This Chapter “Concept Notes on Molecular Basis of Inheritance for NEET” is taken from our Book:

ISBN : 9789385846854

Product Name : ACE Biology for NEET/ AIPMT/ AIIMS Medical Entrance Exam Vol. 2 (class 12) 3rd Edition (English, Paperback, Dr. Ramesh C Narang, Dr. Sahil Agarwal)

Product Description : "ACE Biology for NEET/ AIPMT/ AIIMS Medical Entrance Exam Vol. 2 (class 12) 3rd Edition is a newly Scientifically revised book for guaranteed success in NEET Common medical entrance exam. The book is developed on an objective pattern following the chapter plan as per the NCERT books of class 12. The book is updated with the Class 12 Biology section of the 2016 NEET/ AIPMT Phase I Solved paper. The book contains 16 chapters in all. Each chapter provides exhaustive point-wise theory for better retention. This is the unique selling point of the book. Most of the books provide detailed theory with huge paragraphs which makes it really cumbersome for the students to study from such a book. This book provides the complete chapters in the form of point-wise notes prepared by expert faculties thus making it India's first STUDENT FRIENDLY book in Biology. The theory is supplemented with At a Glance, Well labeled Diagrams, Illustrations, Illustrated pictures, Connecting Concepts, Checkpoints etc followed by a set of 3 MCQ exercises for practice. The first exercise is completely based on the NCERT book. The second exercise presents a window to competitive exams, where questions of past years of the leading medical exams are covered. The third exercise is ""TEST YOURSELF"" which is a collection of best questions for practice. The explanations to the selected questions of the third exercise are provided immediately at the end of each chapter. The book follows the latest AIPMT syllabus as approved by the CBSE Board. The book is a must for every Medical aspirant. It is one of the most student friendly book for Biology."
NUCLEIC ACIDS (DNA & RNA)

- They are ‘Informational molecules’ of universal occurrence.
- Present in all cells and viruses.
- They are ‘polymers of nucleotides’ and hence Macromolecules. (The structural unit of nucleic acids is Nucleotide).

Chemical Structure of Nucleic Acid

The nucleic acid on hydrolysis yields 1–Pentose Sugar, 2-types of heterocyclic nitrogenous bases (Purines and Pyrimidines) and phosphoric acid.

<table>
<thead>
<tr>
<th>Nucleic Acid</th>
<th>Purines</th>
<th>Pyrimidines</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA</td>
<td>Adenine and Guanine</td>
<td>Cytosine and Thymine</td>
</tr>
<tr>
<td>RNA</td>
<td>Adenine and Guanine</td>
<td>Cytosine and Uracil</td>
</tr>
</tbody>
</table>
I. PURINES

II. PYRIMIDINES

Following are the important differences between DNA & RNA:

<table>
<thead>
<tr>
<th>DNA</th>
<th>RNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Double stranded</td>
<td>1. Generally single stranded</td>
</tr>
<tr>
<td>2. Sugar-Deoxyribose</td>
<td>2. Sugar-Ribose</td>
</tr>
<tr>
<td>3. Pyrimidines - Cytosine and Thymine</td>
<td>3. Pyrimidines – Cytosine and Uracil</td>
</tr>
<tr>
<td>4. Cytosines are equal to Guanines</td>
<td>4. Cytosines are not equal to Guanines (being single stranded)</td>
</tr>
<tr>
<td>5. Base pairs in millions</td>
<td>5. Base pairs usually 100 to 5000</td>
</tr>
</tbody>
</table>

SUGARS IN NUCLEIC ACIDS

**DEOXYRIBONUCLEIC ACID (DNA)**

- Mainly localised in nucleus.
- Small amount of D.N.A. is also present in mitochondria and chloroplast.

**NUCLEOSIDES**

The combination of pentose sugar with nitrogenous bases (Purines or pyrimidines) is called nucleoside.

i. **Nucleosides of purines**
   - Adenine – Adenosine
   - Guanine – Guanosine

ii. **Nucleosides of pyrimidines**
   - Cytosine – Cytidine
   - Thymine (in DNA) – Thymidine
   - Uracil (in RNA) – Uridine
Phosphate ester of a nucleoside is called nucleotide. Each nucleotide consists of nitrogenous base, pentose sugar and one or more phosphate groups.

i. **Nucleotides of purines**
- Adenosine + 1-phosphate group – Adenosine Monophosphate (AMP) or Adenylic acid
- Adenosine + 2-phosphate groups – Adenosine Diphosphate (ADP)
- Adenosine + 3-phosphate groups – Adenosine Triphosphate (ATP)
- Guanosine + 1-phosphate group – Guanosine Monophosphate (GMP) or Guanylic acid

ii. **Nucleotides of pyrimidines**
- Cytidine + 1-phosphate group - Cytidine Monophosphate (CMP) or Cytidylia acid
- Cytidine + 2-phosphate groups – Cytidine Diphosphate (CDP)
- Cytidine + 3-phosphate groups – Cytidine Triphosphate (CTP)
- Thymidine + 1 Phosphate gp. - Thymidine monophosphate or Thymidylac acid
- Thymidine + 2 phosphate groups – Thymidine Diphosphate (TDP)
- Thymidine + 3-phosphate groups – Thymidine Triphosphate (TTP)
- Uracil + 1 phosphate gp. - Uridine Monophosphate or Uridyllic acid
- Uracil + 2-phosphate groups – Uridine Diphosphate (UDP)
- Uracil + 3-phosphate groups – Uridine Triphosphate (UTP)

- Nucleic acids (DNA & RNA) are polymers of the nucleotides (Nucleoside monophosphate)
- The nucleotides are acids and are negatively charged at neutral pH.
- The carbons of pentose sugars are primed as 1’, 2’, 3’, to distinguish them from the carbons of nitrogenous bases.
- Nucleotides are joined together by **phosphodiester linkage** between 5’ and 3’ carbon atoms of pentose sugar. The chain of nucleic acid is abbreviated from 5’ end to 3’ end, in left to right order.

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**Connecting Concepts**

ATP (Adenosine Triphosphate) is also a nucleotide. It contains 1-Adenine base, 1-Ribose sugar and 3-phosphate bonds. It is energy-rich compound, and is also called as ‘energy currency’. Its II and III bonds are energy rich bonds, each releasing 31 kJ energy per mol.

Edwin Chargaff reported that net amount of adenine was equal to thymine (A = T) and amount of Guanine was equal to cytosine (G = C).

This means that total number of purines is equal to the total number of pyrimidines (A + G = T + C).

As the base composition in DNA of different species varies, the AT/CG ratio also varies from species to species.

**AT/CG ratio** = 1.52 in human and 0.93 in *E. coli*.
Double Helical Structure of DNA

- To explain base equivalence (A/T, G/C) and other properties of DNA, Watson and Crick (1953), based on X-ray diffraction studies, proposed double helical structure of DNA.
- Such structure has 2 right handed helical polynucleotide chains (strands) around a central axis resembling a spiral staircase.
- The two strands of helical are anti parallel, means 5′ → 3′.
- Phosphodiester bonds (Sugar-phosphate groups) are oriented in opposite direction in 2-strands, i.e., the 5′ end of one strand is opposite to the 3′ end of the other strand.
- The bases are held like steps (rungs) of spiral staircase by hydrogen bonds.
- The phosphodiester bonds (with sugar) form rails or the sides of ladder.
- These bonds connect 2-nucleotides. Between A & T there are 2 hydrogen bonds (A = T) and in between C & G there are 3 hydrogen bonds (C ≡ G).
- The C ≡ G base pair has more stability due to triple bond, as compared to the A = T base pair.
  - The diameter of double helical structure of DNA is 2 nm (20 Å)
  - Total distance from 1 base pair to another base pair (step or rise) = 0.34 nm (3.4 Å)
  - Total base pairs in 1 complete turn (pitch) = 10 (in B-type DNA)
  - The distance covered in 10 steps or 10 base pairs or 1 complete turn (Pitch) = 3.4 nm (34 Å)
- On the basis of number of base pairs and right or left handedness of helicals the DNAs are of more than 12-forms. The main forms or types of DNA are

<table>
<thead>
<tr>
<th>Types of DNA</th>
<th>Type of Helics</th>
<th>No. of Base pairs per turn</th>
<th>Properties</th>
</tr>
</thead>
<tbody>
<tr>
<td>A – Type</td>
<td>Right Handed</td>
<td>11</td>
<td>Most stable and most common form. (Described by Watson and Crick.)</td>
</tr>
<tr>
<td>B – Type</td>
<td>Right Handed</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>C – Type</td>
<td>Right Handed</td>
<td>9 ½</td>
<td>C &amp; D types occur under artificial conditions</td>
</tr>
<tr>
<td>D – Type</td>
<td>Right Handed</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td>Z – Type</td>
<td>Left Handed</td>
<td>12 (6-nucleotides)</td>
<td>Sugar phosphate rail is Zig-Zag, hence named ‘Z’ DNA Pitch 45Å, diameter 18Å.</td>
</tr>
</tbody>
</table>

Connecting Concepts

RNA is double stranded in reoviruses wound tumour virus, rice dwarf virus and mycophages.

- On heating, the 2-strands of DNA separate from each other (called Melting), and on cooling they again hybridize (called Annealing).
- The temperature at which the 2-strands separate completely is known as its melting temperature (Tm) which is specific for each sequence.
- If one sample of DNA has more Tm, this means it has more C = G pairs (having stronger bonds, i.e. 3-hydrogen bonds, difficult to break).

RIBONUCLEIC ACID (RNA)

- It has single helical structure and is mainly of 3-types.
1. **m-RNA (Messenger RNA)**
   - ~5% of total RNA.
   - Base sequence complementary to one DNA strand.
   - Length varies according to the length of the polynucleotide used.
   - Generally exists for a short time.
   - Life span of 1-4 minutes (shortest life).
   - Number of nucleotides generally more than 1500, so it is the longest RNA.

2. **r-RNA (Ribosomal RNA)**
   - 80% of total RNA.
   - Base sequence is similar in all organisms.
   - Synthesized in nucleolar organizing region (NOR) of the DNA.
   - Life span of several days (longest life).
   - Most stable RNA.
   - The enzyme Ribozyme is also a r-RNA.

3. **t-RNA (Transfer RNA)**
   - 15% of total RNA.
   - Average 80 nucleotides per molecule.
   - Smallest of all RNAs.
   - More than 20 different t-RNA may be present in a given cell.
   - Easily soluble, so called soluble RNA (s-RNA) also.
   - Transfers amino acid from cytoplasm to the ribosomal machinery.
   - Acquires Clover leaf structure by folding upon itself.
   - The unusual bases present in tRNA are Dihydouracil, Pseudouridine and Hypoxanthine, inosine etc. This causes coiling of otherwise single-stranded t-RNA into L shaped form or c lover like form.

### Prokaryotic DNA Packaging

- DNA of bacteria such as *E. coli* is a circular, double stranded molecule which contain 4.6 million base pairs.
- The circular DNA is packaged into nucleoid where it is organized into loops or domains bound to a central protein. Scaffold DNA actually is super coiled, i.e., twisted upon itself and complexed with 7 DNA binding proteins like HU, HLP and HNS. These are histone like basic protein (HLP).

### Eukaryotic DNA Packaging

- DNA is organized into beaded structure called nucleosome.
- There is a set of positively charged, basic proteins called histones which are rich in basic amino acids – lysine and arginine. They have positively charged side chains.
- Histones organize into unit of 8 molecules called histone octamer.
- Negatively charged DNA is wrapped around positively charged octamer to form nucleosome.
- One histone octamer has 8 histones.

### Check Point

1. Write the correct value or number of:
   (i) Pitch of B-DNA
   (ii) Base pairs per turn in A-DNA
   (iii) Percentage of r-RNA
   (iv) AT/CG ratio in human.
DNA packaging is best explained by – **Solenoid model**.

- There are 5 classes of histone called H1, H2A, H2B, H3 and H4.
- H1, H2A & H2B are rich in lysine and H3 & H4 are rich in arginine.
- Most conserved histones are \( H_3 \) and \( H_4 \), \( H_1 \) is least conserved.
- One nucleosome (DNA + histone octamer) attaches to other nucleosome with the help of linker DNA associated with H1 protein.
- Histone octamer has 2 molecule each of histone H2A, H2B, H3 and H4.
- DNA takes 1.8 left handed turns around octamer.
- DNA length is shortened about seven fold by winding around nucleosome.

![Structure of Nucleosome](image)

**Fig. 6.1 : Structure of Nucleosome**

- A typical nucleosome contains 200 bp of DNA helix.
- Nucleosome forms chromatin in the form of **bead on string**.
- Chromatin condense/super coil at metaphase stage to form chromosomes.
- Packaging of chromatin to chromosomes occurs with the help of additional set of proteins called **NHC (non-histone chromosomal) proteins**.
- NHC are high molecular weight protein having amino acids - tyrosine & tryptophan.
- On the basis of packaging, chromatin is classified into 2 types – euchromatin and heterochromatin.

(a) **Euchromatin**
   - (i) Transcriptionally active.
   - (ii) Loosely packed, rich in gene concentration.
   - (iii) Lightly stained.

(b) **Heterochromatin**
   - (i) Transcriptionally inactive.
   - (ii) Densely packed.
   - (iii) Darkly stained.

![Bead on a string-structure of chromatin](image)

**Fig. 6.2 : Bead on a string-structure of chromatin**

- Order of packaging is
DNA → Histone octamer → Nucleosome → 6 nucleosome → Solenoid → 7 solenoid → 30 nm fibre → Chromatin → Protein scaffold/nuclear matrix → Radial loops → packaging → Chromosome.

### DNA AS GENETIC MATERIAL

There are many experiments which successfully proved DNA as genetic material. Some of the early experiment are as follows

#### Griffith's Experiment of Bacterial Transformation

- Frederick Griffith (in 1928), a British Medical officer described the phenomenon of bacterial transformation.
- He carried out experiment with Streptococcus pneumoniae (bacterium causing pneumonia) which is used to infect mice.
- It has 2 types of colonies on culture plate – S (smooth due to mucous polysaccharide which makes it infective) and R (rough strain, mucous polysaccharide absent).
- **Steps of experiment are** –
  - S strain (Virulent) → injected into mice → Mice die
  - R strain (Non-virulent) → injected into mice → Mice survive
  - S strain (Heat killed) → injected into mice → Mice survive
  - S strain (Heat killed) + R strain (Live) → injected into mice → Mice die
- By using S Strain (heat killed) and R strain (live) it was concluded that R strain has been transformed by some material of S strain which makes R strain virulent and enable to synthesize smooth polysaccharide. This must be due to transfer of genetic material from S → R strain.

#### Establishment of biochemical nature of transforming genetic material

- Ostwald Avery, Colin Macleod and McCarty in 1933-34 revealed the chemical nature of the transforming substance to be DNA.
- They purified DNA, RNA, protein from heat killed S strain to see which of them could transform R cells → S cells.
- They also observed that protein digesting enzyme (Protease) and RNA digesting (RNase) have no effect on transformation whereas digestion of DNA with DNase would not cause transformation.
- This finding established that transforming genetic material is DNA.

#### Hershey-Chase experiment

- Hershey & Chase (1962) discovered that DNA is the genetic material of bacteriophage.
- Virus which infect bacteria are called bacteriophage.
- Hershey & Chase experimented with T₂ phage which attacks the bacterium E. coli.
- Some virus made to grow on culture containing radioactive sulphur and some on radioactive phosphorus.
- Virus growing on radioactive phosphorus containing culture plate → Radioactive DNA.
- Virus growing on radioactive sulphur containing culture plate → Radioactive protein coat.
- Radioactively labelled sulphur virus infect E. coli bacteria → No radioactivity in bacteria.
- Radioactively labelled phosphorus virus infect E. coli → Radioactivity in E. coli.
- These findings indicated that protein did not enter the bacteria from the viruses but DNA from virus particle enters bacteria as genetic material because of which radioactivity is discovered in bacteria.
Properties of Genetic Material

- Genetic material must fulfill the following criteria:
  - Stably inheritable.
  - Chemically and structurally stable.
  - Stably replicable (undergo replication).
  - Should undergo evolution (mutation/recombination/variation).
  - Should follow Mendel’s laws of inheritance.

Stability of DNA over RNA

- Base pairing/Stacking/Complementarity makes DNA structurally and chemically stable.
- **Denaturation** – Separation of 2 DNA strands in heat conditions.
- **Renaturation** – Restoring of DNA double strands in restored conditions.
  - 2' OH group present at every nucleotide in RNA is reactive group which is prone to nucleophilic attack and makes RNA labile and unstable.
  - RNA has been proved to work in enzymatic fashion – named as ribozyme, and hence proving it be to be more reactive.
  - Presence of thymine instead of uracil in DNA makes it additionally stable, helping in DNA repair and making it suitable as genetic material.
  - DNA is preferred for storage of genetic information and RNA is more suitable for transmission of genetic information.
  - First nucleic/genetic material from evolutionary point of view is thought to be RNA because
    (i) It is catalytic as ribozyme [catalyzing post transcriptional tRNA modifications].
    (ii) For biocatalysis, RNA was replaced by protein enzymes. The proteins are more stable, efficient and catalyse varied type of reaction.
(iii) Single stranded RNA could have given rise to double stranded DNA which is found to be more stable and less susceptible to mutation.

- The concept of central dogma in molecular biology was proposed by Francis Crick (1958). It proposes unidirectional or one way flow of information from DNA to RNA & then to protein.

\[
\text{DNA} \xrightarrow{\text{Transcription}} \text{mRNA} \xrightarrow{\text{Translation}} \text{Polypeptide (protein)}
\]

- Temin reported that retroviruses operates reverse of flow of information or teminism inside the host cells in which the entire process is catalyzed by reverse transcriptase. This is represented as

\[
\text{RNA} \rightarrow \text{DNA} \rightarrow \text{mRNA} \rightarrow \text{Protein}
\]

### Replication

- Formation of new DNA strand from old DNA is called DNA replication or DNA duplication. It occurs just prior to cell division.

- Replication of DNA is semiconservative i.e. from one DNA molecule, two new DNA molecules are produced. In each new DNA molecule, one strand is of parental type and another is formed as new.

- Semiconservative replication of chromosome was experimentally proved by Taylor (1957) in Vicia Faba using triradiated thymidine.

- It is also experimentaly proved by Meselson and Stahl by conducting following experiment:
  
  (a) Culturing *E. coli* for many generations in N\textsuperscript{15} containing culture.
  
  (b) N\textsuperscript{15} was incorporated as nitrogenous base in newly synthesized DNA.
  
  (c) Heavy DNA separated from normal by centrifugation in CsCl (cesium chloride) density gradient.
  
  (d) *E. coli* cells having N\textsuperscript{15} was transferred to N\textsuperscript{14} medium.
  
  (e) Extraction of DNA from *E. coli* cells in step (d) and measured density of ds DNA in CsCl centrifugation.

- **Results of experiment**: After one generation, resultant DNA was hybrid with one strand having N\textsuperscript{15} isotope and other having N\textsuperscript{14}.

- DNA extracted after recycling of procedure produced 2 types of DNA– hybrid and light.
**Mechanism of DNA replication**

DNA polymerase enzyme is responsible for the template directed polymerisation of deoxyribonucleotide triphosphate. It is of 3 types in prokaryotes.

(i) **DNA polymerase I** – DNA repair after replication completes and 5’→3’ polymerisation activity.

(ii) **DNA polymerase II** – Catalyze 5’→3’ synthesis + 3’→5’ exonuclease activity.

(iii) **DNA polymerase III** – DNA synthesis in 5’→3’ direction + 3’→5’ and 5’→3’ exonuclease activity.

Exonuclease activity of polymerases due to which mismatched nucleotide is removed is called **proof reading**.

In eukaryotes, five different DNA-polymerases have been identified — DNA polymerases α, β, γ, δ and ε.

**Requirements of enzyme are**

- All four dNTPs (dATP, dGTP, dTTP and dCTP ), Mg^{2+}.
- DNA template to be copied by DNA polymerase.
- A RNA primer with a free 3’ OH end that can be extended by DNA polymerase enzyme.

**Steps of replication**

- DNA replication occurs during S phase of cell cycle. It requires template and DNA polymerase along with primer.
- DNA double helix is unwound by helicase enzyme and single stranded (ss) DNA is stabilized by SSB-single stranded binding protein.
- **DNA topoisomerase** allows the helix to unwind without causing extensive rotation of the chromosome.
- DNA replication begins at a specific site called ori (origin) which has recognition site for DNA polymerase, which also provides site for attachment of RNA primer.
- RNA primer is essential for DNA replication because without the presence of RNA primer, DNA polymerases cannot add nucleotides. RNA primer is synthesized at 5’ end of new DNA.
- The enzyme which form RNA from DNA are called RNA polymerase. The synthesis of RNA primer is brought about by enzyme primase.
- In **bacterial chromosome**, replication starts at a single origin and both strands of a double helix serve as template for DNA synthesis which proceeds outwards in both directions from single origin (i.e., it is bidirectional).
- Region of DNA undergoing replication forms replication bubble/replication eye having replicating fork moving in opposite direction.
- dsDNA is antiparallel, one strand runs in 5’-3’ direction and its complementary strand runs in 3’-5’. New DNA strand is made against each template strand. DNA polymerase polymerises DNA only in 5’-3’ direction. So template strand with 3’-5’ orientation, new DNA strand is form in continuous manner in 5’-3’ direction. This DNA is called **leading strand**.
- Template strand which has 5’→3’ orientation, DNA polymerase synthesizes short stretches of new DNA (about 1000 nucleotides long) in 5’-3’ direction and then joins these pieces together. These small fragments are called okazaki fragments and new DNA strand made in this discontinuous manner is called **lagging strand**. Okazaki fragments are joined by DNA ligase.
TRANSCRIPTION

- Process of copying genetic information from DNA to RNA is called transcription.
- At a time only one DNA strand is being transcribed into RNA.
- The strand of DNA with polarity 3' → 5' act as template strand and the DNA strand with polarity 5' → 3' act as coding strand.
  
  e.g. 3' – ATGCATGCATGCATGC – 5' → template strand.  
  5' – TACGTACGTACGTACG – 3' → coding strand.
- Transcription is carried out by DNA dependent RNA polymerase.
- Transcription unit is the segment of deoxyribonucleic acid between the sites of initiation & termination of transcription.
- Transcription unit has 3 regions in the DNA.
  (i) A promoter – where RNA polymerase binds.  
  (ii) A structural gene – which will undergo transcription.  
  (iii) A terminator – a site where transcription will end.
- RNA transcription requires enzyme RNA polymerase, DNA template, all four types of ribonucleoside triphosphates (ATP, GTP, CTP & UTP), divalent metal ions Mg$^{2+}$ or Mn$^{2+}$ as cofactor, rho ($\rho$) factor etc.
- RNA polymerase can initiate transcription at specific DNA sequences known as promoters. It then produces an RNA chain which is complementary to the DNA strand used as template.
- RNA polymerase has five polypeptides – $\sigma$, $\beta$, $\beta'$, $\alpha$ and $\omega$.
- Chain of $\beta$, $\beta'$, $\alpha$ & $\omega$ constitute the core enzyme.
- $\sigma$ or sigma factor recognises the promoter region while the remaining core enzymes takes part in transcription.

Process of Transcription:

- Initiation: RNA polymerase recognizes a specific site on DNA, upstream from gene that will be transcribed, called a promoter site and then unwinds DNA locally by recognising –35 sequence.
- **Elongation**: Core enzyme contains polymerization catalytic unit within β subunit. The first nucleotide in RNA transcript is usually pppG and pppA. RNA polymerase then synthesizes rRNA in 5' → 3' direction, using ATP, CTP, GTP, UTP as precursor.

**Transcription Bubble**:
- Region of unwound DNA undergoing transcription.
- RNA transcript forms a transient DNA-RNA hybrid then pulls away from template as transcription proceeds.
- DNA is wound ahead of transcription bubble and after the transcription complex has passed, DNA rewinds.

**Termination**:
- Transcription continues till a termination sequence in form of **GC rich/palindromic region** is reached. DNA of this palindrome is self complementary and basepair internally to form **hairpin structure**. Termination sequence is located downstream/towards 3' end of coding strand.
- **Rho factor** helps in termination of RNA synthesis.

**RNA processing**
- **In prokaryotes**, mRNA transcribed from protein coding genes requires no modification prior to translation. In fact, many mRNA molecules begin to translate even before RNA synthesis has finished.
- **Ribosomal RNA** (rRNA) and **transfer RNA** (tRNA) are synthesized as precursor molecule that do not require **post-transcriptional processing**.

**Fig. 6.8**: Process of Transcription in Bacteria

**Differences between prokaryotic and eukaryotic transcription**
- RNA polymerase of one type in prokaryotes coding for all 3 types of RNA.
- In eukaryotes, RNA polymerase are of 3 types –
  (i) RNA polymerase I : transcribes rRNA (28S, 18S, 5.8S)
  (ii) RNA polymerase II : transcribes mRNA (hnRNA-heterogenous RNA)
  (iii) RNA polymerase III : transcribes tRNA, 5S rRNA and SnRNA (small nuclear RNAs)
- **Transcription and translation** takes place in same compartment (there is no separate cytosol and nucleus in bacteria). So transcription and translation are coupled in bacteria where as in **eukaryotes** transcription and translation occur in nucleus and cytosol respectively and thus compartmentalized.
- RNA produced in **bacteria/prokaryotes** do not undergo extensive processing whereas pre mRNA, rRNA and tRNA in eukaryotes undergo extensive processing.
• In prokaryotes: No splitting event takes place. But in eukaryotes – primary transcript has both exons and introns and introns are non-functional. Now it is subjected to process called **splicing** where **introns are removed** and exons are **joined in defined manner**.

- **Capping**: Unusual nucleotide (methyl guanosine triphosphate) is added to 5' end of mRNA forms cap. CCA segment is also added to t-RNA as terminal addition for specific function.

- **Tailing**: Adenylate residues [200-300] are added at 3' end of a template in independent manner. Fully processed **hnRNA**, now called **mRNA** which is transported out of nucleus for translation.

- *In vitro* RNA was firstly synthesized by Ochoa.

- **RNA splicing**: Intron sequences are removed by process known as splicing and ligates the ends of exon sequences together.

- **RNA editing**: The sequence of an mRNA molecule may be changed after synthesis and processing by RNA editing.
  Example: In *trypanosoma* mitochondrial RNA, half of uridines in final mRNA are acquired after editing.

- **Gene**: A gene is defined as the functional unit of inheritance.

- **DNA sequence coding for a polypeptide** is a **cistron**.

- **Structural gene** that codes for one polypeptide as in eukaryotes is called **monocistronic**.

- **Structural gene** that codes for more than one polypeptide as in prokaryotes is called **polycistronic**.

- **Split gene**: Structural gene that has coding/expressed sequences called **exons** alternating with intervening sequences **introns** are called spilt genes eg. eukaryotic genes.

**GENETIC CODE**

• Transfer of genetic information from a polymer of nucleotides to a polymer of amino acids is called **translation**. This is accomplished with the help of genetic code which is row of three consecutive nucleotides – coding for 20 amino acids.

• Codon exists on mRNA, corresponding anticodon exists on tRNA. Protein synthesis occurs with the help of r-RNA.

**Salient features of genetic code –**

(a) **Triplet nature**: Genetic codes are triplet as three adjacent bases codes for one amino acid. 64 possible codons are there. 61 code for 20 amino acids and 3 do not code for any amino acid. These are called **stop codon** – UAA, UAG, UGA.

(b) **Initiation codon**: This codon code for initiating the synthesis of polypeptide chain **AUG** and **GUG** (rarely) are initiating codons. **AUG** codes for methionine and GUG for raline.

(c) **Degeneracy of codon**: One amino acid is coded by several codons. As a result of degeneracy, a mutation that changes only a single nucleotide in DNA, changes a single nucleotide in corresponding mRNA, has no effect on amino acid sequence of the encoded polypeptide.

(d) **Wobble position**: During protein synthesis, each **codon** is recognized by a triplet of base, called **anticodon** present in a specific tRNA molecule. Each base in codon pairs with its complementary base in anticodon. However, the pairing of 3rd base of codon is less stringent than rest of 2 bases. This 3rd position is called **wobble position** for e.g. UCU and UCC both code for serine as only last nucleotide is different while UCU code for serine while UAU codes for tyrosine.

(e) **Universality of code**: Amino acids in all living organism coded by the same codons except some mitochondrial codons.

(f) **Reading frame**: Since the sequence of mRNA molecule is read in group of three nucleotides [codon] from 5' end, it can be read in three possible reading frame. Usually there is only one reading frame include several termination (stop) codons.
**Fig. 6.9**: The Codons for the various Amino Acids

<table>
<thead>
<tr>
<th>First Position</th>
<th>Second Position</th>
<th>Third Position</th>
</tr>
</thead>
<tbody>
<tr>
<td>U</td>
<td>U</td>
<td>C</td>
</tr>
<tr>
<td>U</td>
<td>C</td>
<td>A</td>
</tr>
<tr>
<td>A</td>
<td>G</td>
<td>U</td>
</tr>
<tr>
<td>U</td>
<td>U</td>
<td>C</td>
</tr>
<tr>
<td>U</td>
<td>C</td>
<td>A</td>
</tr>
<tr>
<td>A</td>
<td>G</td>
<td>U</td>
</tr>
</tbody>
</table>

*Reading frame 1:*

UUA UGA GCG CUA AAC
Leu Stop* Ala Leu Asn
— Not possible

*Reading frame 2:*

UUU AUU GAG CGC UAA AU
Tyr Glu Arg Stop*
— Not possible

*Reading frame 3:*

UU AUG ACG GCU AAA U
Met Ser Ala Lys
— Produces functional protein

(g) **Overlapping genes**: Usually one sequence of base encodes only a single protein, however in some bacteriophage DNA, genes overlap, with each gene being in a different reading frame. This is overlapping gene.

(h) **Continuity of codons**: Codons are read in mRNA in a continuous fashion, there are no punctuations.

(i) **Specificity of codon**: One codon codes for only one amino acid.
- Genetic code was deciphered by many researchers such as Khorana, Nirenberg and Mothali.

**tRNA: THE ADAPTOR MOLECULE**

- tRNA is intermediate link between reading of codons on mRNA and formation of amino acid chain for protein.
- tRNA is also called adaptor or supernatant RNA, soluble RNA (sRNA).
- Adaptor role was assigned to tRNA by Francis Crick. The first person to determine the base sequence of a tRNA molecule was Robert Kolley.
- tRNA has 4 arms, folded into clover leaf like structure and amino acid acceptor branch. Clover leaf secondary structure is due to internal base pairing.

**Structure of tRNA**:

In t-RNA, about half of the nucleotides are base paired to produce paired stems. Five regions are unpaired or single stranded. These are:

(i) **Anticodon loop** contains 7 bases out of which 3 nucleotides forms anticodon which will form base pair with complementary codon in mRNA during translation.

(ii) **D/DHU arm** with **D loop** contains dihydrouracil – an unusual pyrimidine. It is binding site for attaching aminoacyl synthetase enzyme.

(iii) **T/ψC arm** : Pseudouracil (ψ) is the modified base present in T ψ C. This loop is binding site of ribosomes.
(iv) **Variable arm**: With 3-21 nucleotide.
(v) **Amino acid acceptor stem**: Site where amino acid attaches at 3' OH group of CCA sequence.

- 3D structure of tRNA was proposed by S. H. Kim in 1973.
- tRNA helps to transport amino acids from the surrounding cytoplasm to the site of protein synthesis.

**TRANSLATION**

- The process of decoding the message from mRNA to protein is called translation (protein synthesis).
- The main step in protein synthesis are **initiation, elongation & termination of polypeptide chain**.
- During translation, mRNA is read in 5' → 3' direction. Aminoacyl tRNA carry specific amino acid and recognises the corresponding codons on mRNA.
- Polypeptide chain is synthesized in N → C terminal.
- It requires ATP to activate tRNA and form aminoacyl tRNA. Catalyzed out by **activating enzymes**, known as **aminoacyl tRNA synthetases**. In the presence of ATP, an amino acid combines with its specific aminoacyl-tRNA synthetase. Mg^{2+} is required in this reaction.
- It produces **amino-acyl-adenylate-enzyme complex**. The energy made available to amino acid during its activation is later used in formation of peptide bonds.

\[
\begin{align*}
\text{Amino acid} & + \text{ATP} + \text{E} & \xrightarrow{\text{Mg}^{2+}} & \text{AA~AMP} - \text{E} + \text{PPI} \\
& & & \text{Pyrophosphate}
\end{align*}
\]

- **Aminoacylation of tRNA**. The complex reacts with tRNA specific for the amino acid to form aminoacyl-tRNA complex. Enzyme and AMP are released. tRNA complexed with amino acid is sometimes called **charged tRNA**. The amino acid is linked to 3-OH-end of tRNA through its –COOH group,

\[
\begin{align*}
\text{AA~AMP} - \text{E} + \text{tRNA} & \rightarrow \text{AA~tRNA} + \text{AMP} + \text{E} \\
& \text{aminoacyl adenylate enzyme}
\end{align*}
\]

- **Initiation**. It requires factors called **initiation factors**. There are three initiation factors in prokaryotes – IF3, IF2 and IF1, Eukaryotes have nine initiation factors – eIF2, eIF3, eIF1, eIF4A, eIF4B, eIF4C, eIF4D, eIF5, eIF6.

Out of these IF3 or eIF2 is attached to smaller subunit of ribosomes in the dissociated state.

- mRNA attaches itself to smaller subunit of ribosomes in the region of its cap. The nucleotides complementary to the nucleotides present at the 3' end of tRNA.

- The attachment is such that initiation codon of mRNA (AUG or GUG) comes to lie at P-site.

- Initiation factor already present in smaller subunit catalyses the reaction (eIF2 in eukaryotes and IF3 in prokaryotes).

\[
\begin{align*}
40S - \text{Subunit} + \text{mRNA} & \xrightarrow{\text{eIF2}} 40 \, S - \text{mRNA} \\
& \text{Aminoacyl tRNA complex specific for the initiation codon (methionine-tRNA or valine-tRNA) reaches the P-site.}
\end{align*}
\]

- Anticodon (e.g., UAC) forms temporary hydrogen bonds with the initiation codon (e.g., AUG) of mRNA.

- The codon-anticodon recognition occurs in the presence of initiation factor eIF3 in eukaryotes and IF2 in prokaryotes. The step also requires energy which is provided by GTP.

\[
\begin{align*}
40S - \text{mRNA} + \text{tRNA}_M^e & \xrightarrow{\text{eIF3}} GTP \rightarrow 40 \, S - \text{mRNA} - \text{tRNA}_M^e \\
& \text{Aminoacyl tRNA complex specific for the initiation codon (methionine-tRNA or valine-tRNA) reaches the P-site.}
\end{align*}
\]
In the presence of Mg\(^{2+}\), the larger subunit of ribosome now combines with 40S-mRNA-tRNA\(^{\text{Met}}\) complex to form intact ribosomes.

Coming together of the two subunits of ribosomes is called association. The intact ribosomes encloses the mRNA-tRNA complex present at the P-site but keeps the A-site exposed.

\[
\text{40S} - \text{mRNA} + \text{tRNA}^{\text{Met}} + 60S \xrightarrow{\text{efF}1, \text{efF}4} 80S - \text{mRNA} - \text{tRNA}^{\text{Met}}
\]

Each ribosome has 3 binding sites for tRNA:
- A site – Acceptor site. Incoming amino acyl tRNA binds at A site.
- P site – Peptidyl site. tRNA linked to growing polypeptide chain.
- E site – Exit site. It binds diacylated tRNA to be release from ribosome.

### Elongation

- **Amino acyl tRNA binding**: Acylated tRNA corresponding to 2nd codon binds to A site as ribosome in presence of elongation factor, using GTP.
- **Peptide bond formation**: Formation of peptide bond between C terminal of amino acyl tRNA at P site and amino acyl tRNA at A site by enzyme peptidyl transferase which is an RNA - enzyme.

### Translocation

Deacylated tRNA moves from P → E site. It requires the factor translocase and energy from GTP.

- Dipeptidyl tRNA moves A → P site.
- Ribosome moves along mRNA for next codons in A site.
- The cycle is repeated till all the codon have been exposed to A-site. The tRNA released comes back to cytoplasm to pick up another amino acid.

### Termination

- When one of 3 termination/stop codons [UAG, UAA and UGA] are positioned in A site, for which there are no tRNA, termination of translation occurs in presence of release factor (RF) which causes cleaving of bond between polypeptide and tRNA in P site.
- Polypeptide leaves ribosome followed by mRNA and now tRNA ready to start next cycle of translation.
  - Ribosomes attached to RER synthesize proteins which are translocated through the lumen of ER.
  - After synthesis the protein may be incorporated in membrane or may be secreted from the cell.

### Regulation of Gene Expression

- Gene expression is the mechanism at the molecular level by which a gene is able to express itself in the phenotype of an organisms.
In eukaryotes, the regulation could be exerted at:
  (i) Transcriptional level (formation of primary transcript).
  (ii) Processing (RNA splicing) level.
  (iii) Transport of mRNA from nucleus to cytoplasm.
  (iv) Translational level.

There are 2 types of genes on the basis of gene expression:

1. **Constitutive genes**: Housekeeping genes – A number of protein coding genes active in all cells and all the time. They are required for housekeeping functions such as enzymes of glycolysis, citric acid cycle and proteins of electron transport chain.

2. **Facultative/Inducible genes**: Genes which are active only in specific cell type and are responsible for defining the specific character and function of these cells. *e.g.*, Immunoglobulin genes in lymphocytes, myosin in muscle.

   - Mostly genes are regulated at transcriptional level.
   - Many protein coding genes in bacteria are regulated together in operon which serves as a transcriptional unit that are coordinately regulated.

**Gene expression is of three types**:

- It is a regulation which is switched on in response to the presence of substrate. In yeast, lactose metabolising enzymes develop only when the fungus is grown in the medium having lactose. Later on bacteria were also shown to synthesise enzymes depending upon substrate and process is called **induction**.

- **Inducer** is a metabolizable compound that turns on transcription of inducible gene.

- **Constitutive**. A regulation is absent. The genes and hence their enzymes remain operational throughout.

- **Repressible**. It is regulation in which the product of gene activity stops the activity of the gene. Repressor is the proteinaceous component which blocks the activity of operator gene.

- One of the best studied example of gene expression is lactose (lac) **operon**. Its model is given by Jacob & Monod in 1961.

- **Operon**: Operons are segments of genetic material (DNA) which function as single regulated units that can be switched on or switched off.

**Check Point**

1. tRNA is also known as supernatant RNA or soluble RNA.
2. Site where amino acid is attached to tRNA is 5' end.
3. Formation is initiation complex requires 30S subunit, initiation factors, mRNA and tRNA.
4. Constitutive genes are also known as housekeeping genes.
5. Inducer is metabolizable compound that turns off the lac operon.
Lactose or lac operon of *E. coli* contains three (Z, Y, A) structural genes which produces enzymes for the degradation of lactose to glucose & galactose.

- **Z** produces \( \beta\)-galactosidase for splitting lactose into glucose & galactose.
- **Y** produces \( \beta\)-galactoside permease (membrane bound proteins) which is required in entry of the lactose/galactose in the cell.
- **A** produces \( \beta\)-galactoside transacetylase enzyme that transfers an acetyl group from acetyl CoA to \( \beta\)-galactosides.

**Operator gene**: DNA sequence that regulates transcription of the structural genes.

**Regulator gene**: Encodes a protein that recognizes operator sequence.

The regulator gene codes for the repressor protein which blocks the operator.

It has two allosteric sites, one for attaching to operator gene and second for binding to inducer. After coming in contact with inducer the repressor undergoes conformational change in such a way that it is unable to combine with operator.

**Inducer**: It is a chemical (substrate, hormone or some other metabolite) which after coming in contact with the repressor, changes the latter into non-DNA binding state so as to free the operator gene.

The inducer for lac-operon of *Escherichia coli* is lactose (actually allolactose, or metabolite of lactose).

**CAP**: It is activator called catabolic activator protein. It exerts a positive control in lac-operon because in its absence RNA polymerase is unable to recognise promoter gene.

Its gene is located away from the operon but the receptor CAP site occurs near the lac promoter. CAP activates lac genes only when glucose is absent.

**Regulation mechanism of lac operon**

- Few molecules of \( \beta\)-galactosidase in cell before induction converts lactose to allolactose which turns on transcription of these three genes in the lac operon.
- Allolactose is an inducer.
- The repressor of operon is synthesized from I gene. The repressor protein binds to operator region of the operon and prevents RNA polymerase from transcribing the operon.
- Transcription and formation of mRNA occurs in absence of repressor and presence of inducer (Lactose). RNA polymerase binds at the promotor region that lies upstream of structural genes.
- Regulation of the operon by repressor is called negative regulation as it decreases expression of structural gene.
- In positive control of gene expression, regulatory protein binds to DNA and increases rate of transcription. In this case the regulating protein is called an activator.

**Human Genome Project (HGP)**

- HGP established whole genome of human with the help of genetic engineering techniques, cloning techniques and bioinformatics.
- It was an ambitious international project which began in 1990. The goal of projects are :
  1. To develop ways of mapping the human genome at increasing fine level of expression.
  2. To store this information in database and develop tools for data analysis.
- This project was coordinated by U.S. Department of Energy and National Institute of Health. The Wellcome trust (U.K.) became a major partner with contribution from Japan, France, Germany, China and others.
Findings of Human Genome Project

- Identification of 20,000-25,000 genes in human DNA.
- Determination of sequence of 3 billion base pairs that make up human DNA.
- The average gene has 3000 bases, but their sizes vary greatly. The largest human gene is **dystrophin**, which contains 2.4 million bases.
- 99% of genome is identical with each other, genomically speaking, every alive human being is exactly the same.
- Only less than 2% of genome is exons, the protein coding sequences.
- Approximately 1 million copies of short 5 to 8 bp long repeated sequence cluster around the centromere and near the ends of chromosome known as **junk DNA**.
- Repetitive sequences are stretches of DNA sequences that are repeated many times, sometimes hundred to thousand times. They are thought to have no direct coding functions, but they shed light on chromosome structure, dynamics and evolution.
- Chromosome 1 has most genes (2968), and the Y has the fewest (231).
- Scientists have identified about 1.4 million locations where single-base DNA differences (SNPs – **single nucleotide polymorphism**, pronounced as ‘snips’) occur in humans. This information promises to revolutionise the processes of finding chromosomal locations for disease-associated sequences and tracing human history.

Implications of Human Genome Project (HGP)

- Sequence more than 1200 genes that are responsible for common cardiovascular ailments, endocrine disease like diabetes, neurological disorder like Alzheimer, deadly coma and many more.
- HGP holds a key to design drugs, genetically modified diets and finding our genetic identity.
- Many non-human model organisms such as bacteria, yeast, **Caenorhabditis elegans** (a free living non pathogenic nematode), **Drosophila** (fruit fly), plants (rice and **Arabidopis**) have also been sequenced.

DNA FINGERPRINTING

- The technique of DNA fingerprinting was developed by **Dr. Alec Jeffrey** in 1984.
- It is a technique generally using repeated sequences (repetitive DNA) in the human genome that produces a pattern of band that is unique for every individuals.

Principle of DNA fingerprinting

- Every individual organism is unique. DNA sequences has some specific regions in DNA called repetitive DNA → which are short stretch repeated many times.
- These short nucleotide repeats vary in number from person to person and are called **variable number of tandem repeat** (VNTR). The VNTR of 2 persons may be of same length and sequence at certain sites, but vary at others.
- A child might inherit a chromosome with 6 tandem repeats from mother and six tandem repeated 4 times from father. This is an example of **DNA polymorphism**. Polymorphism arised due to mutation.
- VNTR/Satellite DNA/repetitive DNA are distinguished as different peaks from bulk genomic DNA during density gradient centrifugation. Bulk DNA forms a major peak and other satellite DNA makes small peaks.
- VNTR belongs to class of satellite DNA referred to as minisatellite. Size of VNTR varies from 1 to 20 bp.
- Pattern of VNTR probe hybridisation in autoradiogram gives many bands of different size.
- These pattern differ from individual to individual except in case of monozygotic twins.
Techniques for DNA fingerprinting

- DNA is extracted from cells like blood/semen/skin/follicle root of hair in a high speed refrigerated centrifugal.
- Amplification of DNA by PCR.
- Restriction digestion of sample DNA.
- Electrophoresis through gel (agarose polymer).
- Visualization of DNA fragments by staining with dye and observation under UV lamps.
- Double stranded DNA is split into ssDNA using alkaline chemicals.
- Separated DNA sequences are transferred to nylon or nitrocellulose sheet over gel. This is called southern blotting.
- Nylon sheet is immersed into bath having probe/marker.
- Probe/marker are radioactive, synthetic DNA fragments of known sequences are added.
- The probe targets a specific nucleotide sequences which are complementary to VNTR sequences and hybridize there.
- X ray film is exposed to nylon sheet containing radioactive probe. Dark band appear at probe sites which are scanned using scanner.

![Diagram of DNA fingerprinting](image)

Fig. 6.13 : Schematic representation of DNA fingerprinting : Few representative chromosomes have been shown to contain different copy number of VNTR. The two alleles (paternal and maternal) of a chromosome also contain different copy numbers of VNTR. It is clear that the banding pattern of DNA from crime scene matches with individual B, and not with A.

Application of DNA fingerprinting

- Identification of criminals in forensic laboratories.
- Determination of paternity disputes/legal cases.
- Verification of migrants from one country to another.
- Identification of racial groups to map biological evolution.

Check Point

1. Operons are the segments of _______ which function as _______ unit.
2. Regulator gene code _______ that recognizes _______.
3. Only less than _______ percent of DNA codes for protein.
4. Separated DNA sequences are transferred to nylon or nitrocellulose sheet, the process is called _______.
5. DNA fingerprinting is used to identify _______ to map _______.

Fill in the blanks

1. Operons are the segments of _______ which function as _______ unit.
2. Regulator gene code _______ that recognizes _______.
3. Only less than _______ percent of DNA codes for protein.
4. Separated DNA sequences are transferred to nylon or nitrocellulose sheet, the process is called _______.
5. DNA fingerprinting is used to identify _______ to map _______.
1. During infection of *E. coli* cells by bacteriophage T₂,
   (1) proteins are the only phage components that actually enter the infected cell.
   (2) both proteins and nucleic acids enter the cell.
   (3) only proteins from the infecting phage can also be detected in progeny phage.
   (4) only nucleic acids enter the cell.

2. The correct order of events for synthesis of the lagging strand is
   (1) Primase adds RNA primer, DNA polymerase III creates a stretch, DNA polymerase I removes the primer, and ligase seals the gaps.
   (2) Primase adds primer, DNA polymerase I removes the primer, DNA polymerase extends the segment, and ligase seals the gap.
   (3) Ligase adds bases to the primase, the primase generates the polymerase 1, polymerase III adds to the stretch, helicase winds the DNA.
   (4) Helicase unwinds the DNA, primase creates a primer, DNA polymerase I elongates the stretch, DNA polymerase III removes the primer, and ligase seals the gaps in the DNA.

3. Identify A, B and C of a nucleosome.
   ![Core of histone molecules diagram]
   (1) A – DNA; B – H1 histone; C – Histone octamer
   (2) A – H1 histone; B – DNA; C – Histone octamer
   (3) A – Histone octamer; B – RNA; C – H1 histone
   (4) A – RNA; B – H1 histone; C – Histone octamer

4. Human Genome Project (HGP) is closely associated with the rapid development of a new area in biology called as
   (1) biotechnology
   (2) bioinformatics
   (3) biogeography
   (4) bioscience

5. Match the following and choose the correct option –
<table>
<thead>
<tr>
<th><strong>Column I</strong></th>
<th><strong>Column II</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>I. Helicase</td>
<td>(p) Joining of nucleotides</td>
</tr>
<tr>
<td>II. Gyrase</td>
<td>(q) Opening of DNA</td>
</tr>
<tr>
<td>III. Primase</td>
<td>(r) Unwinding of DNA</td>
</tr>
<tr>
<td>IV. DNA polymerase III</td>
<td>(s) RNA priming</td>
</tr>
</tbody>
</table>

6. Satellite DNA
   (1) is classified in many categories such as micro-satellites, minisatellites, etc. on the basis of base composition length of segments and number of repetitive units.
   (2) normally does not code for any protein.
   (3) shows polymorphism.
   (4) forms the basis of DNA finger printing.

7. Polymorphism in DNA sequence
   (1) is the basis of genetic mapping of human genome.
   (2) arises due to mutation.
   (3) is the basis of DNA finger printing.
   (4) None of the above

8. Before the discovery of DNA, why was the hereditary material thought to be made of proteins and not nucleic acids?
   (1) Nucleic acids are made up of 20 different bases, while proteins are made up of only 5 amino acids.
   (2) Protein subunits can combine to form larger proteins.
   (3) Proteins seemed to be much more diverse chemically.
   (4) Proteins can be enzymes.

9. What are the three major properties of genes that are explained by the structure of DNA?
   (1) They contain information, direct the synthesis of proteins, and are contained in the cell nucleus.
   (2) They contain nitrogenous bases, direct the synthesis of RNA, and are contained in the cell nucleus.
   (3) They encode the organisms phenotype, are passed on from one generation to the next, and contain nitrogenous bases.
   (4) They contain information, replicate exactly, and change to produce a mutation.

10. DNA replication in eukaryotes differs from replication in bacteria because
    (1) synthesis of the new DNA strand is from 3’ to 5’ in eukaryotes and from 5’ to 3’ in bacteria
    (2) synthesis of the new DNA strand is from 5’ to 3’ in eukaryotes and from 3’ to 5’ in bacteria
    (3) there are many replication forks in each eukaryotic chromosome and only one in bacterial DNA
    (4) synthesis of the new DNA strand is from 5’ to 3’ in eukaryotes and is random in prokaryotes.

11. The error rate of changing an incorrect base with another incorrect base during proofreading is
12. RNA primers are necessary in DNA synthesis because
   (1) DNA polymerase can only add to an existing strand of nucleotides.
   (2) DNA polymerase can only add to an existing RNA strand.
   (3) DNA primase is the first enzyme in the replication complex.
   (4) All of the above

13. If a nucleotide lacking a hydroxyl group at the 3' end is added to a PCR, result would be
   (1) no additional nucleotides would be added to a growing strand containing that nucleotide.
   (2) strand elongation would proceed as normal.
   (3) nucleotides would only be added at the 5' end.
   (4) *Thermus aquaticus* DNA polymerase would be denatured.

14. SNP which is pronounced as “snips” stands for
   (1) small nuclear protein
   (2) single nucleotide particle
   (3) single nucleotide polymorphism
   (4) small nicking points

15. The difference(s) between mRNA and tRNA is / are that –
   I. mRNA has more elaborated 3-dimensional structure due to extensive base-pairing.
   II. tRNA has more elaborated 3-dimensional structure due to extensive pairing.
   III. tRNA is usually smaller than mRNA.
   IV. mRNA bears anticodon but tRNA has codons.
   (1) I, III (2) I, II, III, IV (3) II, III (4) I, II, III

16. DNA replication is
   (1) conservative and discontinuous.
   (2) semiconservative and semidiscontinuous.
   (3) semiconservative and discontinuous.
   (4) conservative.

17. The termination triplet in translation is
   (1) UAU (2) UAA (3) UAC (4) UGC

18. A nucleotide is formed by
   (1) purines, pyrimidines and phosphate
   (2) purines, sugar and phosphate
   (3) nitrogen base, sugar and phosphate
   (4) pyrimidines, sugar and phosphate

19. The process of transfer of genetic information from DNA to RNA/formation of RNA from DNA is
   (1) transversion (2) transcription (3) translation (4) translocation

20. *Escherichia coli* fully labelled with $^{15}$N is allowed to grow in $^{14}$N medium. The two strands of DNA molecule of the first generation bacteria have
   (1) different density and do not resemble with their parent DNA
   (2) different density but resemble with their parent DNA
   (3) same density and resemble with their parent DNA
   (4) same density but do not resemble with their parent DNA

21. The process of translation is
   (1) ribosome synthesis (2) protein synthesis
   (3) DNA synthesis (4) RNA synthesis

22. During DNA replication, the strands separate by
   (1) DNA polymerase
   (2) topoisomerase
   (3) unwindase/helicase
   (4) gyrase

23. Because most of the amino acids are represented by more than one codon, the genetic code is
   (1) overlapping (2) wobbling
   (3) degenerate (4) generate

24. Who proved that DNA is basic genetic material?
   (1) Griffith (2) Watson
   (3) Boveri and Sutton (4) Hershey and Chase

25. Initiation codon of protein synthesis (in eukaryotes) is
   (1) GUA (2) GCA
   (3) CCA (4) AUG

26. Protein helping in opening of DNA double helix in form of replication fork is
   (1) DNA gyrase (2) DNA polymerase I
   (3) DNA ligase (4) DNA topoisomerase

27. DNA template sequence of CTGATAGC is transcribed over mRNA as
   (1) GUCTUTCG (2) GACUAUCG
   (3) GAUTATUG (4) UACTATCU

28. In *Escherichia coli*, lac operon is induced by
   (1) lactose (2) promoter gene
   (3) β-galactosidase (4) I-gene

29. The wild type *E. coli* cells are growing in normal medium with glucose. They are transferred to a medium containing only lactose as sugar. Which of the following changes takes place?
   (1) The lac operon is repressed
   (2) All operons are induced
   (3) The lac operon is induced
   (4) *E.coli* cells stop dividing

30. Okazaki fragments are seen during
   (1) transcription (2) translation
   (3) replication (4) transduction
1. In some viruses RNA is present instead of DNA indicating that
   (1) their nucleic acid must combine with host DNA before
   replication.
   (2) they cannot replicate.
   (3) there is no hereditary information.
   (4) RNA can act to transfer heredity.

2. **Lac** operon is
   (1) arabinose operon (2) repressible operon
   (3) inducible operon (4) overlapping genes

3. Double hydrogen bonds occur in DNA between
   (1) adenine and thymine
   (2) uracil and thymine
   (3) adenine and guanine
   (4) thymine and cytosine

4. Hydrogen bonds between cytosine and guanine are
   (1) 1 (2) 2
   (3) 3 (4) 4

5. Hereditary information is indicated by
   (1) number of nucleic acids.
   (2) position of nucleic acids.
   (3) sequence of nucleic acids.
   (4) All the above

6. A mutation at one base of first codon of a gene forms a
   nonfunctional protein is
   (1) nonsense mutation
   (2) reverse mutation
   (3) frame shift mutation
   (4) mis-sense mutation

7. DNA synthesis can be measured by estimating incorporation
   of radio-labelled
   (1) uracil (2) ribose sugar
   (3) thymidine (4) adenine

8. tRNA recognises ribosome by
   (1) T π C loop (2) DHU loop
   (3) anticodon (4) AA-site.

9. Enzyme required for removing RNA primer during DNA
   replication is
   (1) primase (2) ligase
   (3) DNA polymerase I (4) DNA polymerase III

10. DNA is present in
    (1) nucleus (2) chloroplasts
    (3) mitochondria (4) All the above

11. Beadle and Tatum produced mutant strain of *Neurospora*
    by
    (1) X-rays (2) UV rays
    (3) Beta rays (4) Gamma rays

12. Maximum formation of RNA occurs in
    (1) cytoplasm (2) nucleoplasm
    (3) nucleolus (4) ribosome

13. Regulated unit of genetic material is termed as
    (1) operon (2) regulator gene
    (3) operator gene (4) okazaki segment

14. Circular DNA is found in
    (1) viruses
    (2) bacteria, chloroplasts and mitochondria
    (3) chloroplasts and mitochondria alone
    (4) All the above

15. The process of multiplication of DNA from DNA is known
    as
    (1) replication (2) duplication
    (3) transcription (4) translation

16. DNA acts as a template for synthesis of
    (1) DNA
    (2) RNA
    (3) Both DNA and RNA
    (4) Protein

17. Code transfer for synthesis of polypeptide involves
    (1) DNA, tRNA, rRNA and mRNA.
    (2) mRNA, tRNA, rRNA and DNA.
    (3) tRNA DNA, mRNA and rRNA.
    (4) DNA, mRNA, tRNA and amino acids.

18. A gene that takes part in the synthesis of polypeptide is
    (1) structural gene (2) regulator gene
    (3) operator gene (4) promoter gene

19. Which nitrogen base is absent in RNA?
    (1) Adenine (2) Cytosine
    (3) Thymine (4) Guanine

20. Codon AUG specifies
    (1) methionine (2) valine
    (3) tyrosine (4) phenylalanine

21. Nucleoside is
    (1) nitrogen base + phosphate
    (2) phosphate + sugar
    (3) nitrogen base + sugar
    (4) nitrogen base + sugar + phosphate
22. Okazaki fragments give rise to Okazaki fragments give rise to [BHU 1986, Kerala 2001]
   (1) master strand (2) sense strand
   (3) lagging strand (4) leading strand

23. Nonsense codon takes part in [DPMT 2001]
   (1) terminating message of gene controlled protein synthesis.
   (2) formation of unspecified amino acids.
   (3) Conversion of sense DNA into non-sense one
   (4) Releasing tRNA from polypeptide chain

24. Operon model of gene regulation and organisation of prokaryotes was proposed by [MP PMT’93, 2000, 01]
   (1) Meselson and Stahl (2) Wilkins and Franklin
   (3) Beadle and Tatum (4) Jacob and Monod

25. The scientists involved in discovery of DNA as chemical basis of heredity were [MP PMT 2002]
   (1) Hershey and Chase
   (2) Griffith and Avery
   (3) Avery, MacLeod and McCarty
   (4) Watson and Crick

26. Frame shift mutation occurs when [AIIMS 2002]
   (1) base is deleted or added
   (2) base is added
   (3) base is deleted
   (4) anticodons are not present

27. Change in sequence of nucleotides of DNA is [CBSE 2002]
   (1) mutagen (2) recombination
   (3) mutation (4) translation

28. Replacement of a purine base with another purine base is [JIPMER 2002]
   (1) somatic mutation (2) addition mutation
   (3) deletion mutation (4) substitution mutation

29. Barbara McClintock is famous for her work on [Har. PMT 2002]
   (1) rice (2) wheat
   (3) maize (4) sugarcane

30. Triplet UUU codes for [Orissa 2003]
   (1) leucine (2) methionine
   (3) phenylalanine (4) glycine.

   (1) protein (2) DNA
   (3) all parts (4) Both (1) and (2)

32. Information flow or central dogma of modern biology is [Keral 2000, Orissa 2003, AMU 2003, Manipal 2004]
   (1) RNA → Proteins → DNA
   (2) DNA → RNA → Proteins
   (3) RNA → DNA → Proteins
   (4) DNA → RNA → Proteins.

33. Polypeptide chain in eukaryotes is initiated by [AMU 1997, 2005]
   (1) glycine (2) leucine
   (3) methionine (4) lysine.

34. Supercoiled DNA occurs in [Wardha 2005]
   (1) prokaryotes as well as eukaryotes
   (2) prokaryotes only
   (3) eukaryotes only
   (4) none of these

35. Antibiotic inhibiting interaction between tRNA and mRNA during protein synthesis in bacteria is [CBSE 2006]
   (1) tetracycline (2) neomycin
   (3) erythromycin (4) streptomycin

36. Ligase is an enzyme required for [BHU 1994, AIIMS 1994, COMED–K’s 2006]
   (1) breaking of DNA (2) joining DNA bits
   (3) renaturation of DNA (4) proof reading

37. One gene one enzyme hypothesis was proposed by [Orissa 2007]
   (1) Khorana and Nirenberg
   (2) Beadle and Tatum
   (3) Bateson and Punnet
   (4) Bridges

   (1) UUG, UAG and UCG
   (2) UAA, UAG and UGA
   (3) UUG, UGC and UCA
   (4) UCG, GCG and ACC

   (1) peptide bonds (2) phosphodiester bonds
   (3) hydrogen bonds (4) S – S bonds

40. C-value paradox is [CPMT 2007]
   (1) diploid DNA content
   (2) haploid DNA content
   (3) variation in C-value
   (4) constancy of C-value

41. DNA is acidic due to [MP PMT 2007]
   (1) sugar (2) purine
   (3) phosphoric acid (4) pyrimidine

42. RNA polymerase III transcribes [COMED-K’s 2008]
   (1) tRNA (2) ssDNA
   (3) mRNA (4) reverse transcriptase

43. Larger subunit of ribosome produces [COMED- K’s’08]
   (1) gyrase (2) RNA-polymerase
   (3) topoisomerase (4) peptidyl transferase

44. The area of unwinding and separation of DNA strands during replication is called [CPMT 2009, Orissa 2009]
   (1) origin (2) initiation point
   (3) primer (4) replication fork
45. Variable part of DNA molecule is [Orissa 2009]
(1) phosphate  (2) sugar
(3) nitrogen base  (4) All the above

46. T.O. Diener discovered a: [CBSE PMT 2009]
(1) free infectious DNA
(2) infectious protein
(3) bacteriophage
(4) free infectious RNA

47. What is not true for genetic code? [CBSE PMT 2009]
(1) It is nearly universal
(2) It is degenerate
(3) It is unambiguous
(4) A codon in mRNA is read in a non contiguous fashion

48. Removal of introns and joining the exons in a defined order in a transcription unit is called: [CBSE PMT 2009]
(1) capping (2) transformation
(3) splicing (4) tailing

49. Semi-conservative replication of DNA was first demonstrated in: [CBSE PMT 2009]
(1) Escherichia coli
(2) Streptococcus pneumoniae
(3) Salmonella typhimurium
(4) Drosophila melanogaster

50. Whose experiments cracked the DNA and discovered unequivocally that a genetic code is a ‘triplet’ [CBSE PMT 2009]
(1) Hershey and Chase
(2) Morgan and Sturtevant
(3) Beadle and Tantum
(4) Nirenberg and Mathaei

51. Select the two correct statements out of the four (a–d) given below about lac operon.
(i) Glucose or galactose may bind with the repressor and inactivate it
(ii) In the absence of lactose the repressor binds with the operator region
(iii) The z-gene codes for permease
(iv) This was elucidated by Francois Jacob and Jacque Monod

The correct statements are:
(1) (ii) and (iii)  (2) (i) and (iii)
(3) (ii) and (iv)  (4) (i) and (ii)

52. What would be the correct base sequence in mRNA for the given DNA strand?
5′ – AATGCCTTAAGC – 3′ [Kerala PMT 2009]
(1) 5′ – GCUUAAGGCAAU – 3′
(2) 5′ – UUACGGAAATTCG – 3′
(3) 3′ – UUACCGGAAUCG – 5′
(4) 3′ – AAUGCCUUAUUCG – 5′

53. In DNA of certain organisms, guanine constitutes 20% of the bases. What percentage of the base would be adenine? [Kerala PMT 2009]
(1) 0%  (2) 10%
(3) 20%  (4) 30%

54. The process of transformation was discovered by [Kerala PMT 2009]
(1) Maurice H.F. Wilkins and Rosalind E. Franklin
(2) M. Meselson and F.W. Stahl
(3) James Watson and Francis Crick
(4) Fredrick Griffith

55. Which of the following codons has no tRNA? [Kerala PMT 2009]
(1) UAA  (2) UAU
(3) UGU  (4) UGC

56. Methyl guanosine triphosphate is added at 5′ end of hn RNA in a process of [AMU 2010]
(1) tailing (2) splicing
(3) capping (4) None of the above

57. 5′ end of a polynucleotide contains [Orissa 2010]
(1) hydroxyl group  (2) methyl group
(3) carboxyl group  (4) phosphate group

58. Nucleosome is [HPPMT. 2010]
(1) intron interrupted DNA
(2) double helix DNA
(3) negatively charged DNA wrapped around positively charged histone octomer
(4) satellite DNA

59. The one aspect which is not a salient feature of genetic code, is its being: [CBSE PMT 2010]
(1) degenerate (2) ambiguous
(3) universal (4) specific

60. Satellite DNA is useful tool in: [CBSE PMT 2010]
(1) organ transplantation
(2) sex determination
(3) forensic science
(4) genetic engineering

61. Which one of the following does not follow the central dogma of molecular biology? [CBSE PMT 2010]
(1) Pea  (2) Mucor
(3) Chlamydomonas  (4) HIV

62. In the Lac operon system, b-galactosidase is coded by [Kerala PMT 2010]
(1) a-gene  (2) i-gene
(3) l-gene  (4) z-gene

63. Match the codons with their respective amino acids and choose the correct answer [Kerala PMT 2010]
(1) A – 3; B – 4; C – 1; D – 5; E – 2
(2) A – 3; B – 1; C – 4; D – 5; E – 2
(3) A – 3; B – 4; C – 5; D – 1; E – 2
(4) A – 2; B – 4; C – 1; D – 5; E – 3
(e) A – 2; B – 4; C – 1; D – 3; E – 5

64. In bacteria, the formation of peptide bond during translation is effected by [Kerala PMT 2010]
(1) lysozyme  (2) ribozyme
(3) nucleosome  (4) microsome
65. Locations or sites in the human DNA where single base DNA differences occur are called  
(Kerala PMT 2010)  
(1) repetitive DNA (2) VNTR  
(3) SNP (4) SSCP  

66. The technique of DNA finger printing was initially developed by  
(Kerala PMT 2010)  
(1) Ian Wilmut (2) Hargobind Khorana  
(3) Jacque Monod (4) Alec Jeffreys  

67. The process of copying genetic information from one strand of the DNA into RNA is termed as  
(Kerala PMT 2010)  
(1) translation (2) transamination  
(3) replication (4) transcription  

68. Consider the following statements  
(Kerala PMT 2010)  
I. r-RNA provides the template for synthesis of proteins  
II. t-RNA brings amino acids and reads the genetic code  
III. DNA polymerase binds to promoter and initiates transcription  
IV. A segment of DNA coding for polypeptide is called intron  
(1) I and III are correct  
(2) I and II are correct  
(3) I, II and III are correct  
(4) II and III are correct  

69. During Meselson and Stahl’s experiments, heavy DNA was distinguished from normal DNA by centrifugation in  
(Kerala PMT 2010)  
(1) CsOH gradient (2) 14NH4Cl  
(3) 15NH4Cl (4) CsCl gradient  

70. The process of removal of introns and joining of exons is called  
(Kerala PMT 2010)  
(1) capping (2) tailing  
(3) termination (4) splicing  

71. In a DNA percentage of thymine is 20%. What is the percentage of guanine?  
(AFMC 2011)  
(1) 20% (2) 40%  
(3) 30% (4) 60%  

72. The codon for anticodon '-UUUA-' is  
(JIPMER-2011)  
(1) '-AAU-' (2) '-UAAA-'  
(3) '-AAAU-' (4) '-UAAU-'  

73. The Okazaki fragments in DNA chain growth  
(JIPMER-2011)  
(1) polymerize in the 3' - to - 5' direction and forms replication fork  
(2) prove semi-conservative nature of DNA replication  
(3) polymerize in the 5' - to - 3' direction and explain 3' - to - 5' DNA replication  
(4) result in transcription.  

74. One gene-one enzyme relationship was established for the first time in  
(JIPMER-2011)  
(1) Neurospora crassa  
(2) Salmonella typhimurium  
(3) Escherichia coli  
(4) Diplococcus pneumonia  

75. Allelic sequence variations where more than one variant (allele) at a locus in a human population with a frequency greater than 0.01 is referred to as  
(Kerala PMT 2011)  
(1) incomplete dominance  
(2) multiple allelism  
(3) SNP  
(4) DNA polymorphism  

76. The double helical model of the DNA was proposed by Watson and Crick based on what data produced by Wilkins and Franklin?  
(Kerala PMT 2011)  
(1) hybridization (2) DNA sequencing  
(3) Southern blotting (4) Fourier’s transformation  

77. The pyrimidine base which confers additional stability to DNA over RNA is  
(Kerala PMT 2011)  
(1) adenine (2) guanine  
(3) cytosine (4) thymine  

78. Methyl guanosine triphosphate is associated with  
(Kerala PMT 2011)  
(1) point mutation (2) tautomerism  
(3) capping (4) Okazaki fragments  

79. Which of the following statements are correct?  
(Kerala PMT 2011)  
(i) RNA polymerase I transcribes rRNAs  
(ii) RNA polymerase II transcribes snRNAs  
(iii) RNA polymerase III transcribes hnRNA  
(iv) RNA polymerase I transcribes hnRNAs  
(1) (i) and (ii) are correct  
(2) (i) and (iii) are correct  
(3) (i), (ii) and (iv) are correct  
(4) (i) and (iv) are correct  

80. Match the enzyme in column I with its function in column II and select the correct option.  
(Kerala PMT 2011)  
(1) A – 2, B – 1, C – 4, D – 3  
(2) A – 3, B – 4, C – 1, D – 2  
(3) A – 2, B – 4, C – 1, D – 3  
(4) A – 1, B – 2, C – 4, D – 3  

81. The inducer for switching ‘on’ the lac operon in bacteria is  
(Kerala PMT 2011)  
(1) presence of lactose  
(2) number of bacteria  
(3) presence of structural genes in the bacteria  
(4) presence of sucrose  

82. Select the incorrect statement(s).  
(Kerala PMT 2011)  
1. Six codons do not code for any amino acid.  
2. Codon is read in mRNA in a contiguous fashion.  
3. Three codons function as stop codons.  
4. The initiator codon AUG codes for methionine.  
(1) 1, 2 and 4 are incorrect  
(2) 1, 2 and 3 are incorrect  
(3) 2, 3 and 4 are incorrect  
(4) 1 alone is incorrect
83. Alec Jeffreys developed the DNA fingerprinting technique. The probe he used was [Kerala PMT 2011]
(1) ribozyme (2) sex chromosomes (3) SNP (4) VNTR

84. Automated DNA sequencers, work on the principle of the method developed by [Kerala PMT 2011]
(1) Erwin Chargaff (2) Maurice Wilkins (3) Frederick Sanger (4) Francis Crick

85. Which one of the following also acts as a catalyst in a bacterial cell? [CBSE PMT 2012]
(1) 5 sr RNA (2) sn RNA (3) hn RNA (4) 23 sr RNA

86. Removal of RNA polymerase III from nucleoplasm will affect the synthesis of: [CBSE PMT 2012]
(1) t RNA (2) hn RNA (3) m RNA (4) r RNA

87. Which one of the following is not a part of a transcription unit in DNA? [CBSE PMT 2012]
(1) The inducer (2) A terminator (3) A promoter (4) The structural gene

88. If one strand of DNA has the nitrogenous base sequence ATCTG, what would be the complementary RNA strand sequence [CBSE PMT 2012]
(1) TTAGU (2) UAGAC (3) AACTG (4) ATCGU

89. Removal of introns and joining of exons in a defined order during transcription is called: [CBSE PMT 2012]
(1) Looping (2) Inducing (3) Slicing (4) Splicing

90. Read the following four statements (A-D).
(1) In transcription, adenosine pairs with uracil.
(2) Regulation of lac operon by repressor is referred to as positive regulation.
(3) The human genome has approximately 50,000 genes.
(4) Haemophilia is a sex-linked recessive disease. How many of the above statements are correct? [CBSE PMT 2012M]
(1) Two (2) Three (3) Four (4) One

91. Which of the following forms the basis of DNA Fingerprinting? [CBSE PMT 2012M]
(1) The relative proportions of purines and pyrimidines in DNA.
(2) Satellite DNA occurring as highly repeated short DNA segments.
(3) The relative difference in the DNA occurrence in blood, skin and saliva.
(4) The relative amount of DNA in the ridges and grooves of the fingerprints.

92. Which one of the following correctly represents the manner of replication of DNA? [AIHMS 2012]
C. Two nucleosides are linked through $3'\text{--}5'\text{-}N\text{-glycosidic}$ linkage.
D. Negatively charged DNA is wrapped around positively charged histone octamer to form nucleosome.
E. The chromatin that is more densely packed and stains dark is called euchromatin.

(1) A, B and C alone are wrong
(2) D alone is wrong
(3) C and E alone are wrong
(4) A alone is wrong

100. Who used the frequency of recombination between gene pairs on the same chromosome as a measure of the distance between genes and mapped their position on the chromosome? [Kerala PMT 2012]
(1) Gregor Mendel  (2) Correns
(3) Tschermark  (4) Alfred Sturtevant

101. Select the correct statement regarding protein synthesis. [Kerala PMT 2012]
(1) When the small subunit of the ribosome encounters an mRNA the process of translation begins.
(2) Peptidase catalyses the formation of peptide bond.
(3) UTRs are present between the start codon and stop codon.
(4) At the end of translation the release factor binds to the initiation codon.

102. Which among the following codons does not have tRNAs? [Kerala PMT 2012]
(1) start codon  (2) AUG
(3) GGG  (4) stop codon

103. The behaviour of the chromosomes was parallel to the behaviour of genes during meiosis was noted by [Kerala PMT 2012]
(1) Correns  (2) Tschermark
(3) Sutton and Boveri  (4) de Vries

104. The enzyme required to catalyze the polymerization of deoxynucleotides is [Kerala PMT 2012]
(1) DNA ligase  (2) DNA polymerase
(3) b-galactosidase  (4) transacetylase

105. To which of the following factors, RNA polymerase binds transiently to initiate transcription? [Kerala PMT 2012]
(1) rho  (2) beta
(3) gamma  (4) sigma

106. The enzyme(s) responsible for the transcription of snRNAs in eukaryotes is/are [Kerala PMT 2012]
(1) RNA polymerase I  (2) RNA polymerase I and II
(3) RNA polymerase II  (4) RNA polymerase III

107. The presence and position of which one of the following defines the template and coding strands in a transcription unit? [Kerala PMT 2012]
(1) Repressor  (2) Operator
(3) Structural gene  (4) Promoter

108. ABO blood groups are determined by three different alleles. How many genotypes and phenotypes are possible? [Kerala PMT 2012]

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1) 3</td>
<td>1</td>
</tr>
<tr>
<td>(2) 6</td>
<td>4</td>
</tr>
<tr>
<td>(3) 4</td>
<td>6</td>
</tr>
<tr>
<td>(4) 9</td>
<td>7</td>
</tr>
</tbody>
</table>

109. The codon which has dual function is [Kerala PMT 2012]
(1) UGA  (2) UUU
(3) AUG  (4) AAA

110. Choose the wrong statement. [Kerala PMT 2012]
(1) VNTR belong to a class of mini-satellite DNA.
(2) DNA sequencers work on the principle developed by Frederick Sanger
(3) HGP was coordinated by US Department of Energy and the National Institute of Health.
(4) DNA fingerprinting involves identifying similarities in repetitive DNA

111. In lac operon, the genes a,i,y and z code respectively for [Kerala PMT 2012]
(1) respressor protein, permease, b-galactosidase, transacetylase
(2) transacetylase, permease, b-galactosidase, repressor protein
(3) permease, transacetylase, repressor protein, b-galactosidase
(4) transacetylase, repressor protein, permease, b-galactosidase

112. In humans, most number of genes are located on chromosome [Kerala PMT 2012]
(1) 1  (2) 6
(3) X  (4) 21

113. The diagram shows an important concept in the genetic implication of DNA. Fill in the blanks A to C. [NEET 2013]
(1) A-translation B - transcription C-Erwin Chargaff
(2) A-transcription B - translation C-Francis Crick
(3) A-translation B - extension C-Rosalind Franklin
(4) A-transcription B - replication C-James Watson

114. Which enzymes will be produced in a cell in which there is a nonsense mutation in the lac Y gene? [NEET 2013]
(1) Lactose permease
(2) Transacetylase
(3) Lactose permease and transacetylase
(4) b-galactosidase

115. Human Genome Project (HGP) is closely associated with the rapid development of a new area in biology called as [AIIMS 2013]
(1) biotechnology  (2) bioinformatics
(3) biogeography  (4) bioscience

116. Assertion : DNA is associated with proteins.
Reason : DNA binds around histone proteins that form a pool and the entire structure is called a nucleosome. [AIIMS 2013]
(1) If both Assertion and Reason are correct and Reason is the correct explanation of Assertion.
(2) If both Assertion and Reason are correct, but Reason is not the correct explanation of Assertion.
(3) If Assertion is correct but Reason is incorrect.
(4) If Assertion is incorrect but Reason is correct.

117. Read the statements regarding structure of polynucleotide chain and choose the correct option. [Kerala PMT 2013]
1. A nitrogenous base is linked to the pentose sugar through a phospho-diester linkage.
2. Two nucleotides are linked through 3’-5’ N-glycosidic linkage to form a dinucleotide.
3. The polynucleotide backbone is formed by sugar and phosphate.
4. A phosphate group is linked to 5’-OH of a nucleoside through a N-glycosidic linkage to form a nucleotide.
   (1) 4 alone is correct
   (2) 3 alone is correct
   (3) 1, 3 and 4 alone are correct
   (4) 1 and 4 alone are correct
   (e) 1 and 2 alone are correct

118. Avery, MacLeod and McCarty inhibited bacterial transformation by using the enzyme [Kerala PMT 2013]
(1) RNase (2) Ligase
(3) DNase (4) DNA polymerase

119. Choose the wrong statement regarding translation [Kerala PMT 2013]
   (1) The process of translation of mRNA to protein begins only when the small ribosomal subunit encounters mRNA.
   (2) The 23SrRNA acts as a catalyst for the formation of peptide bond in prokaryotes.
   (3) The additional sequences of mRNA that are not translated are present only at the end.
   (4) For initiation, ribosomes binds to the mRNA at the start codon.

120. Identify the wrong statement about RNA [Kerala PMT 2013]
   (1) RNA was the first genetic material to evolve in the living systems.
   (2) Apart from being a genetic material, it is also a catalyst.
   (3) DNA evolved from RNA with chemical modifications.
   (4) RNA being a catalyst is non-reactive and stable.

121. Identify the wrong statement [Kerala PMT 2013]
   (1) In prokaryotes, the structural gene is polycistronic.
   (2) In eukaryotes, structural genes have interrupted coding sequences.
   (3) Eukaryotes have split gene arrangement.
   (4) Intervening sequences appear in mature RNA.

122. A ‘transcription unit’ in DNA is defined primarily by the (i) promoter (ii) structural gene (iii) adenylate residues (iv) Okazaki fragments (v) terminator
   Choose the correct option [Kerala PMT 2013]
   (1) iii and v only (2) i, ii and v only
   (3) iv only (4) ii and v only

123. AUG codes for [Kerala PMT 2013]
   (1) Methionine (2) Serine
   (3) Arginine (4) Valine

124. Select the correct sequence of steps in DNA fingerprinting involving southern blot hybridization using radiolabeled VNTR as a probe. [Kerala PMT 2013]
   I. Hybridization using labelled VNTR probe.
   II. Isolation of DNA.
   III. Transferring (blotting) of separated DNA fragments to synthetic membranes, such as nitrocellulose or nylon.
   IV. Detection of hybridized DNA fragments by autoradiography.
   V. Separation of DNA fragments by electrophoresis.
   VI. Digestion of DNA by restriction endonucleases
   (1) I, V, VI, II, III and IV
   (2) II, VI, V, III, I and IV
   (3) V, I, VI, III, IV and II
   (4) II, I, V, VI, IV and III

125. Which RNA picks up specific amino acid from the amino acid pool in the cytoplasm to the ribosome during protein synthesis? [Kerala PMT 2013]
   (1) tRNA (2) mRNA
   (3) rRNA (4) SnRNA
   (e) hnRNA

126. The heavy isotope used for proving semi-conservative replication of DNA by Meselson and Stahl was [Kerala PMT 2013]
   (1) 15N (2) 14N
   (3) 14C (4) 31N

127. Read the statements regarding the lac operon and choose the correct option. [Kerala PMT 2013]
   1. An inducer regulates the switching on and off of the lac operon.
   2. The repressor protein dissociates from the operator region and prevents RNA polymerase from transcribing the operon.
   3. In the presence of lactose, the repressor is activated by interaction with lactose.
   4. RNA polymerase has access to the promoter and transcription proceeds only when the repressor is inactivated.
   (1) 1 and 2 alone are correct
   (2) 2 alone is correct
   (3) 3 and 4 alone are correct
   (4) 1 and 4 alone are correct

128. The enzyme in bacteria which acts as a catalyst for the formation of peptide bond during translation is [Kerala PMT 2013]
   (1) 28S rRNA (2) polymerase
   (3) ribozyme (4) lysozyme

129. Choose the wrong statement regarding the observations drawn from the Human Genome Project [Kerala PMT 2013]
194

(1) Repetitive sequences are stretches of RNA.
(2) Less than 2 per cent of the genome codes for protein.
(3) Chromosome ‘Y’ has the fewest number of genes.
(4) SNPs help in tracing human history.

130. Which one of the following is wrongly matched?
[AIPMT 2014]
(1) Transcription – Writing information from DNA to tRNA.
(2) Translation – Using information in mRNA to make protein.
(3) Repressor protein – Binds to operator to stop enzyme synthesis.
(4) Operon – Structural genes, operator and promoter.

131. Transformation was discovered by: [AIPMT 2014]
(1) Meselson and Stahl
(2) Hershey and Chase
(3) Griffith
(4) Watson and Crick

132. Select the correct option: [AIPMT 2014]

<table>
<thead>
<tr>
<th>Direction of RNA synthesis</th>
<th>Direction of reading of the template DNA strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>(1) 5’—3’</td>
<td>3’—5’</td>
</tr>
<tr>
<td>(2) 3’—5’</td>
<td>5’—3’</td>
</tr>
<tr>
<td>(3) 5’—3’</td>
<td>5’—3’</td>
</tr>
<tr>
<td>(4) 3’—5’</td>
<td>3’—5’</td>
</tr>
</tbody>
</table>

133. Commonly used vectors for human genome sequencing are: [AIPMT 2014]
(1) T-DNA
(2) BAC and YAC
(3) Expression Vectors
(4) T/A Cloning Vectors

134. A man with blood group 'A' marries a woman with blood group 'B'. What are all the possible blood groups of their offsprings ? [AIPMT 2015]
(1) A, B and AB only
(2) A, B, AB and O
(3) O only
(4) A and B only

135. In sea urchin DNA, which is double stranded, 17% of the bases were shown to be cytosine. The percentages of the other three bases expected to be present in this DNA are :- [AIPMT 2015]
(1) G 17%, A 16.5%, T 32.5%
(2) G 17%, A 33%, T 33%
(3) G 8.5%, A 50%, T 24.5%
(4) G 34%, A 24.5%, T 24.5%

136. The movement of a gene from one linkage group to another is called : [AIPMT 2015]
(1) Duplication
(2) Translocation
(3) Crossing over
(4) Inversion

137. Gene regulation governing lactose operon of E.coli that involves the lacI gene product is : [AIPMT 2015]
(1) Negative and inducible because repressor protein prevents transcription
(2) Negative and repressible because repressor protein prevents transcription
(3) Feedback inhibition because excess of β-galactosidase can switch off transcription
(4) Positive and inducible because it can be induced by lactose

138. The chromosomes in which centromere is situated close to one end are: [AIPMT 2015]
(1) Acrocentric
(2) Telocentric
(3) Sub-metacentric
(4) Metacentric

139. Multiple alleles are present : [AIPMT 2015]
(1) At different loci on the same chromosome
(2) At the same locus of the chromosome
(3) On non-sister chromatids
(4) On different chromosomes

140. An abnormal human baby with 'XXX' sex chromosomes was born due to : [AIPMT 2015]
(1) formation of abnormal ova in the mother
(2) fusion of two ova and one sperm
(3) fusion of two sperms and one ovum
(4) formation of abnormal sperms in the father

141. A pleiotropic gene:
(1) is a gene evolved during Pliocene.
(2) controls a trait only in combination with another gene
(3) controls multiple traits in an individual.
(4) is expressed only in primitive plants

142. A gene showing codominance has:
(1) alleles tightly linked on the same chromosome
(2) alleles that are recessive to each other
(3) both alleles independently expressed in the heterozygote
(4) one allele dominant on the other

143. The enzyme used to join the fragments of DNA during the process of replication is : [AMU’s 2015]
(1) DNA polymerase
(2) DNA ligase
(3) Endonuclease
(4) Helicase

144. Semi-conservative replication of DNA was first demonstrated in : [AMU’s 2015]
(1) Escherichia coli
(2) Streptococcus pneumoniae
(3) Drosophila melanogaster
(4) Salmonella typhimurium

145. The transfer of genetic material from one bacterium to another via viruses is called: [AMU’s 2015]
(1) Transformation
(2) Conjugation
(3) Recombination
(4) Transduction

146. Which of the following DNA polymerase of prokaryotes have both 3’–5’ and 5’–3’ exonuclease activity. [AMU’s 2015]
(1) DNA Pol-II
(2) DNA Pol-I
(3) DNA Pol-IV
(4) DNA Pol-III
147. Which of the following is correct regarding RNA processing. [AMU’s 2015]
(1) In capping, methyl guanosine triphosphate is added to 3 end of hnRNA
(2) RNA polymerase I transcribes tRNA in eukaryotes
(3) In tailing, adenylate residues are added at 3 end of hnRNA
(4) Three types of RNA polymerase catalyse the transcription of three different types of RNAs in most bacteria

148. Splicing the process where [AMU’s 2015]
(1) exons are removed from growing t-RNA strand
(2) introns are removed from growing polypeptide chain
(3) introns are removed from heterogenous nuclear RNA
(4) exons are removed from mRNA

149. Who postulated the chromosome basis of linkage? [UPCPMT 2015]
(1) Bateson (2) Bridges
(3) Griffith (4) Morgan

150. Which one of the following terms is usual to explain the acquisition of new genes in mammalian cells due to up take of naked DNA? [UPCPMT 2015]
(1) Translation (2) Transformation
(3) Transtection (4) Conjugation

151. The process of synthesis of messenger RNA on the DNA template is called [UPCPMT 2015]
(1) Replication (2) Transcription
(3) Translation (4) Reverse transcription

152. The okazaki fragments on the lag are joined together by the enzyme [UPCPMT 2015]
(1) DNA primase (2) DNA polymerase
(3) DNA ligase (4) Helicase

153. Meselson and Stahl used a isotope to demonstrate semiconservative nature of DNA duplication which isotope did they use? [UPCPMT 2015]
(1) $^{12}$C (2) $^3$H
(3) $^{32}$P (4) $^{15}$N

154. Who for the first time experimentally demonstrated that only DNA of the bacteriophage enters the host cell and not the phage protein? [UPCPMT 2015]
(1) Beadle and Tatum (2) Hershey and Chase
(3) Jacob and Monad (4) Luria and Delbruck

155. Semi conservative replication of eucaryotic genetic material was first demonstrated by Taylor et al using root tip cells of: [UPCPMT 2015]
(1) Vicia faba (2) Pism sativum
(3) Vigna aconitifolia (4) Arabidopsis thaliana
1. Topoisomerase is involved in
   (1) producing RNA primer.
   (2) joining of DNA segments.
   (3) producing nick in DNA.
   (4) separation of DNA strands.

2. In DNA replication, the primer is
   (1) small deoxyribonucleotide polymer.
   (2) small ribonucleotide polymer.
   (3) helix destabilising protein.
   (4) enzyme taking part in joining nucleotides to their complementary template bases.

3. DNA strand is synthesised in the direction
   (1) 5' → 3'
   (2) 3' → 5'
   (3) 1' → 4'
   (4) 6' → 1'

4. Okazaki segments are
   (1) small segments of RNA.
   (2) small peptides.
   (3) small DNA segments.
   (4) small DNA segments formed over DNA template running in 3' → 5' direction.

5. In proof reading during DNA replication
   (1) wrong nucleotides are inserted.
   (2) wrong nucleotides are taken out.
   (3) wrong nucleotides are removed and correct ones inserted.
   (4) mutations are prevented.

6. Nonsense codons take part in
   (1) helping protein synthesis.
   (2) termination gene message for polypeptide synthesis.
   (3) initiating gene message for polypeptide synthesis.
   (4) synthesis of nonprotein amino acids.

7. Transcription involves
   (1) protein synthesis over ribosomes.
   (2) removal of worn out organelles by lysosomes.
   (3) synthesis of RNA over DNA.
   (4) synthesis of DNA over DNA.

8. A mutant strain of Neurospora which fails to grow on a minimal medium unless supplemented with a nutrient is called
   (1) auxotroph
   (2) autotroph
   (3) heterotroph
   (4) prototroph

9. Components of an operon are
   (1) operator, promoter and regulator genes.
   (2) regulator, promoter, operator and structural genes.
   (3) operator, regulator and structural genes.
   (4) regulator, promoter and structural genes.

10. Cistron is
    (1) functional unit of DNA.
    (2) functional unit of RNA.
    (3) nonfunctional unit of DNA.
    (4) nonfunctional unit of RNA.

11. House keeping genes
    (1) produce antibodies.
    (2) constantly operate for cellular activity.
    (3) form hormones.
    (4) function only at the time of reproduction.

12. Anticodon is made of
    (1) three adjacent nitrogen bases.
    (2) unpaired triplet bases on mRNA.
    (3) paired triplet of nitrogen bases on tRNA.
    (4) unpaired triplet of nitrogen bases at one end of tRNA.

13. Experimental material used by Hershey and Chase for proving that DNA controls heredity was
    (1) Diplococcus pneumoniae
    (2) Salmonella typhimurium
    (3) T2 phage
    (4) TMV

14. A codon specifies the same amino acid in Brassica and Homo sapiens because codons are
    (1) nonoverlapping
    (2) commaless
    (3) universal
    (4) nonambiguous

15. In eukaryotes mRNA is synthesised with the aid of
    (1) RNA polymerase III
    (2) RNA polymerase II
    (3) RNA polymerase I
    (4) Reverse transcriptase

16. A bacterium grown over medium having radioactive 35S incorporates radioactivity in
    (1) carbohydrates
    (2) proteins
    (3) DNA
    (4) RNA

17. New strand formation on a DNA template can be initiated only by
    (1) DNA polymerase I
    (2) DNA polymerase III
    (3) RNA primer
    (4) DNA primer

18. In streptococcus pneumoniae
    (1) virulent form is smooth
    (2) virulent form is rough
    (3) nonvirulent form is capsulated
    (4) all forms are rough

19. VNTRs are
    (1) variable number of tandem repeats.
    (2) very narrow tandem repeats.
    (3) variable noncistronic transposon repeats.
    (4) valuable noncistrionic transposic regions.

20. DNA probes used in finger printing are
    (1) highly sensitive electron microscope
    (2) UV beams
    (3) DNA segments having radioactive isotopes
    (4) X-ray scanners

21. Process used for amplification or multiplication of DNA for finger printing is
    (1) polymerase chain reaction
    (2) nesslerisation
    (3) southern blotting
    (4) northern blotting
22. DNA finger printing can resolve
   (1) identification of a person
   (2) paternity dispute
   (3) maternity dispute
   (4) All the above

23. DNA replication in eukaryotes commences
   (1) from both ends of a chromosome simultaneously
   (2) several sites along DNA of a chromosome simultaneously.
   (3) from centromere to either end.
   (4) from one end of chromosome to the other.

24. Genetic code determines
   (1) sequence of amino acids in protein chain
   (2) variations
   (3) constancy of morphological traits
   (4) structural pattern

25. In operon concept, the operator gene combines with
   (1) regulator protein to switch off structural gene transcription.
   (2) regulator protein to switch on structural gene transcription.
   (3) inducer to switch off structural gene transcription.
   (4) regulator gene to switch off structural gene transcription.

26. Eukaryotes differ from prokaryotes in mechanism of DNA replication due to
   (1) different enzymes for opening of strands.
   (2) DNA primers instead of RNA primers.
   (3) unidirectional rather than bidirectional.
   (4) discontinuous rather than semidiscontinuous.

27. DNA template sequence of CTGATAGC is transcribed over mRNA as
   (1) GUCTUTCG
   (2) GACUAUCG
   (3) GAUTATUG
   (4) UACTATCU

28. Reverse transcriptase is
   (1) RNA dependent RNA polymerase
   (2) DNA dependent RNA polymerase
   (3) DNA dependent DNA polymerase
   (4) RNA dependent DNA polymerase

29. What is true of Watson and Crick’s model of DNA. It is duplex with
   (1) 10 base pairs and 3.4 Å distance for every turn
   (2) 10 base pairs and 3.4 Å distance for each turn of spiral
   (3) 20 base pairs and 34 Å for each turn
   (4) None of the above

30. Which step of translation does not consume high energy phosphate bond?
   (1) Translocation
   (2) Peptidyl transferase reaction
   (3) Amino acid activation
   (4) Aminoacyl tRNA binding to A-site

31. Determination of one amino acid by more than one codon is due to
   (1) redundancy of genetic code.
   (2) continuous nature of genetic code.
   (3) punctuation in genetic code.
   (4) universal nature of genetic code.

32. The processes by which DNA forms mRNA and mRNA forms protein are respectively
   (1) translation and transcription
   (2) transcription and replication
   (3) transcription and translation
   (4) replication and translation

33. In which of the following will DNA melt at the lowest temperature?
   (1) 5’ – AAIAAAGC – 3’
   3’ – TTATTTGC – 5’
   (2) 5’ – AATGCTGC – 3’
   3’ – TTACGACG – 5’
   (3) 5’ – ATGCTGAI – 3’
   3’ – TACGACTA – 5’
   (4) 5’ – GCATAGCT – 3’
   3’ – CGTATCGA – 5’

34. Which is true according to Chargaff’s rule?
   (1) A + G = T + C
   (2) A = C
   (3) G = T
   (4) \( \frac{A + T}{C + G} = 1 \)

35. tRNA takes part in
   (1) transfer of genetic code to cytoplasm.
   (2) carry amino acids to ribosomes.
   (3) collection of RNA in ribosomes.
   (4) copy the genetic code from DNA in nucleus.

36. In Escherichia coli, the product of i gene combines with
   (1) operator gene to switch off structural genes.
   (2) inducer gene to switch off structural genes.
   (3) operator gene to switch on structural genes.
   (4) regulator gene to switch off structural genes.

37. Lactose operon produces enzymes
   (1) \( \beta \)-galactosidase, permease and glycogen synthetase.
   (2) \( \beta \)-galactosidase, permease and transacetylase.
   (3) Permease, glycogen synthetase and transacetylase.
   (4) \( \beta \)-galactosidase, permease and phosphoglucose isomerase.

38. During elongation of polypeptide chain, sigma factor is
   (1) functionless.
   (2) retained for specific function.
   (3) released for re-use.
   (4) required during closing of chain.

39. During replication of DNA
   (1) the two daughter molecules develop from both the parental strands.
   (2) RNA functions as template.
   (3) one strand from parent and one strand freshly formed in the two daughter molecules.
   (4) one daughter receives both the parental strands while the other daughter receives newly formed strands.

40. Similarity between DNA and RNA is that both have
   (1) similar sugars
   (2) similar mode of replication
   (3) similar pyrimidines
   (4) polymers of nucleotides
41. Okazaki fragments are
(1) RNA primers
(2) short DNA fragments on leading strand
(3) short DNA fragments on lagging strand
(4) DNA fragments from radiation action

42. Heat killed pathogenic NL cells and live nonpathogenic cells are mixed and injected into mice. The result would be
(1) mice develop disease and die.
(2) mice die without developing disease.
(3) mice remain healthy.
(4) 50% mice develop disease and die

43. Extraneural DNA occurs in
(1) chloroplast and lysosome
(2) mitochondria and ribosome
(3) chloroplast and mitochondrion
(4) peroxisome and ribosome

44. Gene and cistron are sometimes used as synonyms because
(1) one gene contains one cistron.
(2) one gene contains many cistrons.
(3) one gene contains no cistron.
(4) one cistron contains many genes.

45. Evolution was termed RNA world due to discovery of
(1) absence of RNAs in some cells.
(2) genomic RNA.
(3) RNA enzymes.
(4) synthesis of proteins by mRNA, tRNA and rRNA

46. Jacob and Monod proposed operon concept on the basis of their study of lactose metabolism in Escherichia coli. The concept is applicable to
(1) all prokaryotes only.
(2) all prokaryotes and some eukaryotes.
(3) all prokaryotes and all eukaryotes.
(4) all prokaryotes and some protozoans.

47. Chargaff's rules are applicable to
(1) single stranded RNA
(2) single stranded DNA and RNA
(3) single stranded DNA
(4) double stranded DNA

48. What is correct?
(1) mRNA is polycistronic in eukaryotes and monocistronic in prokaryotes
(2) mRNA is polycistronic in both eukaryotes and prokaryotes
(3) mRNA is monocistronic in both eukaryotes and prokaryotes.
(4) mRNA is polycistronic in prokaryotes and monocistronic in eukaryotes.

49. Genetic code is
(1) triplet, universal, ambiguous and degenerate.
(2) triplet, universal, nonambiguous and nondegenerate.
(3) triplet, universal, nonambiguous and degenerate.
(4) triplet, universal, ambiguous and non-degenerate.

50. Which of the following is the Pribnow box?
(1) 5’TATAAT3’
(2) 5’TATTA3’
(3) 5’ATAAT3’
(4) 5’ATATTA3’

51. Telomere and euarkaryotic chromosome possesses short segments of
(1) guanine rich repeats.
(2) thymine rich repeats.
(3) cytosine rich repeats.
(4) adenine rich repeats.

52. Operon is
(1) sequence of three nitrogen bases determining a single amino acid.
(2) a set of closely placed genes regulating a metabolic pathway in prokaryotes.
(3) segment of DNA specifying a polypeptide.
(4) gene responsible for switching on and switching off of other genes.

53. Clover leaf secondary structure of tRNA has a loop for
(1) three nucleotides of a codon.
(2) three nucleotides of an anticodon.
(3) no nucleotides
(4) Both (1) and (2)

54. Transcription
(1) starts at initiator region and ends at stop region.
(2) starts at operator region and ends at telomeric end.
(3) starts at promoter region and ends at terminator region.
(4) starts at CAAT box and ends at TATA box.

55. Protein synthesis in an animal cell occurs
(1) on cytosolic ribosomes only.
(2) on ribosomes attached to E.R. and nuclear envelope.
(3) on ribosomes present in nucleolus as well as cytoplasm.
(4) on ribosomes present both in cytoplasm as well as mitochondria.

56. In lac operon, structural gene ‘Z’ syntheses
(1) β-galactosidase
(2) galactosidase permease
(3) galactosidase transacetylase
(4) None of the above

57. Which antibiotic inhibits peptide bond formation?
(1) Streptomycin
(2) Tetracycline
(3) Chloramphenicol
(4) Neomycin

58. DNA replication is semiconservative as
(1) only non-parent strand acts at template.
(2) both strands of new molecule are synthesized de novo.
(3) one of the strand in each new molecule is parental and the other is new.
(4) daughter strands are dispersive.

59. Antisense technology is
(1) use of complementary RNA to stop expression of specific gene.
(2) RNA polymerase producing DNA.
(3) a cell with foreign antigen used for synthesis of antigens.
(4) production of somaclonal variants in tissue culture.

60. Crossing over that results in genetic recombination in higher organisms occurs between
(1) sister chromatids of a bivalent.
(2) nonsister chromatids of a bivalent.
(3) two daughter nuclei.
(4) two different bivalents.

61. After a mutation at a gene locus, a character of an organism changes due to change in
(1) protein structure.
(2) DNA replication.
(3) protein synthesis pattern.
(4) RNA transcription pattern.
62. During replication of a bacterial chromosome DNA synthesis starts from an origin of replication site and
(1) RNA primers are involved.
(2) is facilitated by telomerase.
(3) moves in one direction of the site.
(4) moves in bi-directional way.

63. In transgenics, expression of transgene in target tissue is determined by
(1) enhancer (2) transgene
(3) promoter (4) reporter

64. The most likely reason for development of resistance against pesticides in insect damaging a crop is
(1) random mutations
(2) genetic recombination
(3) directed mutations
(4) acquired heritable changes

65. Mutations which alter nucleotide sequence within a gene are
(1) frame shift mutations
(2) base pair substitutions
(3) Both (1) and (2)
(4) None of these

66. A child of blood group O cannot have parents of blood groups
(1) A and A (2) AB and O
(3) A and B (4) B and B

67. A naturally occurring coding strand composed of alternating C and U residues would result in the formation of
(1) a polypeptide containing alternating leu and ser residues.
(2) a polypeptide containing either leu or ser residues.
(3) a polypeptide containing only ser residues.
(4) a polypeptide containing only leu residues.

68. Which RNA is short lived?
(1) \( m \) – RNA
(2) \( t \) – RNA
(3) \( r \) – RNA
(4) \( sn \) – RNA

69. Which one is a purine pair?
(1) Uracil, Guanine
(2) Cytosine, Thymine
(3) Adenine, Guanine
(4) Adenine, Thymine

70. Which one of the following group of codons is called as degenerate codons?
(1) UAA, UAG and UGA
(2) GUA, GUG, GCA, GCG and GAA
(3) UUC, UUG, CCU, CAA and CUG
(4) UUA, UUG, CUU, CUC, CUA and CUG
EXERCISE 1 : NCERT BASED QUESTIONS

1. (4) 2. (1) 3. (1) 4. (2) 5. (4)
6. (2) 7. (4) 8. (3) 9. (4) 10. (3)
11. (4) 12. (1) 13. (1) 14. (3) 15. (3)
16. (3) 17. (2) 18. (3) 19. (2) 20. (1)
21. (2) 22. (3) 23. (3) 24. (4) 25. (4)
26. (1) 27. (2) 28. (1) 29. (3) 30. (3)

EXERCISE 2 : WINDOW TO COMPETITIVE EXAMS

1. (4) 2. (3) 3. (1) 4. (3) 5. (4)
6. (4) 7. (3) 8. (1) 9. (3) 10. (4)
11. (1) 12. (3) 13. (1) 14. (2) 15. (1)
16. (3) 17. (4) 18. (1) 19. (4) 20. (1)
21. (3) 22. (3) 23. (1) 24. (4) 25. (3)
26. (1) 27. (3) 28. (4) 29. (3) 30. (3)
31. (2) 32. (4) 33. (3) 34. (1) 35. (2)
36. (2) 37. (2) 38. (2) 39. (3) 40. (2)
41. (3) 42. (1) 43. (1) 44. (1) 45. (3)
46. (4) 47. (4) 48. (4) 49. (1) 50. (4)
51. (3) 52. (3) 53. (4) 54. (4) 55. (1)
56. (3) 57. (1) 58. (3) 59. (2) 60. (3)
61. (4) 62. (4) 63. (1) 64. (2) 65. (3)
66. (4) 67. (4) 68. (4) 69. (4) 70. (4)
71. (3) 72. (3) 73. (3) 74. (1) 75. (e)
76. (4) 77. (4) 78. (3) 79. (4) 80. (2)
81. (1) 82. (4) 83. (4) 84. (3) 85. (4)
86. (1) 87. (1) 88. (2) 89. (4) 90. (1)
91. (2) 92. (4) 93. (1) 94. (1) 95. (1)
96. (2) 97. (2) 98. (2) 99. (3) 100. (4)
101. (1) 102. (4) 103. (3) 104. (2) 105. (4)
106. (4) 107. (4) 108. (2) 109. (3) 110. (4)
111. (4) 112. (1) 113. (2) 114. (4) 115. (2)
116. (1) 117. (2) 118. (3) 119. (3) 120. (4)
121. (4) 122. (2) 123. (1) 124. (2) 125. (1)
126. (1) 127. (4) 128. (3) 129. (1) 130. (1)
131. (3) 132. (1) 133. (2) 134. (2) 135. (2)
136. (2) 137. (1) 138. (1) 139. (2) 140. (1)
141. (3) 142. (3) 143. (2) 144. (1) 145. (4)
146. (1) 147. (3) 148. (3) 149. (4) 150. (1)
151. (2) 152. (3) 153. (4) 154. (2) 155. (1)

EXERCISE 3 : TEST YOURSELF

1. (3) 2. (2) 3. (1) 4. (4) 5. (3)
6. (2) Three of the 64 codons, namely, UAA, UAG and UGA, do not specify any amino acid. They are called the nonsense or terminator, codons. Either of these stops synthesis of the polypeptide chain.

7. (3) 8. (1) 9. (2) 10. (1) 11. (2)
12. (4) 13. (3) 14. (3) 15. (2) 16. (2)
17. (3) 18. (1) Griffith (1928) injected into mice with virulent or smooth strain (s-type, smooth colony with mucilage) form Streptococcus pneumoniae. The mice died due to pneumonia.
19. (1) In human genome, there are about 200,000 satellite loci. These simple tandem repeats of short sequences are called “variable number tandem repeats” (VNTRs). These repeats are inherited from the parents, and are used as genetic markers in a personal identity test.
20. (3) 21. (1) 22. (4) 23. (2) 24. (1)
25. (1) 26. (1) 27. (2)
28. (4) In the case of reverse transcription DNA is synthesized from RNA in retrovirus and the enzyme which catalyze this reaction is reverse transcriptase or RNA dependent DNA polymerase.
29. (1) 30. (2) 31. (1) 32. (3) 33. (1)
34. (1) The base ratio A + T / G + C may vary from one species to another, but is constant for a given species. This ratio can be used to identify the source of DNA, and can help in classification.
35. (2) tRNAs pick up specific amino acid from amino acid pool and carry over the mRNA strand.
36. (1) 37. (2) 38. (1) 39. (3) 40. (4)
41. (3) 42. (1) 43. (3) 44 (1) 45 (3)
46 (3) 47 (4) 48 (4) 49. (3)
50. (1) Pribnow box is a conserved region in the promoter part of DNA ahead of area where RNA polymerase attaches.
51. (1) 52. (2)
53. (2) Clover leaf secondary structure of rRNA has a loop for three unpaired bases (triplet of base) whose sequence is complementary with a codon in mRNA.
54. (3) Formation of mRNA from DNA is called as transcription. The segment of DNA involved in transcriptions is cistron, which have a promoter region where initiation is started and terminator region where transcription ends. Enzyme involved in transcription is RNA polymerase-II.
55. (4) 56. (1) 57. (3) 58. (3) 59. (1)
60. (2) 61. (1) 62. (4) 63. (4) 64. (4)
65. (3) 66. (2) 67. (1) 68. (1)
69. (3) DNA (deoxyribose nucleic acid) consists of 3 different molecules phosphate, 5- carbon deoxyribose sugar and nitrogenous base. The nitrogenous base may be a 9- membered, double purine,  i.e.,  adenine (A) or Guanine (G), or a 6- membered, single - ringed pyrimidine,  i.e.,  thymine (T) or cytosine (C).
70. (4)