

NEET Biology Mastery: Human Genome Project (HGP) MCQs

Comprehensive Question Bank Covering All NEET Formats

Type 1: Single-Option Correct MCQs (Fundamental Concepts)

Q1. The Human Genome Project (HGP) was officially launched in which year?

- A) 1980
- B) 1990
- C) 1995
- D) 2003

Answer: B) 1990

Explanation: The HGP was a 13-year mega-project launched in 1990 as a collaborative international research initiative under the primary coordination of the U.S. Department of Energy and the National Institutes of Health (NIH).

Q2. Which of the following was NOT a goal of the Human Genome Project?

- A) To identify all the approximately 20,000–25,000 genes in human DNA.
- B) To sequence the genomes of selected model organisms.
- C) To eliminate all genetic diseases directly.
- D) To address the ethical, legal, and social issues (ELSI) arising from the project.

Answer: C) To eliminate all genetic diseases directly

Explanation: The HGP was an informational mapping and sequencing initiative. While it serves as the foundation for modern gene therapies and clinical diagnostics, its direct scope was not immediate therapeutic elimination of all diseases.

Q3. Which was the last human chromosome to be completely sequenced during the HGP?

- A) Chromosome 1
- B) Chromosome 11
- C) Chromosome 21
- D) Chromosome X

Answer: A) Chromosome 1

Explanation: Chromosome 1 is the largest human autosome, housing the maximum number of genes (2,968). Due to its massive structural complexity and density, its definitive sequence assembly was completed last, in May 2006.

Q4. Sequencing the whole set of a genome containing both coding and non-coding regions, followed by assigning functional roles to different regions, is known as:

- A) Expressed Sequence Tags (ESTs)
- B) Sequence Annotation
- C) RFLP Analysis
- D) Single Nucleotide Polymorphisms (SNPs)

Answer: B) Sequence Annotation

Explanation: Blindly sequencing the absolute whole genome without bias towards coding segments, and then systematically cataloging functional segments later, is called Sequence Annotation. Tagging only expressed parts as cDNA is called Expressed Sequence Tags (ESTs).

Type 2: Statement-Based / Assertion & Reason MCQs

Q5. Identify the incorrect statement regarding the findings of the Human Genome Project:

- A) The human genome contains approximately 3×10^9 base pairs.
- B) Less than 2% of the genome codes for proteins.
- C) The average gene consists of 3,000 bases, but sizes vary greatly.
- D) Total number of genes is estimated at 1,40,000, much higher than previous estimates.

Answer: D) Total number of genes is estimated at 1,40,000, much higher than previous estimates.

Explanation: The HGP surprised researchers by revealing that the human genome contains only around 30,000 genes. This was significantly lower than pre-project estimates which ranged from 80,000 to 1,40,000 genes.

Q6. Given below are two statements:

Statement I: Repetitive sequences make up a very large portion of the human genome.

Statement II: Repetitive sequences have direct coding functions for essential metabolic enzymes.

Choose the correct option:

- A) Both Statement I and Statement II are correct.
- B) Both Statement I and Statement II are incorrect.
- C) Statement I is correct but Statement II is incorrect.
- D) Statement I is incorrect but Statement II is correct.

Answer: C) Statement I is correct but Statement II is incorrect.

Explanation: While highly repetitive elements comprise a dominant chunk of human genomic infrastructure, they do not directly code for proteins or operational enzymes. They are useful for understanding chromosomal mechanics, evolution, and pedigree history.

Type 3: Match the Columns (High Yield for NEET)

Q7. Match Column-I with Column-II and select the correct option:

Column-I (Feature / Concept)	Column-II (Scientific Detail)
(a) Mega Project Cost	(i) Chromosome Y

(b) Fewest Genes	(ii) ~9 billion USD
(c) Most Genes	(iv) Chromosome 1
(d) SNP positions	(iii) 1.4 million locations

Options:

- A) a-(ii), b-(i), c-(iv), d-(iii)
- B) a-(ii), b-(iv), c-(i), d-(iii)
- C) a-(iii), b-(i), c-(iv), d-(ii)
- D) a-(iv), b-(i), c-(ii), d-(iii)

Answer: A) a-(ii), b-(i), c-(iv), d-(iii)

Explanation: Total HGP deployment capital reached roughly 9 billion USD (planned at \$3 per base pair for ~3 billion bp). Chromosome Y has the fewest mapped loci (231), Chromosome 1 holds the highest payload (2968), and polymorphic single nucleotide targets are spread over roughly 1.4 million recorded locations.

Type 4: Methodological & Vector-Based MCQs

Q8. Which of the following specialized vectors were commonly used for cloning genomic DNA fragments during the sequencing phase of the HGP?

- A) pBR322 and pUC19
- B) BAC (Bacterial Artificial Chromosome) and YAC (Yeast Artificial Chromosome)
- C) Ti Plasmid and Retroviruses
- D) Lambda phage and Cosmid

Answer: B) BAC (Bacterial Artificial Chromosome) and YAC (Yeast Artificial Chromosome)

Explanation: Human DNA fragments are incredibly long compared to typical prokaryotic plasmid targets. To clone large human inserts stably, high-capacity host-vector complexes like Bacterial Artificial Chromosomes (BAC) and Yeast Artificial Chromosomes (YAC) were deployed.

Q9. The automated DNA sequencers used in the Human Genome Project worked on the principle of a method developed by:

- A) Alec Jeffreys
- B) Frederick Sanger
- C) Watson and Crick
- D) Kary Mullis

Answer: B) Frederick Sanger

Explanation: High-throughput automated sequencing platforms rely fundamentally on modifications of the chemical chain-termination method engineered by dual Nobel laureate Frederick Sanger.

Type 5: Numerical / Analytical MCQs

Q10. If the total human genome consists of approximately 3×10^9 base pairs, and any two unrelated humans are 99.9% identical in their genetic sequence, what is the absolute number of base pair differences between them?

- A) 3×10^6 bp
- B) 3×10^7 bp

- C) 3×10^8 bp
- D) 3×10^5 bp

Answer: A) 3×10^6 bp

Explanation: If 99.9% is completely sequence-identical, the remaining individual variance equates to exactly 0.1%. Calculation: 0.1% of $(3 \times 10^9) = (0.1 / 100) * 3,000,000,000 = 3,000,000$, which equals 3×10^6 base pair differences.