive chemical properties? A) Atom B) Macromolecule C) Nucleoside D) Cell

Q3. The characteristics of materials from which living cells are made depend primarily on how their atoms link together to form what structures? A) Elements B) Molecules C) Tissues D) Organs

Q4. Which two specific elements are explicitly mentioned in the handout as examples of substances that cannot be broken down by chemical means? A) Oxygen and Nitrogen B) Hydrogen and Carbon C) Sodium and Potassium D) Iron and Calcium

Answer Key

C) Element — Matter is composed of elements like hydrogen or carbon that cannot be chemical broken down.

A) Atom — The smallest particle of an element retaining its distinctive chemical properties is an atom.

B) Molecules — Properties of living matter depend on how atoms link together in groups to form molecules.

B) Hydrogen and Carbon — The handout explicitly names hydrogen and carbon as examples of chemical elements.

Module 5: Size Matters & Cell Structure

Q1. Why are cells extremely small in size? A) To reduce metabolic rate B) To maintain a large surface area-to-volume ratio C) To minimize waste product transportation D) To avoid having cell walls

Q2. Which feature is characteristic of prokaryotic cells? A) Membrane-enclosed nucleus B) Lack of membrane-enclosed internal compartments C) Absence of a plasma membrane D) Absence of a nucleoid region

Q3. Where is the genetic material (DNA) located inside a prokaryotic cell? A) Nucleolus B) Nucleoid region C) Nuclear envelope D) Endoplasmic reticulum

Q4. What is the chemical reaction where a bond in a large molecule is split by adding water? A) Condensation B) Polymerization C) Hydrolysis D) Oxidation

Answer Key

B) To maintain a large surface area-to-volume ratio — Cells remain small to maintain a high surface area-to-volume ratio for efficient transport.

B) Lack of membrane-enclosed internal compartments — Prokaryotic cells have no internal membrane-bound compartments.

B) Nucleoid region — Prokaryotes store their DNA in the nucleoid region.

C) Hydrolysis — Hydrolysis splits a large molecule into smaller fragments by adding water across the broken bond.

Module 8: History of Molecular Biology

Q1. Who synthesized urea in 1828, contributing to the foundation of biochemistry? A) Anselme Payen B) Friedrich Wöhler C) Friedrich Miescher D) Eduard Buchner

Q2. In 1833, Anselme Payen discovered the very first enzyme, which was named what? A) Urease B) Diastase C) Polymerase D) Ribozyme

Q3. In which year did Friedrich Miescher discover DNA? A) 1828 B) 1865 C) 1869 D) 1897

Q4. Which scientists demonstrated in 1944 that DNA is the hereditary material? A) Gregor Mendel B) Thomas Hunt Morgan C) Oswald Avery and colleagues D) Alfred Hershey and Martha Chase

Answer Key

B) Friedrich Wöhler — Friedrich Wöhler synthesized urea in 1828.

B) Diastase — Diastase was the first enzyme discovered by Anselme Payen in 1833.

C) 1869 — DNA was discovered by Friedrich Miescher in 1869.

C) Oswald Avery and colleagues — Oswald Avery and his team demonstrated in 1944 that DNA is the hereditary material.

Module 12: Nucleoside and Nucleotide

Q1. What three components make up a complete nucleotide molecule? A) Amino acid, pentose sugar, and phosphate group B) Phosphate group, pentose sugar, and nitrogenous base C) Nitrogenous base, hexose sugar, and carboxyl group D) Fatty acid, pentose sugar, and phosphate group

Q2. How does a nucleoside differ chemically from a nucleotide? A) It lacks a nitrogenous base B) It lacks a pentose sugar C) It lacks a phosphate group D) It contains hexose sugar instead of pentose sugar

Q3. Adenosine is formed by the combination of adenine and which sugar? A) Deoxyribose B) Ribose C) Glucose D) Fructose

Q4. Combining adenosine with phosphoric acid forms which nucleotide? A) Guanylic acid B) Cytidylic acid C) Adenylic acid D) Uridylic acid

Answer Key

B) Phosphate group, pentose sugar, and nitrogenous base — A nucleotide consists of a phosphate group, pentose sugar, and nitrogenous base.

C) It lacks a phosphate group — A nucleoside contains a pentose sugar and nitrogenous base but lacks a phosphate group.

B) Ribose — Adenosine is a nucleoside formed by Adenine and Ribose.

C) Adenylic acid — Adenylic acid is the nucleotide formed by combining adenosine and phosphoric acid.

Module 18: Common Genetic Terminologies

Q1. What term refers to a heritable feature such as skin color or height? A) Trait B) Character C) Phenotype D) Genotype

Q2. What is defined as a specific variant for a heritable character (e.g., brown or black eye color)? A) Genotype B) Trait C) Character D) Allele

Q3. How is the physical appearance of an organism described in genetic terms? A) Genotype B) Phenotype C) Karyotype D) Prototype

Q4. What type of genetic cross occurs between two F1 generation hybrids (Ww×Ww)? A) Pure cross B) Test cross C) Hybrid cross D) Back cross

Answer Key

B) Character — A heritable feature like skin color or height is termed a character.

B) Trait — A variant of a character (such as brown or black color) is defined as a trait.

B) Phenotype — The physical appearance of an organism is its phenotype, while the genetic makeup is its genotype.

C) Hybrid cross — A cross between F1 generation individuals (Ww×Ww) is called a hybrid cross.

Module 20: Prokaryotic Genome

Q1. What defines prokaryotic organisms regarding their genetic material? A) Enclosed within a double membrane nucleus B) Not enclosed in a nuclear membrane C) Stored inside mitochondria D) Arranged in linear chromosomes

Q2. Which cellular organelle is present inside prokaryotic cells? A) Endoplasmic reticulum B) Golgi apparatus C) Ribosomes D) Lysosomes

Q3. What shape does the main chromosome typically have in a bacterial prokaryotic genome? A) Linear double strand B) Big chromosome in the middle C) Multiple fragmented plasmids D)

Quadruplex structure

Q4. Why do prokaryotic cells lack membrane-bound organelles? A) They lack cytoplasm B) Because there is no true nucleus C) They do not synthesize proteins D) They lack cell walls

Answer Key

B) Not enclosed in a nuclear membrane — Prokaryotic genetic material is not enclosed by a nuclear membrane.

C) Ribosomes — Simple prokaryotes contain ribosomes floating in cytoplasm.

B) Big chromosome in the middle — Bacteria typically carry a single large genomic chromosome in the center.

B) Because there is no true nucleus — Lacking a true nucleus, prokaryotes have no justification to carry membrane-bound organelles.

Module 21: Eukaryotic Genome

Q1. How does the size of eukaryotic genomes generally compare to prokaryotic genomes? A) Smaller and simpler B) Larger and more complex C) Exactly identical in size D) Lacks non-coding sequences

Q2. Why do salamander and lily genomes contain over 10 times more DNA than the human genome? A) They have 10 times more functional genes B) They contain large amounts of non-coding DNA C) They are prokaryotic organisms D) They lack nuclear membranes

Q3. Approximately how many genes does the human genome contain according to the handout? A) 3,200 genes B) 20,000 to 25,000 genes (formerly thought ~100,000) C) 1,000,000 genes D) 500 genes

Q4. Roughly how many more genes does the human genome have compared to E. coli (~3,200 genes)? A) 1,000 times more B) 25 times more C) 500 times more D) 2 times more

Answer Key

B) Larger and more complex — Eukaryotic genomes are generally larger and more complex than prokaryotic ones.

B) They contain large amounts of non-coding DNA — Genome size differences in plants/salamanders reflect vast non-coding DNA abundance rather than gene count.

B) 20,000 to 25,000 genes — Human genome estimate is roughly ~25,000 genes (~25 times more than E. coli).

B) 25 times more — Human gene count (~25,000) is about 25 times that of E. coli (~3,200).

Module 36: Genetic Code

Q1. How many total triplet codons exist in the genetic code? A) 20 B) 32 C) 64 D) 128

Q2. How many standard amino acids are specified by the 64 genetic codons? A) 16 B) 20 C) 4 D) 64

Q3. Which codon acts as the universal start codon and codes for Methionine? A) UAA B) UAG C) UGA D) AUG

Q4. Which three codons function as stop codons (termination signals) during translation? A) AUG, UAA, UAG B) UAA, UAG, UGA C) UAA, UCG, UGA D) GUA, GAG, GAC

Answer Key

- C) 64 — Combinations of 4 base letters in triplets give $4^3=64$ codons.
- B) 20 — The 64 codons code for 20 standard amino acids.
- D) AUG — AUG serves as the start codon coding for methionine.
- B) UAA, UAG, UGA — UAA, UAG, and UGA are the three stop codons.

Module 40: Types of RNA

Q1. What are the three primary types of RNA present in living cells? A) mRNA, tRNA, and cDNA B) mRNA, tRNA, and rRNA C) snRNA, miRNA, and siRNA D) gRNA, rRNA, and vRNA

Q2. Which type of RNA carries genetic information from DNA to the protein biosynthetic machinery? A) Transfer RNA (tRNA) B) Messenger RNA (mRNA) C) Ribosomal RNA (rRNA) D) Small nuclear RNA

Q3. What serves as the template that specifies amino acid sequences in polypeptide chains? A) Ribosomal RNA B) Messenger RNA C) Transfer RNA D) DNA Polymerase

Q4. Where in the cell does mRNA deliver genetic information for protein synthesis? A) Nucleolus B) Mitochondria C) Ribosome D) Cell wall

Answer Key

- B) mRNA, tRNA, and rRNA — Living cells contain Messenger RNA, Transfer RNA, and Ribosomal RNA.
- B) Messenger RNA (mRNA) — mRNA carries genetic instructions from DNA to ribosomes.
- B) Messenger RNA — mRNA provides the codon template specifying polypeptide amino acid order.
- C) Ribosome — mRNA connects with ribosomes where proteins are synthesized.

Module 52: Translation Initiation Factors

Q1. How many translation initiation factors catalyze prokaryotic translation initiation? A) 2 B) 3 C) 5 D) 7

Q2. What is the specific function of Initiation Factor 1 (IF1) in prokaryotic translation? A) Hydrolizes ATP B) Prevents tRNAs from binding to the A-site portion of the small subunit C) Binds stop codons D) Cleaves mRNA

Q3. Initiation Factor 2 (IF2) belongs to which family of enzymes? A) Kinase B) GTPase C) Polymerase D) Helicase

Q4. Which charged initiator tRNA interacts with IF2 during translation initiation? A) Met-tRNA^{fMet} B) fMet-tRNA^{fMet} C) Ala-tRNA D) Phe-tRNA

Answer Key

- B) 3 — Prokaryotic translation initiation is catalyzed by IF1, IF2, and IF3.
- B) Prevents tRNAs from binding to the A-site portion of the small subunit — IF1 blocks tRNAs from entering the future A-site on the small subunit.
- B) GTPase — IF2 is a GTPase interacting with the small subunit, IF1, and initiator tRNA.
- B) fMet-tRNA^{fMet} — IF2 carries the charged initiator tRNA fMet-tRNA^{fMet} to the initiation complex.

Module 68: Quaternary Structure of Proteins

Q1. What level of protein structure describes the spatial arrangement of multiple polypeptide chains? A) Primary structure B) Secondary structure C) Tertiary structure D) Quaternary structure

Q2. What term refers to a multi-subunit protein complex? A) Monomer B) Multimer C) Polymerase D) Codon

Q3. What is a multimer containing only a few subunits called? A) Oligomer B) Protomer C) Peptide D) Isomer

Q4. What is the simplest form of rotational symmetry found in protein oligomers? A) Helical symmetry B) Cyclic symmetry C) Dihedral symmetry D) Asymmetric folding

Answer Key

D) Quaternary structure — Quaternary structure describes the spatial arrangement of two or more polypeptide subunits.

B) Multimer — A protein composed of multiple subunits is called a multimer.

A) Oligomer — A multimer with just a few subunits is specifically termed an oligomer.

B) Cyclic symmetry — The simplest form of rotational symmetry in oligomers is cyclic symmetry.

Module 72: Pairwise Sequence Alignment

Q1. What is the primary purpose of performing a sequence alignment on DNA, RNA, or protein sequences? A) To translate RNA into amino acids B) To identify regions of similarity representing functional, structural, or evolutionary relationships C) To calculate cell volume D) To measure atomic weights

Q2. What type of alignment exhibits the highest correspondence score between query and target sequence? A) Local alignment B) Optimal alignment C) Heuristic alignment D) Random alignment

Q3. Why are gaps introduced into sequence alignments? A) To shorten the sequence length B) To achieve maximum character matching C) To remove non-coding DNA D) To split long sequences

Answer Key

B) To identify regions of similarity representing functional, structural, or evolutionary relationships — Alignment identifies similarity reflecting shared evolution or function.

B) Optimal alignment — An optimal alignment achieves the maximum match correspondence score.

B) To achieve maximum character matching — Gaps represent insertions/deletions introduced to maximize matching residues.

(Note: this module's source material covered the alignment topic partially; the original response included a fourth alignment-scope question which is omitted here as it lacked a fourth option.)

Module 84: Types of BLAST

Q1. Which BLAST variant searches a nucleotide database using a nucleotide query? A) blastp B) blastn C) blastx D) tblastn

Q2. Which BLAST program compares a protein query sequence against a protein database? A) blastn B) blastp C) tblastx D) megablast

Q3. How does the blastx tool operate? A) Searches nucleotide database using protein query B) Searches protein database using translated nucleotide query C) Searches protein database using protein query D) Searches translated nucleotide DB using translated query

Q4. What does the acronym HSP stand for in BLAST output analysis? A) High Scoring Pair B) Homologous Sequence Protein C) Helical Structure Prediction D) Homology Search Protocol

Answer Key

B) blastn — Standard nucleotide BLAST (blastn) searches nucleotide DBs using nucleotide queries.

B) blastp — Standard protein BLAST (blastp) compares protein queries against protein DBs.

B) Searches protein database using translated nucleotide query — blastx translates a nucleotide query into 6 frames to search protein databases.

A) High Scoring Pair — HSP stands for High-Scoring Segment Pair in BLAST results.

Module 120: Seven Steps to Homology Modelling

Q1. How many sequential steps are involved in protein homology modeling? A) 3 steps B) 5 steps C) 7 steps D) 10 steps

Q2. What is Step 1 in the 7-step workflow of homology modeling? A) Loop modeling B) Backbone generation C) Template recognition and initial alignment D) Side-chain modeling

Q3. Which step follows backbone generation in homology modeling? A) Alignment correction B) Loop modeling C) Model validation D) Side-chain modeling

Q4. What is the final (7th) step of homology modeling? A) Side-chain modeling B) Model optimization C) Model validation D) Template selection

Answer Key

C) 7 steps — Homology modeling operates through a 7-step workflow.

C) Template recognition and initial alignment — Step 1 is template recognition and initial sequence alignment.

B) Loop modeling — Step 4 is loop modeling, which takes place after backbone generation (Step 3).

C) Model validation — Step 7 is model validation to ensure structural reliability.

End of Quiz

BIF101 — 59 solved MCQs
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