

NEET- 2020- 45 Days Crash Course



Date : 24th Aug 2020



Chapter Name : MOLECULAR BASIS OF INHERITANCE



Lecture Outline :
QUIZ

If there are 999 bases in an RNA that codes for a protein with 333 amino acids and the base at position 901 is deleted such that the length of the RNA becomes 998 bases, how many codons will be altered?

NEET-2017

(A) 1

(B) 11

(C) 33

(D) 333

$$999 - 901 = 98 \text{ bases.}$$

3 bases - 1 codon

$$98 \text{ bases} - \frac{98}{3} = \underline{33 \text{ codons}}$$

Solution

Ans [C]

33 codons will be altered if the 901st base is deleted and RNA has only 998 bases instead of 999 bases.

Total bases present in RNA = 999

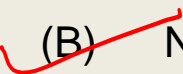
Bases left after deletion of 901st base in RNA = $999 - 901 = 98$

Number of codon present in $98 = 33$

(Approximately as three codons code for one amino acid).

DNA fragments are

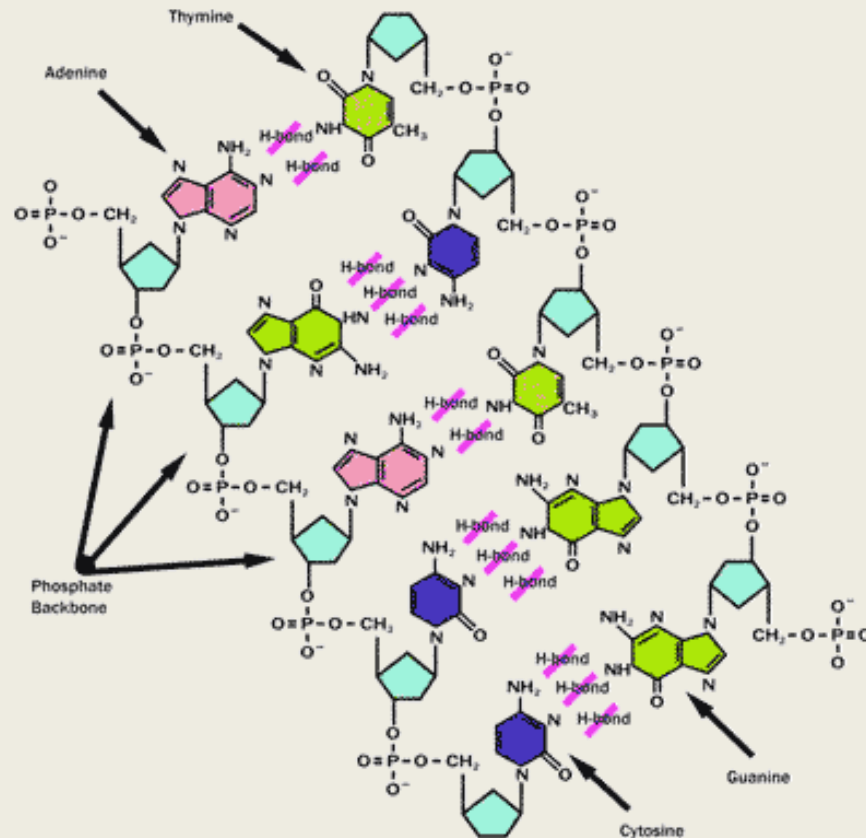
NEET-2017

- (A) Positively charged
-  (B) Negatively charged
- (C) Neutral
- (D) Either positively or negatively charged depending on their size

Solution

Ans [B]

DNA fragments are negatively charged molecules. The reason why DNA is negatively charged is the phosphate (PO_4^-) group that constitutes every nucleotide.



During DNA replication, Okazaki fragments are used to elongate

NEET-2017

- (A) The leading strand towards replication fork
- (B) The lagging strand towards replication fork
- (C) The leading strand away from replication fork
- ☒ (D) The lagging strand away from replication fork

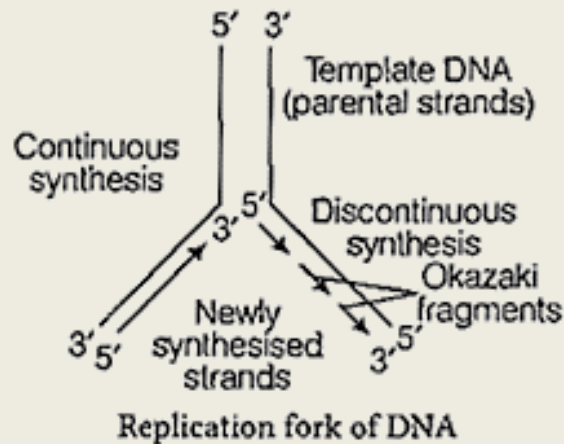
→ lagging strand

3' - 5' away
from Replication
fork →

Solution

Ans [D]

Okazaki fragments are short segments of replicating DNA. These have 1000-2000 bp in prokaryotes and 100-200 bp in eukaryotes. These fragments are used to elongate the lagging strand away from the replication fork.



Spliceosomes are not found in cells of

NEET-2017

(A) Plants

(B) Fungi

(C) Animals

(D) ~~Bacteria~~

No post transcriptional modⁿ
in prokaryotes

Solution

Ans [D]

Spliceosome is a large molecular complex found in nucleus of eukaryotic cells of plants, animals and fungi, etc. It is assembled from snRNAs and protein complexes that plays an important role in splicing of introns. Spliceosome is absent in cells of bacteria.

The final proof for DNA as the genetic material come from the experiments of

NEET-2017

- (A) Griffith
- (B) Hershey and chase
- (C) Avery, Macleod and McCarty
- (D) Hargobind Khorana

Radioactive
phage
Transduction

Solution

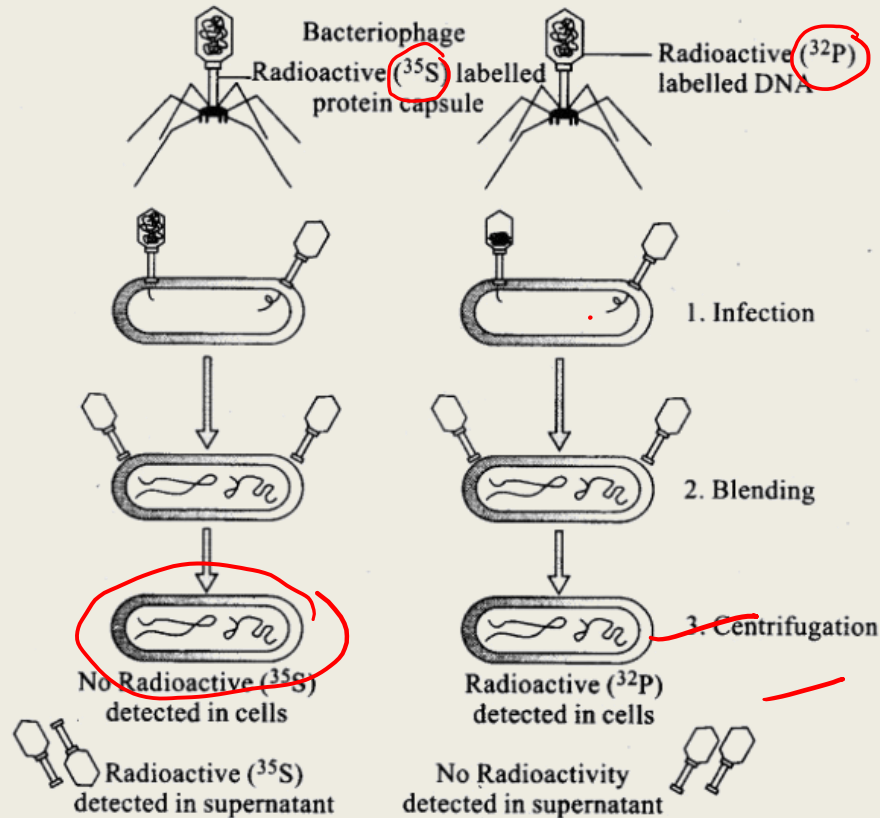
Ans [B]

trip

Hershey and Martha Chase (1952) - proof that DNA is the genetic material.

Alfred Griffith's experiment proved the existence of genetic material.

Avery, MacLeod and McCarty - determine the biochemical nature of transforming principle.



The Hershey-Chase experiment

DNA is the genetic material

The association of histone H1 with a nucleosome indicates

NEET-2017

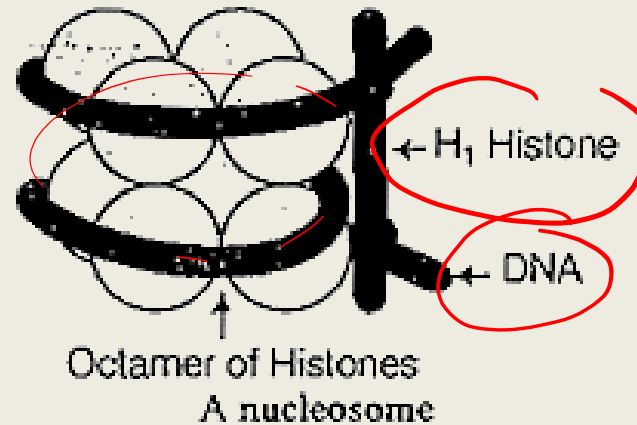
- (A) Transcription is occurring
- (B) DNA replication is occurring
- ☒ (C) The DNA is condensed into chromatin fibre
- (D) The DNA double helix is exposed

Histone protein · Octamers + DNA
→
Chromosome

Solution

Ans [C]

The linker DNA, consisting of H1 histone connects two adjacent nucleosomes. They together constitute chromatosome. It gives rise to a chromatin fibre after further condensation.



Histone Octamer

Which of the following RNAs should be most abundant in animals cell ?

NEET-2017

(A) rRNA

(B) tRNA

(C) mRNA

(D) ~~mRNA~~

— Ribosomal
RNA

Solution

Ans [A]

RNA – (rRNA, tRNA and mRNA).

rRNA is the most abundant form of RNA - responsible for coding and protein synthesis and associated with ribosomes. **mRNA** provides the template for translation.

tRNA brings amino acids and reads the genetic code.

Taylor conducted the experiments to prove semi-conservative mode of chromosome replication on

NEET-2016

(A) *Vinca rosea*

~~(B) *Vicia faba*~~



(C) *Drosophila melanogaster*

(D) *E. coli*



Solution

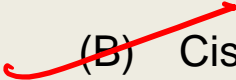
Ans [B]

The use of radioactive thymidine to detect the semiconservative mode of replication of newly synthesised DNA in the chromosomes was performed on *Vicia faba* by Taylor and colleagues in 1958.

The equivalent of a structural gene is

NEET-2016

(A) Muton

 (B) Cistron



(C) Operon

(D) Recon

Solution

Ans [B]

Cistron is the segment of DNA which determines the synthesis of complete polypeptide. Eukaryotic structural gene is monocistronic whereas prokaryotic structural gene is polycistronic.

Muton - Smallest unit of DNA in which mutation occurs.

Operon - Functional unit of genomic DNA containing a cluster of genes under control of single promoter.

Recon - Smallest unit of DNA for recombination.

Which of the following rRNAs act as structural RNA as well as ribozyme in bacteria ?

NEET-2016

- (A) 5 srRNA
- (B) 18 srRNA
- (C) 23 srRNA
- (D) 58 srRNA

Solution

Ans [C]

Bacterial cells use their 23 srRNA as an enzyme during protein synthesis. This is the only non-proteinaceous enzyme known so far.

A molecule that can act as a genetic material must fulfill the traits given below, except

NEET-2016

- (A) It should be able to express itself in the form of 'Mendelian characters'
- (B) It should be able to generate its replica
- ~~(C) It should be unstable structurally and chemically~~ *should be stable*
- (D) It should provide the scope for slow changes that are required for evolution

Solution

Ans [C]

The criteria that a molecule must fulfil to act as a genetic material are as following :

- (1) It should be able to replicate
- (2) It should be chemically and structurally stable
- (3) It should provide the scope for slow changes, i.e. mutations which are required for evolution
- (4) It should be able to express itself in the form of 'Mendelian characters'

DNA-dependent RNA polymerase catalyses transcription on one strand of the DNA which is called the

NEET-2016

~~(A) Template strand~~

(B) Coding strand

(C) Alpha strand

(D) Anti strand

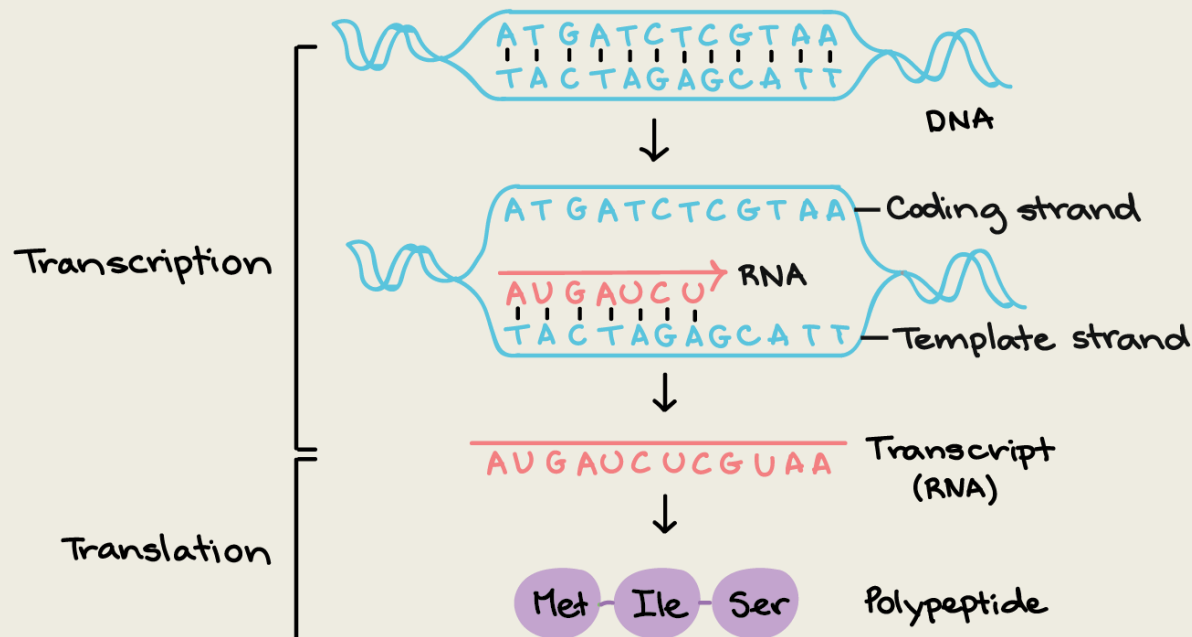
3' - 5'

Solution

Ans [A]

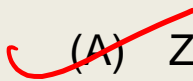
DNA dependent RNA polymerase catalyses transcription on one strand of the DNA called a template strand.

A template can be considered as one of those strands of DNA which decodes its information directly through RNA polymerase.



Which of the following is not required for any of the techniques of DNA fingerprinting available at present ?

NEET-2016

 (A) Zinc finger analysis

(B) Restriction enzymes

(C) DNA-DNA hybridisation

(D) Polymerase chain reaction

Solution

Ans [A]

A zinc finger is a small protein structural motif that is characterised by the co-ordination of one or more Zn ions in order to stabilise the folds.

Which one of the following is the starter codon ?

NEET-2016

(A) UGA

(B) UAA

(C) UAG

☒ (D) AUG

— codes for methionine

Solution

Ans [D]

AUG is the start codon. It also codes for amino acid called methionine which is the first amino acid in a polypeptide chain. UAA, UAG and UGA are stop codons and are meant for termination of polypeptide chain during protein synthesis.

Which one of the following is not applicable to RNA ?

NEET-2015

- (A) Complementary base pairing (B) 5' phosphoryl and 3' hydroxyl ends
(C) Heterocyclic nitrogenous bases (D) ~~Chargaff's rule~~

Not applicable to
RNA

Solution

Ans [D]

Chargaff's rule is not applicable to RNA because it is single stranded and doesn't have complementary base pairs.

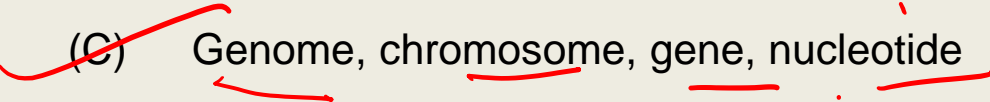
The rule states that DNA from any cell of all organisms should have a 1: 1 ratio (base pair rule) of pyrimidine and purine bases, i.e. the amount of guanine is equal to cytosine and the amount of adenine is equal to thymine.

Identify the correct order of organisation of genetic material from largest to smallest.

(A) Chromosome, gene, genome, nucleotide

NEET-2015

(B) Genome, chromosome, nucleotide, gene

 (C) Genome, chromosome, gene, nucleotide

(D) Chromosome, genome, nucleotide, gene

Solution

Ans [C]

The correct order of organisation of genetic material from largest to smallest is as follow:
Genome, chromosome, gene, nucleotide.

Genome is the total genetic material of an individual.

Chromosome is a packed and organized structure containing most of the DNA of a living organism.

Gene is a segment of DNA that encodes for a protein.

Nucleotide is one of the structural components, or building blocks, of DNA and RNA.

Satellite DNA is important because it

NEET-2015

- (A) Codes for proteins needed in cell cycle
- ☒ (B) Shows high degree of polymorphism in population and also the same degree of polymorphism in an individual, which is heritable from parents to children
- (C) Does not code for proteins and is same in all members of the population
- (D) Codes for enzymes needed for DNA replication.

Basis of finger
printing

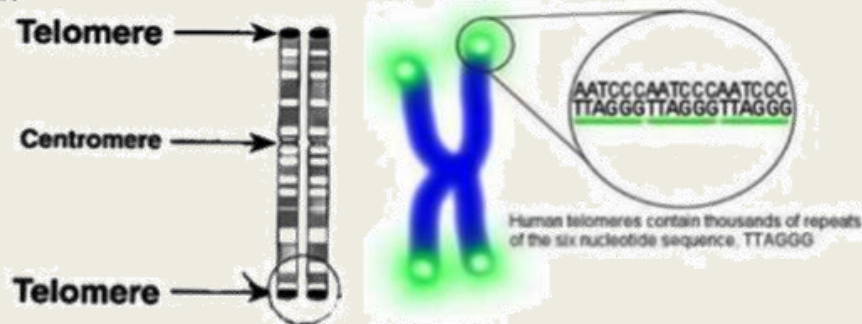
Solution

Ans [B]

Satellite DNA forms the minor peak after centrifugation of DNA. These are repetitive DNA sequences that do not code for any protein. They show high degree of polymorphism and are heritable from parents to children, thus forming the basis of DNA fingerprinting.

Satellite DNA

- Unit - 5-300 bp depending on species.
 - Repeat - 10^5 - 10^6 times.
 - Location - Generally heterochromatic.
 - Examples - Centromeric DNA, telomeric DNA.
- There are at least 10 distinct human types of satellite DNA.



Transformation was discovered by

NEET-2014

(A) Meselson and Stahl

(B) Hershey and Chase

~~(C) Griffith~~

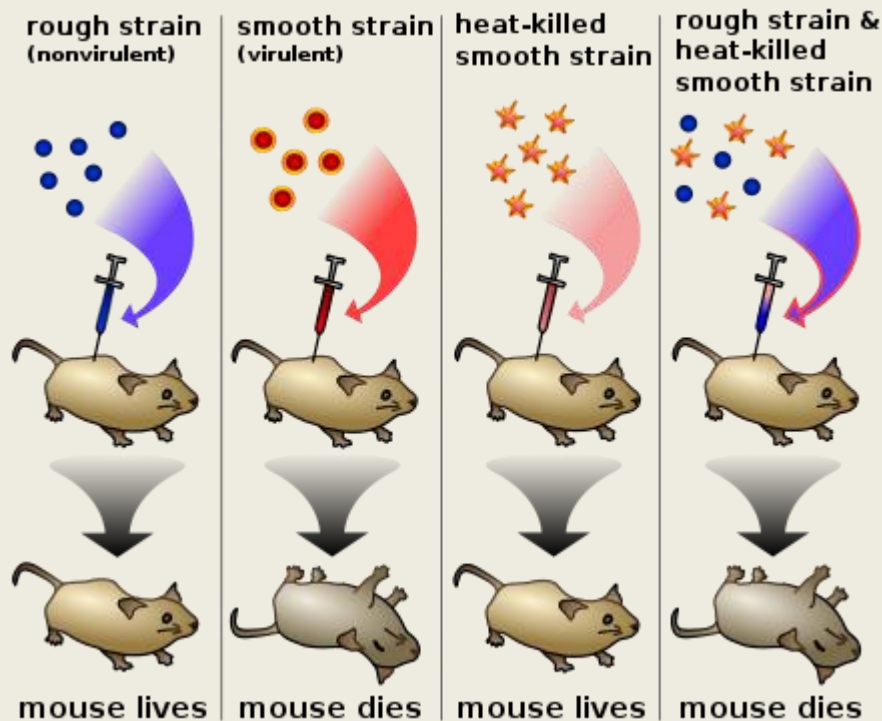
(D) Watson and Crick

- 1928

Solution

Ans [C]

Transformation was discovered by F Griffith (1928). He isolated the DNA as genetic material that inherit the genetic information between two generation using two strain of Pneumococcus bacteria type III S(smooth) and type II R (rough) strain which infect mice.



An analysis of chromosomal DNA using the Southern hybridisation technique does not use

NEET-2014

(A) Electrophoresis

(B) Blotting

(C) Autoradiography

(D) PCR

*on nitrocellulose
membrane*

↳ X-ray film

Solution

Ans [D]

Southern hybridisation is a technique used in molecular biology for detection of a specific DNA sequence in DNA samples in which excepting PCR we use all three methods such as electrophoresis, blotting and autoradiography. Because PCR is the method used for amplification of DNA sample. In vitro clonal propagation is characterised by PCR and RAPD.

Commonly used vectors for human genome sequencing are

NEET-2014

- (A) T-DNA
- (B) BAC and YAC
- (C) Expression vectors
- (D) T/A cloning vectors

Solution

Ans [B]

Commonly used vector for human genome sequencing are **BAC (Bacterial Artificial Chromosome)** and **YAC (yeast artificial chromosome)**.

BAC is used for transforming and cloning in bacteria (e.coli) and YAC are genetically engineered chromosomes derived from the DNA of the yeast, *Saccharomyces cerevisiae*, which is then ligated into a bacterial plasma.