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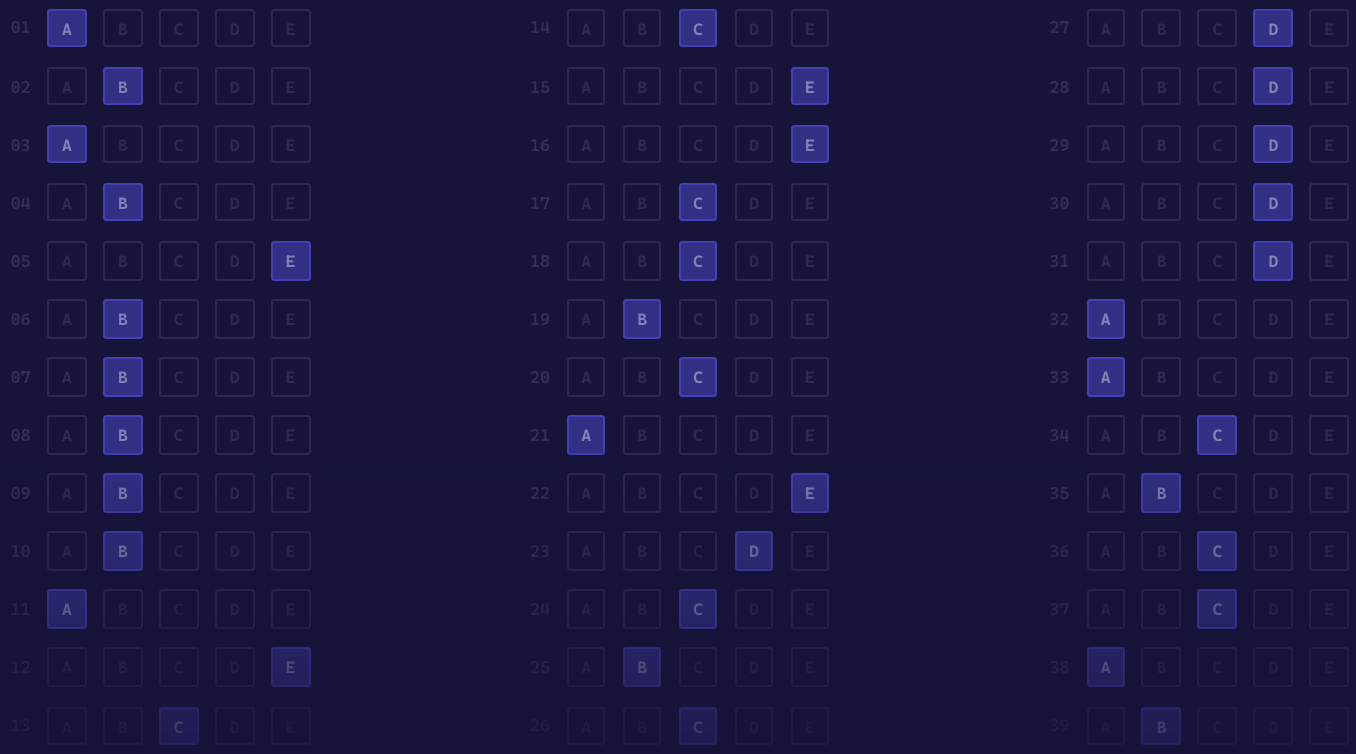

PRACTICE QUESTIONS

Saudi Commission For Health Specialties (SCFHS)

GENBI

Genomic & Biotechnology

EDITION	QUESTIONS	FORMAT
Demo	9	Limited Edition PDF

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Before you begin

What this is

9 practice questions for Saudi Commission For Health Specialties (SCFHS) `GENBI`, each with its answer key and an explanation. Answer a question before you read its key — the explanation is worth more once you have committed.

If something looks wrong

Send us three things and we will check it:

- the exam code, `GENBI`
- the question number
- the email address on your order

Write to **support@mometrix.net**. We reply within one business day.

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QUESTION 1 MULTIPLE CHOICE

Which of the following are core features that distinguish eukaryotic genomes from prokaryotic genomes? (Choose two.)

A **Presence of introns within most protein-coding genes**

B Circular chromosome structure as the default genomic organization

C **Histone-associated chromatin packaging of nuclear DNA**

D Coupled transcription and translation in the cellular cytoplasm

ANSWER **A · C**

WHY Eukaryotic genomes are typically organized into linear chromosomes packaged with histones into chromatin, and most protein-coding genes contain introns that are removed by splicing. Prokaryotic genomes are usually a single circular molecule (B) and perform coupled transcription and translation (D). Therefore, A and C are the correct distinguishing features.

QUESTION 2 MULTIPLE CHOICE

Which of the following are valid applications of the polymerase chain reaction (PCR) in a clinical genomics laboratory? (Choose two.)

A **Amplifying a specific DNA region for downstream Sanger sequencing**

B Determining the three-dimensional structure of a protein from its gene

C **Detecting pathogen DNA such as Mycobacterium tuberculosis in patient samples**

D Directly measuring the absolute quantity of mRNA transcripts without a reverse-transcription step

ANSWER **A · C**

WHY PCR is widely used to amplify defined DNA targets prior to Sanger sequencing (A) and to detect pathogen DNA in clinical specimens, including M. tuberculosis (C). Protein 3D structure is determined by methods such as X-ray crystallography or cryo-EM, not PCR (B). mRNA quantification requires reverse transcription to cDNA before PCR; PCR amplifies DNA, not RNA directly (D).

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QUESTION 3 SINGLE CHOICE

Which sequencing approach is best suited for sequencing entire human genomes at relatively low cost and high throughput in a modern clinical genomics workflow?

A Sanger sequencing of individual PCR amplicons

B **Whole-genome next-generation sequencing (NGS) on a short-read platform**

C Manual chain-termination analysis using radiolabeled ddNTPs

D Northern blotting followed by autoradiography

ANSWER B

WHY Whole-genome short-read next-generation sequencing platforms (e.g., Illumina-based systems) are the standard for large-scale human genome sequencing because they provide high throughput at a low cost per base. Sanger sequencing (A, C) is accurate but lower throughput and more expensive per base, and Northern blotting (D) analyzes RNA, not DNA sequence.

QUESTION 4 SINGLE CHOICE

In a typical variant-calling pipeline for human whole-genome sequencing data, which file format is the standard for storing the genomic variants identified in a sample?

A BAM

B FASTA

C **VCF**

D PDB

ANSWER C

WHY VCF (Variant Call Format) is the widely adopted standard for storing germline and somatic variants such as SNVs and indels with their genomic positions and annotations. BAM stores sequence alignments (A), FASTA stores raw reference or read sequences (B), and PDB stores protein three-dimensional structures (D).

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QUESTION 5 SINGLE CHOICE

A patient is found to carry a pathogenic BRCA1 variant during whole-genome sequencing performed for an unrelated indication. Which principle best guides the clinician's duty regarding this incidental finding?

A Withhold all results because the test was not performed for hereditary cancer assessment

B Disclose the actionable BRCA1 finding because it is an established, clinically actionable incidental finding

C Share the full raw genomic data publicly to advance research

D Only disclose results if a family member independently requests the information

ANSWER B

WHY Professional bodies such as the ACMG recommend returning clinically actionable incidental (secondary) findings, including pathogenic BRCA1 variants, when the patient has not opted out. Withholding actionable findings (A) is not appropriate; publicly releasing raw data breaches confidentiality (C); and the patient's right to their own information does not depend on a relative's request (D).

QUESTION 6 SINGLE CHOICE

Which clinical scenario most appropriately warrants pharmacogenomic testing to guide drug selection and dosing?

A Selecting an antibiotic for an uncomplicated urinary tract infection

B Determining warfarin dosing based on CYP2C9 and VKORC1 genotypes

C Choosing an antihypertensive based on the patient's age

D Diagnosing a fractured bone based on radiography

ANSWER B

WHY Warfarin dosing is strongly influenced by CYP2C9 (metabolism) and VKORC1 (sensitivity) genotypes, and pharmacogenomic-guided dosing is recommended by clinical guidelines. Antibiotic selection in UTI (A) is driven by susceptibility, not host genotype; antihypertensive choice based on age (C) and fracture diagnosis by imaging (D) are not pharmacogenomic indications.

QUESTION 7 SINGLE CHOICE

A single-nucleotide change that converts a codon into a premature stop codon is best classified as which type of mutation?

A Missense mutation

B Silent mutation

C Nonsense mutation

D Frameshift mutation

ANSWER C

WHY A nonsense mutation is a point substitution that creates a premature stop codon, typically truncating the protein. Missense changes one amino acid for another (A), silent mutations do not change the amino acid (B), and frameshift mutations result from insertions or deletions not in multiples of three that alter the downstream reading frame (D).

QUESTION 8 SINGLE CHOICE

A disease phenotype appears in every generation, affects males and females equally, and is transmitted from an affected parent to approximately 50% of offspring regardless of sex. Which inheritance pattern does this most likely represent?

A Autosomal recessive

B Autosomal dominant

C X-linked recessive

D Mitochondrial

ANSWER B

WHY Autosomal dominant traits typically appear in every generation, affect both sexes equally, and show a 50% transmission risk from an affected heterozygote to each offspring. Autosomal recessive traits often skip generations (A), X-linked recessive primarily affects males and skips through carrier females (C), and mitochondrial inheritance comes exclusively from the mother and affects all her children (D).

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QUESTION 9 SINGLE CHOICE

Which technique is most appropriate for measuring the expression level of thousands of mRNA transcripts simultaneously in a single experiment?

A **RNA sequencing (RNA-seq)**

B Southern blotting

C DNA footprinting

D Chromatin immunoprecipitation (ChIP) without sequencing

ANSWER **A**

WHY RNA-seq uses high-throughput sequencing of cDNA derived from the sample's RNA to quantify transcript abundance across the entire transcriptome in a single experiment. Southern blotting detects specific DNA fragments (B), DNA footprinting identifies protein-binding sites on DNA (C), and ChIP without sequencing identifies protein-bound DNA regions but does not quantify expression (D).

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