

NEET Biology: Human Genome Project (HGP) Masterbank - Vol 2

Advanced High-Yield Practice Sets (Strictly Based on NCERT Lines)

Type 1: Single-Option Correct MCQs (Advanced Facts)

Q1. Besides humans, several non-human organisms have also been completely sequenced. Which of the following sets represents non-human organisms sequenced during or as an offshoot of the HGP?

- A) *Drosophila melanogaster*, *Caenorhabditis elegans*, *Arabidopsis*, Rice
- B) *Panthera tigris*, *Mus musculus*, *Plasmodium*, *Amoeba*
- C) *Escherichia coli*, *Neurospora crassa*, Frog, *Hydrilla*
- D) HIV, Bacteriophage T4, Pea plant, Maize

Answer: A) *Drosophila melanogaster*, *Caenorhabditis elegans*, *Arabidopsis*, Rice

Explanation: Non-human organisms sequenced include bacteria, yeast, *Caenorhabditis elegans* (a free-living non-pathogenic nematode), *Drosophila* (fruit fly), plants (rice and *Arabidopsis*).

Q2. The branch of biology that directly emerged from the massive data management demands of the Human Genome Project is:

- A) Biomonitoring
- B) Biosystematics
- C) Bioinformatics
- D) Bioremediation

Answer: C) Bioinformatics

Explanation: The enormous quantity of data generated required high-speed computational tools for storage, retrieval, and analysis, leading to the rapid growth of Bioinformatics.

Type 2: Statement-Based / Assertion & Reason MCQs

Q3. Given below are two statements:

Statement I: The functions are unknown for over 50 per cent of the discovered genes.

Statement II: Chromosome 1 has 231 genes and the Y chromosome has 2968 genes.

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: Statement I is a direct factual line from NCERT. Statement II is incorrect because Chromosome 1 has the most genes (2968) and Chromosome Y has the fewest (231).

Q4. Assertion (A): The Human Genome Project is considered a 'Mega Project'.

Reason (R): If the cost of sequencing was US \$3 per base pair, the total estimated cost of the project was roughly 9 billion US dollars.

Choose the correct option:

- A) Both (A) and (R) are true and (R) is the correct explanation of (A).
- B) Both (A) and (R) are true but (R) is NOT the correct explanation of (A).
- C) (A) is true but (R) is false.
- D) Both (A) and (R) are false.

Answer: A) Both (A) and (R) are true and (R) is the correct explanation of (A).

Explanation: The cost parameters (3 USD per base pair for 3×10^9 base pairs totaling 9 billion USD) directly explain why it required unprecedented financial scale and international coordination, defining it as a 'Mega Project'.

Type 3: Match the Columns (Advanced Grid Layout)

Q5. Match Column-I with Column-II and select the correct option:

Column-I (Methodology / Term)	Column-II (NCERT Context)
(a) ESTs	(i) Sequencing all coding & non-coding elements blindly
(b) Sequence Annotation	(ii) High-throughput sequencing of RNA tags as cDNA
(c) Frederick Sanger	(iii) Single nucleotide position polymorphic changes
(d) SNPs	(iv) Method of chemical amino acid and base sequencing

Options:

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

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

Explanation: Expressed Sequence Tags (ESTs) target active regions via cDNA copies of RNA. Sequence Annotation deals with blind total sequencing. Frederick Sanger formulated chain-termination sequencing mechanisms, and SNPs reflect unique single-base differences.