Human DNA	3.3×10^9 bp of nucleotides in the DNA of haploid chromosomes
Nucleotides	**N-glycosidic linkage-** Nitrogenous base is attached to OH of 1'C of deoxyribose or ribose sugar **Phosphoester linkage-** Phosphate group attached to OH of 5'C of deoxyribose or ribose sugar
Polynucleotide	Two nucleotides are joined by 3'-5' phosphodiester linkage. OH of 3'C of pentose sugar of one nucleotide is attached to the phosphate group of 5'C of another nucleotide

5’ end of polynucleotides	Free Phosphate group at 5’C of the pentose sugar
3’ end of polynucleotides	Free OH group at 3’C of the pentose sugar
Friedrich Miescher	Identified DNA in 1869 Named it ‘Nuclein’ Present in nucleus and acidic

Maurice Wilkins and Rosalind Franklin	Obtained DNA images from X-ray crystallography
James Watson and Francis Crick	Proposed the double-helix model of DNA in 1953
Erwin Chargaff	Elucidated that the DNA contains equal amounts of adenine and thymine and in the same way guanine and cytosine

DNA double helix	Antiparallel strands, coiled in a right-handed fashion Backbone- sugar-phosphate Bases are bonded by hydrogen bonds and projected inside Adenine bonds to thymine by two hydrogen bonds Guanine bonds to cytosine by three hydrogen bonds Pitch- 3.4 nm and 10 bp in each turn
Central Dogma	Proposed by Francis Crick in 1958 The flow of genetic information from DNA → RNA → Protein

Nucleoid	Found in prokaryotes The region where DNA is concentrated within a cell associated with positively charged proteins
Histones	Positively charged basic proteins, rich in lysine and arginine eight molecules of histones associated with DNA to form a nucleosome
Nucleosome	DNA associated with histones octamer 200 bp of DNA in each nucleosome Appear as beads on chromatin threads

Euchromatin	Loosely packed and lightly stained part of chromatin Shows active transcription
Heterochromatin	Densely packed and darkly stained part of chromatin Inactive for transcription
Transforming principle	Frederick Griffith in 1928 He concluded that there was some transforming principle in the heat-killed S-strain, which transformed R strain *Streptococcus pneumoniae* to virulent

Avery, MacLeod and McCarty	Demonstrated that the DNA caused the bacterial transformation They showed that proteases and RNAases did not affect transformation, whereas DNAase inhibit transformation
Alfred Hershey and Martha Chase	Unequivocal proof of DNA as genetic material in 1952 They worked on bacteriophages Radioactive ^{35}S labelled- protein capsule Radioactive ^{32}P labelled- DNA
RNA as a genetic material	Present in many viruses known as retrovirus E.g. TMV, QB bacteriophage, etc. ds RNA- reovirus, etc.

Semiconservative DNA replication	Proposed by Watson and Crick Experimentally proved by Matthew Meselson and Franklin Stahl in 1958 using ^{15}N isotope in the growing medium for *E.coli* Taylor and colleagues worked on *Vicia faba* using radioactive thymidine
DNA-dependent DNA polymerase	Main enzyme for replication Polymerisation in 5'→3' direction
DNA ligase	Join the DNA strand, which is synthesised discontinuously during replication

DNA helicase	Unwind DNA at the origin of replication forming replication fork
Transcription	Synthesis of RNA from DNA Template strand- 3'→5' DNA Coding strand- 5'→3' DNA, has the same sequence as newly synthesised RNA strand
DNA-dependent RNA polymerase	Catalyses transcription Polymerisation in 5'→3' direction

Transcription unit	Reference point with respect to the coding strand (5'→3', DNA) Promoter- present at 5' end of a structural gene, RNA polymerase binds here Terminator- at 3' end of the coding strand
Cistron	A segment of DNA coding for polypeptide Monocistronic- eukaryotes Polycistronic- prokaryotes
Exons	Coding sequence of DNA expressed in mature and processed RNA

Introns	Interrupted sequence which are spliced in mature RNA
Translation	Formation of polypeptide from RNA mRNA- template for protein synthesis tRNA- adapter molecule, brings amino acids and reads codon on mRNA rRNA- structural and catalytic role
Eukaryotic transcription	RNA polymerase I - 28S, 18S, 5.8S rRNA RNA polymerase II - hnRNA (mRNA precursor) RNA polymerase III - tRNA, 5S rRNA, snRNA

hnRNA processing	**Splicing -** removal of introns and joining together of exons **Capping -** addition of methyl guanosine triphosphate at 5' end **Tailing -** addition of adenylate residues (200-300) at 3' end
Marshall Nirenberg	Deciphered first the 64 triplet codons for 20 amino acids present in protein
Start codon	AUG Codes for Methionine

Stop codons	UAA, UAG, UGA They do not code for any amino acids
tRNA	**Structure-** 2° structure like clover leaf, 3° like inverted L Anticodon loop- complementary mRNA codon for specific codon Acceptor arm- binds to amino acid DHU loop, TψC loop and variable loop **Function-** Adapter molecule, brings amino acid for translation and reads codon
Translation	Occurs in cytoplasm First step is charging of tRNA, aminoacylation or binding of tRNA to amino acid Peptide bond formation takes place between the amino acid of growing chain and newly brought amino acid in two sites present in large subunit of ribosomes

Ribozyme	Catalytic RNA 28S rRNA in bacteria
Untranslated regions (UTR)	Regions on mRNA, which are not translated Present on both 5’ and 3’ ends Required for efficient translation
Francois Jacob and Jacque Monod	First elucidated transcriptionally regulated system in *lac* operon

Operon	Present in prokaryotes Contains multiple genes, which are regulated by a promoter and an operator E.g. *lac* operon, *val* operon, *his, ara, trp,* operon, etc.
lac operon	i gene- repressor (negative regulation) Structural genes- **z** - beta-galactosidase (β-gal) **y** - permease **a** - transacetylase Inducer - lactose or allolactose
Human genome project (HGP)	Started in 1990, Completed in 2003 3 x 10^9 base pairs (haploid) 20,000-25,000 genes Largest gene- Dystrophin gene of the X chromosome (2.4 million bp) Smallest gene- SRF/TDY gene of the Y chromosome (14 bp)

SNPs	Single nucleotide polymorphism Single base differences exist at 1.4 million places in the human genome
Sequence annotation	Assigning different regions of genome according to function
Expressed Sequence Tags (ESTs)	Identifying all the genes, which are expressed as RNAs

DNA Fingerprinting	Developed by Sir Alec Jeffreys Involves identifying of repeated DNA sequences Satellite DNA forms smaller peaks and shows a high degree of polymorphism
VNTR	Variable number of tandem repeats Mini-satellite Number and position differs from person to person Flanked by restriction sites
Southern blotting	Transfer of electrophoresis separated DNA to nitrocellulose or nylon membrane and detection by probe hybridisation Used to detect DNA sample in blood or tissue