Collegedunia NCERT Formula Sheet

The Quick Revision Reference for Class 12 Biology (NCERT 2026-27 / Latest Edition)

Chapter 5: Molecular Basis of Inheritance

Key Facts | Definitions | Calculations | NEET Extensions

Also see for this chapter: **NCERT Solutions** | **Revision Notes** | **Exemplar Solutions**

Key Numerical Facts — Molecular Basis of Inheritance

Distance between two adjacent bp	0.34 nm $= 0.34 \times 10^{-9}$ m
Pitch (one full turn) of B-DNA helix	3.4 nm; $\approx$ **10** bp per turn
Bacteriophage ϕX174 genome	**5386** nucleotides
Bacteriophage lambda genome	**48502** base pairs (bp)
***E. coli* genome**	4.6×10^6 bp
Human haploid DNA content	3.3×10^9 bp
Length of DNA in a mammalian cell	$\approx$ **2.2** metres
Typical nucleus diameter	$\approx 10^{-6}$ m
Nucleosome DNA content	$\approx$ **200** bp wrapped on a histone octamer
A–T base pair	2 hydrogen bonds
G–C base pair	3 hydrogen bonds
***E. coli* replication rate**	$\approx$ **2000** bp per second (replicates in 18 min)
Total codons / coding / stop	**64** total $= 61$ coding $+3$ stop
Capping nucleotide (hnRNA)	methyl guanosine triphosphate at $5'$-end
Tailing (poly-A) residues	**200–300** adenylates at $3'$-end
Human genome size (HGP)	**3164**.7 million bp
Estimated human genes (HGP)	$\approx$ **30**,000 ($< 2\%$ of genome codes for protein)
Inter-individual base identity	**99**.9% bases identical between any two humans
Identified SNP sites	$\approx$ **1**.4 million locations
VNTR size range	0.1 to 20 kb

This chapter is mostly conceptual but carries several exam-critical **calculations** (DNA length, bp counts, codon combinatorics, base-ratio from Chargaff's rule). This sheet condenses every NCERT subsection (5.1–5.10) into compact "definition + key-fact + calculation" boxes and quick-recall tables so the whole chapter can be revised in minutes before NEET or the board exam.

1 5.1 The DNA

This section gathers the polynucleotide structure, the DNA length calculation, Chargaff's base-ratio rule, the Watson–Crick double-helix parameters, and the packaging of DNA into nucleosomes and chromatin.

Polynucleotide chain — structure

Nucleotide $=$ **nitrogenous base** $+$ **pentose sugar** $+$ **phosphate**.

Purines: **Adenine, Guanine** (double ring). Pyrimidines: **Cytosine, Thymine** (DNA), **Uracil** (RNA).

Linkages: base–sugar $=$ **N-glycosidic**; sugar–phosphate $=$ phosphoester; nucleotide–nucleotide $=$ $3'$–$5'$ **phosphodiester**.

Chain has a free **phosphate at $5'$-end** and a free **OH at $3'$-end**. RNA differs by a $2'$-OH and uracil in place of thymine.

DNA length calculation

$L = (\text{number of bp}) \times 0.34 \times 10^{-9}$ m

Mammalian cell: 6.6×10^9 bp $\times 0.34 \times 10^{-9}$ m ≈ 2.2 m.

Uses 0.34 nm per bp. The 2.2 m of DNA must fold into a $\sim 10^{-6}$ m nucleus, hence packaging is essential.

Chargaff's rule — base ratios

In double-stranded DNA: $A = T$ and $G = C$.

$$\frac{A+G}{T+C} = 1$$ (purines $=$ pyrimidines)

Worked use: if $C = 20\%$ then $G = 20\%$, so $A + T = 60\%$, giving $A = T = 30\%$. Pairing makes the two strands **complementary**.

Watson–Crick double helix — parameters

Two **antiparallel** strands: one $5' \rightarrow 3'$, the other $3' \rightarrow 5'$.

Right-handed coil; pitch $= 3.4$ nm; ≈ 10 bp per turn; rise per bp $= 0.34$ nm.

A=T (2 H-bonds), **G≡C** (3 H-bonds); a purine always pairs a pyrimidine $\Rightarrow$ uniform strand spacing.

Base-pair stacking plus H-bonds stabilise the helix. Proposed by Watson & Crick (1953) using Wilkins & Franklin's X-ray data.

Packaging of DNA

Nucleosome $=$ DNA (≈ 200 bp, negatively charged) wrapped on a **histone octamer** (8 basic, positively charged histones rich in lysine & arginine).

Nucleosomes $\rightarrow$ "beads-on-string" $\rightarrow$ **chromatin** fibre $\rightarrow$ chromosome (with NHC proteins).

Euchromatin: loosely packed, light-staining, **transcriptionally active**. **Heterochromatin:** densely packed, dark, inactive. Prokaryotes: DNA + positive proteins in the **nucleoid**.

DNA vs RNA — structure

DNA: deoxyribose sugar, thymine, double-stranded, stable, stores information.
RNA: ribose ($2'$-OH), uracil, mostly single-stranded, reactive/labile, catalytic; acts as messenger, adapter, structural and catalytic molecule.

2 5.2 The Search for Genetic Material

This section covers the three landmark experiments that proved DNA is the genetic material and the criteria a genetic material must satisfy.

Griffith's transforming principle (1928)

Streptococcus pneumoniae: **S strain** (smooth, virulent, mice die) vs **R strain** (rough, non-virulent, mice live).

Heat-killed S $\rightarrow$ mice live. Heat-killed S $+$ live R $\rightarrow$ **mice die** (live S recovered).

R was **transformed** by a "transforming principle" from heat-killed S; biochemical nature not yet identified.

Avery, MacLeod & McCarty (1933–44)

Purified protein, RNA, DNA from heat-killed S. Only **DNA** transformed live R into S.

Proteases & RNases did **not** stop transformation; **DNase did** stop it.

Conclusion: **DNA is the transforming/hereditary material** (still not universally accepted).

Hershey–Chase experiment (1952)

Bacteriophages on **radioactive ^{32}P** (labels **DNA**) and on **radioactive ^{35}S** (labels **protein coat**).

After infection: ^{32}P (DNA) **enters** bacteria; ^{35}S (protein) stays **outside**.

Unequivocal proof: **DNA**, not protein, is the genetic material passed from virus to bacterium.

Criteria for a genetic material

A genetic material must: (i) **replicate** (generate its replica); (ii) be chemically and structurally **stable**; (iii) allow slow **mutation** for evolution; (iv) **express** as Mendelian characters. DNA is more stable than RNA (no $2'$-OH; thymine adds stability; double strand allows repair), so DNA is the better genetic material; RNA is better for transmission/expression.

3 5.3 RNA World & 5.4 Replication

This section states the RNA-world idea, the semiconservative model, the Meselson–Stahl proof, and the enzymes of the replication fork.

RNA world

RNA was the first genetic material: it acted as genetic material and as a catalyst (ribozyme). Being reactive (catalytic), RNA was unstable; **DNA evolved from RNA** with modifications (thymine, double strand, repair) for greater stability.

Semiconservative replication

Each new DNA double helix $=$ **one parental** strand $+$ **one newly synthesised** strand.

Predicted by Watson & Crick (1953) from base complementarity; each strand acts as a template.

Meselson–Stahl proof (1958)

E. coli grown on ^{15}**N** (heavy), shifted to ^{14}**N** (light); DNA separated on CsCl density gradient.

Gen I (20 min): all **hybrid** (^{15}N–^{14}N) density.

Gen II (40 min): **half hybrid** $+$ **half light**.

Confirms semiconservative replication. Taylor's *Vicia faba* experiment proved the same for chromosomes.

Replication machinery

Main enzyme: **DNA-dependent DNA polymerase**; polymerises only $5' \rightarrow 3'$.

Site $=$ **replication fork**; starts at **origin of replication** (*ori*).

Continuous synthesis on the $3' \rightarrow 5'$ template; **discontinuous** (fragments) on the $5' \rightarrow 3'$ template, joined by **DNA ligase**.

Deoxyribonucleoside triphosphates act as substrate **and** energy source. *E. coli* rate ≈ 2000 bp/s. Eukaryotic replication is in **S-phase**.

Replication is NOT fully conservative or dispersive

The Meselson–Stahl Gen I result (all-hybrid) rules out the **conservative** model; the Gen II result (half light + half hybrid) rules out the **dispersive** model. Only **semiconservative** fits both.

4 5.5 Transcription

This section covers the transcription unit, template vs coding strand, the three types of RNA, and hnRNA processing.

Transcription & transcription unit

Transcription = copying genetic information from one DNA strand into RNA (adenine pairs **uracil**).

Transcription unit = **Promoter** (binds RNA polymerase, towards $5'$/upstream) + **Structural gene** + **Terminator** (towards $3'$/downstream).

Only **one** segment and **one** strand are copied (avoids two different proteins and double-stranded RNA).

Template vs coding strand

Template strand: polarity $3' \to 5'$; actually copied.

Coding strand: polarity $5' \to 3'$; same sequence as RNA (T for U); not copied.

RNA built from the template is complementary; reference points are defined on the **coding strand**.

RNA polymerase & factors (bacteria)

Single DNA-dependent **RNA polymerase** catalyses all RNA; it only does **elongation**.

+ **Initiation factor (σ, sigma)** → initiation. + **Termination factor (ρ, rho)** → termination.

Steps: Initiation → Elongation → Termination. In bacteria, transcription & translation are **coupled** (no nucleus).

Eukaryotic RNA pols & hnRNA

Three nuclear RNA polymerases process hnRNA into mature mRNA:

RNA pol **I** → rRNAs (28S, 18S, 5.8S); RNA pol **II** → hnRNA (mRNA precursor); RNA pol **III** → tRNA, 5S rRNA, snRNAs.

hnRNA processing: **splicing** (introns removed, exons joined) + **capping** (methyl guanosine triphosphate at $5'$) + **tailing** (200–300 adenylates at $3'$).

Exons appear in mature mRNA; **introns** do not. Split-gene arrangement is an ancient (RNA-world) feature.

RNA polymerases — "1 ribosome, 2 messenger, 3 transfer"

Pol **I** → r**R**NA (**r**ibosomes). Pol **II** → **m**RNA precursor (**m**essenger). Pol **III** → **t**RNA + small RNAs (**t**ransfer). Order I-II-III = large-medium-small product size.

5 5.6 Genetic Code

This section covers the codon combinatorics, the salient features of the code, mutations, and tRNA as the adapter molecule.

Codon combinatorics

Number of codons $= 4^3 = 4 \times 4 \times 4 = 64$.

$64 = 61$ coding codons $+3$ stop codons (UAA, UAG, UGA).

George Gamow argued the code must be a **triplet** (4 bases, 20 amino acids). A doublet ($4^2 = 16$) is too few; a triplet ($4^3 = 64$) is enough.

Salient features of the genetic code

Triplet; **degenerate** (an amino acid may have > 1 codon); read **continuously, no punctuation**; nearly **universal**.

AUG = codes Methionine **and** acts as **initiator**. Stop codons: **UAA, UAG, UGA**.

Exceptions to universality occur in some mitochondrial and protozoan codons.

Mutation & genetic code

Point mutation: single bp change; e.g., glutamate → valine in β-globin causes **sickle-cell anaemia**.

Frameshift: insertion/deletion of 1 or 2 bases shifts the reading frame from that point onward.

Insertion/deletion of **three** (or multiples of three) bases adds/removes whole amino acids; frame is restored beyond that point.

tRNA — the adapter molecule

tRNA has an **anticodon loop** (bases complementary to the codon) and an **amino acid acceptor end**.

Specific tRNA per amino acid; a special **initiator tRNA**; **no tRNA for stop codons**.

Secondary structure = clover-leaf; actual 3-D structure = inverted L. Postulated by Crick as the adapter.

Degenerate ≠ ambiguous

"Degenerate" means one amino acid can have several codons — it does **not** mean one codon codes several amino acids. Each codon specifies **exactly one** amino acid (or a stop signal).

6 5.7 Translation & 5.8 Regulation

This section covers translation, charging of tRNA, the role of the ribosome, and regulation of gene expression including the *lac* operon.

Translation

Translation = polymerisation of amino acids into a polypeptide; order set by mRNA codons; bond = **peptide bond** (energy-requiring).

Charging / aminoacylation: amino acid + ATP → activated → linked to cognate tRNA.

Ribosome (rRNA + ∼80 proteins) provides the platform; **23S rRNA** in bacteria is the ribozyme catalysing peptide-bond formation.

Translational unit & steps

Translational unit = mRNA flanked by **start codon (AUG)** and a **stop codon**, with **UTRs** at $5'$ (before start) and $3'$ (after stop).

Steps: **Initiation** (ribosome + initiator tRNA at AUG) → **Elongation** (codon-by-codon) → **Termination** (release factor at stop codon).

UTRs are not translated but are required for **efficient translation**.

The *lac* operon

Polycistronic: regulatory gene *i* + promoter + operator + structural genes ***z, y, a***.

z → β-galactosidase; *y* → permease; *a* → transacetylase; *i* → **repressor**.

Inducer = lactose/allolactose. No lactose ⇒ repressor binds operator ⇒ operon **off**. Lactose present ⇒ repressor inactivated ⇒ operon **on** (**negative regulation**).

Levels of regulation (eukaryotes)

Gene expression can be regulated at: (i) **transcriptional** level, (ii) **processing** (splicing) level, (iii) **transport** of mRNA to cytoplasm, (iv) **translational** level. In prokaryotes, control of **transcription initiation** is the predominant site.

NEET Extension — *lac* operon one-liners

- *i* gene = "inhibitor" (repressor), **not** "inducer".
- Repressor is made **constitutively** (all the time).
- Glucose & galactose **cannot** act as inducers.
- Jacob & Monod elucidated the first transcriptionally regulated system.

7 5.9 Human Genome Project (HGP)

This section covers the aims, methodology, timeline, and the salient features of the human genome.

HGP — scale & cost

Human genome $\approx 3 \times 10^9$ bp; at $3/bp $\Rightarrow$ total cost ≈ 9 billion US dollars.

In typed form (1000 letters/page, 1000 pages/book) ≈ 3300 books for one cell.

Launched **1990**; **13-year** project; completed **2003**; led to **Bioinformatics**.

HGP — methodology

ESTs (Expressed Sequence Tags): focus on **expressed** genes.

Sequence Annotation: sequence the whole genome (coding $+$ non-coding), assign functions later.

Vectors: **BAC** (bacterial) & **YAC** (yeast) artificial chromosomes; sequencing by **Sanger**'s method.

Sequences aligned by computer programs; chromosome 1 finished last (May 2006).

Salient features of the human genome

Size $= 3164.7$ million bp; average gene ≈ 3000 bases (largest $=$ **dystrophin**, 2.4 Mb).

$\approx 30{,}000$ genes; $<$ **2%** codes protein; 99.9% bases identical between humans.

Chromosome 1: most genes (**2968**); Y: fewest (**231**); ≈ 1.4 million **SNP** sites.

Functions unknown for $>$ **50%** of genes; repetitive sequences dominate the genome.

8 5.10 DNA Fingerprinting

This section covers the basis (polymorphism, satellite/repetitive DNA), the technique steps, and VNTR-based fingerprinting.

Basis — polymorphism & satellite DNA

Bulk DNA forms the major peak; **satellite DNA** forms small peaks (micro-/mini-satellites) on density-gradient centrifugation.

Polymorphism: an inheritable mutation present in a population at frequency > 0.01 (more than one allele at a locus).

Satellite DNA is non-coding, highly **polymorphic**, same in every tissue of an individual — ideal for identification.

Technique (Alec Jeffreys) — steps

Probe $=$ **VNTR** (Variable Number of Tandem Repeats), a mini-satellite. Steps:

(i) isolation of DNA $\rightarrow$ (ii) digestion by **restriction endonucleases** $\rightarrow$ (iii) separation by **electrophoresis** $\rightarrow$ (iv) **blotting** (Southern) to nylon/nitrocellulose $\rightarrow$ (v) hybridisation with labelled VNTR probe $\rightarrow$ (vi) detection by **autoradiography**.

VNTR copy number varies chromosome-to-chromosome; size 0.1–20 kb $\Rightarrow$ characteristic band pattern.

Applications

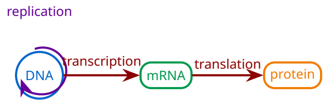
Same for every tissue of one individual; differs between individuals **except identical (monozygotic) twins**.

Sensitivity boosted by **PCR**. Uses: **forensics**, **paternity testing**, population & genetic diversity studies.

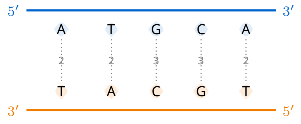
Polymorphisms are inherited parent → child, so banding patterns can establish parentage.

9 Core Recall Diagrams

Two visuals carry relationships that prose alone cannot: the Central Dogma flow and the antiparallel base-pairing rule.



Central Dogma (Crick)



Antiparallel pairing
A=T (2 H-bonds), G≡C (3 H-bonds)

Read the Full Revision Notes

Quick Reference Summary

Class 12 Biology — Chapter 5 Molecular Basis of Inheritance

Term	One-line recall
Nucleotide	Base + pentose sugar + phosphate
Phosphodiester bond	$3'$–$5'$ link joining nucleotides
Chargaff's rule	$A = T$, $G = C$; $(A+G)/(T+C) = 1$
B-DNA helix	Pitch 3.4 nm, ∼10 bp/turn, 0.34 nm/bp
A=T / G≡C	2 H-bonds / 3 H-bonds
Nucleosome	∼200 bp on a histone octamer
Euchromatin / Heterochromatin	Loose, active / dense, inactive
Griffith	Transforming principle (S/R, mice)
Avery–MacLeod–McCarty	DNA is the transforming material
Hershey–Chase	^{32}P/^{35}S phages ⇒ DNA is genetic material
Semiconservative	1 old strand + 1 new strand
Meselson–Stahl	^{15}N→^{14}N, CsCl; hybrid then half-light
DNA polymerase	DNA-dependent; $5' \to 3'$ only
Okazaki / DNA ligase	Discontinuous fragments joined by ligase
Transcription unit	Promoter + structural gene + terminator
Template strand	$3' \to 5'$, actually copied
Coding strand	$5' \to 3'$, same as RNA (T for U)
σ / ρ factors	Initiation / termination of transcription
hnRNA processing	Splicing + capping + tailing
Genetic code	$4^3 = 64$; 61 coding + 3 stop; triplet, degenerate
AUG	Met + initiator codon
Stop codons	UAA, UAG, UGA
tRNA	Adapter; anticodon loop + acceptor end
Ribozyme	23S rRNA catalyses peptide bond
lac operon	*i*-p-o-*z*-*y*-*a*; lactose = inducer; negative regulation
HGP	1990–2003; ∼3164.7 Mb; ∼30,000 genes
SNP	∼1.4 million single-base difference sites
DNA fingerprinting	VNTR/satellite DNA polymorphism (Jeffreys)
VNTR	Mini-satellite probe; size 0.1–20 kb

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Same chapter — other resources:

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- Ch 4: Principles of Inheritance and Variation
- Ch 6: Evolution
- Class 12 Biology — All Chapters