Collegedunia NCERT Formula Sheet

The Ultimate Formula Reference for Class 12 (12th) Chemistry — NCERT 2026-27

Chapter 10: Biomolecules

Carbohydrates · Glucose / Fructose · Di- & Polysaccharides · Amino Acids · Proteins · Enzymes · Vitamins · Nucleic Acids · JEE & NEET

Quick Reference — Biomolecule Classes & Key Units

Biomolecule / Group	Formula / unit	Key feature
Carbohydrate (general)	$C_x(H_2O)_y$	Optically active polyhydroxy aldehyde/ketone or hydrolyses to one
Monosaccharide (hexose)	$C_6H_{12}O_6$	Cannot be hydrolysed; e.g. glucose, fructose, galactose
Disaccharide	$C_{12}H_{22}O_{11}$	2 monosaccharides joined by glycosidic linkage
Polysaccharide	$(C_6H_{10}O_5)_n$	Many monosaccharides; e.g. starch, cellulose, glycogen
α-Amino acid	R–CH(NH_2)–COOH	20 natural; chiral at C_α (not glycine); L-configuration
Peptide linkage	–CO–NH–	Amide bond between –COOH and –NH_2 (loss of H_2O)
DNA sugar	β-D-2-deoxyribose	2′-OH replaced by H
RNA sugar	β-D-ribose	2′-OH present
DNA bases / RNA bases	A, G, C, T / A, G, C, U	T only in DNA; U replaces T in RNA
Nucleoside	Base + sugar	N-glycosidic bond at C1′
Nucleotide	Base + sugar + phosphate	Phosphate ester at C5′ of sugar
Zwitter ion	^+H_3N–CHR–COO^-	Amphoteric form of amino acid in aqueous solution
Fat-soluble vitamins	A, D, E, K	Stored in liver & adipose tissue
Water-soluble vitamins	B-group, C	Excreted in urine (B_{12} stored)

1 Carbohydrates — Definition & Classification

NCERT Section 10.1 fixes the modern structure-based definition of a carbohydrate and splits them by hydrolysis behaviour (mono- / oligo- / poly-saccharide) and by reducing power.

Modern definition

Optically active polyhydroxy aldehydes or ketones, or compounds that produce such units on hydrolysis.
Old empirical formula: $\mathbf{C_x(H_2O)_y}$ ("hydrates of carbon").
Counter-examples: CH_3COOH fits $C_x(H_2O)_y$ but is **not** a carbohydrate; rhamnose $C_6H_{12}O_5$ is a carbohydrate but does **not** fit.
Use the **functional-group** definition — the empirical formula is only a memory aid.

Classification by hydrolysis

(i) Monosaccharide — cannot be hydrolysed further (about 20 in nature); e.g. glucose, fructose, ribose.
(ii) Oligosaccharide — yields 2–10 monosaccharide units; di-, tri-, tetra-saccharide; commonest are disaccharides (sucrose, maltose, lactose).
(iii) Polysaccharide — many monosaccharide units; e.g. starch, cellulose, glycogen, gums — generally **not sweet** ("non-sugars").
Classified further by C count: aldo- / keto- triose, tetrose, pentose, hexose (Table 10.1).

Reducing vs non-reducing sugars

Reducing sugar reduces Fehling's solution / Tollens' reagent.
All **monosaccharides** (aldose or ketose) are reducing.
Maltose, lactose (disaccharides) are reducing — free hemiacetal –CHO can open.
Sucrose is *non-reducing* — both anomeric –OH locked in the glycosidic linkage.
Ketoses (fructose) still test positive: in alkali they tautomerise (ketone $\rightarrow$ enediol $\rightarrow$ aldose).

2 Glucose — Structure, Cyclic Form & Reactions

NCERT 10.1.2 establishes the open-chain Fischer structure of D-(+)-glucose by six chemical evidences and explains why mutarotation and four "unexplained" facts force the cyclic pyranose hemiacetal.

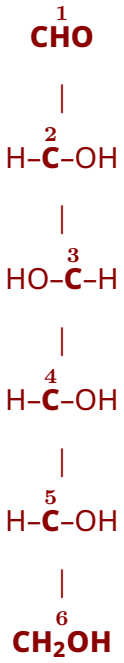
Preparation of glucose

From sucrose (lab): $\mathbf{C_{12}H_{22}O_{11} + H_2O \longrightarrow [H^+]\ C_6H_{12}O_6\ (glucose) + C_6H_{12}O_6\ (fructose)}$
From starch (commercial): $\mathbf{(C_6H_{10}O_5)_n + n\,H_2O \longrightarrow [H_2SO_4,\ 393\ K,\ 2\text{–}3\ atm]\ n\,C_6H_{12}O_6}$
The starch route gives pure glucose only — no fructose contamination.

Six evidences for the open chain (Fischer)

1. Mol. formula: $C_6H_{12}O_6$.
2. HI / Δ (prolonged) $\rightarrow$ n-hexane $\Rightarrow$ **straight 6-C** chain.
3. NH_2OH $\rightarrow$ oxime; **HCN** $\rightarrow$ cyanohydrin $\Rightarrow$ presence of $>C{=}O$.
4. Br_2/H_2O (mild) $\rightarrow$ **gluconic acid** (mono-COOH) $\Rightarrow$ –CHO group.
5. $(CH_3CO)_2O$ $\rightarrow$ **glucose pentaacetate** $\Rightarrow$ **five** –OH on five different C.
6. HNO_3 (strong) $\rightarrow$ **saccharic acid** (di-COOH) $\Rightarrow$ terminal $-CH_2OH$ at the other end.
Combined verdict: glucose = $\mathbf{CHO-(CHOH)_4-CH_2OH}$, an aldohexose with five –OH on five different C.

Open-chain D-(+)-glucose



D-(+)-glucose: –CHO at C1, $-CH_2OH$ at C6; **four chiral centres** (C2–C5).
D $\Rightarrow$ –OH on the *lowest* chiral C (C5) on the **right** (vs D-glyceraldehyde). *(+)* $\Rightarrow$ dextrorotatory.
D / L $=$ relative configuration; (+) / $(-)$ $=$ measured rotation. The two labels are independent.

Cyclic pyranose form, mutarotation & specific rotations

α-D-(+)-glucopyranose $\rightleftharpoons$ open chain $\rightleftharpoons$ β-D-(+)-glucopyranose.
Ring closure: –OH at **C5** attacks –CHO at **C1** $\Rightarrow$ **six-membered O-ring** (pyranose, NCERT Fig. 10 cyclic).
α-form: m.p. **419 K**, anomeric –OH *axial* (below ring in Haworth), $[\alpha]_D = +112°$ (crystallised at 303 K from conc. soln.).
β-form: m.p. **423 K**, anomeric –OH *equatorial* (above ring), $[\alpha]_D = +19°$ (hot saturated soln. at 371 K).
Equilibrium mixture (via open chain in solution): $[\alpha]_D = +52.7°$ — this slow drift is **mutarotation**.
The former –CHO carbon (C1) becomes the new chiral **anomeric C**. α and β differ *only* at C1 and are **anomers**. β-form predominates ($\sim$64%) at equilibrium because the equatorial –OH is less sterically strained.

Reagent $\rightarrow$ product map for glucose

Glucose $\longrightarrow$ [HI, Δ] n-hexane
Glucose $\longrightarrow$ [NH_2OH] glucose oxime ; **Glucose** $\longrightarrow$ [HCN] cyanohydrin
Glucose $\longrightarrow$ [Br_2/H_2O] **gluconic acid** (COOH–$(CHOH)_4$–CH_2OH)
Glucose $\longrightarrow$ [$(CH_3CO)_2O$] **glucose pentaacetate**
Glucose $\longrightarrow$ [HNO_3] **saccharic acid** (COOH–$(CHOH)_4$–COOH)
Open-chain CANNOT explain: negative Schiff's test, no $NaHSO_3$ adduct, pentaacetate + NH_2OH $\rightarrow$ no reaction, two crystalline forms with mutarotation. These force the **cyclic hemiacetal** structure.

Gluconic acid vs saccharic acid

Mild oxidant (Br_2/H_2O) attacks only –CHO $\Rightarrow$ mono-carboxylic **gluconic** acid (proves –CHO).
Strong oxidant (HNO_3) attacks –CHO *and* terminal $-CH_2OH$ $\Rightarrow$ di-carboxylic **saccharic** acid (proves 1° –OH at the other end). Don't swap the reagents.

3 Fructose, Anomers & Haworth Projection

NCERT 10.1.2.2 introduces D-(–)-fructose, the only ketohexose in the syllabus, and its five-membered furanose ring; the same section pins down the meaning of anomers and the Haworth orientation convention.

D-(–)-fructose

Open chain (ketohexose, mol. formula $C_6H_{12}O_6$ — same as glucose):
$\mathbf{CH_2^{1}OH-C^{2}(=O)-CHOH^{3}-CHOH^{4}-CHOH^{5}-CH_2^{6}OH}$
D-series (–OH on C5 right in Fischer), **laevorotatory**, $[\alpha]_D = -92.4°$.
Cyclic form: –OH at **C5** attacks >C=O at **C2** $\Rightarrow$ **five-membered** ring $=$ **β-D-fructofuranose** (and α).
Fructose ring = **5-membered (furanose)**; glucose ring = **6-membered (pyranose)** — single biggest exam discriminator.

Anomers, epimers, anomeric C, Haworth rule

Anomeric C = former carbonyl C (C1 in aldoses, C2 in ketoses); carries one –OH and one –H after cyclisation.
Anomers = pair of cyclic isomers differing in configuration *only* at the anomeric C:
α-form: anomeric –OH **below** the ring (Haworth); β-form: anomeric –OH **above** the ring.
Epimers = pair of diastereomers differing at *exactly one* non-anomeric chiral C:
Glucose / mannose $\Rightarrow$ **C2 epimers**; glucose / galactose $\Rightarrow$ **C4 epimers**.
Pyran (1 O + 5 C) $\rightarrow$ **pyranose**; furan (1 O + 4 C) $\rightarrow$ **furanose** sugars. Reducing test (Fehling's / Tollens') requires a **free anomeric –OH**; ketoses pass because they tautomerise to enediol $\rightarrow$ aldose in alkali.

Ring-size memory aid
"**G**lucose $\rightarrow$ **G**reat (**6**-ring) pyranose"; "**F**ructose $\rightarrow$ **F**ive-ring furanose".

D / L vs (+) / (−)

D, L label the *relative configuration* (vs D- or L-glyceraldehyde) — they describe *geometry*, not direction of rotation. **(+), (−)** label the *measured optical rotation*. Independent: D-(–)-fructose is D-series but laevorotatory.

4 Disaccharides — Sucrose, Maltose, Lactose

NCERT 10.1.3 fixes the three textbook disaccharides by their constituent monosaccharides and the position of the glycosidic linkage.

Glycosidic linkage

Bond formed when the anomeric –OH of one monosaccharide reacts with an –OH of another, with loss of H_2O:
$\mathbf{Sugar_1-OH + HO-Sugar_2 \rightarrow Sugar_1-O-Sugar_2 + H_2O}$
An **ether-like C–O–C bridge** between two sugar carbons; cleaved by H^+ or specific enzymes (sucrase, maltase, lactase).

Sucrose (cane sugar) — non-reducing

$\mathbf{C_{12}H_{22}O_{11} + H_2O \longrightarrow}$ [H^+ or invertase] **D-(+)-glucose + D-(−)-fructose** (equimolar).
Linkage: **C1 of α-D-glucose ↔ C2 of β-D-fructose** — both anomeric –OH used $\Rightarrow$ **non-reducing**.
$[\alpha]_{\text{sucrose}} = +66.5°$; after hydrolysis: $+52.5°$ (glu) $+(-92.4°)$ (fru) $= -39.9° \Rightarrow$ sign *inverts* $\Rightarrow$ "**invert sugar**".

Maltose & lactose — reducing

Maltose: two α-D-glucose units; linkage **C1(I)–C4(II)**; free hemiacetal –OH at C1 of unit II $\Rightarrow$ **reducing**.
Lactose (milk sugar): β-D-galactose + β-D-glucose; linkage **C1 (galactose)–C4 (glucose)**; free hemiacetal at C1 of glucose $\Rightarrow$ **reducing**.
Rule: if both anomeric –OH are used in the glycosidic linkage $\Rightarrow$ non-reducing (sucrose); otherwise reducing (maltose, lactose).

JEE/NEET extension — invert sugar

Acidic / enzymatic hydrolysis of sucrose is called **inversion** because the optical rotation flips sign. The 1:1 glucose:fructose mixture is *sweeter* than sucrose; honey is largely invert sugar.

5 Polysaccharides — Starch, Cellulose, Glycogen

NCERT 10.1.4 covers the three NCERT polysaccharides. All three are polymers of D-glucose; only the *stereochemistry* (α vs β) and the *linkage position* differ.

Starch = Amylose + Amylopectin

General formula $\mathbf{(C_6H_{10}O_5)_n}$.
Amylose (15–20%, water-soluble): *unbranched* chain of 200–1000 α-D-glucose units; **C1–C4 α-linkage** ($\alpha 1 \rightarrow 4$).
Amylopectin (80–85%, water-insoluble): *branched*; main chain **C1–C4 α** ($\alpha 1 \rightarrow 4$), with **$\alpha 1 \rightarrow 6$** branches *every ∼25–30 glucose units*.
Storage carbohydrate in plants; chief dietary glucose source. Iodine test: **deep blue** with I_2/KI.

Cellulose — structural β-linkage

Linear polymer of **β-D-glucose**; **C1–C4 β-glycosidic** linkage; unbranched.
Most abundant organic compound in the plant kingdom; cell-wall material.
Humans lack **β-glucosidase $\Rightarrow$ indigestible** to humans.
Industrial uses: wood, cotton fibre, paper, rayon, lacquers. Difference from starch is solely the **β- vs α-linkage**.

Glycogen — "animal starch"

Polymer of α-D-glucose; same linkages as amylopectin (C1–C4 main, C1–C6 branches) but **more highly branched**.
Stored in **liver, muscles, brain**; also in yeast and fungi.
Instant glucose reserve: when blood glucose drops, hydrolytic enzymes release D-glucose from glycogen.

α vs β linkage

Animals digest α, animals can't digest β.
Starch / glycogen: **α-1,4** ($\pm$ α-1,6 branches) — digestible.
Cellulose: **β-1,4** — indigestible to humans.

6 Amino Acids — Structure & Zwitter Ion

NCERT 10.2.1–10.2.2 introduces the 20 natural α-amino acids that build proteins, their dual –NH_2/–COOH functionality, the zwitter-ionic form, and the essential vs non-essential split.

General α-amino acid

$$\mathbf{R-\overset{\displaystyle NH_2}{\underset{|}{CH}}-COOH}$$ (R = side chain)

Greek-letter classification by –NH_2 position: α, β, γ, δ, ...
Only α-amino acids occur in proteins (20 in the standard set — NCERT Table 10.2).
The α-C carries (–NH_2, –COOH, –R, –H), so it is **chiral** in every amino acid *except glycine* (R = H).

Acidic / basic / neutral / aromatic / sulphur & essential

Acidic (extra –COOH in R): Asp, Glu. **Basic** (extra –NH_2/guanidino/imidazole in R): Lys, Arg, His.
Aromatic (R contains a benzene/indole/phenol ring): Phe, Tyr, Trp. **Sulphur-containing**: Cys (–SH), Met (–S–CH_3).
Cyclic / imino acid: Pro — the only amino acid with a *secondary* amine (–NH– fused into a 5-ring), so it breaks helices.
Neutral: Gly, Ala, Val, ...(count side-chain groups only — backbone –NH_2/–COOH is common to all).
Essential (body cannot synthesise — 10 in NCERT, marked $*$ in Table 10.2):
Val, Leu, Ile, Thr, Met, Phe, Trp, Lys, Arg, His. (Mnemonic **PVT TIM LH + Arg**; Arg is conditionally essential.)
Non-essential (body makes): Gly, Ala, Ser, Cys, Tyr, Asn, Gln, Asp, Glu, Pro.

Zwitter ion, amphoteric behaviour & isoelectric point (pI)

$\mathbf{R-CH(NH_2)-COOH \rightleftharpoons R-CH(\overset{+}{N}H_3)-COO^-}$ (**zwitter ion**: net charge 0, both $+$ and $-$ present)

Amphoteric: reacts with acid (gives $\mathbf{R-CH(\overset{+}{N}H_3)-COOH}$, cation) and with base (gives $\mathbf{R-CH(NH_2)-COO^-}$, anion).
Isoelectric point (pI): pH at which the amino acid exists *entirely* as the zwitter ion; **net charge** $= 0$; mobility in an electric field is zero.
Neutral AA: $\mathrm{pI} = \dfrac{\mathrm{pK_{a,\,\alpha\text{-}COOH}} + \mathrm{pK_{a,\,\alpha\text{-}NH_3^+}}}{2}$. Acidic AA $\Rightarrow$ low pI (avg of two –COOH pK_a); basic AA $\Rightarrow$ high pI (avg of two –NH_3^+ pK_a).
Because of the zwitter-ionic salt-like nature, amino acids are **high-melting, water-soluble, crystalline solids** — unlike free amines or carboxylic acids of similar size. Natural proteins are built from **L-amino acids**.

7 Proteins — Peptide Bond & Structure

NCERT 10.2.3 builds proteins as linear polymers of α-amino acids joined by peptide (amide) bonds and lays out the 1°, 2°, 3°, 4° hierarchy.

Peptide bond — geometry and counting

Bond formed between –COOH of one amino acid and –NH_2 of the next, with loss of H_2O:
$\mathbf{H_2N-CH_2-COOH + H_2N-CH(CH_3)-COOH}$
$\longrightarrow$ $[-H_2O]$ $\mathbf{H_2N-CH_2-\boxed{CO-NH}-CH(CH_3)-COOH}$ (Gly–Ala)
Peptide linkage = the amide group **–CO–NH–**.
Planarity & restricted rotation: the C–N bond has **~40% double-bond character** (resonance with C=O), so the 6 atoms $\mathbf{C_\alpha-CO-NH-C_\alpha}$ are **coplanar**. The two C_α residues sit in the **trans**

configuration (lower steric clash) in almost all peptides (exception: Xaa–Pro junctions).
Counting: 2 AA = dipeptide; 3 = tripeptide; $>$10 = **polypeptide**; $>$100 residues or $M > 10\,000$ u $=$ **protein**.
Boundary is fuzzy: **insulin** (51 AA) is conventionally called a protein because of its defined 3-D conformation.

Four levels of protein structure with geometric parameters

Primary (1°): the *covalent* amino-acid **sequence** of the polypeptide (determined by the gene); peptide bonds only.
Secondary (2°): regular local fold stabilised by H-bonds between peptide $>$C$=$O and –N–H. Two motifs:
• **α-helix:** *right-handed* screw; *intra*-chain H-bonds; **3.6 residues / turn**; **pitch $=$ 5.4 Å**; **rise $=$ 1.5 Å/ residue** (Fig. 10.4).
• **β-pleated sheet:** chains stretched flat side by side; *inter*-chain H-bonds; strands run either **parallel** (same N$\rightarrow$C direction) or **antiparallel** (opposite, slightly more stable) (Fig. 10.5).
Tertiary (3°): overall 3-D fold (fibrous or globular); stabilised by **H-bonds, disulphide –S–S– (Cys–Cys), salt bridges, hydrophobic packing, van der Waals**.
Quaternary (4°): multimeric assembly of ≥ 2 polypeptide sub-units.
• **Haemoglobin: 2α + 2β** chains (4 sub-units), each with a haem–Fe^{2+}.
• **Insulin:** 2 chains, A (**21 aa**) + B (**30 aa**); held by **2 inter-chain –S–S–** bridges + **1 intra-A –S–S–**.
Sequence $\rightarrow$ folding $\rightarrow$ shape $\rightarrow$ function. Side chains do *not* participate in 2° H-bonding — only the peptide-bond $>$C$=$O and –NH–.

Fibrous vs globular proteins

Fibrous: polypeptide chains run *parallel*, held by H-bonds and –S–S– bridges $\Rightarrow$ fibre-like, **insoluble** in water. Examples: **keratin** (hair, wool, silk), **myosin** (muscles).
Globular: chains coil into roughly *spherical* shape $\Rightarrow$ **soluble** in water. Examples: **insulin, albumins**.
Function follows shape: fibrous $=$ structural; globular $=$ enzymes / transport / hormones.

Denaturation of proteins

Heat, pH change, strong acid / base, organic solvent, urea, or heavy-metal salts break H-bonds, salt bridges, hydrophobic packing and –S–S– links $\Rightarrow$ globule unfolds, helix uncoils, sub-units dissociate.
2°, 3° and 4° structures destroyed; 1° (covalent peptide sequence) preserved.
Examples: coagulation of **egg-white on boiling**; **curdling of milk** (lactic acid lowers pH, casein denatures).
Denatured protein retains its sequence but loses biological activity — peptide bonds are *not* broken in denaturation.

Native vs denatured

NCERT *native protein* = the unique 3-D structure with biological activity; *not* a synonym for "natural / unprocessed". After boiling, egg-white is still a protein but no longer *native* — 1° intact, function lost.

8 Enzymes — Biological Catalysts

NCERT 10.3 treats enzymes as globular proteins that catalyse biochemical reactions with very high specificity. Naming is by substrate + "-ase".

Enzymes — key facts

Almost all enzymes are **globular proteins**.
Specific for *one* reaction *and one* substrate.
Named after the substrate or reaction class; ending **-ase**.
Maltase: $\mathbf{C_{12}H_{22}O_{11}}$ **(maltose)** $\longrightarrow$ [maltase] $2\,\mathbf{C_6H_{12}O_6}$ **(glucose)**
Other examples: **invertase / sucrase** (sucrose $\rightarrow$ glucose + fructose); **lactase** (lactose $\rightarrow$ glucose + galactose); **zymase** (glucose $\rightarrow$ ethanol + CO_2); **pepsin / trypsin** (proteins $\rightarrow$ amino acids).

Mechanism — activation-energy lowering

Like a chemical catalyst, an enzyme *lowers* E_a without being consumed.
Sucrose hydrolysis (NCERT data):
E_a with H^+ (chemical acid) $= 6.22\ \text{kJ mol}^{-1}$
E_a with sucrase (enzyme) $= 2.15\ \text{kJ mol}^{-1}$
Enzyme drops E_a to roughly **one-third** of the chemical value — this is why enzymatic reactions go at body temperature and ordinary pH.

JEE/NEET extension — Lock-and-Key / Induced-Fit & inhibitors

Substrate binds the enzyme's specific **active site**. **Lock-and-key** (Fischer): rigid complementary fit. **Induced-fit** (Koshland): active site reshapes around the substrate. Either way, the enzyme–substrate complex (ES) is the key intermediate.
Inhibitors: (i) **Competitive** — inhibitor mimics substrate, binds the *same active site*, blocks productive binding; reversed by raising [S]. (ii) **Non-competitive (allosteric)** — inhibitor binds a *different site*, distorts the active site; not reversed by raising [S].

9 Vitamins — Classification & Deficiency Table

NCERT 10.4 defines vitamins as organic compounds required in small amounts in the diet for specific biological functions, and splits them into fat-soluble and water-soluble groups.

Vitamin groups

Vitamins (from *vital* + *amine*): organic compounds required in *small amounts* in the diet; most cannot be synthesised in the human body (gut bacteria can make a few).
(i) Fat-soluble: A, D, E, K — soluble in fats / oils, insoluble in water; **stored in liver and adipose tissue**.
(ii) Water-soluble: B-group (B_1, B_2, B_6, B_{12}, ...) and **C** — excreted in urine; *must be supplied regularly* (exception: $\mathbf{B_{12}}$ **is stored** in the liver).
Excess vitamins (especially A, D) are also harmful — do not self-prescribe.

NCERT Table 10.3 (expanded) — Vitamin / chemical name / source / deficiency disease

Vitamin	Chemical name	Source	Deficiency disease
A	Retinol	Fish-liver oil, carrots, butter, milk	Xerophthalmia, **night blindness**
B_1	Thiamine	Yeast, milk, green veg., cereals	**Beri-beri**
B_2	Riboflavin	Milk, egg-white, liver, kidney	**Cheilosis** (cracked lips)
B_3	Niacin (nicotinic acid)	Liver, meat, fish, peanuts	**Pellagra** (3D: dermatitis, diarrhoea, dementia)
B_5	Pantothenic acid	Yeast, liver, eggs, vegetables	Burning-feet syndrome
B_6	Pyridoxine	Yeast, milk, egg yolk, cereals	**Convulsions**
B_7	Biotin (vitamin H)	Egg yolk, liver, gut flora	Dermatitis, hair loss
B_9	Folic acid	Leafy vegetables, liver	**Anaemia** (megaloblastic)
B_{12}	Cobalamin (contains **Co**)	Meat, fish, egg, curd	**Pernicious anaemia**
C	Ascorbic acid	Citrus, amla, leafy vegetables	**Scurvy** (bleeding gums)
D	Calciferol	Sunlight, fish, egg yolk	**Rickets** (children), **osteomalacia** (adults)
E	Tocopherol	Wheat-germ & sunflower oils	RBC fragility, sterility, muscular dystrophy
K	Phylloquinone	Green leafy vegetables	Increased blood-clotting time

Fat vs water-soluble

"**ADEK** float in oil" $\Rightarrow$ fat-soluble are **A, D, E, K**. Everything else (B-group + C) is water-soluble. The one stored water-soluble vitamin is **B**$_{12}$.

10 Nucleic Acids — DNA & RNA

NCERT 10.5 defines nucleic acids as polymers of nucleotides, lays out the sugar / base / phosphate composition, and contrasts DNA and RNA at every level.

Composition — complete hydrolysis

Complete hydrolysis of a nucleic acid gives:
1. Pentose sugar: β-D-2-deoxyribose in DNA; β-D-ribose in RNA.
2. Phosphoric acid: H_3PO_4.
3. Nitrogenous bases:
DNA: **A, G, C, T** (adenine, guanine, cytosine, thymine).
RNA: **A, G, C, U** (uracil replaces thymine).
Purines (2 fused rings): A, G. **Pyrimidines** (single 6-ring): C, T, U.

Nucleoside vs nucleotide — with examples

Nucleoside: *base* + *sugar* — base attached at **C1′** of pentose via an N-glycosidic bond.
e.g. **adenosine** = adenine + ribose; **deoxyguanosine** = guanine + 2-deoxyribose.
Nucleotide: *base* + *sugar* + *phosphate* — phosphate esterified at **C5′** of the sugar (i.e. phosphate ester of a nucleoside).
e.g. **AMP** = adenosine + phosphate; **dGMP** = deoxyguanosine + phosphate.
Phosphodiester linkage: joins the 3′-OH of one sugar to the 5′-OH of the next $\Rightarrow$ backbone = sugar–phosphate–sugar–phosphate–...; bases project sideways.
Nucleic acids are also called **polynucleotides**.

Watson–Crick double helix — base pairing & geometry

DNA = **two** polynucleotide chains wound about each other in a *double helix* (Watson–Crick, **1953**; NCERT Fig. 10.7).
Strands are **complementary** and *antiparallel* (one 5′ $\rightarrow$3′, other 3′ $\rightarrow$5′); bases pair across the helix:
$\mathbf{A \cdots T}$ (**2 H-bonds**) and $\mathbf{G \cdots C}$ (**3 H-bonds**). Hence A:T = G:C = 1:1 in any DNA (**Chargaff's rule**).
B-form geometry (right-handed): 10 bp / turn; **pitch = 3.4 nm**; **rise = 0.34 nm / bp**; **diameter = 2 nm**.
In **RNA**: $\mathbf{A \cdots U}$ replaces A–T (RNA is usually single-stranded but can fold back on itself locally).
Complementarity is the molecular basis of **replication** — each strand templates its partner. Each Watson–Crick pair is *purine–pyrimidine* (size match): two purines would be too bulky; two pyrimidines, too short.

DNA vs RNA — one-glance comparison

Feature	DNA	RNA
Sugar	2-deoxyribose	ribose
Bases	A, G, C, **T**	A, G, C, **U**
Strand(s)	double helix (antiparallel)	single strand (usually)
Location	nucleus (chiefly)	cytoplasm + nucleus
Function	heredity / blueprint	protein synthesis
Types	one	m-RNA, r-RNA, t-RNA
Self-replicates?	yes	no

Three types of RNA & central dogma

m-RNA (messenger): *template* that carries the coded message from DNA to ribosome (codon = 3 bases).
r-RNA (ribosomal): *structural* + *catalytic* component of the ribosome (the actual site of protein synthesis).
t-RNA (transfer): carries an *anticodon* that pairs with the m-RNA codon and *brings the correct amino acid* for translation.
Central dogma: DNA $\xrightarrow{\text{replication}}$ DNA $\xrightarrow{\text{transcription}}$ m-RNA $\xrightarrow{\text{translation (ribosome + tRNA + rRNA)}}$ Protein.
DNA functions = **heredity** (replication) + **gene expression** (transcription). RNA functions = executing the protein-synthesis instructions.

T vs U; ribose vs deoxyribose

DNA has **T (thymine)** and **2-deoxyribose** (–H at 2′).
RNA has **U (uracil)** and **ribose** (–OH at 2′).
The extra 2′-OH makes RNA chemically more labile — this is why RNA has a short cellular lifetime.

JEE/NEET extension — purine vs pyrimidine pairing

Each Watson–Crick pair is **purine–pyrimidine** (size match): A–T, G–C, A–U. Two purines would be too bulky; two pyrimidines, too short. The 1:1 purine:pyrimidine ratio is a direct consequence.

Quick Reference — Linkage & Structure Map

Item	Key structural facts
Glucose / Fructose	Both $C_6H_{12}O_6$. Glu: aldohexose, D-(+), 4 chiral C, pyranose; $[\alpha]_D$ $\alpha = +112°$, $\beta = +19°$, eq. $+52.7°$. Fru: ketohexose, D-(–), furanose; $[\alpha]_D = -92.4°$
Sucrose / Maltose / Lactose	Suc: α-glu(C1)–β-fru(C2), **non-reducing**, $[\alpha]_D = +66.5°$. Mal: 2 α-glu, C1–C4 α, reducing. Lac: β-gal(C1)–β-glu(C4), reducing, "milk sugar"
Amylose / Amylopectin	Amy: 200–1000 α-glu, C1–C4 α, unbranched, soluble (15–20%). Amp: C1–C4 main + C1–C6 branches every $\sim$25–30 units, insoluble (80–85%)
Cellulose / Glycogen	Cel: β-glu, C1–C4 β, unbranched, indigestible to humans. Gly: "animal starch", like amylopectin but more highly branched; liver / muscles / brain
Anomers / Epimers	Anomers = differ only at anomeric C (C1 aldose, C2 ketose). Epimers = differ at one non-anomeric C: glu/man at C2, glu/gal at C4
α-Amino acid / Zwitter ion / pI	R–CH(NH_2)–COOH; chiral at C_α (except Gly); L-series in proteins. Zwitter: ^+H_3N–CHR–COO^-; pI = pH of net-zero charge; neutral AA $pI = (pK_{a1} + pK_{a2})/2$
Essential AA (10)	Val, Leu, Ile, Thr, Met, Phe, Trp, Lys, Arg, His (PVT TIM LH + Arg)
Peptide bond	–CO–NH–; planar (40% double-bond character), trans configuration; loss of H_2O
1° / 2° / 3° / 4°	Sequence / α-helix (R-handed, 3.6 aa/turn, pitch 5.4 Å, rise 1.5 Å), β-sheet (parallel / antiparallel) / 3-D fold via –S–S–, salt bridges, hydrophobic / sub-units: Hb ($2\alpha+2\beta$), insulin (A 21+B 30, 2 inter + 1 intra –S–S–)
Denaturation	2°/3°/4° lost; 1° preserved; egg-white coag., milk curdling
Enzymes	Globular protein catalysts; suffix -ase; lower E_a (sucrose: 6.22 $\rightarrow$ 2.15 kJ mol^{-1}); lock-and-key / induced-fit; competitive vs non-competitive inhibitors
Vitamins	Fat-sol. A, D, E, K (stored in liver / adipose). Water-sol. B-group + C (excreted; B_{12} stored). Key: A–night blind., D–rickets, K–clotting, B_1–beri-beri, B_3–pellagra, B_{12}–pernic. anaemia, C–scurvy
DNA	Double helix (W-C 1953); deoxyribose; A,G,C,T; A=T (2H), G≡C (3H); 10 bp/turn, pitch 3.4 nm, rise 0.34 nm/bp, diameter 2 nm; antiparallel; heredity
RNA	Single strand; ribose; A,G,C,U; m-RNA (template), t-RNA (anticodon, brings aa), r-RNA (ribosome)
Nucleoside / Nucleotide	Base+sugar at C1′ (e.g. adenosine) / + phosphate at C5′ (e.g. AMP); chained by 3′–5′ phosphodiester backbone
Purines / Pyrimidines	Purines (bicyclic): A, G. Pyrimidines (monocyclic): C, T (DNA), U (RNA); each W-C pair = purine–pyrimidine

End of Class 12 Chemistry — Chapter 10 — Biomolecules — Formula Sheet.
Collegedunia NCERT Resource Library — 2026-27 Syllabus.