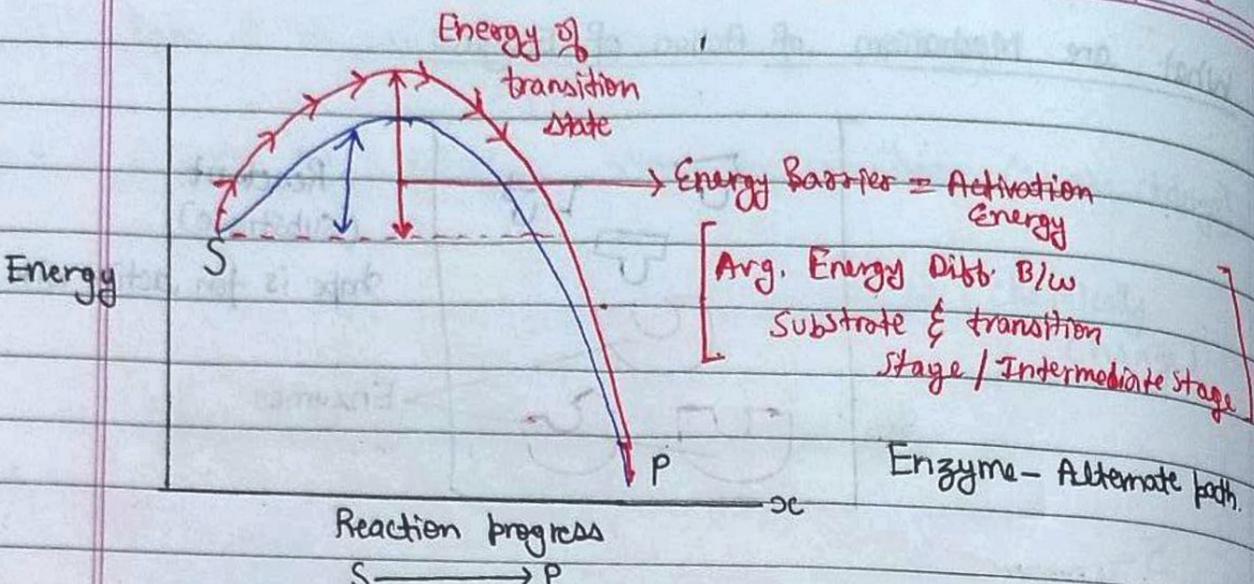
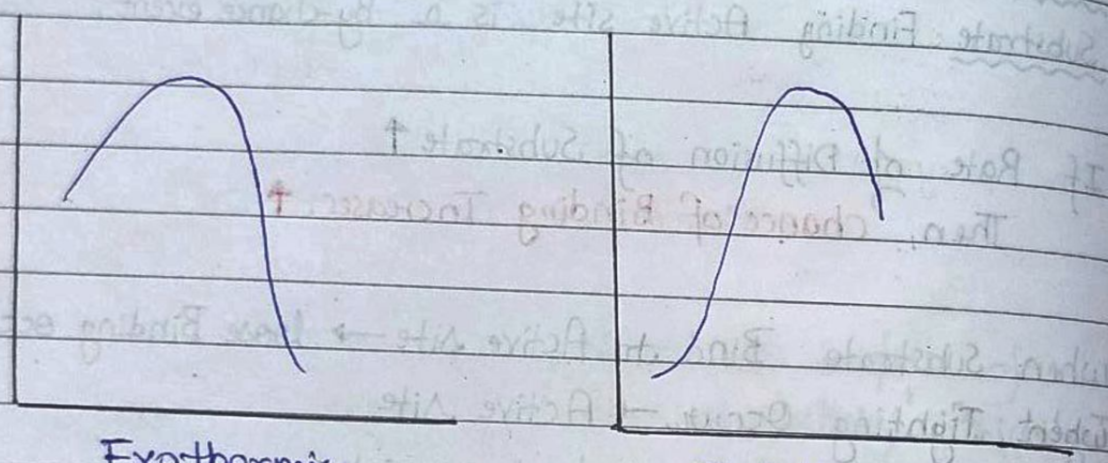


Enzyme- Alternate path.



Exothermic

Endothermic

Feature of Enzymes :-

1. Chemical nature :- made up of Protein
   since "protein" have more diversity so it was prefered over RNA

2. Medium in which it Act :- Act in Aquous Medium.

3. Specificity :- • Enzyme Active site → Fix chemical group
↓
So, Fix type of chemical Rxn.

• Enzyme active site shape specific.

4 Selectivity :-

Glucose ⟶ Pyruvate $\xrightarrow{\text{Pyruvate Dehydrogenase}}$ Acety COA

Pyruvate $\xrightarrow{\text{lactate Dehydrogenase}}$ Lactic Acid

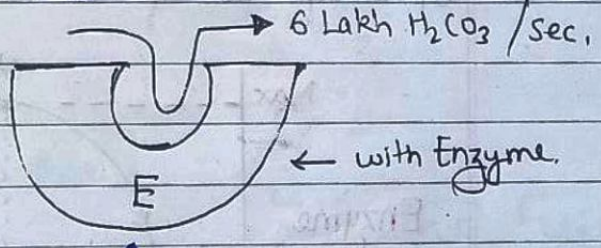
Pyruvate $\xrightarrow{\text{Pyruvate Decarboxylase}}$ Acetaldehyde

So, out of various possibility Enzyme can select any one.

5. Turn over number ⟶ no: of Product per unit time from single substrate.

→ Enzyme is very Efficient.

$H_2O + CO_2 \longrightarrow H_2CO_3$
without Enzyme
200 molecules / hour



(max or High turn over no: enzyme = Carbonic Anhydrase)

Factors Affecting Enzyme Activity :-
|
Speed / work Ability

1. Temperature
2. PH
3. Substrate concentration
4. Presence of inhibitor

1. Temperature

→ Every Enzyme to work at a particular temp.

Temp. at which Enzyme act maximally ↓ Known as Optimum temperature

[many organism over time – 37°c – optimum temp.]

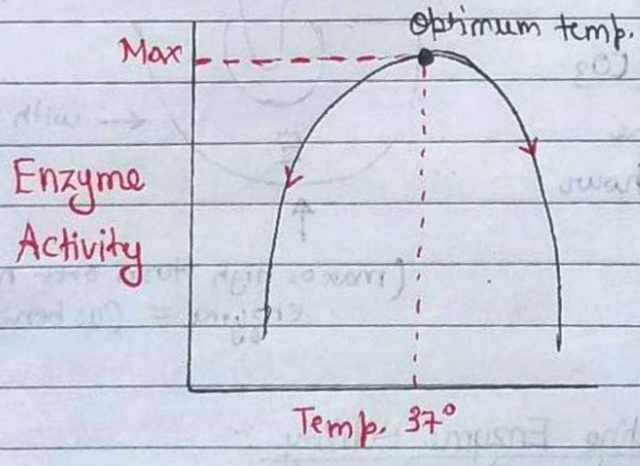
Low temp – Below 10°c ⟶ Substrate Diffusion ↓

Enzyme Activity – decreases.

* In this condition Enz. is less Active.

Above 50°c ⟶ Enzyme structure destroy – Denature (shape destroy)

Optimum = 37°c



→ 37°c – optimum

27°c — Enz. Activity ↓ (Decreases)

47°c — En. " ↓ (Decreases)

$\boxed{Q_{10} = 2}$

27° ← Rate half – 37° → half 47°

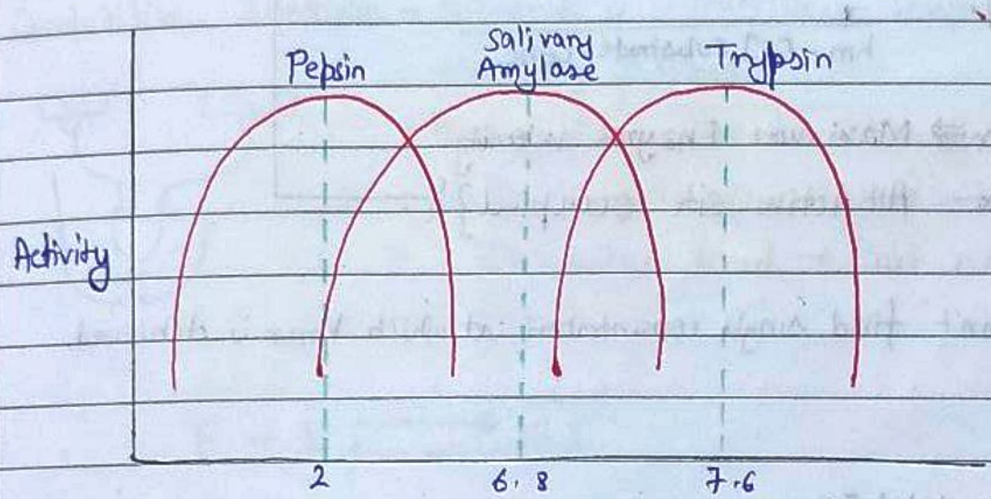
Double → ← Double

DELTA Pg No.

2. PH → Enzyme Final folding
it is balance of charge in 3° structure. → This Balance is maintain optimum PH,

* Optimum PH is that PH, where Enzyme shape is maintain → Maximum work

* PH other than optimum — Enzyme Activity → Decrease

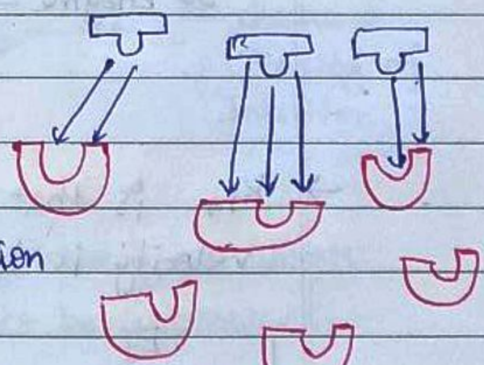


3. Substrate Concentration

→ No: of substrate is always Greater than no: of Enzyme.

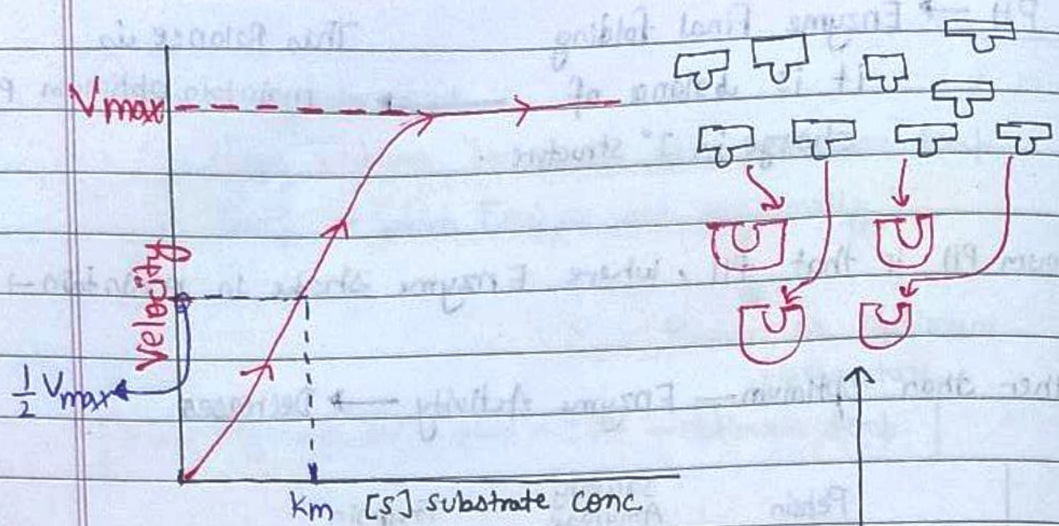
→ Substrate move to Enzyme — "Diffusion".

→ Substrate concentration Increase → Rate of Diffusion Increases



↓

Chance of E&S Combination Increase → Enzyme Velocity Increases



Vmax ⇒ Maximum Enzyme velocity.

{Vmax – All Active site occupied}

- We can't find single concentration at which Vmax is Achieved.

* Assume total Enzyme

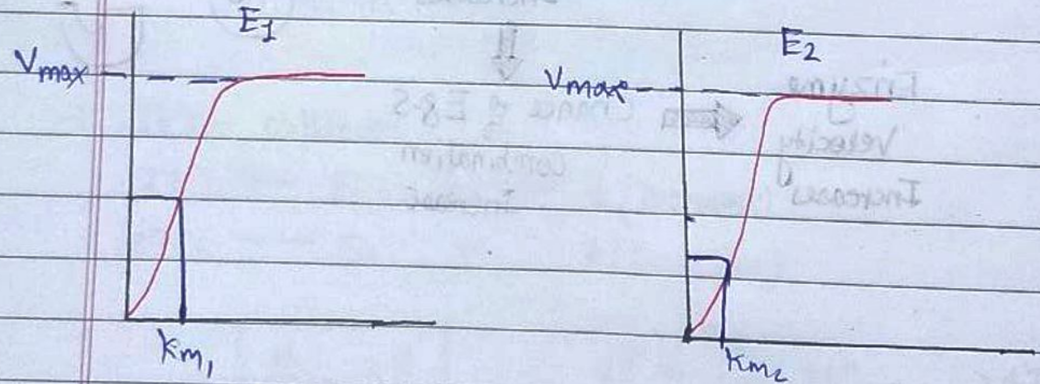
100 Enzyme ⟶ Vmax ~~is~~ → All 100 are working.

$\frac{1}{2}$ Vmax

↓

50 Enzyme ⟶ $\frac{1}{2}$ Vmax functional

→ Km is that substrate concentration at which velocity is half of Vmax.



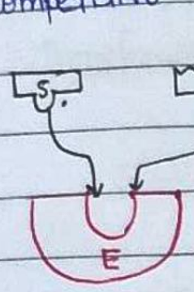
E_2 Enzyme low km → This means :-

At low substrate conc, more velocity
Hence, Enzyme forms more product.

Presence of Inhibitor

* Any chemical which can decrease Enzyme Activity.

(a) Competitive Inhibition - substrate & Inhibitor - shape similar But chemically Different



- Binding occur due to shape of substrate.
- Both compete for Active site.
- Inhibitor bind → But not tight Binding occur.

$$E + I \rightleftharpoons E.I$$

→ Competitive inhibition can be Decreased by

S → 100 I = 10 ⟶ 1/10 chance of Binding

Enzyme -

Substrate Increase to 1000 ⟶ $\frac{1}{100}$ chance of Binding of Inhibitor.

Vmax - Unchange

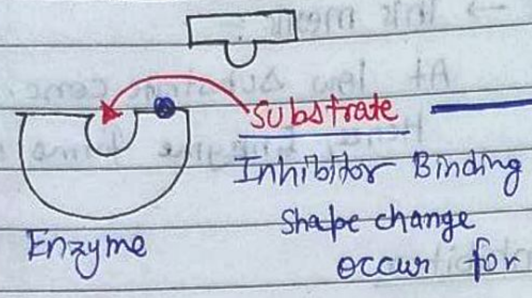
Km → Increase - Because for same velocity substrate Con^c need to be increase.

Example → Succinate $\xrightarrow[\text{Dehydrogenase (Enzyme)}]{\text{Succinate}}$ Fumarate (Product)

↓
Substrate

Malonate ⇒ I (Inhibitor) compete with substrate (Succinate)

Non-competitive Inhibition :-



Substrate ⟶ Some Enzyme non-functional.

Inhibitor Binding

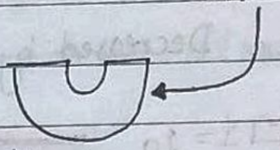
Shape change occur for enzyme.

V_{max} - decrease
K_m - Unchanged

Ex :- Cytochrome oxidase (Complex IV)
Block by cyanine

Feedback Inhibition - Product of Rxn. Try to stop it's own conversion.

Glucose + ATP ⟶ G.-6-P + ADP



Hexokinase

NOMENCLATURE OF ENZYMES

IUB - Enz. catalysed Rxn ;- 6 category (-13) - (subcategory).

Class :-

I. O - Oxidoreductase
II. T - Transferase
III. H - Hydrolase
IV. L - Lyase
V. I - Isomerase
VI. L - Ligase

Date
DELTA Pg No.

I. oxidoreductase :- oxidation and Reduction Rxn.

$$\text{Pyruvate} \xrightarrow{\text{oxidation}} \text{Acety COA}$$

$$NAD^+ \longrightarrow NADH$$

(Pyruvate Dehydrogenase)

II. Transferase :- Group transfer b/w two substrates

$$S' - G + S \longrightarrow S - G + S'$$

(Ex :- Aminotransferase)

III. Hydrolases :-
↳ Digestive Enzyme - Amylase, pepsin, Lipase

C-N, C-O, Ether, Ester, peptide, Glycosidic.
Break bond → H_2O Add.

IV. Lyase :- Double bond Introduce. without Removing H_2O.

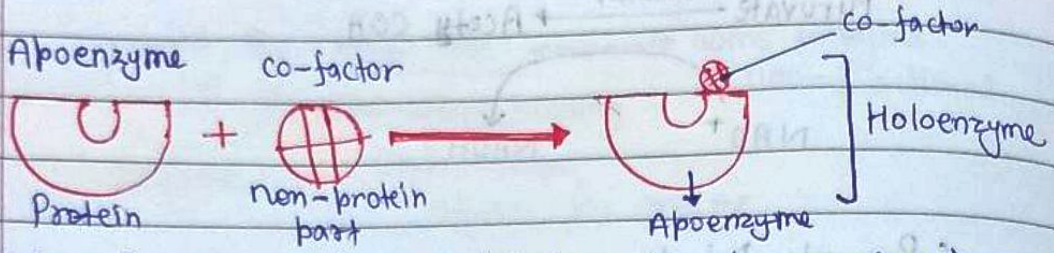
$$\underset{X}{C} - \underset{Y}{C} \longrightarrow C=C + XY \text{ (not water)}$$

V. Isomerase :-
↳ Isomerise → Positional, structural and optical Isomer.

3PGA → 2PGA

VI. Ligase :-
↳ Bond link → C-N, C-O, C-H, C-Halide
DNA Ligase → DNA link

COFACTOR



→ Many Enzyme work as catalyst without any requirement.
→ Some Enzyme Req. Co-factor (non-protein part)

$$\boxed{\text{Apoenzyme + cofactor = Holoenzyme}}$$

Co-factor

- Inorganic (Metal ion)
- Organic
  - Co-enzyme
  - Prosthetic group

In organic

RUBISCO
PEPCASE
Hexokinase
Pyruvate Dehydrogenase
} Mg^{+2}

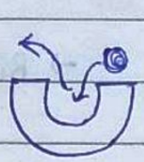
Carbonic Anhydrase
Alcohol Dehydrogenase
Carboxypeptidase
} Zn

Date
DELTA Pg No.

Nitrogenase] Fe, Mo

Nitrate Reductase] Mo

Organic



Coenzyme
→ It is organic
→ Bind transiently During Rxn. only.

NAD - Nicotin Amidedinucleotide
NADP
FAD

→ Coenzymes are Derivative of vitamin.
Niacin → NAD
↳ coenzyme.

Prosthetic group
→ Tightly Bound / covalently Bound

→ Remove from active site
Enzyme Denature.

Ex:- Heme prosthetic group For Peroxidase, catalase

$H_2O_2 \longrightarrow H_2O + O_2$

→ If we Remove prosthetic Group or Coenzyme. Catalytic Activity lost.

Q:- which of the following statements is correct with reference to enzymes?

(a) $\boxed{\text{Holoenzyme = Apoenzyme + Co enzyme.}}$
(b) Coenzyme = Apoenzyme + Holoenzyme
(c) Holoenzyme = Coenzyme + cofactor.
(d) Apoenzyme = Holoenzyme + coenzyme

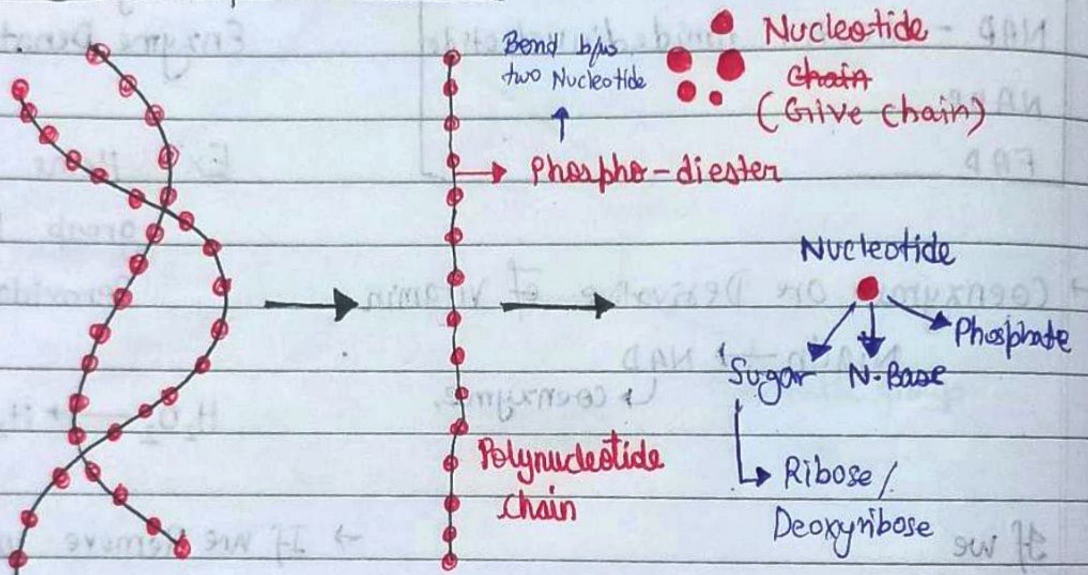
(Neet 2017)

NUCLEIC ACID

Ex. of Nucleic Acid :-

DNA	RNA
→ Genetic material in all living cell.	→ Ribosenucleic Acid
→ Deoxyribosenuelic acid	

Structure of Nucleic Acid :-

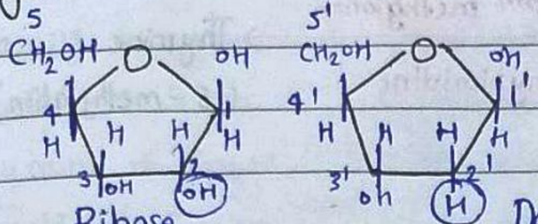


→ 2 Nucleotide chain

Nucleotide (3- component)

- Sugar
- N.B (Nitrogenous - Base)
- Phosphate.

1. Sugar — 5C ⟶ Aldose $C_5H_{10}O_5$ (Ribose)

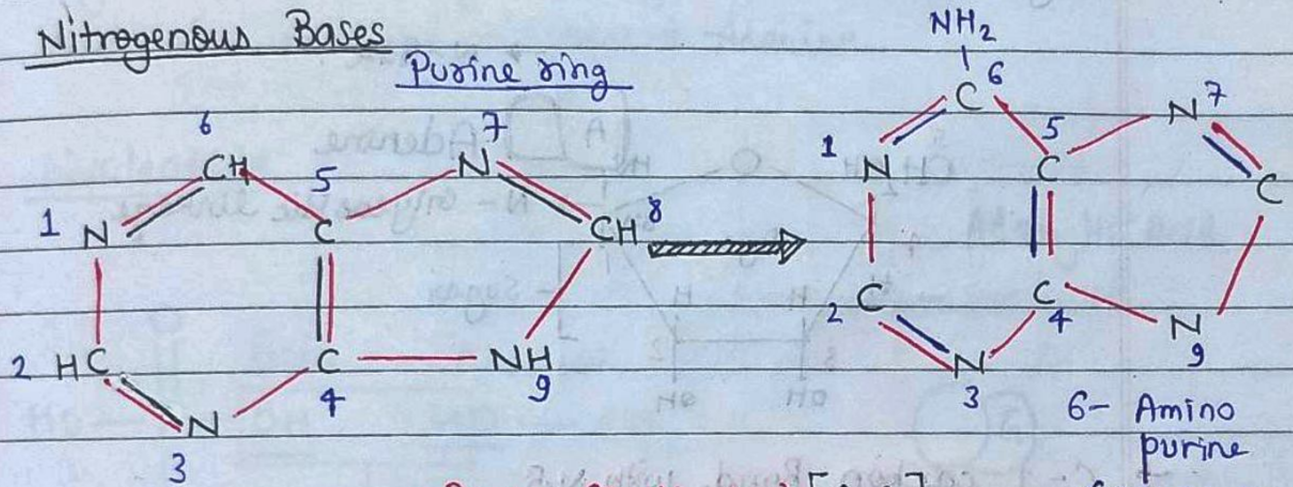


Ribose Deoxyribose

(4C, 1O → Furan)

2. Nitrogenous Bases

Purine ring

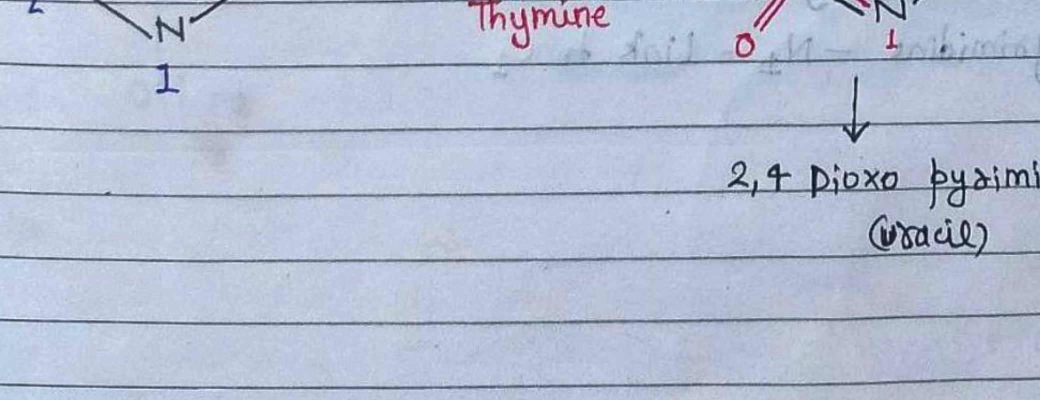


6- Amino purine (Adenine)

2Amino, 6 oxopurine (Guanine)

Nitrogenous Bases → Purine (Double ring) [A, G]
→ Pyrimidine (single ring) [C, U, T]

Pyrimidine :-



Cytosine

Uracil

Thymine

2,4 Dioxo pyrimidine (Uracil)

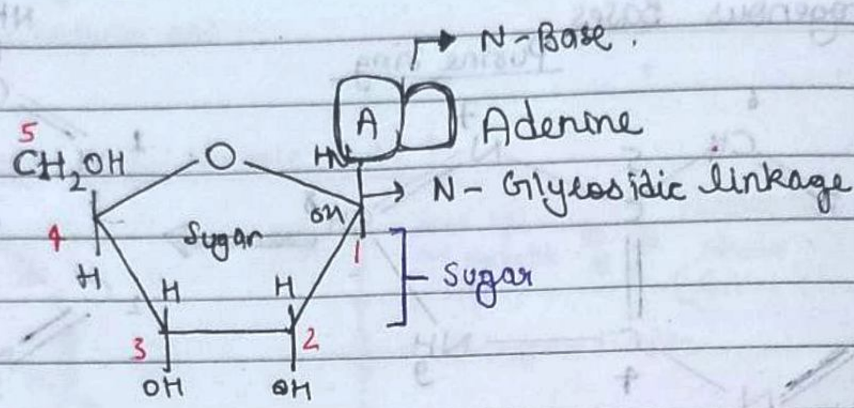
S+S → O glycosidic
S+N → N "

Date
DELTA Pg No

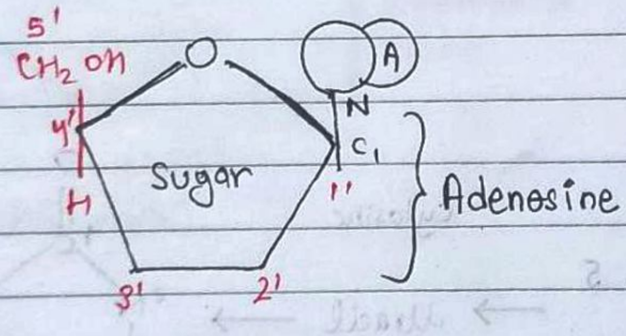
Cytosine $\xrightarrow{\text{4th amethylation}}$ U $\xrightarrow{\text{5th methylation}}$ Thymine
2, 4, Dioxophyrimidine (5-methylation)

Nucleoside

Sugar + N.B



→ C-1 carbon Bond with N.B
→ Bond - N-Glycosidic.



- Purine - N_9 - Link to C1
- Pyrimidine - N_1 - Link to C_1

Alcohol + Acid = ester bond

Date
DELTA Pg No.

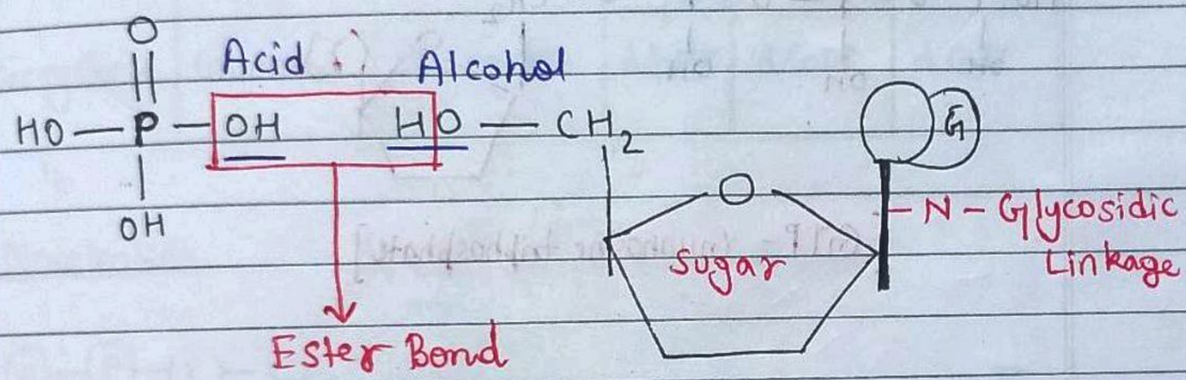
N.B + Sugar = Nucleoside

i. Adenine + Sugar → Adenosine
ii. Guanine + Sugar → Guanosine } Purine
iii. Cytosine + Sugar → Cytidine
iv. Thymine + Sugar → Thymidine
v. Uracil + Sugar → Uridine } - Pyrimidine

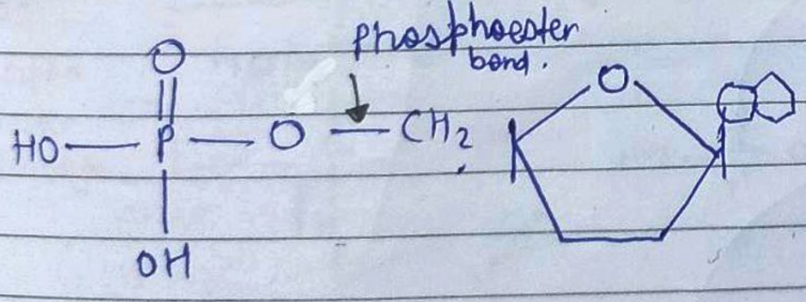
→ deoxyadenosine – Sugar deoxyribose + Adenine.
→ Adenosine – Sugar – Ribose + Adenine.

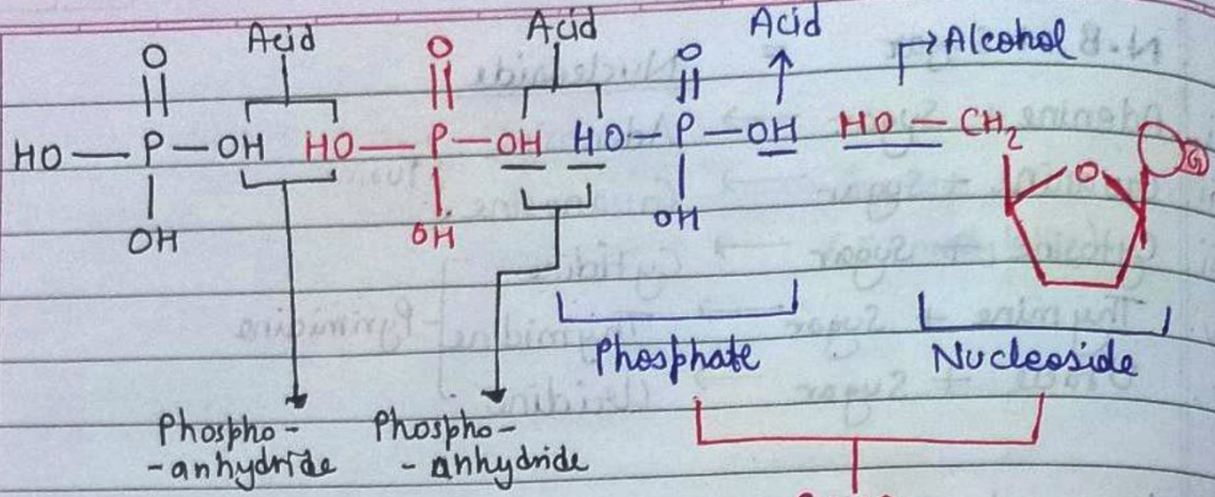
Nucleotide

Adenylic Acid.



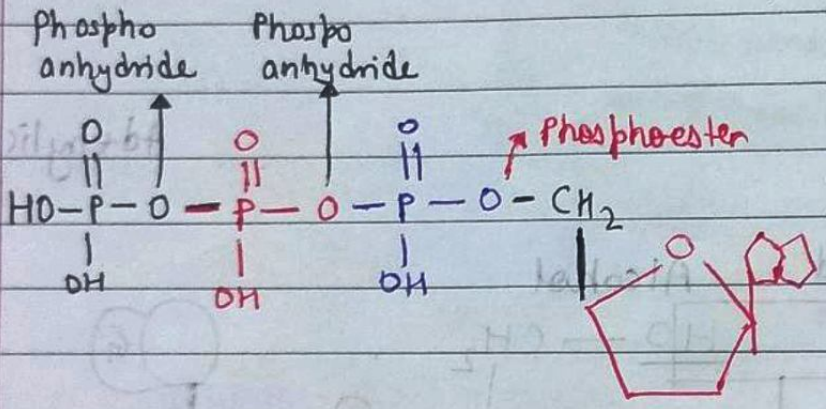
* Ester Bond form b/w Acid and Alcohol.





GMP
(Guanosine mono phosphate)

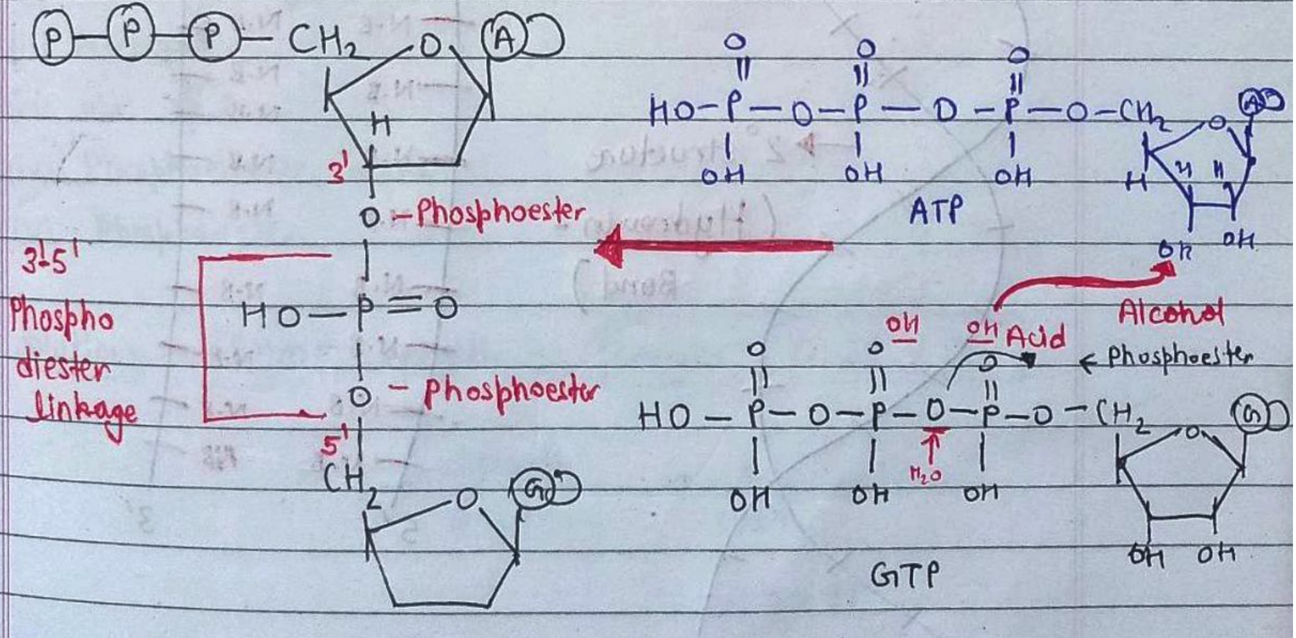
Phosphoester bond



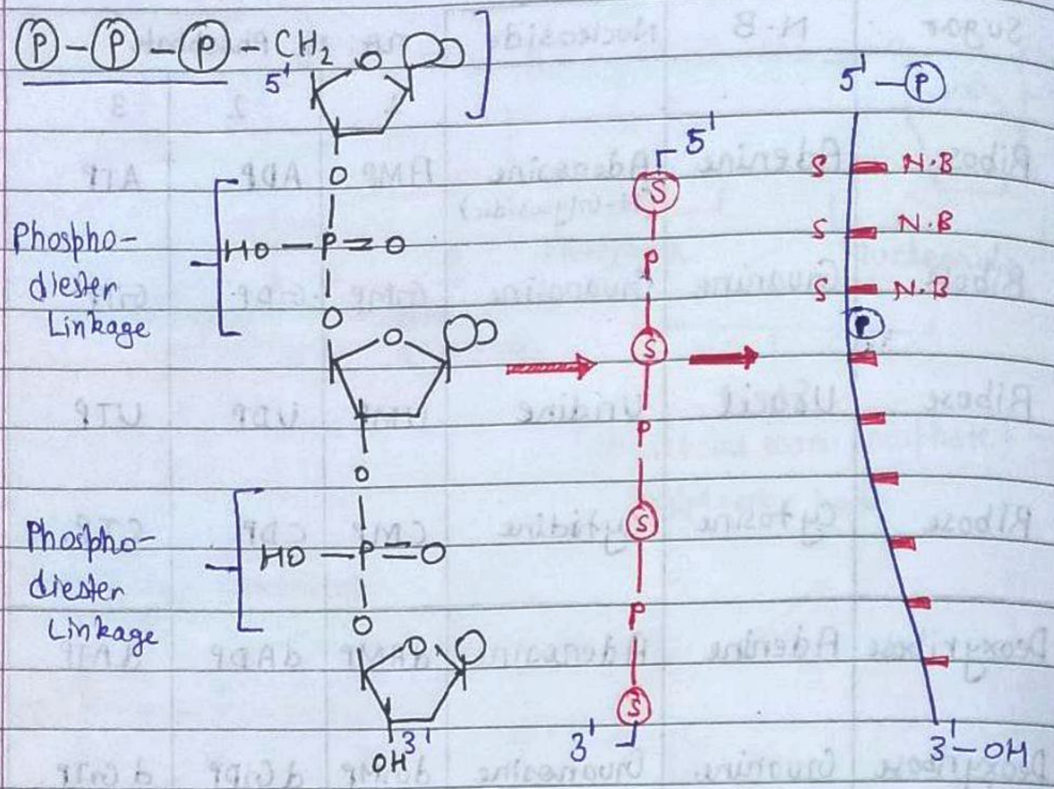
[GTP- Guanosine triphosphate]

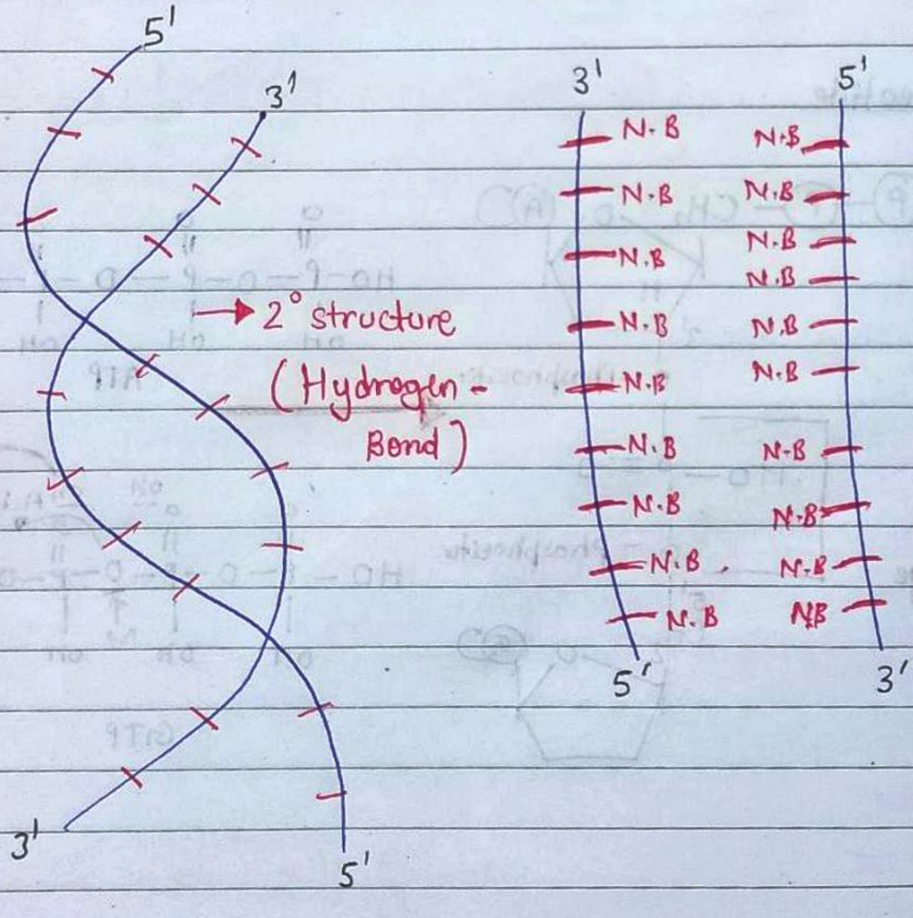
Sugar	N.B	Nucleoside	no: of Phosphate		
			1	2	3
Ribose	Adenine	Adenosine (N-Glycosidic)	AMP	ADP	ATP
Ribose	Guanine	Guanosine	GMP	GDP	GTP
Ribose	Uracil	Uridine	UMP	UDP	UTP
Ribose	Cytosine	Cytidine	CMP	CDP	CTP
Deoxyribose	Adenine	Adenosine	dAMP	dADP	dATP
Deoxyribose	Guanine	Guanosine	dGMP	dGDP	dGTP

Dinucleotide



R·H·coil

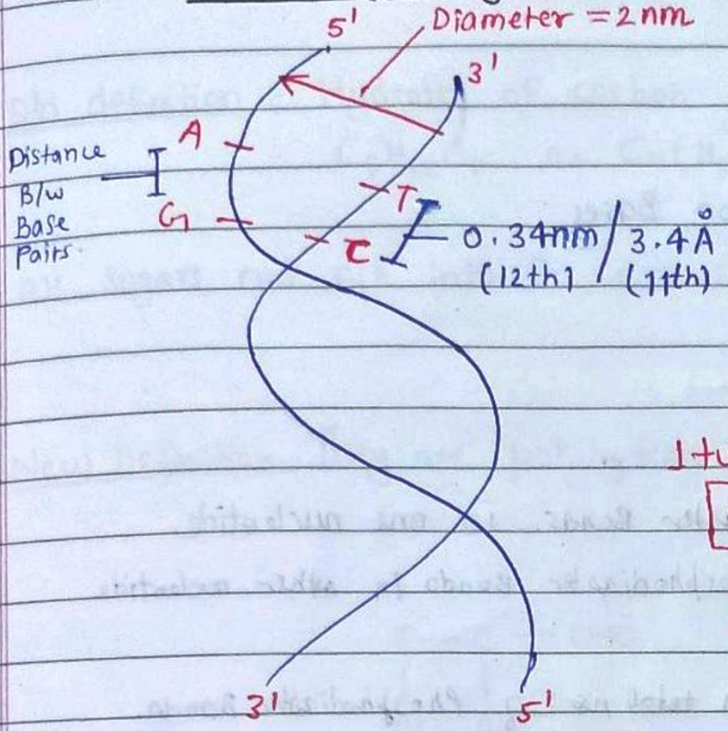

Ⓟ–Ⓟ–Ⓟ–CH_2
5'
Phospho-
diester
Linkage
Phospho-
diester
Linkage
$OH^{3'}$
5'
3'
5'–Ⓟ
N·B
3'–OH


5'
3'
2° structure
(Hydrogen-
Bond)
3'
5'
N·B

A-T are base pairs
G-C are base pairs

Date
DELTA Pg No

Feature of B type DNA



[Z-type - Left handed DNA]

Right handed coil

$\boxed{1 \text{ turn} = 10 \text{ B.P}}$

1 turn Pitch = 3.4 nm

$\boxed{100 \text{ BP} = 10 \text{ turn} \times 10 \text{ BP}}$

$\boxed{100 \text{ BP} \times 0.34 \text{ nm} = 34 \text{ nm}}$

Ques: In a 68 nm DNA if Percentage of guanine is 30 than calculate

(i) Percentage of A
(ii) H-Bond
(iii) No: of A.
(iv) Phosphodiester bond.
(v) Phosphoester.

Solution:- 68 nm = length — $\boxed{\text{length} = 0.34 \times \text{BP}}$

$$BP = \frac{\text{length}}{0.34 \text{ nm}} = \frac{68}{0.34} \times 100$$

$$= 200 \text{ BP}$$

G = 30% ; C = 30%
A = 20% ; T = 20%

200 BP
↓
400 Bases

(iii). A = 20% of 400 Bases

$\boxed{A = 80}$

T = 80

G = 30% of 400 Bases

G = 120

C = 120

(iv) 200 − 1

= 199 Phosphodiaster Bonds in one nucleotide

and also 199 Phosphodiaster Bonds in other nucleotide

So, 398 are in total no: of Phosphodiaster Bonds.

(v) Phosphoester = 2(398)

= 796

(ii) H- Bond

A = 80×2 = 160

G = 120×3 = 360

= 520

A ⎤
T ⎦ 2 H-Bond

G ⎤
C ⎦ 3 H- Bond

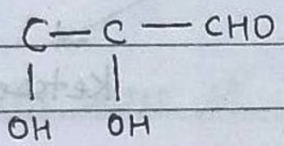
CARBOHYDRATE

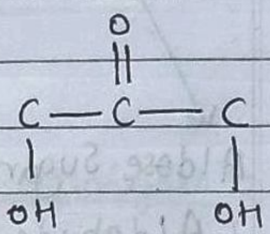
Old definition :- Hydrates of carbon

$C_6H_{12}O_6$ or $C_n(H_2O)n$

All sugars not Fit into it.

New Definition They are polyhydroxy ketone or Aldehyde.





Polyhydroxy ketone and aldehyde

→ no: of carbon → Minimum→3, Maximum →7

Sugar – saccharide → sweet in taste.

→ optically active

$\underbrace{C_3}_{\text{Sugar}} — \underbrace{C_7}_{\text{Sugar}}$

↳ chiral Carbon

↓

Optically Active

[Min:- Triose, Max. heptose].

(Maximum Sugar:- dexorotatory).

(Fructose:- Laevorotatory).

$$HOH_2C - \overset{\overset{O}{\|}}{C} - CH_2OH$$

Optically inactive,
↓
3c — Ketose
(Dihydroxyacetone)

on the basis of :-
<u>Classification</u> → Functional group

Aldose Sugar
(Aldehyde)

Ketose

✓ 3c — Glycealdehyde ✓ 3c — Dihydroxyaccetone

4c — Erythrose , 4c — Erythrose

✓ 5c — Ribose ✓ 5c — Ribulose

✓ 6c — [Glucose ✓ 6c —] Fructose

✓ 7c — Galactose ✓ 7c — Sedoheptulose

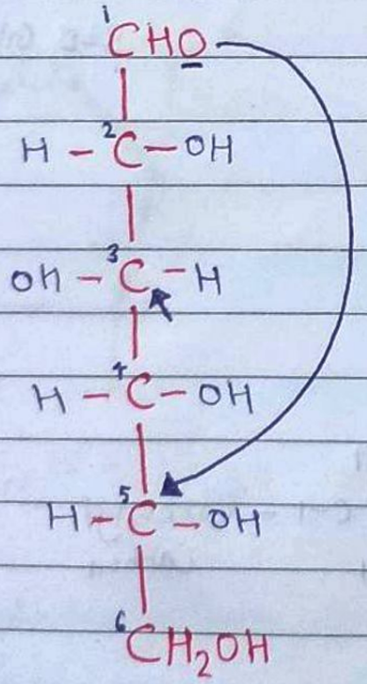
Classification – on the bases of "No: of carbon"

1. 3C – Triose → Glyceraldehyde, Dihydroxyacetone
2. 4C – Tetrose
3. 5C – Pentose
4. 6C – Hexose → Glucose, Galactose → Aldose; Fructose → Ketose
5. 7C – Heptose

Classification – on the bases of Product of Hydrolysis :-

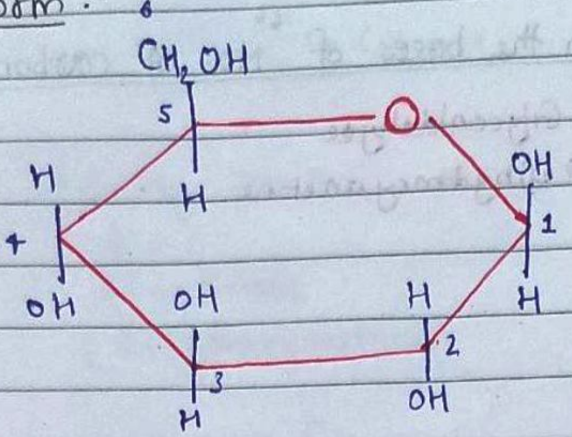
Monosaccharide – Not further Hydrolysed. → Hexose

open chain (Glucose) 6C.



(D – Glucose)

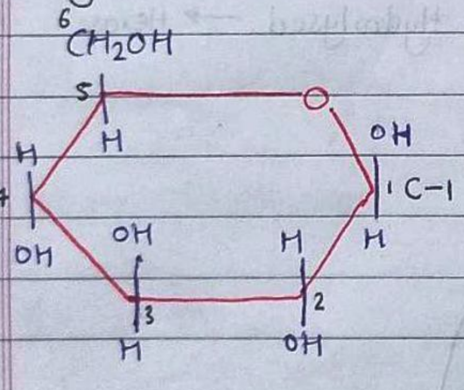
Ring form :-



$5\underline{C}$ (in Ring)
$1\underline{O}$ (in Ring)
→ Pyran ring

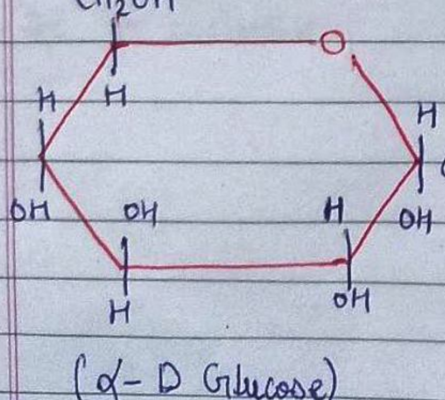
Glucose :-

Ring form - α-D Glucose, β-D Glucose



α-D Glucose, β-D Glucose] Anomer.

(β - D Glucose)

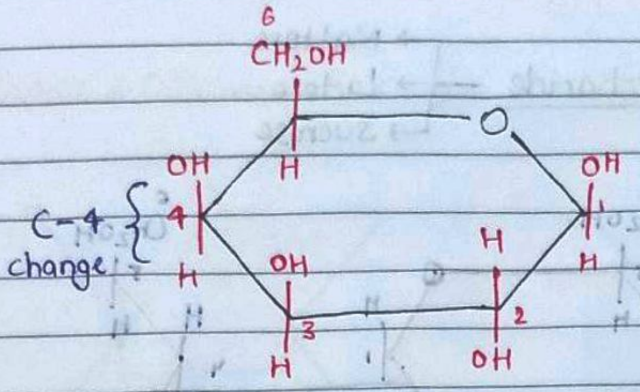


C-1 - Carbonyl Carbon

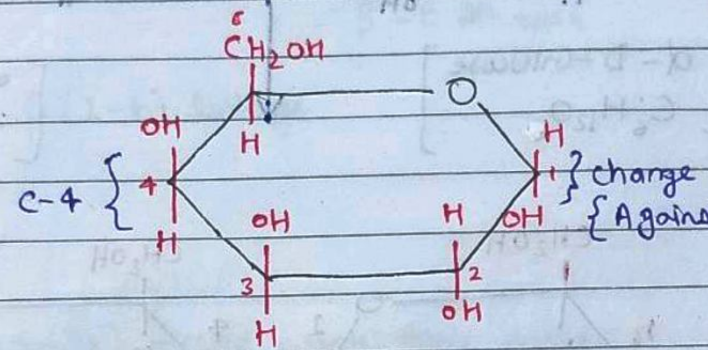
(α - D Glucose)

β-D Glucose & β-D Galactose → Epimer

Galactose [Along trend]

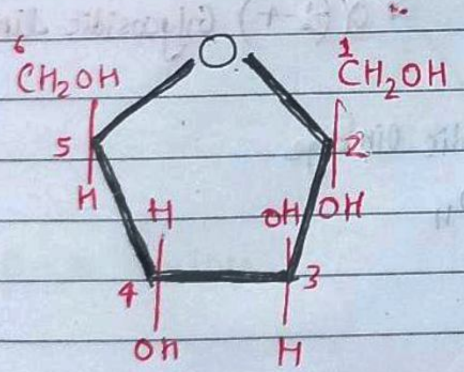


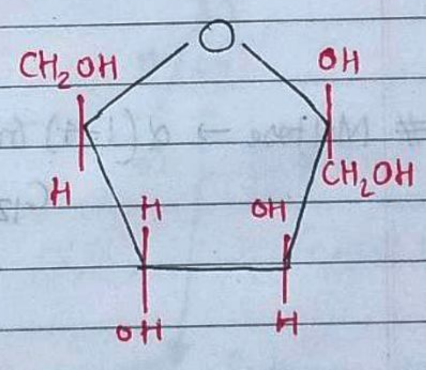
(β-D Galactose)



(α-D Galactose)

Fructose — Furan Ring (6C - Ketose) — Ring - 4C.



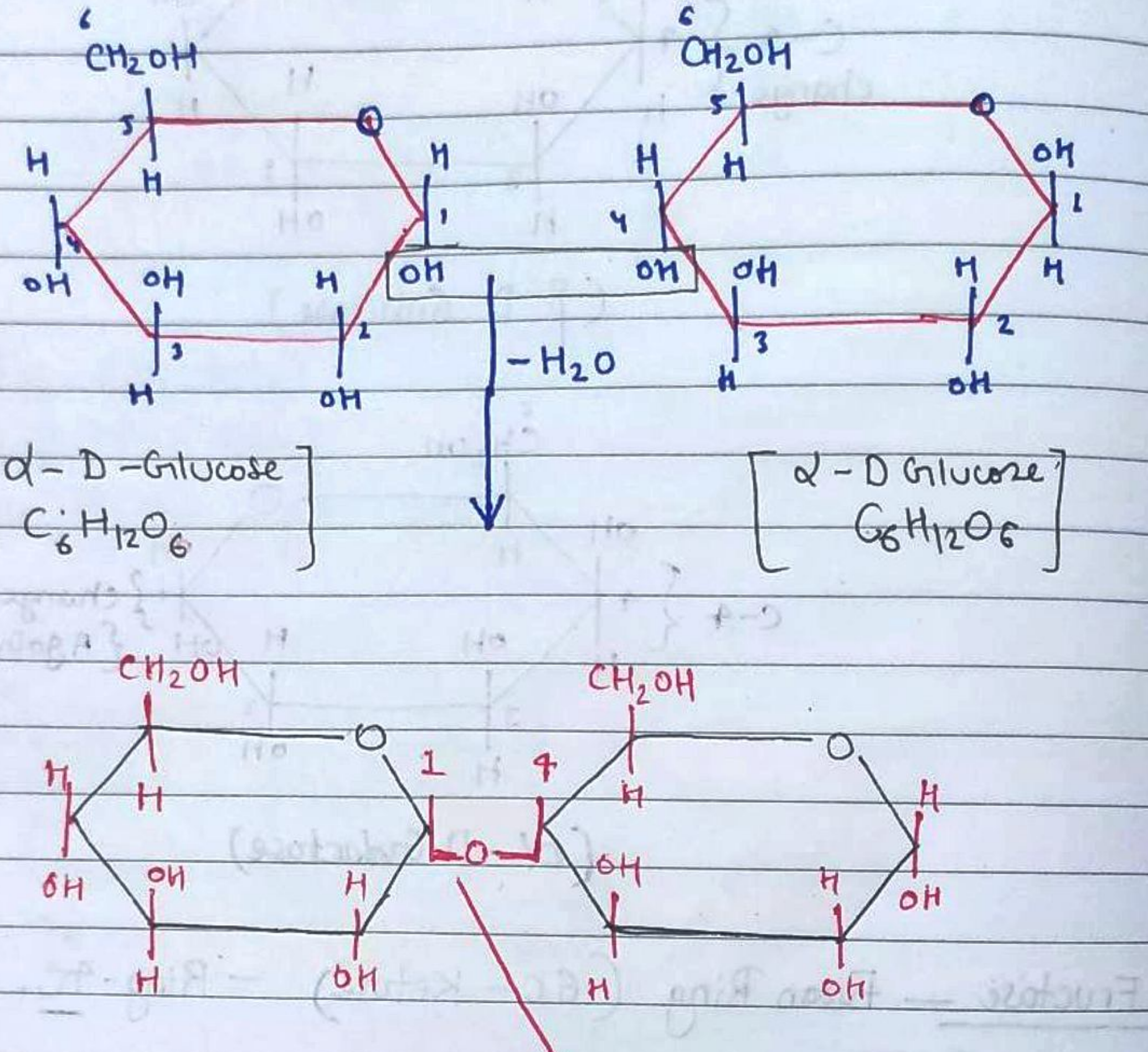


(Along trend = α-D fructose) (β-D Fructose)

* Glucose and Galactose → Anomeric / carbonyl carbon — C1

* Fructose ——————→ Anomeric carbon / Carbonyl carbon — C2

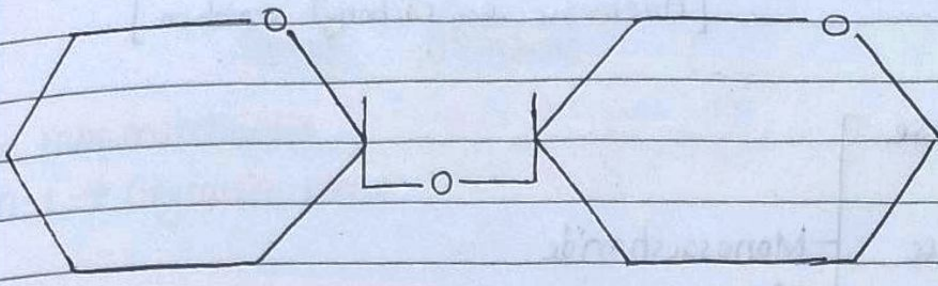
Disaccharide → Maltose
→ Lactose
→ sucrose



Maltose → α (1-4) Glycosidic linkage
$C_{12}H_{22}O_{11}$

also known As invert sugar.

Lactose - Galactose + Glucose

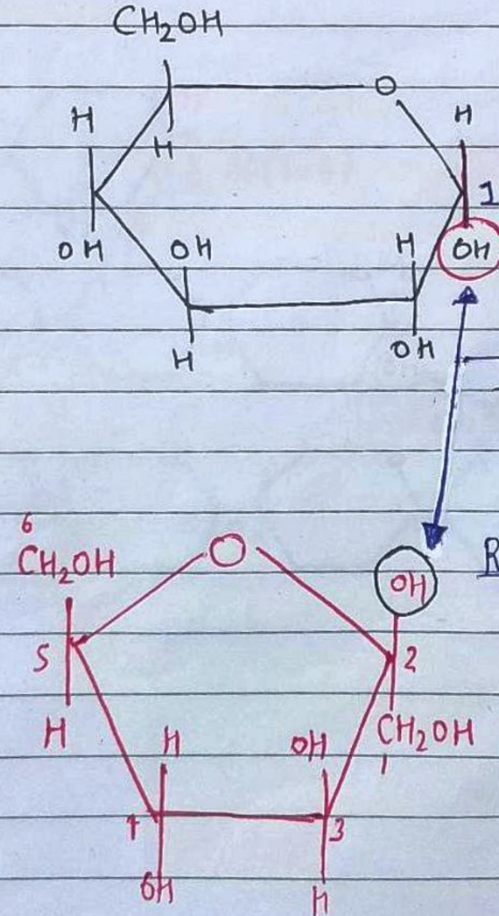


β-D Galactose β - D Glucose

⇒ β (1-4) linkage

Sucrose (Disaccharide) -cane sugar, table sugar

α-D Glucose



(C1 and C2 C involved in Bond for.)

β- D fructose

Glu α 1 - 2 β fruc.

Reducing sugar: Anomeric/ Carbonyl carbon is free and (not involve in Bond)

DELTA Pg No

* <u>Sucrose</u> is non reducing - because - involve in Bond formation.
[Anomeric or carbonyl carbon]

→ Glucose
→ fructose
→ Galactose

] - Monosaccharide (Reducing)

→ Lactose
→ Maltose

] - (free Anomeric carbon) - (Reducing)

POLYSACCHARIDES

Storage / Structural

- n monosaccharide
- n-1 → Glycosidic bond.

Storage

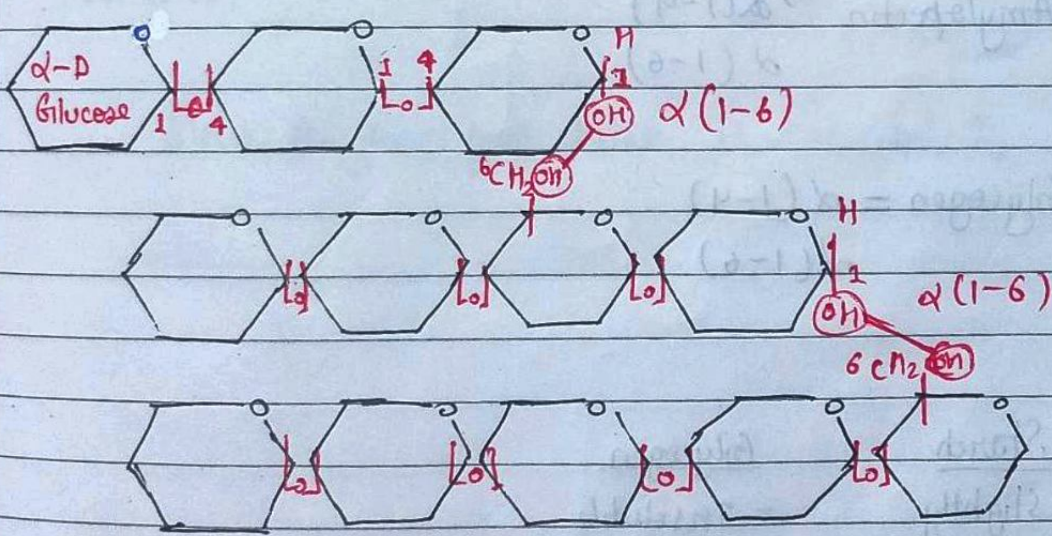
→ Starch
→ Glycogen
→ Inulin - Polymer of fructose
  → Measure GFR

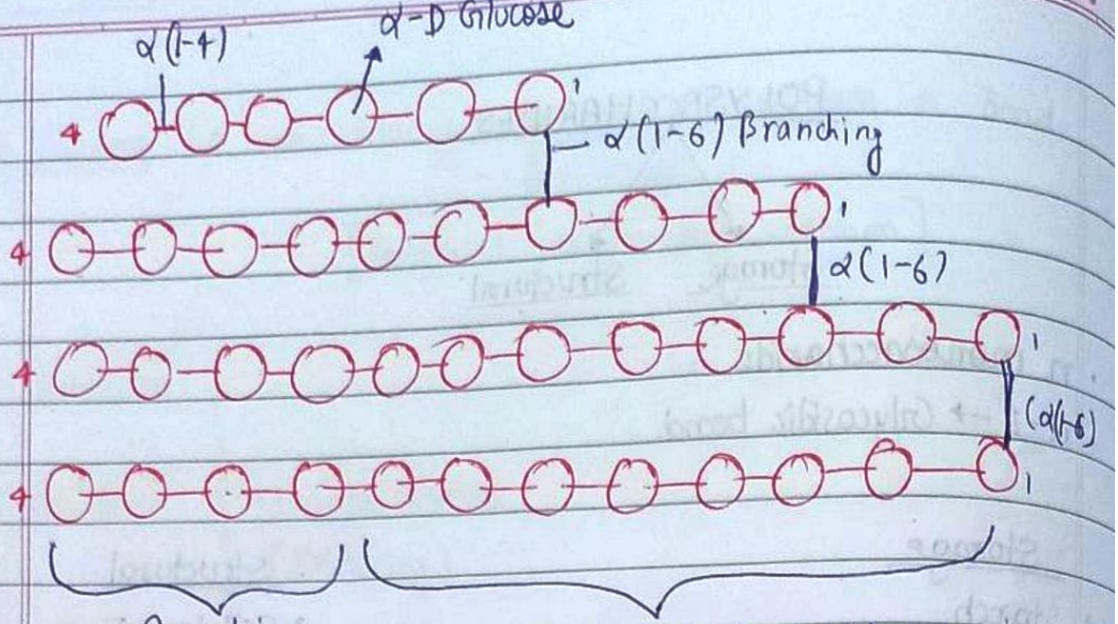
All [Homopolymer]

Structural

→ Cellulose] Homopolymer
→ Chitin]
→ Peptidoglycan (Heteropolymer)

STARCH





Amylose
→ α(1-4) linkage
→ 20% of starch
→ water soluble.

Amylopectin ~ Glycogen
→ α(1-4) α(1-6) Linkage

- Starch → α (1-4), α (1-6)
- Amylose → α (1-4)
- Amylopectin → α(1-4)
  α (1-6)

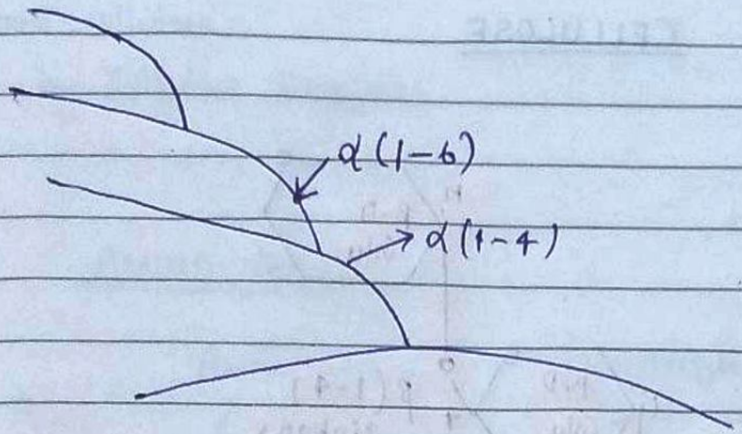
- Glycogen = α(1-4)
  α(1-6)

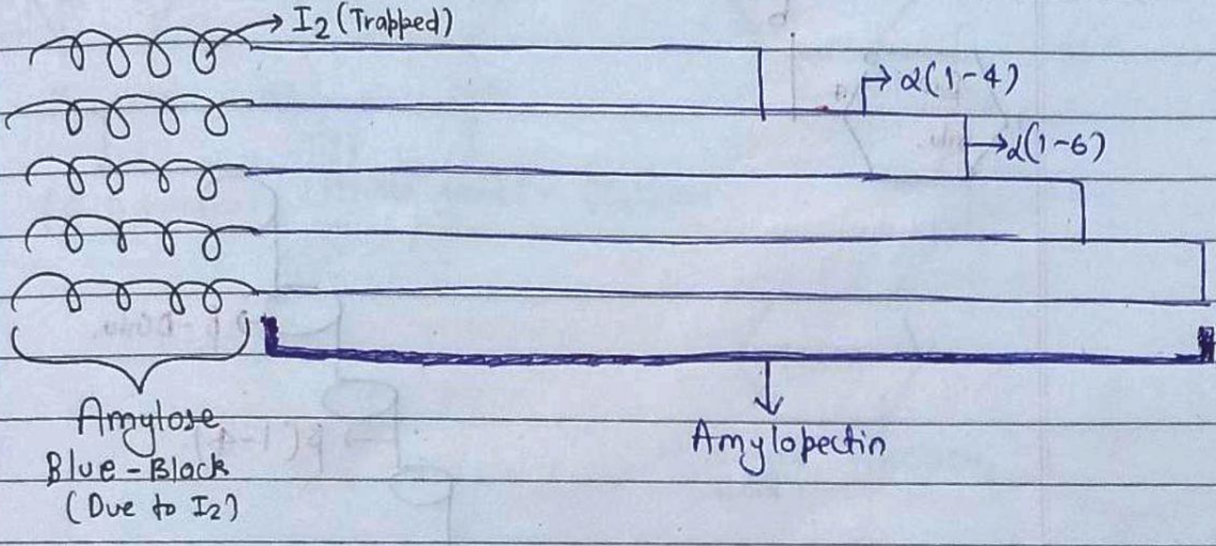
* Starch
- Slightly soluble

Glycogen
- Insoluble completely

→ Solubility :-

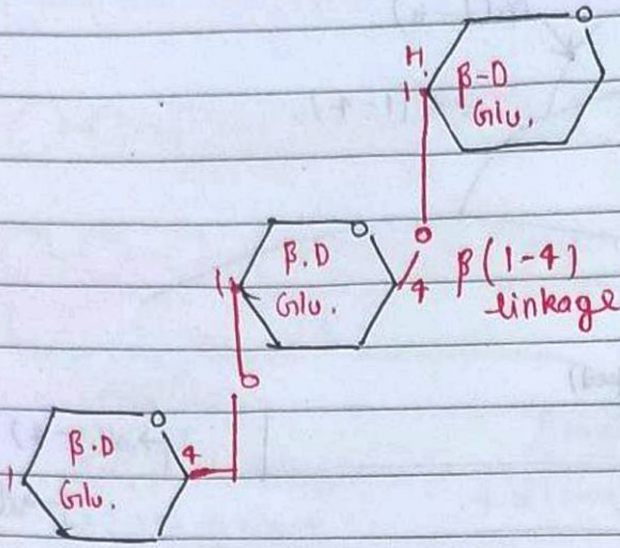
Amylose > starch > Glycogen

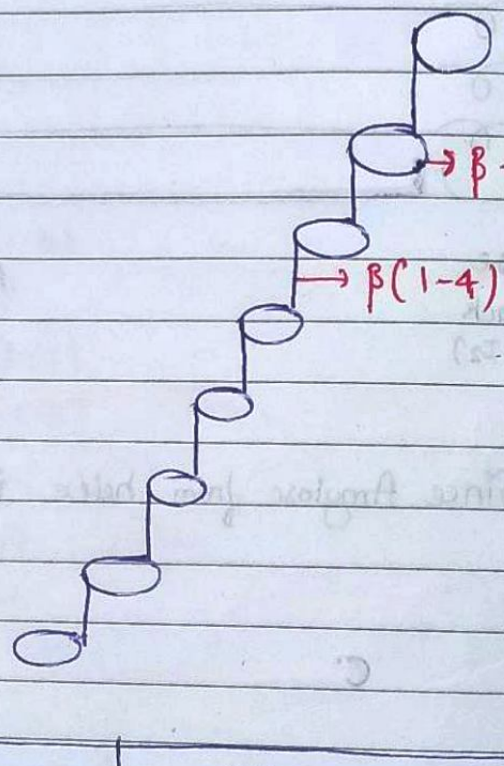




Since Amylose from helix it can trap I_2.

CELLULOSE





Starch	Cellulose
α-D-Glucose	β-D Glucose
α(1-4), α(1-6)	β(1-4)

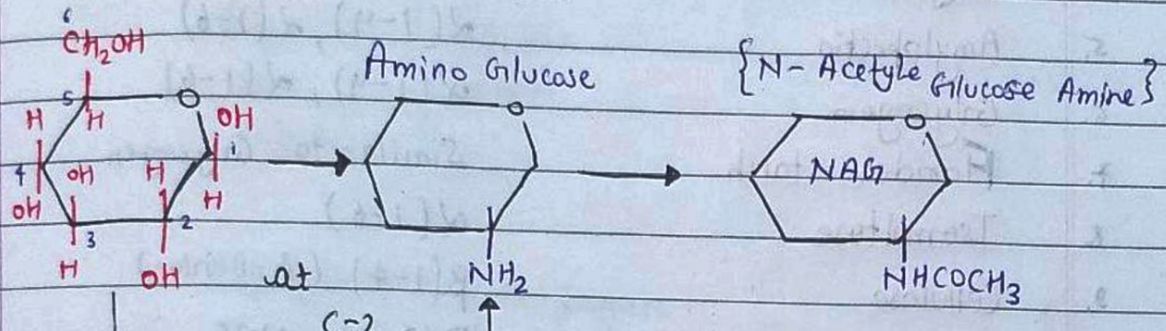
Cellulose :-

→ 90% cotton ;

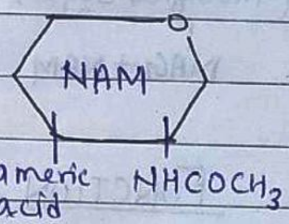
→ Wood - cellulose

→ Digest by Cellulose Enzymes.

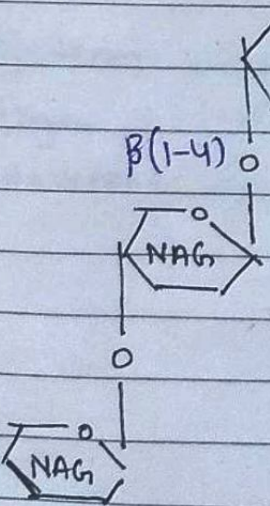
AMINO SUGARS

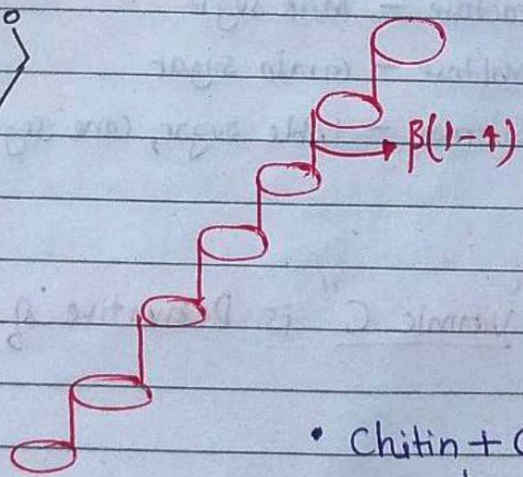


(β - D Glucose)



CHITIN (Homopolymer of NAG





• Chitin + $CaCO_3$

↓

Arthropod Exoskeleton.

	Name of compound	Linkage
1.	Maltose	$\alpha (1-4)$
2.	Lactose	$\beta (1-4)$ Galactose $\downarrow$ Glucose
3.	Starch	$\alpha (1-4)$
4.	Amylose	$\alpha (1-4)$
5.	Amylopectin	$\alpha (1-4)$, $\alpha (1-6)$
6.	Glycogen	$\alpha (1-4)$, $\alpha (1-6)$
7.	Floridean starch	Similar to Glycogen
8.	Isomaltose	$\alpha (1-6)$
9.	Cellulose	$\beta (1-4)$ (β-D Glu.)
10.	Chitin	$\beta (1-4)$ NAG
11.	Peptidoglycan	$\beta (1-4)$

→ (Modified sugar)
NAG + NAM

FUNCTION OR ROLE

- Glucose – Grape sugar, Blood sugar,
- fructose – fruit sugar.
- Lactose – Milk sugar
- Maltose – Grain sugar.
- Sucrose – table sugar, cane sugar.

* "Vitamic C" is Derivative of sugar.

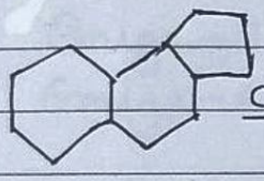
LIPID

→ Soluble in organic solvent, Acid insoluble pool.
M.W less than 800 Dalton.

Example :- Fat, Glycerol, wax, Suberin] Simple lipid.

Lipoprotein, Glycolipid] Conjugate lipid.

Cholestrol - Derived lipid.



C.P.P ring.

→ Cyclo pentano phena antheracene ring.

→ Vitamin D
→ Projesteron
→ Estogen
→ Testosterone

GLYCEROL

- Trihydroxy propane.

$$
\begin{array}{l}
CH_2 - OH \\
\ \ | \\
CH - OH \\
\ \ | \\
CH_2 - OH
\end{array}
$$

Fat → Glycerol

Fat → Fatty acid

FATTY ACID

1. Long chain carboxylic Acid.

Two types

- Saturated fatty acid – single Bond

× • L – Lauric – 12 C

× • M – Mystic – 14 C

✓ • P – Palmitic – 16C

• S – Stearic Acid – 18C

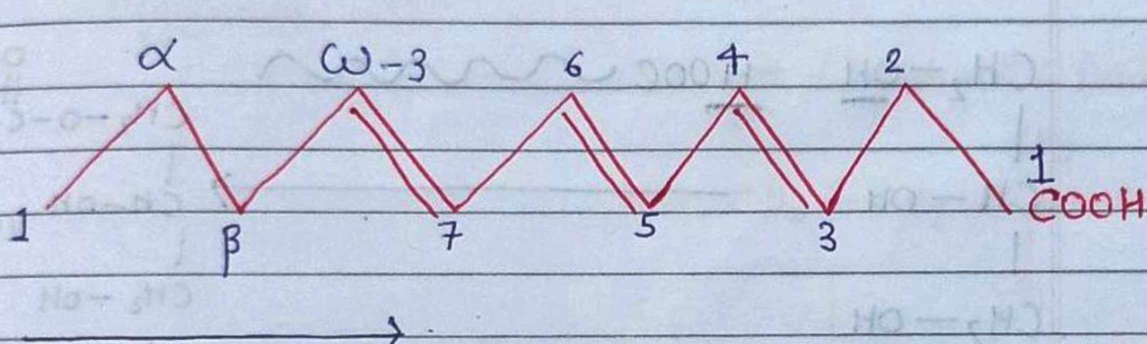
Imp. Ex.(s).

- Unsaturated fatty acid :- (Double Bond)

18C – Oleic Acid – 1 Double Bond] – MUFA – Mono unsaturated Fatty Acids.

18C – Linoleic – 2 Double Bond
18C – Linolenic – 3 Double Bond
20 C – Arachidonic – 20C
4 Double Bond] – PUFA – Poly unsaturated fatty Acids.
(EFA – Essential fatty acids)

OMEGA 3 and OMEGA 6



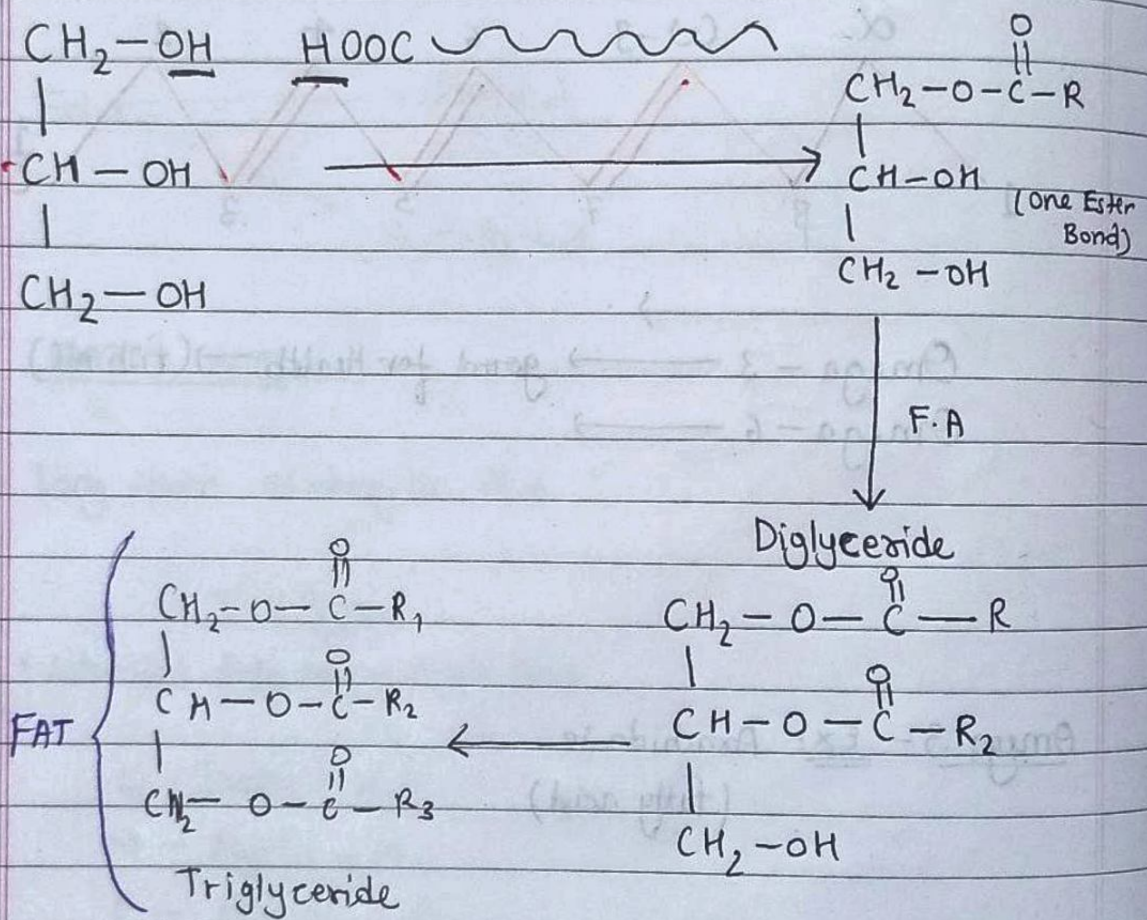
Omega – 3 ⟶ good for Health. ⟶ (fish oil).
Omega – 6 ⟶

Omega 3 :- Ex :- Arachidonic (fatty acid).

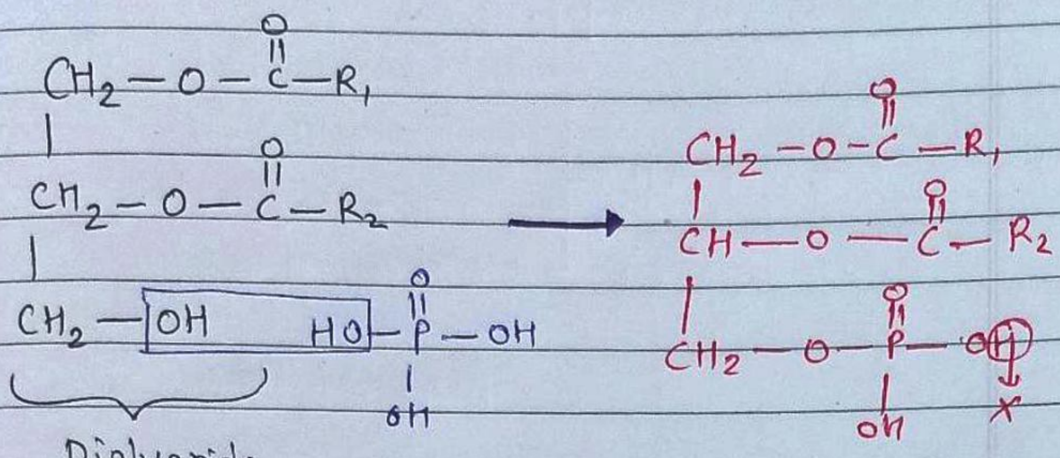
FAT

$$\text{Glyerol} + \text{F.A} \longrightarrow \text{Monoglyceride} \xrightarrow{\text{F.A}} \text{Diglyceride} \xrightarrow{\text{F.A}} \text{Triglyceride}$$

[FAT]



Derived lipid - Phospholipid



Diglyceride

$X = H$ → Phosphatidic Acid.

$X = CH_2 - CH_2 - N(CH_3)_3$

↓

Photidylcholine
(Lechithin).