BIOCHEMISTRY AND METABOLISM

Total hours/week: L:4 T:0 P:0 Marks: Internal: 40 External: 60 Total: 100

Scope: On the successful completion of the course the students will get an overall understanding of structure of atoms and metabolic reactions in a living system.

Objective: This paper presents the study of identification and quantitative determination of the substances, studies of their structure, determining how they are synthesized metabolized and degraded in organisms, and elucidating their role in the operation of the organism.

UNIT-I

18BTU101

Introduction to macromolecules: Amino acids & Proteins: Structure, properties and function of Amino acids and Protein, Amino acid and protein classification. Protein Purification. Denaturation and renaturation of proteins. Fibrous and globular proteins.

UNIT-II

Carbohydrates and Metabolism: Carbohydrates: Structure, Function and properties of Monosaccharides, Disaccharides and Polysaccharides. Bacterial cell wall polysaccharides, Glycoprotein's and their biological functions; Glycolysis: Fate of pyruvate under aerobic and anaerobic conditions. Pentose phosphate pathway and its significance, Gluconeogenesis, Glycogenolysis and glycogen synthesis. TCA cycle.

UNIT-III

Enzymes : Nomenclature and classification of Enzymes, Holoenzyme, apoenzyme, Cofactors, coenzyme, groups, metalloenzymes, monomeric & oligomeric enzymes, activation energy and transition state, enzyme activity, specific activity, common features of active sites, Role of: NAD+, NADP+, FMN/FAD, coenzymes A, Thiamine pyrophosphate, Pyridoxal phosphate, lipoic-acid, Biotin vitamin B12, Tetrahydrofolate and metallic ions. Photosynthesis – Photosystem I and II.

UNIT-IV

Lipids : Structure and functions –Classification, nomenclature and properties of fatty acids, essential fatty acids. Phospholipids, sphingolipids, glycolipids, cerebrosides, gangliosides, Prostaglandins, Cholesterol. β-oxidation of fatty acids.

UNIT-V

Nucleic acids: Structure and functions: Physical & chemical properties of Nucleic acids, Nucleosides & Nucleotides, purines & pyrimidines, Biologically important nucleotides, Double helical model of DNA structure, A, B & Z – DNA, denaturation and renaturation of DNA

References

- 1. Buchanan, B., Gruissem, W., & Jones, R. (2015). *Biochemistry and Molecular Biology of Plants* (2nd ed.). American Society of Plant Biologists.
- 2. Nelson, D.L., & Cox, M.M. (2013). *Lehninger: Principles of Biochemistry* (6th ed.). New York: W.H. Freeman and Company.

- 3. Murray, R.K., Bender, D.A., Botham, K.M.,& Kennelly, P.J., (2012). *Harper's illustrated Biochemistry* (29th ed.). London: McGraw-Hill Medical.
- 4. Berg, J. M., Tymoczko, J. L., & Stryer, L. (2006). *Biochemistry* (6th ed.). Newyork: W.H. Freeman & Company.
 - 5. Hopkins, W.G., & Huner, P.A. (2008). *Introduction to Plant Physiology* (2nd ed.). John Wiley & Sons.

DEPARTMENT OF BIOTECHNOLOGY I B.Sc., BIOTECHNOLOGY – SEMESTER I LECTURE PLAN – BIOCHEMISTRY AND METABOLISM (18BTU101)

S.No Lecture Duration (hr)		Topics	Support materials	
1.	1	Amino acids – Essential amino acids Structures	T1: 67-80	
2.	1	Classification of Amino acids based on properties and functions	T1: 70-71	
3.	1	Protein structure – linear –Primary structure	T1: 1130-1135	
4.	1	Protein structure – helical –secondary structure	T1: 1145-1148	
5.	1	Protein structure – Tertiary structure	T1: 1149-1153	
6.	1	Protein structure – Quaternary structure	T1: 1153-1160	
7.	1	Classification of proteins - Fibrous and Globular Protein	T1: 232-240; T1: 281-282	
8.	1	Protein purification – Size exclusion chromatography	T1: 138-140	
9.	1	Revision	-	
10.	1	Revision	-	
11.	1	Carbohydrates structure, and functions - Monosaccharaides	T1:359-363	
12.	1	Disaccharides and sugar derivaties	T1:367-369	
13.	1	Polysaccharides – Homo and Hetero	T1:365-366	
14.	1	Bacterial cell wall polysaccharides and glycoproteins	T1:375-383	
15.	1	Glycolysis – fate of pyruvate under aerobic and anaerobic condition	T1:593-600	
16.	1	Hexose mono phosphate pathway	T1:892-895	
17.	1	Glycogenesis – Glycogen synthesis;	T1:660-665	
18.	1	Glycogenolysis – Glycogen breakdown	T1:660-665	
19.	1	Gluconeogenesis	T1:667-670	
20.	1	TCA cycle	T1:789-795	
21.	1	Revision	-	

22.	1	Revision	-	
23.	1	Classification of Enzymes	T1: 479-480	
24. 1		Holoenzyme, apoenzyme, Cofactors, coenzyme,	T1: 482-483	
		metalloenzymes		
25.	1	Activation energy and transition state, enzyme	T1: 483-485	
		activity, specific activity, Active sites		
26.	1	Role of: NAD+, NADP+, FMN/FAD, coenzymes A,	T1: 485-487	
		Thiamine pyro phosphate		
27.	1	Pyridoxal phosphate, lipoic-acid, Biotin	T1: 487-490	
28.	1	vitamin B12,Tetrahydrofolate and metallic ions	T1: 492-493	
29.	1	Photosynthesis – Photosystem I	T1: 914-917	
30.	1	Photosynthesis – Photosystem II	T1: 917-921	
31.	1	Revision	-	
32.	1	Revision	-	
33.	1	Classification of lipids – Simple, conjugated and	T1: 386-394	
		derived		
34.	1	Essential fatty acids, Phospholipids	T1: 389-390	
35.	1	Sphingolipids, Glycolipids, cerebrosides	T1: 390-391	
36.	1	Gangliosides, Prostaglandins	T1: 392-393	
37.	1	Cholesterol – Structure and Functions	T1: 392-394	
38.	1	β-oxidation of fatty acids	T1: 951-953	
39.	1	Revision	-	
40.	1	Revision	-	
41.	1	Structure and functions of Nucleic acids - purines &	R1: 82-84	
		pyrimidines		
42.	1	Biologically important nucleotides, Double helical	T1: 85-90	
		model of DNA structure		
43.	1	Watson and Crick model of DNA	T1: 88-90	
44.	1	A, B & Z – DNA	R1: 281-282	
45.	1	Denaturation and renaturation of DNA	T1: 89-92	

46.	1	Revision	-
47.	1	Revision	-

References

T1: Donald Voet and Judith Voet; 2012, Biochemistry, 4th Edition, John Wiley and Sons. Inc.

R1: Daniel L. Nelson and Michael M. Cox; 2005 Biochemistry – Lehininger 5th Edition, W. H. Freeman and Company, Newyork.

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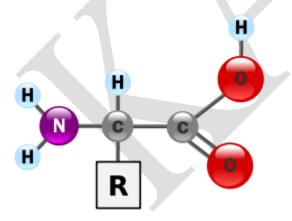
UNIT : I (Introduction to macromolecules)

<u>UNIT I</u>

SYLLABUS

Introduction to macromolecules: Amino acids & Proteins: Structure, properties and function of Amino acids and Protein, Amino acid and protein classification. Protein Purification. Denaturation and renaturation of proteins. Fibrous and globular proteins.

Amino acids are organic compounds containing amine (-NH₂) and carboxyl (-COOH) functional groups, along with a side chain (R group) specific to each amino acid. The key elements of an amino acid are carbon (C), hydrogen (H), oxygen (O), and nitrogen (N), although other elements are found in the side chains of certain amino acids. About 500 naturally occurring amino acids are known (though only 20 appear in the genetic code) and can be classified in many ways. They can be classified according to the core structural functional groups' locations as alpha- (α -), beta- (β -), gamma- (γ -) or delta- (δ -) amino acids; other categories relate to polarity, pH level, and side chain group type (aliphatic, acyclic, aromatic, containing hydroxyl or sulfur, etc.). In the form of proteins, amino acid residues form the second-largest component (water is the largest) of human muscles and other tissues. Beyond their role as residues in proteins, amino acids participate in a number of processes such as neurotransmitter transport and biosynthesis.



The structure of an alpha amino acid in its un-ionized form

In biochemistry, amino acids having both the amine and the carboxylic acid groups attached to the first (alpha-) carbon atom have particular importance. They are known as 2-,

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alpha-, or α-amino acids (generic formula H2NCHRCOOH in most cases, where R is an organic substituent known as a "side chain"); often the term "amino acid" is used to refer specifically to these. They include the 22 proteinogenic ("protein-building") amino acids, which combine into peptide chains ("polypeptides") to form the building-blocks of a vast array of proteins. These are all L-stereoisomers ("left-handed" isomers), although a few D-amino acids ("right-handed") occur in bacterial envelopes, as a neuromodulator (D-serine), and in some antibiotics.

Twenty of the proteinogenic amino acids are encoded directly by triplet codons in the genetic code and are known as "standard" amino acids. The other two ("non-standard" or "non-canonical") are selenocysteine (present in many prokaryotes as well as most eukaryotes, but not coded directly by DNA), and pyrrolysine (found only in some archea and one bacterium). Pyrrolysine and selenocysteine are encoded via variant codons; for example, selenocysteine is encoded by stop codon and SECIS element. *N*-formylmethionine (which is often the initial amino acid of proteins in bacteria, mitochondria, and chloroplasts) is generally considered as a form of methionine rather than as a separate proteinogenic amino acid. Codon–tRNA combinations not found in nature can also be used to "expand" the genetic code and form novel proteins known as alloproteins incorporating non-proteinogenic amino acids.

Many important proteinogenic and non-proteinogenic amino acids have biological functions. For example, in the human brain, glutamate (standard glutamic acid) and gamma-amino-butyric acid ("GABA", non-standard gamma-amino acid) are, respectively, the main excitatory and inhibitory neurotransmitters. Hydroxyproline, a major component of the connective tissue collagen, is synthesised from proline. Glycine is a biosynthetic precursor to porphyrins used in red blood cells. Carnitine is used in lipid transport.

Nine proteinogenic amino acids are called "essential" for humans because they cannot be produced from other compounds by the human body and so must be taken in as food. Others may be conditionally essential for certain ages or medical conditions. Essential amino acids may also differ between species.

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Because of their biological significance, amino acids are important in nutrition and are commonly used in nutritional supplements, fertilizers, and food technology. Industrial uses include the production of drugs, biodegradable plastics, and chiral catalysts.

- Each amino acid is assigned a 3 letter or 1 letter symbol.
- These symbols are commonly used to represent the amino acids in protein structure.
- The 20 amino acids found in proteins are divided into seven distinct groups.
- The different groups of amino acids, their symbols and structures are given.



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Special group prese	Structure	bol	Sym	ne	Name	
dies sollie (Asserbes inche	and the second second	3 letters 1 letter				
Calculation	THE TOTAL	de chains	h aliphatic sid	no acids with	Amii	
	H CH-COOT	G oc	Gly	Glycine	1.	
	CH ₃ CH-COOT	A 500	Ala	Alanine	2.	
Branched chain	H ₃ C CH - CH - COO - NH ₃ + NH ₃ +	٧	Val	Valine	3.	
-COO Branched chain	H ₃ C CH-CH ₂ -CH-COOT NH ₃ ⁺	L DOD-HO	Leu	Leucine	4.	
- Branched chain	CH ₃ CH ₂ CH-CH-COO ⁻ NH ₃	T.	lle	Isoleucine	5.	
	ups	xyl (—OH) gro	taining hydro	no acids con	Amin	
Hydroxyl	CH2-CH-COO- OH NH3	S	Ser	Serine	6.	
O" Hydroxyl	H ₃ C-CH-CH-COOTOH NH ₃ +	Т	Thr	Threonine	7.	
Hydroxyl	See under aromatic	Υ	Tyr	Tyrosine		

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Name	Symbol		Structure	Special group present
	3 letters	1 letter		
II. Sulfur conta	ining amino acid	ls	Delinization of the last of th	
8. Cysteine	Cys	С	CH ₂ -CH-COO ⁻ SH NH ₃	Sulfhydryl
			CH ₂ -CH-COO ⁻ S NH ₃	
Cystine		70	CH ₂ -CH-COO ⁻ S NH ₃ ⁺ S CH ₂ -CH-COO ⁻ NH ₃ ⁺	Disulfide
9. Methioni	ne Met	М	CH ₂ -CH ₂ -CH-COO ⁻ S-CH ₃ NH ₃ ⁺	Thioether
V. Acidic amino	acids and their	amides		
10. Aspartic	acid Asp	D	-OOC-CH ₂ -CH-COO-NH ₃	β-Carboxyl
11. Asparag	ine Asn	N	H ₂ N-C-CH ₂ -CH-COO ⁻ O NH ₃	Amide
12. Glutamio	acid Glu	E	TOOC - CH ₂ - CH ₂ - CH - COOT NH ₃ +	γ-Carboxyl
13. Glutamin	ne Gin	Q	H ₂ N-C-CH ₂ -CH ₂ -CH-COO	Amide
. Basic amino	acids	***************************************		
14. Lysine	Lys	к	ε δ γ β α CH ₂ -CH ₂ -CH ₂ -CH ₂ -CH-CH-CH ₃	OO ε-Amino
15. Arginine	Arg	R	NH-CH ₂ -CH ₂ -CH ₂ -CH-CO C=NH ₂ ⁺ NH ₃ ⁺ NH ₂	Guanidino
16. Histidine	His	н	CH ₂ -CH-COO ⁻ NH ₃ ⁺	Imidazole

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Name	Symbol		Structure	Special group present
	3 letters	1 letter	The Manual Control of the	
/I. Aromatic amino a	ncids			
17. Phenylalanine	Phe	F	-CH ₂ -CH-COOT	Benzene or phenyl
18. Tyrosine	Tyr	Y	HO-CH ₂ -CH-COO-NH ₃	Phenol
19. Tryptophan	Тгр	W	CH ₂ -CH-COO ⁻	Indole
/II. Imino acid			A LINE CONTRACTOR OF THE PARTY	Array (1984) 22
20. Proline	Pro	Р	N coc N	OO Pyrrolidine
(Note : R group is shown	n in red)		н 	

- Amino acids with aliphatic side chains: These are monoamino monocarboxylic acids. This group consists of the most simple amino acids-glycine, alanine, valine, leucine and isoleucine. The last three amino acids (Leu, lle, Val) contain branched aliphatic side chains, hence they are referred to as branched chain amino acids.
- **Hydroxyl group containing amino acids:** Serine, threonine and tyrosine are hydroxyl group containing amino acids. Tyrosine-being aromatic in nature-is usually considered under aromatic amino acids.

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Sulfur containing amino acids: Cysteine with sulfhydryl group and methionine with thioether group are the two amino acids incorporated during the course of protein.

- Acidic amino acids and their amides: Aspartic acid and glutamic acids are dicarboxylic monoamino acids while asparagine and glutamine are their resoective amide derivatives. All these four amino acids possess distinct codons for their incorporation into proteins.
- **Basic amino acids**: The three amino acids lysine, arginine (with guanidino group) and histidine (with imidazole ring) are dibasic monocarboxylic acids. They are highly basic in character.
- **Aromatic amino acids:** Phenylalanine, tyrosine and tryptophan (with indole ring) are aromatic amino acids. Besides these, histidine may also be considered under this category.
- **Imino acids:** Proline containing pyrrolidine ring is a unique amino acid. It has an amino group (=NH), instead of an amino group (-NH2) found in other amino acids. Therefore proline is an amino acid

Classification of amino acids based on polarity:

Amino acids are classified into 4 groups based on their polarity. The polarity in turn reflects the functional role of amino acids in protein structure.

Non-polar amino acids : These amino acids are also referred to as hydrophobic (water hating). They have no charge on the 'R' group. The amino acids included in this group are - alanine, leucine, isoleucine, valine, methionine, phenylalanine, tryptophan and proline.

Polar amino acids with no charge on 'R' group: These amino acids, as such, carry no charge on the 'R'group. They however possess groups such as hydroxyl, sulfhydryl and amide and participate in hydrogen bonding of protein structure. The simple amino acid glycine (where R = H) is also considered in this category. The amino acids in this group are glycine, serine, threonine, cysteine, glutamine, asparagine and tyrosine.

Polar amino acids with positive 'R' group: The three amino acids lysine, arginine and histidine are included in this group.

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Polar amino acids with negative 'R'group: The dicarboxylic

monoamino acids aspartic acid and glutamic acid are considered in this group.

Nutritional classification of amino acids:

The twenty amino acids are required for the synthesis of variety of proteins, besides other biological functions.

However, all these 20 amino acids need not be taken in the diet. Based on the nutritional requirements amino acids are grouped into two classes essential and nonessential.

Essential or indispensable amino acids: The amino acids which cannot be synthesized by the body and, therefore, need to be supplied through the diet are called essential amino acids. They are required for proper growth and maintenance of the individual. The ten amino acids listed below are essential for humans.

Non - essential or dispensable amino acids : The body can synthesize about '10 amino acids to meet the biological needs, hence they need not be consumed in the diet. These are-glycine, alanine, serine, cystein e, aspartate, a sparagnie, glutamate, glutamine, tyrosine and proline.

Amino acid classification based on their metabolic fate:

The carbon skeleton of amino acids can serve as a precursor for the synthesis of glucose.

From metabolic view point, amino acids are divided into three

Glycogenic amino acids: These amino acids can serve as precursors for the formation of glucose or glycogen. e.g. alanine, aspartate, glycine, methionine etc.

Ketogenic amino acids: Fat can be synthesized from these amino acids. Two amino acids leucine and lysine are exclusively ketogenic.

Glycogenic and ketogenic amino acids: The four amino acids isoleucine, phenylalanine, tryptophan, tyrosine are precursors for synthesis of glucose as well as fat.

Chemical reactions of amino acids:

The general reactions of amino acids are mostly due to the presence of two functional groups namely carboxyl (-COOH) group and amino (-NH2) group.

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Reactions due to -COOH group:

Amino acids form salts (-COONa) with bases and esters (-COOR') with alcohols.

Decarboxylation: Amino acids undergo decarboxylation to produce corresponding amines.

This reaction assumes significance in the living cells due to the formation of many biologically important amines.

These include histamine, tyramine and y-amino butyric acid (CABA) from the amino acids histidine, tyrosine and glutamate, respectively.

Reaction with ammonia: The carboxyl group of dicarboxylic amino acids reacts with NH3 to form amide

Aspartic acid + NH, ----- Asparagine

Glutamic acid + NH -----Glutamine

Reactions due to -nh₂ group:

The amino groups behave as bases and combine with acids (e.g. HCI) to form salts (-NHiCl-).

Reaction with ninhydrin: The a-amino acids react with ninhydrin to form a purple, blue or pink colour complex (Ruhemann's purple).

Amino acid + Ninhydrin ------Keto acid +

NH₃+CO₂+Hydrindantin

Hydrindantin + NH₃ + Ninhydrin ------ Ruhemann's purple

Ninhydrin reaction is effectively used for the quantitative determination of amino acids and proteins.

Colour reactions of amino acids: Amino acids can be identified by specific colour reactions

Transamination: Transfer of an amino group from an amino acid to a keto acid to form a new amino acid is a very important reaction in amino acid metabolism.

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Oxidative deamination: The amino acids undergo oxidative deamination to

liberate free ammonia.

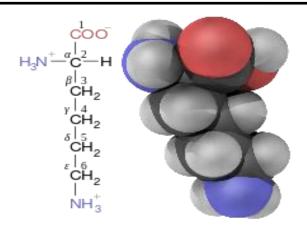
Isomerism

The alpha amino acids are the most common form found in nature, but only when occurring in the L-isomer. The alpha carbon is a chiral carbon atom, with the exception of glycine which has two indistinguishable hydrogen atoms on the alpha carbon. Therefore, all alpha amino acids but glycine can exist in either of two enantiomers, called L or D amino acids, which are mirror images of each other (see also Chirality). While L-amino acids represent all of the amino acids found in proteins during translation in the ribosome, D-amino acids are found in some proteins produced by enzyme posttranslational modifications after translation and translocation to the endoplasmic reticulum, as in exotic sea-dwelling organisms such as cone snails. They are also abundant components of the peptidoglycan cell walls of bacteria, [36] and D-serine may act as a neurotransmitter in the brain. D-amino acids are used in racemic crystallography to create centrosymmetric crystals, which (depending on the protein) may allow for easier and more robust protein structure determination. The L and D convention for amino acid configuration refers not to the optical activity of the amino acid itself but rather to the optical activity of the isomer of glyceraldehyde from which that amino acid can, in theory, be synthesized (D-glyceraldehyde is dextrorotatory; L-glyceraldehyde is levorotatory). In alternative fashion, the (S) and (R) designators are used to indicate the absolute stereochemistry. Almost all of the amino acids in proteins are (S) at the α carbon, with cysteine being (R) and glycine non-chiral. [39] Cysteine has its side chain in the same geometric position as the other amino acids, but the R/S terminology is reversed because of the higher atomic number of sulfur compared to the carboxyl oxygen gives the side chain a higher priority, whereas the atoms in most other side chains give them lower priority.

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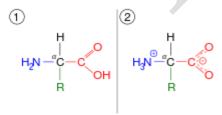
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Lysine with carbon atoms labeled by position

In amino acids that have a carbon chain attached to the α -carbon (such as lysine, shown to the right) the carbons are labeled in order as α , β , γ , δ , and so on. In some amino acids, the amine group is attached to the β or γ -carbon, and these are therefore referred to as *beta* or *gamma amino acids*. Amino acids are usually classified by the properties of their side chain into four groups. The side chain can make an amino acid a weak acid or a weak base, and a hydrophile if the side chain is polar or a hydrophobe if it is nonpolar. The chemical structures of the 22 standard amino acids, along with their chemical properties, are described more fully in the article on these proteinogenic amino acids. The phrase "branched-chain amino acids" or BCAA refers to the amino acids having aliphatic side chains that are non-linear; these are leucine, isoleucine, and valine. Proline is the only proteinogenic amino acid whose side-group links to the α -amino group and, thus, is also the only proteinogenic amino acid containing a secondary amine at this position. ^[34] In chemical terms, proline is, therefore, an imino acid, since it lacks a primary amino group, ^[41] although it is still classed as an amino acid in the current biochemical nomenclature, ^[42] and may also be called an "N-alkylated alpha-amino acid".

Zwitterions



Prepared by Dr. T. Sivaraman, Professor, and Dr. A. A. Arunkumar, Assistant Professor, Department of Biotechnology, KAHE.

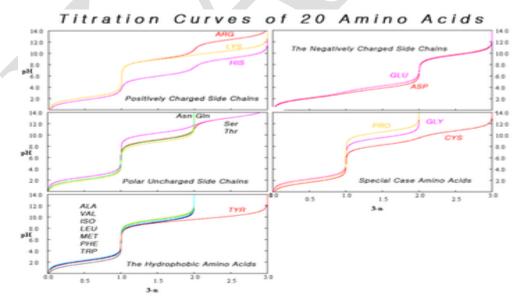
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The α-carboxylic acid group of amino acids is a weak acid, meaning that it releases a hydron (such as a proton) at moderate pH values. In other words, carboxylic acid groups (-CO₂H) can be deprotonated to become negative carboxylates (-CO₂⁻). The negatively charged carboxylate ion predominates at pH values greater than the pKa of the carboxylic acid group (mean for the 20 common amino acids is about 2.2, see the table of amino acid structures above). In a complementary fashion, the α amine of amino acids is a weak base, meaning that it accepts a proton at moderate pH values. In other words, α -amino groups (NH₂-) can be protonated to become positive α -ammonium groups ($^{+}$ NH₃-). The positively charged α -ammonium group predominates at pH values less than the pKa of the α -ammonium group (mean for the 20 common α-amino acids is about 9.4). Because all amino acids contain amine and carboxylic acid functional groups, they share amphiprotic properties. Below pH 2.2, the predominant form will have a neutral carboxylic acid group and a positive α -ammonium ion (net charge +1), and above pH 9.4, a negative carboxylate and neutral α-amino group (net charge -1). But at pH between 2.2 and 9.4, an amino acid usually contains both a negative carboxylate and a positive α -ammonium group, as shown in structure (2) on the right, so has net zero charge. This molecular state is known as a zwitterion, from the German Zwitter meaning hermaphrodite or hybrid. The fully neutral form (structure (1) on the left) is a very minor species in aqueous solution throughout the pH range (less than 1 part in 10⁷). Amino acids exist as zwitterions also in the solid phase, and crystallize with salt-like properties unlike typical organic acids or amines.



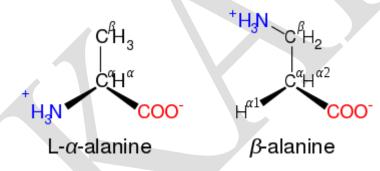
Composite of titration curves of twenty proteinogenic amino acids grouped by side chain

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category. The variation in titration curves when the amino acids can be grouped by category. With the exception of tyrosine, using titration to distinguish among hydrophobic amino acids is problematic. At pH values between the two pKa values, the zwitterion predominates, but coexists in dynamic equilibrium with small amounts of net negative and net positive ions. At the exact midpoint between the two pKa values, the trace amount of net negative and trace of net positive ions exactly balance, so that average net charge of all forms present is zero. This pH is known as the isoelectric point pI, so pI = $\frac{1}{2}(pKa_1 + pKa_2)$. The individual amino acids all have slightly different pKa values, so have different isoelectric points. For amino acids with charged side chains, the pKa of the side chain is involved. Thus for Asp, Glu with negative side chains, $pI = \frac{1}{2}(pKa_1 + pKa_R)$, where pKa_R is the side chain pKa. Cysteine also has potentially negative side chain with pKa_R = 8.14, so pI should be calculated as for Asp and Glu, even though the side chain is not significantly charged at neutral pH. For His, Lys, and Arg with positive side chains, $pI = \frac{1}{2}(pKa_R + pKa_2)$. Amino acids have zero mobility in electrophoresis at their isoelectric point, although this behaviour is more usually exploited for peptides and proteins than single amino acids. Zwitterions have minimum solubility at their isoelectric point and some amino acids (in particular, with non-polar side chains) can be isolated by precipitation from water by adjusting the pH to the required isoelectric point.



PROTEINS

The particular series of amino acids that form a protein is known as that protein's primary structure. This sequence is determined by the genetic makeup of the individual. It specifies the order of side-chain groups along the linear polypeptide "backbone".

Proteins have two types of well-classified, frequently occurring elements of local structure defined by a particular pattern of hydrogen bonds along the backbone: alpha helix and beta sheet. Their number and arrangement is called the secondary structure of the protein. Alpha helices are regular spirals stabilized by hydrogen bonds between the backbone CO group (carbonyl) of one amino acid residue and the backbone

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NH group (amide) of the i+4 residue. The spiral has about 3.6 amino acids per turn, and the amino acid side chains stick out from the cylinder of the helix. Beta pleated sheets are formed by backbone hydrogen bonds between individual beta strands each of which is in an "extended", or fully stretched-out, conformation. The strands may lie parallel or antiparallel to each other, and the side-chain direction alternates above and below the sheet. Hemoglobin contains only helices, natural silk is formed of beta pleated sheets, and many enzymes have a pattern of alternating helices and beta-strands. The secondary-structure elements are connected by "loop" or "coil" regions of non-repetitive conformation, which are sometimes quite mobile or disordered but usually adopt a well-defined, stable arrangement. The overall, compact, 3D structure of a protein is termed its tertiary structure or its "fold". It is formed as result of various attractive forces like hydrogen bonding, disulfide bridges, hydrophobic interactions, hydrophilic interactions, van der Waals force etc. When two or more polypeptide chains (either of identical or of different sequence) cluster to form a protein, quaternary structure of protein is formed. Quaternary structure is an attribute of polymeric (same-sequence chains) or heteromeric (different-sequence chains) proteins like hemoglobin, which consists of two "alpha" and two "beta" polypeptide chains.

Classification of proteins:

Proteins are classified in several ways.

Three major types of classifying proteins based on their function, chemical nature and solubility properties and nutritional importance are discussed here.

Simple proteins: On hydrolysis they yield only the amino acids and occasional small carbohydrate compounds. Examples are: albumins, globulins, glutelins, albuminoids, histones and protamines.

Conjugated proteins: These are simple proteins combined with some non-protein material in the body. Examples are: nucleoproteins, glycoproteins, phosphoproteins, haemoglobins and lecithoproteins.

Derived proteins: These are proteins derived from simple or conjugated proteins by physical or chemical means. Examples are: denatured proteins and peptides

Properties:

Proteins can also be characterized by their chemical reactions. Most proteins are soluble in water, in alcohol, in dilute base or in various concentrations of

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salt solutions.

Proteins have the characteristic coiled structure which is determined by the sequence of amino acids in the primary polypeptide chain and the stereo configuration of the radical groups attached to the alpha carbon of each amino acid.

Proteins are heat labile exhibiting various degrees of lability depending upon type of protein, solution and temperature profile.

Proteins can be reversible or irreversible, denatured by heating, by salt concentration, by freezing, by ultrasonic stress or by aging. Proteins undergo characteristic bonding with other proteins in the so-called plastein reaction and will combine with free aldyhyde and hydroxy groups of carbohydrates to form Maillard type compounds.

Primary Structure of Proteins

The α -carboxyl group of one amino acid is covalently linked to the α -amino group of the next amino acid by an amide bond, commonly known as a peptide bond when in proteins. When two amino acid residues are linked in this way the product is a dipeptide. Many amino acids linked by peptide bonds form a polypeptide.

The repeating sequence of α -carbon atoms and peptide bonds provides the backbone of the polypeptide while the different amino acid side chains confer functionality on the protein. The amino acid at one end of a polypeptide has an unattached α -amino group while the one at the other end has a free α -carboxyl group. Hence, polypeptides are directional, with an N terminus and a C terminus. Sometimes the N terminus is blocked with, for example, an acetyl group.

The sequence of amino acids from the N to the C terminus is the primary structure of the polypeptide. Typical sizes for single polypeptide chains are within the range 100–1500 amino acids, though longer and shorter ones exist.

Secondary structure of Proteins

The highly polar nature of the C=O and N-H groups of the peptide bonds gives the C-N bond partial double bond character. This makes the peptide bond unit rigid and planar,

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though there is free rotation between adjacent peptide bonds.

This polarity also favors hydrogen bond formation between appropriately spaced and oriented peptide bond units. Thus, polypeptide chains are able to fold into a number of regular structures which are held together by these hydrogen bonds. The best known **secondary structure** is the α -helix. The polypeptide backbone forms a right-handed helix with 3.6 amino acid residues per turn such that each peptide N–H group is hydrogen bonded to the C=O group of the peptide bond three residues away. Sections of α -helical

secondary structure are often found in globular proteins and in some fibrous proteins. The β pleated sheet (β - sheet) is formed by hydrogen bonding of the peptide bond N–H and C=O
groups to the complementary groups of another section of the polypeptide chain.

Several sections of polypeptide chain may be involved side-by side, giving a sheet structure with the side chains (R) projecting alternately above and below the sheet. If these sections run in the same direction (e.g. N terminus \rightarrow C terminus), the sheet is **parallel**; if they alternate N \rightarrow C and C \rightarrow N, then the sheet is **antiparallel**. β -Sheets are strong and rigid and are important in structural proteins, for example silk fibroin. The connective tissue protein **collagen** has an unusual **triple helix** secondary structure in which three polypeptide chains are intertwined, making it very strong.

Tertiary structure of Proteins

The way in which the different sections of α -helix, β -sheet, other minor secondary structures and connecting loops fold in three dimensions is the tertiary structure of the polypeptide.

The nature of the tertiary structure is inherent in the primary structure and, given the right conditions, most polypeptides will fold spontaneously into the correct tertiary structure as it is generally the lowest energy conformation for that sequence. However, *in vivo*, correct folding is often assisted by proteins called chaperones which help prevent mis- folding of new polypeptides before their synthesis (and primary structure) is complete.

Folding is such that amino acids with hydrophilic side chains locate mainly on the exterior of the protein where they can interact with water or solvent

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ions, while the hydrophobic amino acids become buried in the interior from which water is excluded. This gives overall stability to the structure.

Various types of non-covalent interaction between side chains hold the tertiary structure together: van der Waals forces, hydrogen bonds, electrostatic salt bridges between oppositely charged groups (e.g. the NH3 + group of lysine and the side chain COO— groups of aspartate or glutamate) and hydrophobic interactions between the nonpolar side chains of the aliphatic and aromatic amino acids.

In addition, covalent disulfide bonds can form between two cysteine residues which may be far apart in the primary structure but close together in the folded tertiary structure. Disruption of secondary and tertiary structure by heat or extremes of pH leads to denaturation of the protein and formation of a random coil conformation.

Quaternary structure of Proteins

Many proteins are composed of two or more polypeptide chains (subunits). These may be identical or different. Hemoglobin has two α -globin and two β -globin chains ($\alpha_2\beta_2$). The same forces which stabilize tertiary structure hold these subunits together, including disulfide bonds between cysteines on separate polypeptides. This level of organization is known as the quaternary structure and has certain consequences.

First, it allows very large protein molecules to be made. Tubulin is a dimeric protein made up of two small, non-identical α and β subunits. Upon hydrolysis of tubulin-bound GTP, these dimers can polymerize into structures containing many hundreds of α and β subunits. These are the microtubules of the cytoskeleton.

Secondly, it can provide greater functionality to a protein by combining different activities into a single entity, as in the fatty acid synthase complex. Often, the interactions between the subunits are modified by the binding of small molecules and this can lead to the allosteric effects seen in enzyme regulation.

Globular or Corpuscular Proteins

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These have an axial ratio (length: width) of less than 10 (usually not over 3 or 4) and, henceforth, possess a relatively spherical or ovoid shape.

These are usually soluble in water or in aqueous media containing acids, bases, salts or alcohol, and diffuse readily. As a class, globular proteins are more complex in conformation than fibrous proteins, have a far greater variety of biological functions and are dynamic rather than static in their activities.

Tertiary and quaternary structures are usually associated with this class of proteins. Nearly all enzymes are globular proteins, as are protein hormones, blood transport proteins, antibodies and nutrient storage proteins.

A simple functional classification of globular proteins is not possible because of 2 reasons: (a) Firstly, these proteins perform a variety of different functions. (b) Secondly, many widely-differing globular proteins perform almost similar functions.

Fibrous or Fibrillar Proteins

These have axial ratios greater than 10 and, henceforth, resemble long ribbons or fibres in shape.

These are mainly of animal origin and are insoluble in all common solvents such as water, dilute acids, alkalies and salts and also in organic solvents. Most fibrous proteins serve in a structural or protective role.

The fibrous proteins are extremely strong and possess two important properties which are characteristic of the elastomers.

They can *stretch* and later recoil to their original length.

They have a tendency to *creep*, *i.e.*, if stretched for a long time, their basic length increases and equals the stretched length but, if the tension on the two ends of the fibril is relaxed, they creep to their shorter and shorter length. A large scar, for example, creeps to a smaller size if there is no tension on the scar. On the contrary, if the scar is in a region of high tension, the scar becomes larger and larger as happens in the skin of a person gradually

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becoming obese. It is a heterogeneous group and includes the proteins of connective tissues, bones, blood vessels, skin, hair, nails, horns, hoofs, wool and silk.

The important examples are:

Collage

ns. These are of mesenchymal origin and form the major proteins of white connective tissues (tendons*, cartilage) and of bone. More than half the total protein in mammalian body is collagen; acted upon by boiling in water, dilute acids or alkalies to produce the soluble gelatins; unique in containing high contents (12%) of hydroxyproline; poor in sulfur since cysteine and cystine are lacking.

Elastins. Also of mesenchymal origin; form the major constituents of yellow elastic tissues (ligaments, blood vessels); differ from collagens in not being converted to soluble gelatins.

Keratins. These are of ectodermal origin; form the major constituents of epithelial tissues (skin, hair, feathers, horns, hoofs, nails); *usually contain large amounts of sulfur in the form of cystine*—human hair has about 14% cystine.

Fibroin. It is the principal constituent of the fibres of silk; composed mainly of glycine, alanine and serine units.

Size exclusion chromatography is used for semi-preparative purifications and various analytical assays. It is a separation technique which takes the advantage of the difference in size and geometry of the molecules. The molecules are separated based on their size. Grant Henry Lathe and Colin R Ruthven was the pioneer of size exclusion chromatography who started this technique for separation of analytes of different size with starch gels as the matrix, later Jerker Porath and Per Flodin introduced dextran gels. Other gel filtration matrices include agarose and polyacrylamide.

Principle: Size exclusion chromatography (SEC) is the separation of mixtures based on the molecular size (more correctly, their hydrodynamic volume) of the components. Separation is achieved by the differential exclusion or inclusion of

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solutes as they pass through stationary phase consisting of heteroporous (pores of different sizes) cross linked polymeric gels or beads. The process is based upon different permeation rates of each solute molecule into the interior of gel particles. Size exclusion chromatography involves gentle interaction with the sample, enabling high retention of biomolecular activity. For the separation of biomolecules in aqueous systems, SEC is referred to as gel filtration chromatography (GFC), while the separation of organic polymers in non-aqueous systems is called gel permeation chromatography (GPC).

The basic principle of size exclusion chromatography is quite simple. A column of gel particles or porous matrix is in equilibrium with a suitable mobile phase for the molecules to be separated. Large molecules are completely excluded from the pores will pass through the space in between the gel particles or matrix and will come first in the effluent. Smaller molecules will get distributed in between the mobile phase of in and outside the molecular sieve and will then pass through the column at a slower rate, hence appear later in effluent.

There are two extremes in the separation profile of a gel filtration column. There is a critical molecular mass (large mass) which will be **completely excluded** from the gel filtration beads. All solutes in the sample which are equal to, or larger, than this critical size will behave identically: they will all eluted in the excluded volume of the column. There is a critical molecular mass (small mass) which will be **completely included** within the pores of the gel filtration beads. All solutes in the sample which are equal to, or smaller, than this critical size will behave identically: they will all eluted in the included volume of the column Solutes between these two ranges of molecular mass will elute between the excluded and included volumes (Fig. 2) Thus, while deciding a size exclusion matrix for protein purification, included and excluded range should be considered. For example: Sephadex G 75 matrix has fractionation range 3-80. This tells that the matrix has included volume range 3 kDa and excluded volume range 80kDa. If protein of interest and impurities both are close to 80 kDa or above they are likely to co-elute in excluded volume. Thus purification will not work. Now you can think what is the use of a size exclusion matrix Sephadax

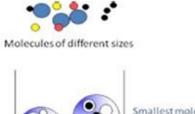
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G25 (range 1- 5kDa)? This is generally used for desalting as all proteins are above 5kDa and comes in excluded volume and salts are eluted late in included volume.

In gel filtration the resolution is a function of column length (the longer the better). However, one drawback is related to the maximum sample volume which can be loaded. The larger the volume of sample loaded, the more the overlap between separated peaks. Generally speaking, the sample size one can load is limited to about 3-5% of the total column volume. Thus, gel filtration is best saved for the end stages of a purification, when the sample can be readily concentrated to a small volume. Gel filtration can also be used to remove salts from the sample, due to its ability to separate "small" from "large" components. Finally, gel filtration can be among the most "gentle" purification methods due to the lack of chemical interaction with the resin.



Smallest molecule moves slowest

Biggest molecules moves fastest

Mechanism of Size Exclusion Chromatography

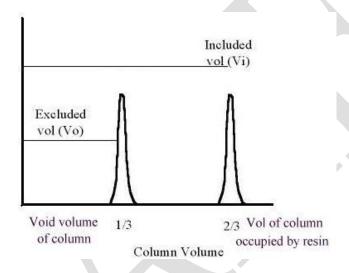
Size exclusion (also known as gel filtration chromatography) is a case of liquid-liquid partition chromatography, in which the solute molecules are get distributed in between two liquid phases, (i) liquid in the gel pores and (ii) liquid outside the gel. The size exclusion may be

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explained by Steric Exclusion Mechanism. As the gel particles contains range of pore sizes, small molecules can enter in large number of pores while the large molecules will get small number of pores into which they can enter. Thus the different fractions of total pore volume are accessible to molecules of different sizes. Thus, molecules with different sizes will differ in distribution coefficient between these two liquid phases [As the small molecules can enter in more pores while larger molecules can enter in pores only larger than the molecular size]



The excluded volume (Vo) is approximately equal to one third of the column volume, the included volume is approximately equal to two thirds of the column volume.

The total volume (Vt) of a column packed with a gel that has been swelled by solvent is given by

$$V_T = V_G + V_I + V_O$$

Where V_G is the volume occupied by the solid matrix of gel, V_I is the volume of solvent held in the pores or interstices and V_G is the free volume outside the gel particles. When mixing or diffusion occurs, the diffusion equilibrium and the retention volume (VR) of the given species is

given by
$$V_R = V_I + K_d V_I$$

where distribution coefficient (K_d) is given by

$$K_d = V_I(acc) / V_T$$

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where V_I(acc) is the accessible pore volume.

 V_T is the total pore volume and V_T is the interstitial volume. The other proposed mechanism is Secondary Exclusion Mechanism. This mechanism states that when a sample containing a mixture of small and large molecules is applied to a gel filtration column, the small molecules diffuse rapidly into the pores of gel, whereas large molecules will find relatively few unoccupied pores and move further down the column till they find the unoccupied pores. This results in the enhancement of separation of small and large molecules.

Denaturation:

The phenomenon of disorganization of native protein structure is known as denaturation.

Denaturation results in the loss of secondary, tertiary and quaternary structure of proteins.

This involves a change in physical, chemical and biological properties of protein molecules.

Agents of denaturation:

Physical agents: Heat, violent shaking, X-rays, UV radiation.

Chemical agents: Acids, alkalies, organic solvents (ether, alcohol), salts of heavy metals (Pb, Hg), urea, salicylate.

Characteristics of denaturation:

The native helical structure of protein is lost.

The primary structure of a protein with peptide linkages remains intact i.e., peptide bonds are not hydrolyzed.

The protein loses its biological activity.

The viscosity of denatured protein (solution) increases while its surface tension decreases.

Denaturation is associated with increase in ionizable and sulfhydryl groups of protein.

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Denatured protein is more easily digested.

Denaturation is usually irreversible.

Careful denaturation is sometimes reversible (known as renaturation).

Denatured protein cannot be crystallized.

Renaturation:

The original structure of a protein is a three-dimensional structure.

The process of returning a denatured protein structure to its original structure and normal level of biological activity, or simply the remodification or folding of an unfolded polypeptide chain of proteins to its normal three-dimensional structure is known as reconstitution of protein.

This reconstitution of a protein structure is also known as renaturation of protein.

In other words, renaturation of proteins is technically the opposite of denaturation of proteins.

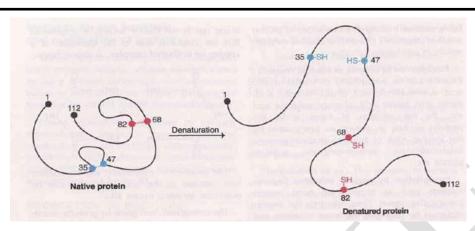
In a renatured protein, the primary structure of the biopolymer remains the same, but the protein which had been denatured (with the help of such agents as chaotropic agents, detergents, heat or reagents) gets restored back to its former native structure (that is the native structure of the protein before it was denatured) and is able to function as effectively as before, because a renatured protein merely undergoes the process of reversal of a denatured protein.

In fact, a renatured protein is able to carry out its functions better, faster and more efficiently, because it is able to pinpoint the level of biological activity that it was going through prior to the process of denaturation.

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Possible questions

PART A

The axial ratio of globular proteins is

A) > 10

B) < 10

C) > 20

D) < 20

The axial ratio of fibrous proteins is

(a) > 10

(b) < 10

(c) > 20

(d) < 20

Biomolecules are

- A) Endogenous
- B) Exogenous
- C) Either endogenous or exogenous
- D) Neither endogenous nor exogenous

Keratin the protein of hair is synthesized from the aminoacid

- A) glycine
- B) Serine
- C) Proline
- D) Methionine

What are amphiphilic molecules?

A) Highly polar

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- B) Highly non-polar
- C) Neutral
- D) Having both polar and non-polar groups

The shape of a water molecule is

- A) Linear
- B) Trigonal
- C) Tetrahedron
- D) Distorted Tetrahedron

The pI of 'Lysine' can be calculated by using the formula

A) pI = (pK2 + pKR)/2

B) pI = (pK1 + pKR)/2

C) pI = (pK1 + pK2)/2

D) pI = (pK1 + pK2 + pKR)/3

PART B

- 1. What is axial ratio?
- 2. Draw 2D structure of an imino acid.
- 3. What is multimeric protein? Give an example.
- 4. Draw a structure of an α -L-amino acid.
- 5. What is reduced protein?

PART C

- 1. Explain the structural architectures of proteins.
- 2. How are amino acids classified on the basis of their metabolic fate and nutritional factors?
- 3. How will you purify proteins by using 'size exclusion chromatography'?
- 4. Draw the structures of any three non-polar amino acids.
- 5. How will you classify the standard amino acids based on their structures and chemical properties?
- 6. What are the unique structural and chemical features of globular proteins?
- 7. What are aromatic amino acids? Draw the structures of any two of them.
- 8. Explain unique features of fibrous and globular proteins in detail.
- 9. How are proteins classified based on their shapes, solubility and secondary structures?
- 10. Draw structures of any three polar amino acids.

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UNIT II

SYLLABUS

Carbohydrates and Metabolism: Carbohydrates: Structure, Function and properties of Monosaccharides, Disaccharides and Polysaccharides. Bacterial cell wall polysaccharides, Glycoprotein's and their biological functions; Glycolysis: Fate of pyruvate under aerobic and anaerobic conditions. Pentose phosphate pathway and its significance, Gluconeogenesis, Glycogenolysis and glycogen synthesis. TCA cycle.

CARBOHYDRATES

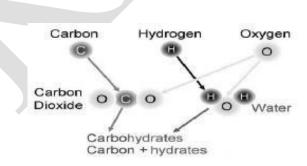
Carbohydrates are polyhydroxylated aldehydes or ketones and their derivatives.

The word "carbohydrate" includes polymers and other compounds synthesized from polyhydroxylated aldehydes and ketones.

They can be synthesized in the laboratory or in living cells. Simple carbohydrates or the entire carbohydrate family may also be called saccharides.

In general carbohydrates have the empirical formula (CH O). The term generated from carbon and hydrate; though some also contain nitrogen, phosphorus, or sulfur.

Chemically, carbohydrates are molecules that are composed of carbon, along with hydrogen and oxygen - usually in the same ratio as that found in water (H O).



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They originate as products of photosynthesis, an endothermic reductive condensation of carbon dioxide requiring light energy and the pigment chlorophyll.

$$nCO_2 + nH_2O + energy C_nH_{2n}O_n + nO_2$$

Typical carbohydrates are composed of strings or chains of monosaccharides - that is, chains of individual sugars.

Importance of carbohydrates

Carbohydrates are of great importance in biology. The unique reaction, which makes life possible on the Earth, namely the assimilation of the green plants, produces sugar, from which originate, not only all carbohydrates but, directly or indirectly, all other components of living organisms.

The carbohydrates are a major source of metabolic energy, both for plants and for animals that depend on plants for food. Aside from the sugars and starch that meet this vital nutritional role, carbohydrates also serve as a structural material (cellulose), a component of the energy transport compound ATP, recognition sites on cell surfaces, and one of three essential components of DNA and RNA.

Classification

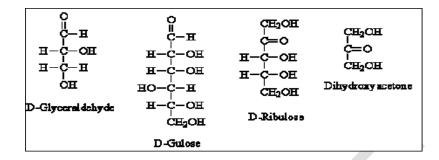
Carbohydrates are called saccharides or, if they are relatively small, sugars. Classifications of carbohydrates are outlined in the following table.

The compounds carbohydrates have common same functional groups, glyceraldehydes and gulose are classifed as aldoses and ribulose and dihydroxyacetone as ketoses. All of these compounds are alcohols with many hydroxyl groups. They are polyhydroxylated and either aldehydes or ketones.

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Monosaccharides

The simplest and smallest unit of the carbohydrates is the monosaccharide, (mono = one, saccharide = sugar) from which disaccharides, oligosaccharides, and polysaccharides are constructed.

Monosaccharides are either aldehydes or ketones, with one or more hydroxyl groups;

the six-carbon monosaccharides glucose (an aldohexose) and fructose (a keto hexose) have five hydroxyl groups.

The carbon atoms, to which hydroxyl groups are attached, are often chiral centers, and stereoisomerism is common among monosaccharides.

Because these molecules have multiple asymmetric carbons, they exist as diastereoisomers, isomers that are not mirror images of each other, as well as enantiomers.

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In regard to these monosaccharides, the symbols D and L designate the absolute configuration of the asymmetric carbon farthest from the aldehyde or keto group.

D-Ribose, the carbohydrate component of RNA, is a five-carbon aldose.

D-Glucose, D-mannose, and D-galactose are abundant six-carbon

aldoses.

It may be noted that D-glucose and D-mannose differ in configuration only at C-2.

Sugars differing in configuration at a single asymmetric center are called epimers.

Thus, D-glucose and D-mannose are epimeric at C-2; D-glucose and D-galactose are epimers with respect to C-4.

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Disaccharides

A disaccharide consists of two monosaccharides joined by an O-glycosidic bond.

Disaccharides can be homo- and heterodisaccharide.

Three most abundant disaccharides are sucrose, lactose, and maltose.

In sucrose the anomeric carbon atoms of a glucose unit and a fructose unit are joined.

Sucrose α-D-glucopyranosyl β-D-fructofuranoside Glc(α1↔2β)Fru

Lactose, the disaccharide of milk, consists of galactose joined to glucose by a β (1 \rightarrow 4) glycosidic linkage.

In maltose, α (1 \rightarrow 4) glycosidic linkage joins two glucose units.

Sucrose and lactose are heterosaccharides and maltose is

homosaccharide.

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Oligosaccharide

An oligosaccharide is a saccharide polymer containing a small number (typically three to ten) of component sugars, and is also known as simple sugars.

They are generally found either O- or N-linked to compatible amino acid side chains in proteins or to lipid moieties.

They (homo-and hetero-oligosaccharides) are also liberated as intermediate products of saccharification by action of glycosidases on polysaccharides.

Polysaccharides

They consist of repeat units of monosaccharides or their derivatives. These units are held by glycosidic bonds. These carbohydrates liberate large number of monosaccharide molecules on hydrolysis. They are colorless and tasteless. So, they are called non-sugars. They are concerned with two important functions - structural and storage of energy. Some examples of polysaccharides are starch, cellulose, glycogen and dextrins. However starch and cellulose are the most important of these.

Polysaccharides are linear as well as branched polymers. The general formula is $(C_6H_{10}O_5)_n$, where 'n' stands for a very large number. The occurrence of branches in polysaccharides is due to the glycosidic linkages formed at any one of the hydroxyl groups of a monosaccharide.

Polysaccharide

Polysaccharides are polymeric carbohydrate molecules composed of long chains of monosaccharide units bound together by glycosidic linkages and on hydrolysis give the constituent monosaccharides or oligosaccharides. They range in structure from linear to highly branched. Examples include storage polysaccharides such as starch and glycogen, and structural polysaccharides such as cellulose and chitin. Polysaccharides are often quite heterogeneous, containing slight modifications of the repeating unit. Depending on the structure, these macromolecules can have distinct properties from their monosaccharide building blocks. They may be amorphous or even insoluble in water. When all the monosaccharides in a polysaccharide are the same type, the polysaccharide is called a

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homopolysaccharide or homoglycan, but when more than one type of monosaccharide is present they are called heteropolysaccharides or heteroglycans.

Amylose is a linear polymer of glucose mainly linked with $\alpha(1\rightarrow 4)$ bonds. It can be made of several thousands of glucose units. It is one of the two components of starch, the other being amylopectin.

Natural saccharides are generally of simple carbohydrates called monosaccharides with general formula $(CH_2O)_n$ where n is three or more. Examples of monosaccharides are glucose, fructose, and glyceraldehyde. Polysaccharides, meanwhile, have a general formula of $C_x(H_2O)_y$ where x is usually a large number between 200 and 2500. When the repeating units in the polymer backbone are six-carbon monosaccharides, as is often the case, the general formula simplifies to $(C_6H_{10}O_5)_n$, where typically $40 \le n \le 3000$. As a rule of thumb, polysaccharides contain more than ten monosaccharide units, whereas oligosaccharides contain three to ten monosaccharide units; but the precise cutoff varies somewhat according to convention. Polysaccharides are an important class of biological polymers. Their function in living organisms is usually either structure- or storage-related. Starch (a polymer of glucose) is used as a storage polysaccharide in plants, being found in the form of both amylose and the branched amylopectin. In animals, the structurally similar glucose polymer is the more densely branched glycogen, sometimes called "animal starch". Glycogen's properties allow it to be metabolized more quickly, which suits the active lives of moving animals.

Cellulose and chitin are examples of structural polysaccharides. Cellulose is used in the cell walls of plants and other organisms, and is said to be the most abundant organic molecule on Earth. It has many uses such as a significant role in the paper and textile industries, and is used as a feedstock for the production of rayon (via the viscose process), cellulose acetate, celluloid, and nitrocellulose. Chitin has a similar structure, but has nitrogen-containing side branches, increasing its strength. It is found in arthropod exoskeletons and in the cell walls of some fungi. It also has multiple uses, including surgical

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threads. Polysaccharides also include callose or laminarin, chrysolaminarin, xylan, arabinoxylan, mannan, fucoidan and galactomannan.

Nutrition polysaccharides are common sources of energy. Many organisms can easily break down starches into glucose; however, most organisms cannot metabolize cellulose or other polysaccharides like chitin and arabinoxylans. These carbohydrate types can be metabolized by some bacteria and protists. Ruminants and termites, for example, use microorganisms to process cellulose. Even though these complex polysaccharides are not very digestible, they provide important dietary elements for humans. Called dietary fiber, these carbohydrates enhance digestion among other benefits. The main action of dietary fiber is to change the nature of the contents of the gastrointestinal tract, and to change how other nutrients and chemicals are absorbed. Soluble fiber binds to bile acids in the small intestine, making them less likely to enter the body; this in turn lowers cholesterol levels in the blood. Soluble fiber also attenuates the absorption of sugar, reduces sugar response after eating, normalizes blood lipid levels and, once fermented in the colon, produces short-chain fatty acids as byproducts with wide-ranging physiological activities (discussion below). Although insoluble fiber is associated with reduced diabetes risk, the mechanism by which this occurs is unknown. Not yet formally proposed as an essential macronutrient (as of 2005), dietary fiber is nevertheless regarded as important for the diet, with regulatory authorities in many developed countries recommending increases in fiber intake.

Starch

Starch is a glucose polymer in which glucopyranose units are bonded by *alpha*-linkages. It is made up of a mixture of amylose (15–20%) and amylopectin (80–85%). Amylose consists of a linear chain of several hundred glucose molecules and Amylopectin is a branched molecule made of several thousand glucose units (every chain of 24–30 glucose units is one unit of Amylopectin). Starches are insoluble in water. They can be digested by breaking the *alpha*-linkages (glycosidic bonds). Both humans and animals have amylases, so they can digest starches. Potato, rice, wheat, and maize are major sources of starch in the human diet. The formations of starches are the ways that plants store glucose.

Glycogen

Glycogen serves as the secondary long-term energy storage in animal and fungal cells, with the primary energy stores being held in adipose tissue. Glycogen is made primarily by the liver and the muscles, but can also be made by glycogenesis within the brain and stomach. Glycogen is analogous to starch, a glucose polymer in plants, and is sometimes referred to as *animal starch*, having a similar

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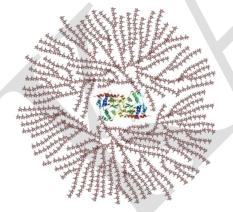
structure to amylopectin but more extensively branched and compact than starch. Glycogen is a polymer of $\alpha(1\rightarrow 4)$ glycosidic bonds linked, with $\alpha(1\rightarrow 6)$ -linked branches. Glycogen is found in the form of granules in the cytosol/cytoplasm in many cell types, and plays an important role in the glucose cycle. Glycogen forms an energy reserve that can be quickly mobilized to meet a sudden need for glucose, but one that is less compact and more immediately available as an energy reserve than triglycerides (lipids). In the liver hepatocytes, glycogen can compose up to eight percent (100–120 g in an adult) of the fresh weight soon after a meal. Only the glycogen stored in the liver can be made accessible to other organs. In the muscles, glycogen is found in a low concentration of one to two percent of the muscle mass. The amount of glycogen stored in the body—especially within the muscles, liver, and red blood cells—varies with physical activity, basal metabolic rate, and eating habits such as intermittent fasting. Small amounts of glycogen are found in the kidneys, and even smaller amounts in certain glial cells in the brain and white blood cells. The uterus also stores glycogen during pregnancy, to nourish the embryo.

Glycogen is composed of a branched chain of glucose residues. It is stored in liver and muscles. It is an energy reserve for animals.

It is the chief form of carbohydrate stored in animal body.

It is insoluble in water. It turns brown-red when mixed with iodine.

It also yields glucose on hydrolysis.



Schematic 2-D cross-sectional view of glycogen. A core protein of glycogenin is surrounded by branches of glucose units. The entire globular granule may contain approximately 30,000 glucose units.

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Cellulose

It is the chief constituent of the cell walls of plants wood contains 45-50% while cotton contains 90-95% cellulose. It is a colourless amorphous solid which decomposes on heating. It is largely linear and its individual strands align with each other through multiple hydrogen bonds. This lends rigidity to its structure. It is thus used effectively as a cell wall material. Cellulose does not reduce Tollens reagent or Fehlings solution. It does not from osazone and is not fermented by yeast. It is not hydrolyzed so easily as starch but on heating with dilute H₂SO₄ under pressure yields only D-glucose.

Cellulose is composed of b-D-glucose units linked by b(1 4) glycosidic bonds. It is a linear chain cellulose on hydrolysis yields a disaccharide cellobcose and then produces b- D-glucose. Due to the lack of an enzyme that can cleave b-glycosidic bonds, all mammals cannot digest cellulose. Large population of cellulolytic bacteria present in the stomach of ruminant mammals like cattle, sheep etc., breaks down the cellulose with the help of enzyme cellulose. It is then digested and converted into glucose.

Structure of cellulose.

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Sugars in the cell wall bacteria

In contrast to eukaryotic cells, bacterial cells have a cell wall in addition to a lipid bilayer membrane. These are essentially carbohydrate polymers, which offer protection from exterior hypotonic condition and the high internal osmotic pressures, preventing swelling and bursting of the cells. The membrane consists of a peptidoglycan.

In Gram positive bacteria

Gram-positive bacteria can be stained with Gram stain. The wall consists of a GlcNAc (b 1->4) MurNAc repeat (like that in chitin which is a polymer of GlcNAc in (b 1->4) links, but in which the OH of lactate is in ether-linkage to C3 to form N-Acetylmuramic acid). A tetrapeptide (Ala-D-isoGlu-Lys-D-Ala) is attached in amide link to the carboxyl group of the lactate in MurNAc. The GlcNAc (b 1->4) MurNAc strands are covalently connected by a pentaglycine bridge through the epsilon amino group of the tetrapeptide Lys on one strand and the D-Ala of a tetrapeptide on another strand.

Techioic acids are often attached to the C6 of MurNAc. Teichoic acid is a polymer of glycerol or ribitol to which alternative GlcNAc and D-Ala are linked to the middle C of the glycerol. Multiple glycerols are linked through phosphodiester bonds. These teichoic acids often make up 50% of the dry weight of the cell wall, and present a foreign (or antigenic) surface to infected hosts. These often serve as receptors for viruses that infect bacteria (bacteriophages).

Glycoproteins are proteins that contain carbohydrate. Proteins destined for an extracellular location are characteristically glycoproteins. For example, fibronectin and proteoglycans are important components of the extracellular

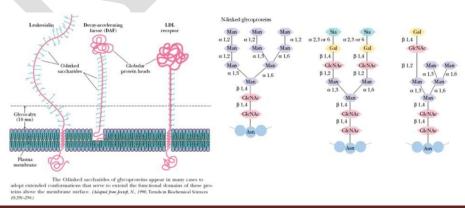
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matrix that surrounds the cells of most tissues in animals. Immunoglobulin G molecules are the principal antibody species found circulating free in the blood plasma. Many membrane proteins are glycosylated on their extracellular segments. Many proteins found in nature are **glycoproteins** because they contain covalently linked oligo- and polysaccharide groups. The list of known glycoproteins includes structural proteins, enzymes, membrane receptors, transport proteins, and immunoglobulins, among others.

Carbohydrate groups may be linked to polypeptide chains via the hydroxyl groups of serine, threonine, or hydroxylysine residues (in **O-linked saccharides**) or via the amide nitrogen of an asparagine residue (in **N-linked saccharides**). The carbohydrate residue linked to the protein in O-linked saccharides is usually an *N*-acetylgalactosamine, but mannose, galactose, and xylose residues linked to protein hydroxyls are also found. Oligosaccharides O-linked to glycophorin involve *N*acetylgalactosamine linkages and are rich in sialic acid residues. N-linked saccharides always have a unique core structure composed of two *N*-acetyl glucosamine residues linked to a branched mannose triad. Many other sugar units may be linked to each of the mannose residues of this branched core. O-Linked saccharides are often found in cell surface glycoproteins and in **mucins**, the large glycoproteins that coat and protect mucous membranes in the respiratory and gastrointestinal tracts in the body. Certain viral glycoproteins also contain O-linked sugars. O-Linked



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saccharides in glycoproteins are often found clustered in richly glycosylated domains of the polypeptide chain.

The Functions of Carbohydrates in the Body

There are five primary functions of carbohydrates in the human body. They are energy production, energy storage, building macromolecules, sparing protein, and assisting in lipid metabolism.

Carbohydrate functions as Bio Fuel

Carbohydrate functions as an energy source of the body and acts as Bio fuel. Step wise details for the process of production of energy are discussed below.

Polysaccharides such as starch and glycogen are first hydrolyzed by enzymes to Glucose.

Glucose is the transported from one cell to another by blood in case of animals and cell sap in case of plants.

Glucose is then oxidized to produce carbon dioxide and water.

Energy is released in this process which is used for functioning of the

cells.

Carbohydrate functions as Primary Source of Energy

The process of production of energy by carbohydrates is described in above steps. Now it is important to note, that fats and proteins can also be burned to provide energy but **carbohydrate functions as primary source of energy**. Fats are only burned if there is non-availability of carbohydrates. When fat is burned in absence of carbohydrates, toxic compounds like called **ketone bodies** are produced. Accumulation of these ketone bodies over long period causes a condition called **Ketosis**. In this condition blood becomes unable to carry oxygen properly and this can be fatal. Thus, one of important function of carbohydrate is help burn fat properly.

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Carbohydrate functions as storage food

Different forms of Carbohydrate are stored in living organism as storage food.

Polysaccharide starch acts as storage food for plants.

Glycogen stored in liver and muscles acts as storage food for animals.

Inulin acts as storage food of dahlias, onion and garlic. Thus carbohydrate performs the function of storing food.

Carbohydrate functions as framework in body

Different Carbohydrates especially Polysaccharides act as framework in living organism.

Cellulose forms cell wall of plant cell along with hemicelluloses and

Pectin

Chitin forms cell wall of fungal cell and exoskeleton of arthropods

Peptidoglycan forms cell wall of bacteria and cyanobacteria.

Thus carbohydrates function as contributing material to the cellular structure.

Carbohydrate functions as Anticoagulant

Heparin is a polysaccharide (carbohydrate) which acts as anticoagulant and prevents intravascular clotting.

Carbohydrate functions as Antigen

Many antigens are glycoprotein (which contains oligosaccharide) in nature and give immunological properties to the blood.

Carbohydrate functions as Hormone

Many Hormones like FSH (Follicular Stimulating Hormone which takes part in ovulation in females) and LH (Leutinizing Hormone) are glycoprotein and help in reproductive processes.

Carbohydrates provide raw material for industry

Carbohydrates are an important component of many industries like textile, paper, lacquers and breweries.

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Other Functions

Agar is polysaccharide used in culture media, laxative and food.

Cellulose acts as roughage of food. It stimulates peristalsis movement and secretion of digestive enzymes.

Hyaluronic acid found in between joints acts as synovial fluid and provides frictionless movement.

Carbohydrate Metabolism Introduction

Glucose is the major form of sugar moiety present in blood and other body fluids. The digestion of food carbohydrates, such as starch, sucrose, and lactose produces the monosaccharides glucose, fructose and galactose, which pass into the blood stream. The study of synthesis (Anabolism) and degradation (Catabolism) of biomolecules is biochemically termed as metabolism.

Anabolism + Catabolism = Metabolism

(Synthesis) (Degradation)

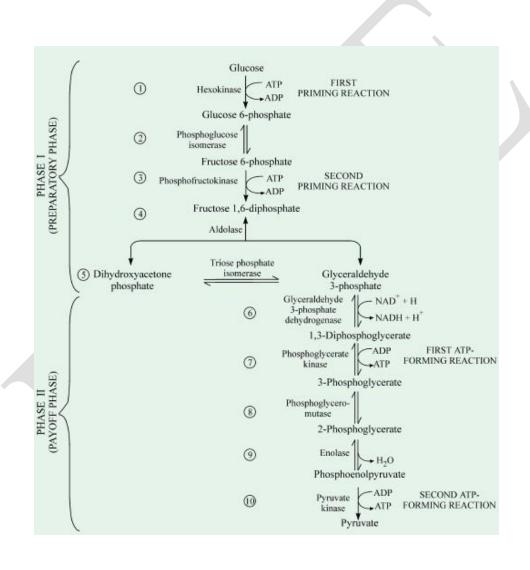
Since glucose is the most important carbohydrate existing in physiological amounts in the body and is easily absorbed from the diet, the metabolism of carbohydrate resolves itself to the study of the metabolism of glucose and its main derivatives. The monosaccharides galactose and fructose are converted to glucose in the liver. All the monosaccharides are completely absorbed in the small intestine.

The glucose in the circulating blood and tissue fluids is drawn upon by all the cells of the body and used for the production of energy. Normally carbohydrate metabolism supplies more than half of the energy requirements of the body. In fact the brain largely depends upon carbohydrate metabolism as a source of energy and quickly ceases to function properly when the blood glucose level falls much below normal.

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Summary of glycolysis

During glycolysis NAD+ is reduced to NADH. At the same time, glyceraldehyde 3-phosphate is oxidized to 1,3-bisphosphoglycerate. To conserve the coenzyme NAD+, NADH must be reoxidized. Under anaerobic conditions this is done when pyruvic acid is converted to lactic acid. In the presence of oxygen, NADH, can be oxidized to NAD+ with the help of the respiratory enzymes.

Energy yield per glucose molecule oxidation

During glycolysis ATP molecules are used and formed in the following reactions (aerobic phase).

Reactions Catalyzed	ATP used	ATP formed
Stage I 1. Glucokinase (for phosphorylation)	1	
2. Phosphofructokinase I (for phosphorylation)	1	
Stage II 3. Glyceraldehyde 3-phosphate dehydrogenase (oxidation of 2 NADH in respiratory chain)		6
Phosphoglycerate kinase (substrate level phosphorylation)		2
Stage IV 5. Pyruvate kinase (substrate level phosphorylation)		2
Total	2	10

Net gain = 8 ATP

Anaerobic phase

In the absence of O2, reoxidation of NADH at glyceraldehyde 3-phosphate dehydrogenase stage cannot take place in respiratory chain. But the cells have limited coenzyme. Hence to continue the glycolysis **NADH must be reoxidized to NAD+**. This is achieved by reoxidation of NADH by conversion of pyruvate to lactate

NADH+H* NAD* ant Professor,
Lactate dehydrogenase Page 17/28

Prepared by Dr. T. Sivaran Department of Biotechnole Pyruvate

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(without producing ATP).

It is to be noted that in the reaction catalyzed by glyceraldehyde 3-phosphate dehydrogenase, therefore, no ATP is produced.

In the anaerobic phase oxidation of one glucose molecule produces 4 - 2 = 2 ATP.

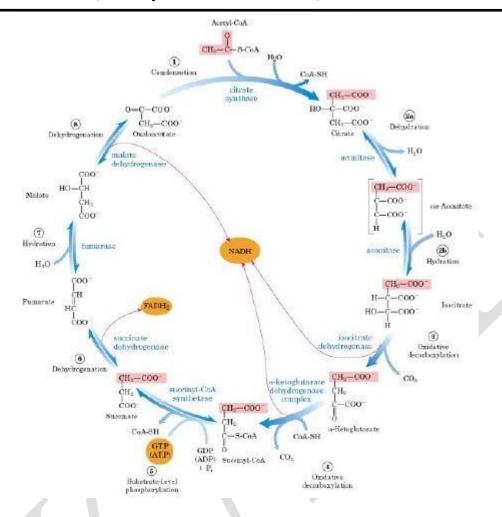
Tricarboxylic acid cycle (TCA cycle)

This cycle is the aerobic phase of carbohydrate metabolism and follows the anaerobic pathway from the stage of pyruvate and is called as citric acid cycle or TCA cycle. The name citric acid cycle stems from citric acid which is formed in the first step of this cycle. This cycle is also named "Kerbs cycle" after H.A. Krebs, an English biochemist who worked on it.

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Under aerobic conditions, pyruvate is oxidatively decarboxylated to acetyl coenzyme A (active acetate) before entering the citric acid cycle. This occurs in the mitochondrial matrix and forms a link between glycolysis and TCA cycle.

PDH-pyruvate dehydrogenase

This reaction is catalysed by the multienzyme complex known as pyruvate

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dehydrogenase complex.

Energy yield from TCA cycle

If one molecule of the substrate is oxidized through NADH in the electron transport chain three molecules of ATP will be formed and through FADH2, two ATP molecules will be generated.

As one molecule of glucose gives rise to two molecules of pyruvate by glycolysis, intermediates of citric acid cycle also result as two molecules.

Reactions	No.of ATP formed
 2 isocitrate → 2 α-ketoglutarate 	
$(2 \text{ NADH} + 2\text{H}^+) (2 \times 3)$	6
 2 α-ketoglutarate→ 2 succinyl CoA 	
(2 NADH + 2H+) (2 × 3)	6
 2 succinyl CoA→2 succinate 	
(2 GTP = 2 ATP)	2
 2 succinate → 2 Fumarate 	
(2 FADH ₂) (2 × 2)	4
 2 malate → 2 oxaloacetate 	
(2 NADH + 2H+) (2 × 3)	6
Total No. of ATP formed	24

HMP shunt pathway

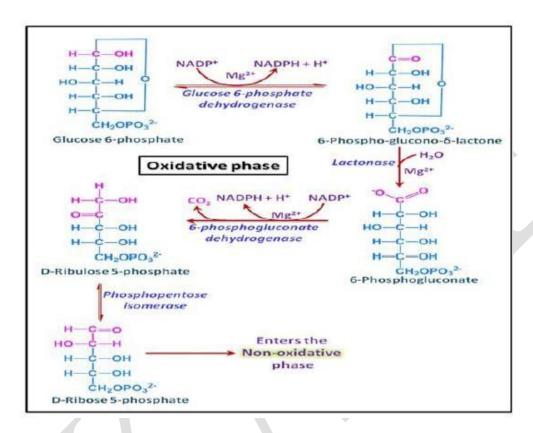
Although glycolysis and citric acid cycle are the common pathways by which animal tissues oxidise glucose to CO2 and H2O with the liberation of energy in the form of ATP, a number of alternative pathways are also discovered. The most important one is Hexose Monophosphate Shunt Pathway (HMP shunt). The pathway occurs in the extra mitochondrial soluble portion of the cells. Unlike glycolysis and Krebs cycle which are primarily concerned with the generation of ATP, HMP shunt generates a different type of metabolic energy - the reducing power. Some of the electrons and hydrogen atoms of fuel molecules are conserved for biosynthetic

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purposes rather than ATP formation. This reducing power of cells is NADPH (reduced nicotinamide adenine dinucleotide phosphate).



The fundamental difference between NADPH and NADH (reduced nicotinamide adenine dinucleotide) is that NADH is oxidised by the respiratory chain to generate ATP whereas NADPH serves as a hydrogen and electron donor in reductive biosynthesis, for example in the biosynthesis of fatty acids and steroids.

Glycogen

Glycogen is the major storage form of carbohydrate in animals and corresponds to starch in plants.It occurs mainly in liver.

Glycogen biosynthesis

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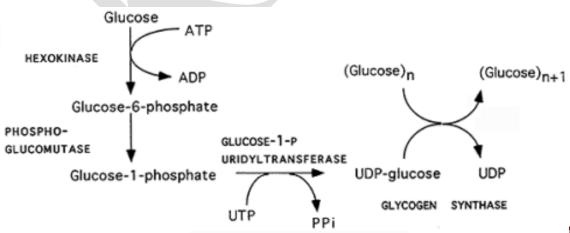
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The process of biosynthesis of glycogen from glucose is known as glycogenesis. This occurs in all the tissues of the body but the major sites are liver and muscles. A considerable amount is synthesised in kidney also.

Glycogenesis is a very essential process since the excess of glucose is converted and stored up as glycogen which could be utilised at the time of requirement. In the absence of this process the tissues are exposed to excess of glucose immediately after a meal and they are starved of it at other times. The following are the various reactions of glycogenesis.

Gluconeogenesis is the reverse process of glycolysis. It involves the conversion of non-carbohydrate molecules into glucose. The non-carbohydrate molecules that are converted in this pathway include pyruvate, lactate, glycerol, alanine, and glutamine. This process occurs when there are lowered amounts of glucose. The production of glucose by this pathway is important to tissues that cannot use any other fuels, such as the brain. The liver is the primary location of gluconeogenesis, but some also occurs in the kidney. This pathway is regulated by multiple different molecules. Glucagon, adrenocorticotropic hormone, and ATP encourage gluconeogenesis. Gluconeogenesis is inhibited by AMP, ADP, and insulin.



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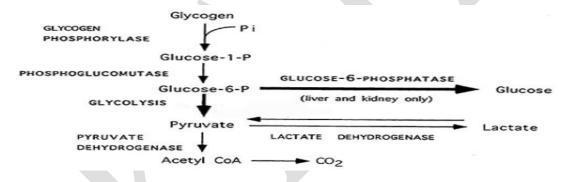
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Glycogenolysis

Glycogenolysis refers to the breakdown of glycogen. In the liver, muscles, and the kidney, this process occurs to provide glucose when necessary. A single glucose molecule is cleaved from a branch of glycogen, and is transformed into glucose-1-phosphate during this process. This molecule can then be converted to glucose-6-phosphate, an intermediate in the glycolysis pathway. Glucose-6-phosphate can then progress through glycolysis. Glycolysis only requires the input of one molecule of ATP when the glucose originates in glycogen. Alternatively, glucose-6-phosphate can be converted back into glucose in the liver and the kidneys, allowing it to raise blood glucose levels if necessary. Glucagon in the liver stimulates glycogenolysis when the blood glucose is lowered, known as hypoglycemia. The glycogen in the liver can function as a backup source of glucose between meals. Adrenaline stimulates the breakdown of glycogen in the skeletal muscle during exercise. In the muscles, glycogen ensures a rapidly accessible energy source for movement.



Gluconeogenesis

Gluconeogenesis is the reverse process of glycolysis. It involves the conversion of non-carbohydrate molecules into glucose. The non-carbohydrate molecules that are converted in this pathway include pyruvate, lactate, glycerol, alanine, and glutamine. This process occurs when there are lowered amounts of glucose. The production of glucose by this pathway is important to tissues that cannot use any other fuels, such as the brain. The liver is the primary location of gluconeogenesis, but some also occurs in the kidney. This pathway is regulated by multiple

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different molecules. Glucagon, adrenocorticotropic hormone, and ATP encourage gluconeogenesis. Gluconeogenesis is inhibited by AMP, ADP, and insulin.

Carbohydrates as fuel

Carbohydrates are a superior short-term fuel for organisms because they are simpler to metabolize than fats or those amino acids (components of proteins) that can be used for fuel. In animals, the most important carbohydrate is glucose. The concentration of glucose in the blood is used as the main control for the central metabolic hormone, insulin. Starch, and cellulose in a few organisms (e.g., some animals (such as termites) and some microorganisms (such as protists and bacteria)), both being glucose polymers, are disassembled during digestion and absorbed as glucose. Some simple carbohydrates have their own enzymatic oxidation pathways, as do only a few of the more complex carbohydrates. The disaccharide lactose, for instance, requires the enzyme lactase to be broken into its monosaccharide components; many animals lack this enzyme in adulthood.

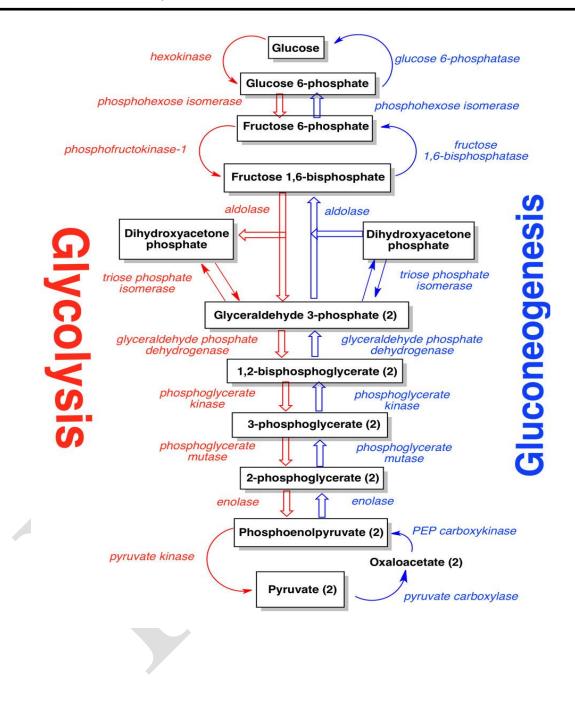
Carbohydrates as storage

Carbohydrates are typically stored as long polymers of glucose molecules with glycosidic bonds for structural support (e.g. chitin, cellulose) or for energy storage (e.g. glycogen, starch). However, the strong affinity of most carbohydrates for water makes storage of large quantities of carbohydrates inefficient due to the large molecular weight of the solvated water-carbohydrate complex. In most organisms, excess carbohydrates are regularly catabolised to form acetyl-CoA, which is a feed stock for the fatty acid synthesis pathway; fatty acids, triglycerides, and other lipids are commonly used for long-term energy storage. The hydrophobic character of lipids makes them a much more compact form of energy storage than hydrophilic carbohydrates. However, animals, including humans, lack the necessary enzymatic machinery and so do not synthesize glucose from lipids (with a few exceptions, e.g. glycerol).

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Cori cycle

In this cycle liver glycogen may be converted into muscle glycogen and vice versa and the major raw material of this cycle is lactate produced by the active

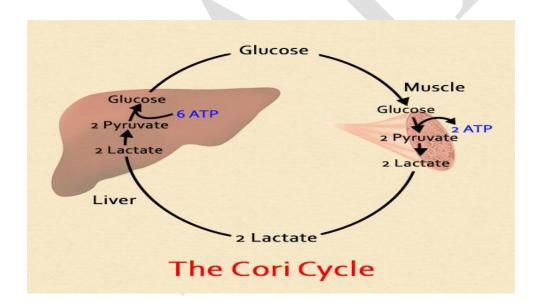
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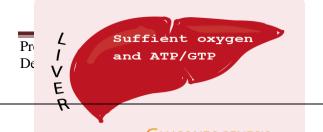
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skeletal muscles. At the time of heavy muscular work or strenuous exercise, O2 supply is inadequate in active muscles but the muscles keep contracting to the maximum. Hence, glycogen stored up in the muscle is converted into lactic acid by glycogenolysis followed by anaerobic glycolysis and thus lactate gets accumulated in the muscle. Muscle tissue lacks the enzyme glucose 6-phosphatase hence it is incapable of synthesizing glucose from lactic acid and the conversion take place only in the liver.

Lactate diffuses out of the muscle and enters the liver through blood. In the liver lactate is oxidised to pyruvate which undergoes the process of gluconeogenesis resulting in the resynthesis of glucose. The glycogen may be once again converted to glucose (glycogenolysis) and may be recycled to the muscle through the blood. The process of gluconeogenesis completes the cycle by converting glucose once again to muscle glycogen.







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Possible questions

PART A

Reducing sugars have following structural and chemical features

- A) Hemiacetal configuration
- B) Exhibit mutarotation
- C) Reduce Tollen's reagent
- D) All the above.

Non-reducing sugars have following structural and chemical features

- A) Acetal configuration
- B) Exhibit mutarotation
- C) Reduce Tollen's reagent
- D) All the above.

The monomeric unit of 'starch' is

- A) β-D-Glucose
- B) a-D-Glucose
- C) a-L-Glucose
- D) B-L-Glucose

The monomeric unit of 'cellulose' is

- A) beta-D-Glucose
- B) alpha-D-Glucose
- C) alpha-L-Glucose

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D) bete-L-Glucose

The net numbers of ATP production of glycolysis under aerobic condition is

- A) 2
- B) 4
- C) 8
- D) 24

The net numbers of ATP production of glycolysis under anaerobic condition is

- A) 2
- B) 4
- C) 8
- D) 24

The net numbers of ATP production in a TCA cycle is

- A) 2
- B) 4
- C) 8
- D) 24

The ----- is an allosteric inhibitor to 'phosphofructokinase'.

- A) ATP
- B) AMP
- C) ADP
- D) All the above

Polyuria is

- A) excessive thirst
- B) excessive appetite
- C) excessive excretion of urine
- D) glucose in urine

PART B

- 1. What do you mean by 'metabolism'?
- 2. List out the enzymes that are involving in the 'preparatory phase'
- 3. Draw the structure of α -D-glucose.
- 4. What is reducing sugar? Give an example.
- 5. What is non-reducing sugar? Give an example.

PART C

- 1. Elaborate structure and properties of a heteropolysaccharide.
- 2. Describe the citric acid cycle in detail.

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UNIT : II (Carbohydrates and Metabolism)

- 3. Enumerate various steps involved in the TCA cycle.
- 4. Explain about the metabolism of glycolysis in detail.
- 5. Write in detail about the glycolysis metabolism.
- 6. Explain about pentose phosphate pathway
- 7. List-out the essential steps involved in the TCA cycle.
- 8. Explain about glycogenolysis in detail.
- 9. Give detailed account on the gluconeogenesis.
- 10. Enumerate various steps involved in glycogenolysis metabolism.



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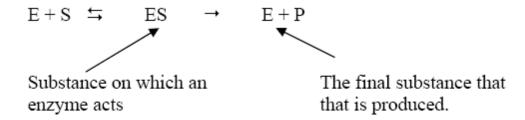
<u>UNIT III</u>

Enzymes : Nomenclature and classification of Enzymes, Holoenzyme, apoenzyme, Cofactors, coenzyme, groups, metalloenzymes, monomeric & oligomeric enzymes, activation energy and transition state, enzyme activity, specific activity, common features of active sites, Role of: NAD+, NADP+, FMN/FAD, coenzymes A, Thiamine pyrophosphate, Pyridoxal phosphate, lipoic-acid, Biotin vitamin B12, Tetrahydrofolate and metallic ions. Photosynthesis – Photosystem I and II.

ENZYME

Enzymes are protein specialized to catalyse biological reactions (Biocatalyse):

- Increase the speed of reactions
- They do not changes in the reaction.
- Very important to life as life depends on biological reactions (example digestion).
- Any change in a single enzyme can have very harmful effects.
- Very specific
- Enzymes (E) act on certain substances which are known as substrate(s). They form an Enzyme-Substance Complex (ES) which is broken or changed to give the Product (P).



CLASSIFICATION/ NOMENCLATURE OF ENZYMES

The most generally accepted classification of enzymes is in term of the reactions they catalyse. Individual enzymes are named by adding the suffix "ase" to the name of the substrate acted upon or to the reaction brought about.

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In the 1960's the International union of Biochemists and molecular Biologist (IUBMB) established a commission on enzyme nomenclature for the ever increasing number enzymes being identified. The commission identified enzymes by the type of reactions they catalysed and defined six major classes.

(1)OXIDOREDUCTASES

These groups of enzyme catalyse the oxidation reduction reaction. They are subdivided into

- (a)Dehydrogenases: which catalyse the removal of 2 atoms of hydrogen from substrates and their transference to a co-acceptor. (They remove 2H to form double bonds).
- (b)Oxidases: They catalyse the direct reduction of oxygen (oxidation).
- (c) Oxygenases: They catalyse the incorporation of oxygen into substrate molecule.
- (d)Oxidative deaminates: they catalyse the oxidation of amino compounds with elimination of a molecule of NH3 ammonia.

Examples:

(2)TRANSFERASES

They bring about the exchange of groups between substrates i.e. group transfer reactions.

 $AB+CD \square \square \square AC+BD$

They are subdivided into:

(a)Amino transferases: These bring about the exchange of amino and keto group between an amino acid and a keto acid.

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- (b)Kinases: These bring about the transfer of a phosphate radical using ATP as the donor or ADP acceptor.
- (c) Phosphorylases: which are phosphorylytic analog of the hydrolytic enzymes. They catalyse the splitting of the substrates with a molecule of phosphoric acid instead of water.
- (d)Glycosyltransferases: These bring about the transfer of a glycosyl group.
- (e) C1-Transferases: These bring about the transfer of an acyl group.

Example:

$$NH_3$$
- CH_3 CH-COO + COO-CO- CH_2 - CH_3 -COO \leftarrow Alanimetransa min ase \rightarrow CH₃-CO-COO + COO- NH_3 CH-CH₂-CH₂-COO

Alanine α -Ketoglutarate Pyruvate Glutamate

(3)HYDROLASES

These groups of enzymes employ water to cleave covalent bonds. They include the digestive enzymes. They catalyze the hydrolytic cleavage of C-C, C-O, C-N, P-O, and certain other bonds, including acid anhydride bonds They catalyse this type of reaction.

$AB + H2O \square \square \square AOH + HB$

This group may be subdivided according to the type of substrates acted on.

- (a) Peptidases are enzymes (proteolytic enzymes or peptide hydrolase) which catalyse the hydrolysis of the peptide bonds.
- (b)Amylases are enzymes (carbohydrases or glycoside hydrolases) which catalyse the hydrolysis of glycosidic bonds.
- (c) Lipases are enzymes which catalyse the hydrolysis of lipids.
- (d)Phosphatases catalyse the hydrolysis of phosphoric acids.

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Examples:

+NH3-CHR1-CO-NH-CHR2-CO-NH-CHR3-CO-NH-CHR4-CO-NH-CHR5-COO-

\$\perispartial* peptidase

*NH₃-CHR¹-COO- + NH₃-CHR²-COO- + NH₃-CHR³-COO- +NH₃-CHR⁴-COO- + NH₃-CHR⁵-COO-

(4)LYASES:

These are enzymes which remove or add groups to substrates non-hydrolytically by electron rearrangement therefore leaving double bond or adding groups to double bonds. They catalyse the cleavage of C-C, C-O, C-N, and other bonds by elimination, leaving double bonds, and also add groups to double bonds. The group however also include the decarboxylases, deaminases, deamidases, dehydrases. It involves the addition of groups to a double bond or formation of double bonds by the removal of group. The reaction may be represented by this scheme:

$$AB \longleftrightarrow A+B$$

For example

$$CH_3$$
- CO - COO + $H \leftarrow Pyrwatedecarboxylaze \rightarrow CH_3$ - COH + CO_2

Pyruvate Acetaldehyde

(5)ISOMERASES

They are enzymes which catalyse the internal rearrangement within a substrate and therefore do not involve the addition or removal of group. These group include; (1)Epimarases which catalyse the inter-conversion of the D and L isomers.

(2) Cis and trans-isomarases which catalyse group transfer between the cis and Trans location of a substrate

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(3) mutases are enzymes which catalyse the intramolecular transfer of a group, specifically a phosphate group.

Example: Fumarate occurs as the Trans isomer while its cis form is called maleate, the enzyme that converts fumarate to malate catalyzes the hydration of the Trans double bond of fumarate but not the cis double bond of maleate (the cis isomer of fumarate). In the reverse direction (from L-malate to fumarate), fumarase is equally stereospecific: D-malate is not a substrate.

(6)LIGASES

Which brings about the formation of different types of covalent bonds to synthesize bio molecules and it requires an input of chemicaal energy which is provided by simultaneously breaking down bio molecules such as ATP. It uses energy from hydrolysis of ATP. Classes include

- (1) synthetases
- (2) synthases
- (3) carboxylases

Example:

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Because of the ever increasing number of newly discovered enzymes, biochemists, by international agreement, have adopted a system for naming and classifying enzymes in the official nomenclature every enzyme is distinctly identifiable by its formal name and by a four component number.

This system divides enzymes into six classes, each with subclasses, based on the type of reaction catalyzed.

Each enzyme is assigned a four-part classification number and a systematic name, which identifies the reaction it catalyzes .e.g Alcohol dehydrogenase in scientific report. It is identified as alcohol NAD+ oxidoreductase, (E.C.1.1.1.1.)

EC means enzyme commission, the lot 1 refers to class 1 (oxidoreductase) and the 2nd 1 refers to the type of group oxidized (1=alcohol) the 3rd 1 the oxidizing agent (1-coenzyme NAD+) and the 4th (1-alcohol dehydrogenase) because official names are often lengthy.

Properties of enzymes

- All enzymes are large and highly specialized globular proteins synthesized in cells.
- Their molecular weight generally ranges from 14000 to 400,000 Da.
- Enzymes are mostly water soluble colloids but some enzymes remain tightly bound to cell membranes.
- An enzyme is a catalyst which speeds up the rate of a specific reaction and while doing so it remains chemically unchanged and without loss of activity at the end of the reaction.
- It is to be emphasized that in an enzyme catalyzed reaction, the chemical equilibrium remains unchanged and the enzyme only speeds up the approach of this equilibrium. As such, enzymes can enhance reaction rates in cells as much as 10¹⁶ times the uncatalyzed rate.
- As stated earlier each type of enzyme has a specific 'active site conformation' that is essential for its catalytic activity.
- The 'active site conformation' includes the presence of some specific amino acid(s) at the active site besides the three dimensional structure of protein.

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- These amino acids are involved in binding of substrate and catalysis of the reaction. In addition, there are some other amino acids at the active site whose side chains help in creating microenvironments at the site.
- Thus, the function of an enzyme depends on spatial arrangement of binding sites, catalytic sites and their microenvironment.

In the process of catalysis, enzyme (E) binds substrate (S) to form enzyme-substrate (ES) complex.

- 'Lock- and- Key' hypothesis: Fischer in 1890 put forward this concept to explain that complementary structural features between E and S are responsible for the formation of ES complex (Fig. 2).
- According to this concept, the structure (or conformation) of enzyme is rigid. The substrate
 nicely fits into the active site (earlier called binding site) just as key fits into a lock. This
 model, however, failed to explain many other behavioural features of enzymes such as,
 high enzyme specificity.

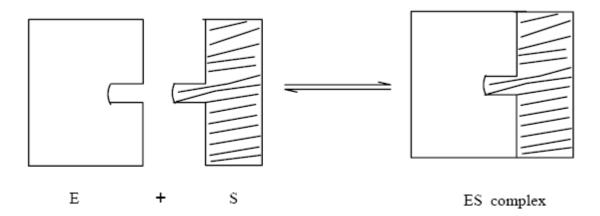


Fig. 2: Enzyme-substrate interaction after 'lock-and-key' hypothesis

'Induced- Fit' hypothesis: Koshland in 1958 suggested that the structures of E and S are complementary to each other only when they exist together in ES form, but not in their free

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existence (Fig.3).

Accordingly, during the binding of substrate to enzyme a conformational change takes place in enzyme and this allows the enzyme to make a grip around substrate. This type of mechanism helps to achieve high degree of specificity for the enzyme.

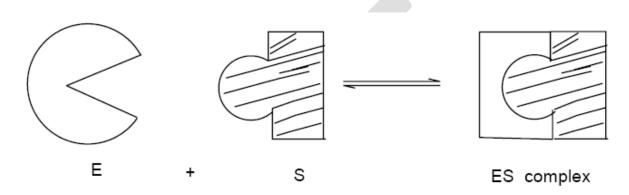


Fig. 3: Enzyme-substrate interaction after 'Induced-Fit' hypothesis

Fig. 3: Enzyme-substrate interaction after 'Induced-Fit' hypothesis

There are some enzymes which require a 'non-protein' part attached to their molecules for the activity. These are called *cofactors*.

The cofactor could be metallic ions or some small molecular weight organic molecules. The nature of binding of a cofactor with the enzyme could be either loose or very tight.

In case the binding is loose the 'non-protein' organic part is called *coenzyme*. On the other hand when binding is very tight (sometimes even covalent) then this is called *prosthetic group*. When metal ions are tightly bound to the enzyme then it is called '**metalloenzyme**'. The examples of some metalloenzymes are given in Table 2.

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Table 2: Some metalloenzymes

Name Enzyme	Metal
Carbonic anhydrase	Zinc
Phenol oxidase	Copper
Carbooxypeptidase A	Zinc
Nitrogenase	Iron and molybdenum
Xanthine oxidase	Molybdenum
Superoxide dismutase	Manganese
Glutathione peroxidase	Selenium
Alcohol dehydrogenase	Zinc
Arginase	Manganese
Ascorbic acid oxidase	Copper
Cytochrome oxidase	Iron, copper
Nitrate reductase	Vanadium
Pyruvate kinase	Potassium, magnesium
Urease	Nickel
Xanthine	Molybdenum, iron
Glutathione peroxidase	Cobalt
Creatine kinase	Manganese
Nickel hydrogenase	Nickel

A fully functional enzyme is called *holoenzyme* which is frequently constituted of a proteinpart and a non-protein part. The protein-part of enzyme is called *apoenzyme* and, as stated above, the non-protein (organic) part is coenzyme.

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Apoenzyme + coenzyme ==== Holoenzyme

- Table 3 shows the various coenzymes and prosthetic groups involved with enzymes.
- There are certain substances which modulate the activity of a holoenzyme. If the activity of enzyme is increased the substance is called *activator*.
- Generally, metal ions are involved in activation of enzyme activity.
- The activation is caused either by binding with substrate or helping in formation of effective ES-complex by bringing suitable conformational changes in enzyme protein. In addition, the metal ion may participate directly in catalytic process. Some of the enzymes requiring metal ions are listed in Table 3.
- Example of non-metal ion as activator of enzyme is that of Cl- for amylase. On the other hand, if the substance decreased the enzyme activity then it is called *inhibitor*. There are a number of substances which cause inhibition of an enzyme catalyzed reaction.

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Table 3: Cofactors, coenzymes and prosthetic groups

Cofactor	Enzyme
Mg ²⁺	Hexokinase
Ni ²⁺	Urease
Mo	Nitrate reductase
Cu ²⁺	Cytochrome oxidase
Mn ²⁺	Arginase
Zn ²⁺	Alcoholic dehydrogenase
Coenzyme	
Nicotinamide adenine dinucleotide	Alcohol dehydrogenase, Lactate
(NAD ⁺)	dehydrogenase
Thiamine pyrophosphate (TPP)	Pyruvate dehydrogenase
Flavin adenine dinucleotide (FAD)	Succinate dehydrogenase
Prosthetic group	
Pyridoxal phosphate	Amino transferases, Glycogen
	phosphorylase
Heme	Cytochrome oxidase

Active site of enzyme

- Enzyme proteins are large molecules and a very small region of the enzyme protein is involved in substrate binding and subsequent catalysis of the reaction. This region is called 'active site' or 'active centre'.
- This site contains certain amino acid residues whose side chains are in specific conformation and participate in the catalyzed reaction.
- At the end of the reaction these side chains assume their original conformation. The amino acids
- present at the active site may appear very close to each other but most often they are widely separated from each other in their location at the level of primary structure of protein.

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• The amino acids are brought close to each other due to folding of protein structure. The side chains of these amino acids are involved to form a part of the pocket located either on the surface of enzyme molecule or forming a deep opening in the enzyme (Fig. 4).

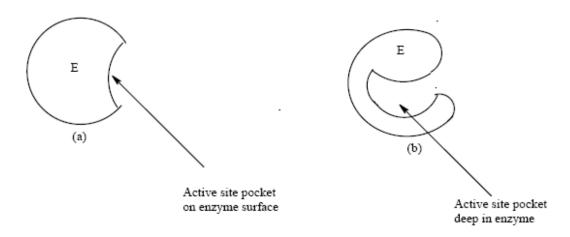


Fig. 4: Location of active sites in enzyme (a) on enzyme surface and (b) deep inside enzyme molecule

- The binding of substrate molecule at this site is facilitated by the flexible nature of this site so that an effective ES-complex is formed.
- The cofactors or coenzymes which are present at the active site facilitate the formation of ES-complex and subsequent catalysis.
- The binding of substrate to enzyme at the active site is due to weak interactions (non-covalent bonds) between the two. The amino acids that are generally involved at the active site for substrate binding and catalysis in various enzymes are cysteine, serine, histidine, aspartate, glutamate, tyrosine, arginine, lysine, etc.

Unit of enzyme activity

• The activity of an enzyme catalyzed reaction is defined in some quantity which indicates an estimate of the rate of that reaction. Thus, activity is expressed as units in many ways because measurement of number of enzyme molecules or its mass is difficult.

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• According to International Commission on Enzymes, 'One International Unit' of enzyme is defined as the amount of enzyme protein that catalyzes formation of one micromole of product in one minute under the conditions of assay (pH, temperature and ionic strength).

- Another definition of unit is in Katal. One Katal is that amount of enzyme which catalyzes
 the conversion of one mole of substrate into product in one second under the experimental
 conditions.
- Arbitrary Unit has a definition and according to which it is that amount of enzyme which transforms one micromole or nano mole or pico mole of substrate into product per minute under the assay conditions.
- However, when enzyme activities are expressed in units as per these definitions then sometimes it is difficult to compare the activities of various enzymes. This becomes relatively a lot easier when activity unit is expressed as specific activity.
- Accordingly, the specific activity is activity units per mg protein i.e. specific activity of enzyme
- A general agreement on expression of specific activity is micromoles per min per mg protein.

Turnover number: When enzyme is fully saturated with substrate then number of substrate molecules converted into product in unit time by one molecule of enzyme is called *turnover over number* (kcat). This is also referred to as 'molecular activity'.

Isoenzymes

- In a number of organisms the existence of different molecular forms of an enzymic protein catalyzing same reaction has been shown. These are called *isoenzymes* or *isozymes*.
- The presence of these isozymes in different organs of an organism suggests the different roles of these enzymic proteins. For example, lactate dehydrogenase (LDH) present in

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different human tissues has five isozymic forms. These forms are commonly separated by gel electrophoresis in five different bands.

• Every band catalyzes the same reaction and these five forms are known as LDH1, LDH2, LDH3, LDH4 and LDH5. These proteins vary in their quaternary structure. All these forms are tetrameric proteins. Two different types of subunits, called H and M are present in variable numbers in each case. There are separate genes for the synthesis of H and M subunits. The relative predominance of these two forms varies in different tissues. For example, H subunits predominate in heart while M subunits predominate in liver and skeletal muscle. The five isozymic forms have the composition as H4, MH3, M2H2 and M3H and M4.

There are enzymes having only one polypeptide unit as structural entity and there are enzymes having more than one polypeptide units. These are named accordingly as;

- **Monomeric enzymes:** If an enzyme is made up of a single polypeptide unit it is called monomeric enzyme.
- Oligomeric enzymes: These enzymes having quaternary structure are made up of two or more polypeptide chains which are linked to each other by non-covalent interactions. These proteins are also called *multimeric* proteins having high molecular weight (usually more than 40,000 Da) and their component polypeptides are called *subunits*.
- All regulatory enzymes are oligomeric enzymes showing the property of *allosteric* regulation.
- If these enzymes are made up of single type of monomer subunits, they are called *homooligomers*.

When subunits are of different kinds then they are termed *hetero-oligomers*. Most of the oligomeric enzymes are made up of either 2 or 4 subunits. The following are examples of some exceptions:

- (i) Glutamine synthetase in *E. coli* has 12 identical subunits.
- (ii) Aspartate transcarbamoylase has two types of subunits in 6+6 numbers.

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Difference between catalysed and uncatalysed reaction:

How enzymes help to increase the reaction rate to such a level by functioning as catalyst could be explained with the help of Fig. 1 which illustrates the energy changes that take place during the conversion of reactants into products.

- The equilibrium of such a reaction is determined by the energy states of reactants and products. These energy states remain unaffected by enzyme action. If the reaction has to proceed then the reactants (or substrate) must be brought to a higher energy level (or state), which is called *transition state*.
- The amount of energy required to bring the substrate to transition state is called *energy of activation*.
- This energy acts as a barrier for the progress of the reaction, thereby limiting the rate of the
- reaction. Catalysts (including enzymes) function by bringing down the activation energy and
- hence increase the rate of reaction.
- The rate of catalyzed reaction both in forward and reverse direction remains same because both these rates have to undergo through same transition state.

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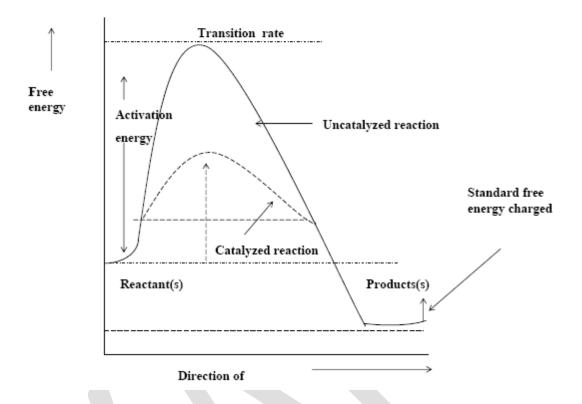


Fig. 1: Need for energy in case of uncatalyzed and enzyme catalyzed reactions

The enzyme catalyzed reactions involve binding of substrate(s) to enzyme (E) at the specific site, called *active site*, to form enzyme substrate complex (ES). This interaction lowers the energy of activation and facilitates formation of new transition state (Fig. 1 broken curve). The substrate while bound to enzyme is converted into product and then released from enzyme. This whole process is represented by following equation:

- Each enzyme is very specific in its function though it is generally depicted by the above equation.
- There are three types of enzyme specificities viz., substrate, stereo chemical and reaction specificity.

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• The extent of substrate specificity varies from enzyme to enzyme.

What are Enzymes, Coenzymes and Cofactors?

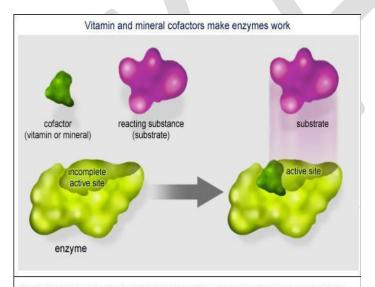
Enzymes are large biological molecules responsible for thousands of metabolic processes that sustain life.

They are highly selective catalyst, greatly accelerating both the rate and specificity of metabolic reactions.

Some enzymes require no chemical groups for activity other than their amino acid residues. Other requires an additional chemical component called a **cofactor** for the required activity.

A **cofactor** is a non-protein chemical compound that is required for the protein's biological activity. These proteins are commonly enzymes, and cofactors can be considered "helper molecules" that assist in biochemical transformations.

Cofactors can be divided into two broad groups: **organic cofactors**, such as flavin or heme, and **inorganic cofactors**, such as the metal ions Mg²⁺, Cu⁺, Mn²⁺, or iron-sulfur clusters.



Many enzymes need a cofactor (vitamin or mineral) to activate them. Without the cofactor, the enzyme can't lock the reacting substance (substrate) into its active site, so the reaction can't take place. Most vitamin deficiency diseases happen this way.

Inorganic cofactor - Metal Ions

Ion	Examples of enzymes containing this
Cupric	Cytochrome oxidase
Ferrous or Ferric	Catalase Cytochrome (via Heme) Nitrogenase Hydrogenase

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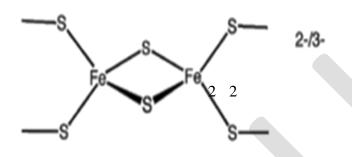
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Magnesium

Glucose 6-phosphatase

Hexokinase

DNA polymerase



A simple [Fe S] cluster containing two iron atoms

and two sulfur atoms, coordinated by four protein cysteine residues.

Organic cofactor

□ □ □ Organic cofactors are small organic molecules (typically a molecular mass less than 1000 Da) that can be either loosely or tightly bound to the enzyme and directly participate in the reaction.

Cofactor	Vitamin	Additiona l componen	Chemical group(s) transferre d	Distribution
NAD ⁺ and NADP ⁺	Niacin (B3)	ADP	Electrons	Bacteria, archaea and eukaryotes

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Coenzyme A	Pantotheni c acid(B5)	ADP	Acetyl group and other	Bacteria, archaea andeukaryotes
Ascorbic acid	Vitamin C	None	Electrons	Bacteria, archaea andeukaryotes
Flavin mononucleotide	Riboflavin (B2)	None	Electrons	Bacteria, archaea andeukaryotes

Coenzyme

- > loosely bound cofactors termed **coenzymes**
- Any of a number of freely diffusing organic compounds that function as cofactors with enzymes in promoting a variety of metabolic reactions.
- ➤ Coenzymes are a type of cofactor and they are bound to enzyme's active sites to aid with their proper functioning.
- > Coenzymes which are directly involved and altered in the course of chemical reactions are considered to be a type of secondary substrate.

Coenzymes as vitamins

	Many coenzymes are closely related to vitamins. Some of them are important growtl
fa	actors.
	Coenzymes are the precursors of vitamins.
	A vitamin is a main component of an coenzyme endowed with bio catalytic functions.
□ □ Coer	nzymes involved in transfer of hydrogens are called hydrogen transferring enzymes
and tho	se which transfer a specific group are known as group transferring coenzymes.

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Coenzymes in Hydrogen transfer reaction

❖ Nicotinamide nucleotide

> These coenzyme involved in hydrogen transfer reaction and form essential components of dehydrogenase.

Biochemical function

- ➤ These NAD+ and NADP are coenzymes of a number of dehydrogenases catalyzing oxidation-reduction reaction.
- ➤ All reaction catalyzed by them reversible

Coenzymes involved in group transfer

* BIOTIN

biotin is a coenzyme belonging to vitamin B2 group which is an essential growth factor for yeast and other microorganism, but is also required by higher organism.

Biochemical function

Biotin is a water soluble vitamin and participate in transfer of carboxyl group.

Role of coenzyme

- The function of coenzymes is to transport groups between enzymes.
- > Chemical groups include hydride ions which are carried by coenzymes such as NAD,
- phosphate groups which are carried by coenzymes such as ATP
- acetyl groups which are carried by coenzymes such as coenzyme A.

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➤ Coenzymes which lose or gain these chemical groups in the course of the reaction are often reformed in the same metabolic pathway.

For example NAD+ used in glycolysis and the citric acid cycle is replaced in the electron transport chain

Function of coenzyme

- The coenzyme is essential for the biological activity of the enzyme.
- A coenzyme is a low molecular weight organic substance, without which the enzyme cannot exhibit any reaction.
- ➤ One molecule of the coenzyme is able to convert a large number of substrate molecules with the help of enzyme.

Salient features of coenzyme

- ➤ Coenzymes are heat stable.
- > They are low-molecular weight substances.
- The coenzymes combine loosely with the enzyme molecules and so, the coenzyme can be separated easily by dialysis.
- ➤ When the reaction is completed, the coenzyme is released from the apo-enzyme, and goes to some other reaction site.

Important coenzyme

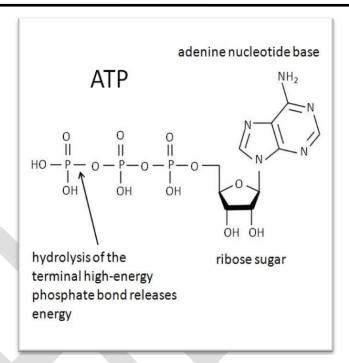
- **❖** Alcohol dehydrogenase
- **❖** Coenzyme A
- **❖** Flavin adenine dinucleotide (FAD)
- **❖** Nicotinamide adenine dinucleotide (NAD)
- **❖** Adenosine triphosphate (ATP)

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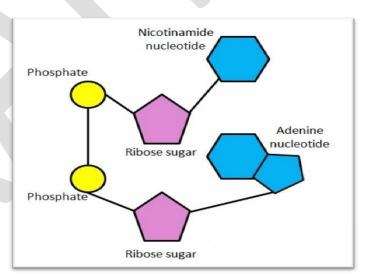
Adenosine triphosphate (ATP)

- The function of ATP is to transport chemical energy within cells for metabolism.
- ➤ ATP is often referred to as the energy currency of cells.
- Adenosine triphosphate is composed of an adenine nucleotide base, a ribose sugar and three phosphate groups.
- > Energy can be released from ATP when the terminal phosphate group is released in a hydrolysis reaction. This is because the energy of ATP is held in the bonds between the phosphate groups and when the broken bonds are it accompanied by a release of energy.



Nicotinamide adenine dinucleotide (NAD)

- NAD is composed of two nucleotides, adenine and nicotinamide.
- The nucleotides are held together by a pair of phosphate groups which act as a bridge and are also bonded to a ribose sugar each.



- > The function of NAD is to carry electrons from one enzyme controlled reaction to another.
- NAD is involved with redox reactions because substrates are either oxidized, in which they lose electrons or are reduced in which they gain electrons.
- NAD is either found as NAD+, which is an oxidizing agent and is involved with

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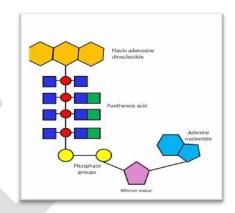
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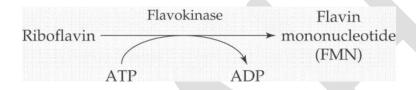
accepting electrons from other molecules.

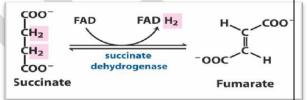
NADH which is used as a reducing agent to donate electrons to other molecule

Flavin adenine dinucleotide (FAD)

- FAD is composed of an adenine nucleotide, a ribose sugar and two phosphate groups.
- FAD can also exist as a monophosphate and is called flavin adenine monophosphate (FMN).
- > FAD is involved with redox reactions.
- ➤ like NAD, FAD can exist in two redox states FAD and FADH.

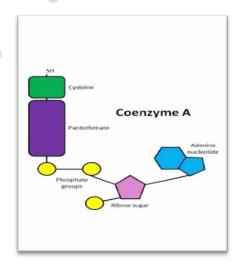






Coenzyme A

- Coenzyme A is a prominent coenzyme of living organism which transfers the acyl group of carboxylic acid.
- ➤ It plays an important role in the metabolism of proteins, carbohydrates and fats which are important reactions that allow the energy from food to be released. For example coenzyme A is required for the oxidation of pyruvate in the citric acid cycle.
- ➤ Coenzyme A is also important in the synthesis of cholesterol and steroid hormones, and is required for the detoxification of a range of harmful drugs that can accumulate in the liver.



Alcohol dehydrogenase

➤ Alcohol dehydrogenase (ADH) is an enzyme

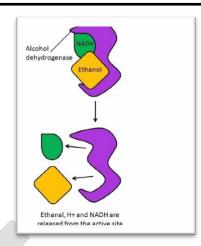
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which uses NAD+ as a coenzyme.

ADH has two binding regions, one where the primary substrate, ethanol binds and one where the coenzyme, NAD+ is able to bind.

The enzyme is responsible for the conversion of ethanol to ethanal. The reaction is an oxidation-reduction reaction and results in the removal of two hydrogen ions and two electrons from ethanol. The hydrogen ions and electrons are added to NAD+ which converts the coenzyme to NADH + H+. This is the first reaction involved with the metabolism of ethanol.

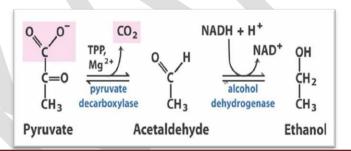


<u>Vitamin B₁ – Thiamine</u>

The active form is thiamin pyrophosphate (TPP)

- Thiamin is rapidly converted to thiamin pyrophosphate (TPP) in small intestine, brain and liver.
- TPP is formed from thiamin by the action of thiamine diphosphotransferase.
- TPP coenzyme is required by enzymes in the decarboxylation of \Box -keto acids.
- Entity Transferred; Aldehydes

TPP as co-enzymes



Pyridoxal Phosphate

PLP is Derivative of Pyridoxine (Vit. B6) involved in.

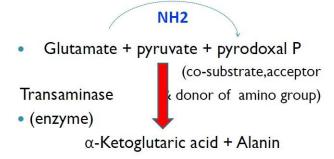
- 1. Transamination reactions required for the synthesis and catabolism of the amino acids.
- 2. Decarboxylation reactions.
- 3. Entity Transferred; Amino Groups(-NH₂)

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Example of co-enzyme in amino acid metabolism



The Two Parts of Photosynthesis Photosystem I and II

Light-dependent and light-independent reactions are two successive reactions that occur during photosynthesis.

Photosynthesis takes place in two sequential stages:

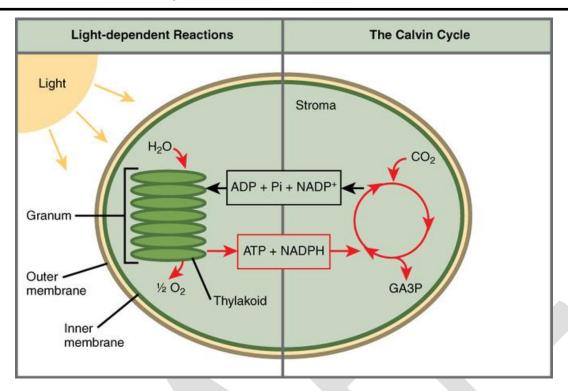
- 1. The light-dependent reactions;
- 2. The light-independent reactions, or Calvin Cycle.

Light-Dependent Reactions

Just as the name implies, light-dependent reactions require sunlight. In the light-dependent reactions, energy from sunlight is absorbed by chlorophyll and converted into stored chemical energy, in the form of the electron carrier molecule NADPH (nicotinamide adenine dinucleotide phosphate) and the energy currency molecule ATP (adenosine triphosphate). The light-dependent reactions take place in the thylakoid membranes in the granum (stack of thylakoids), within the chloroplast.

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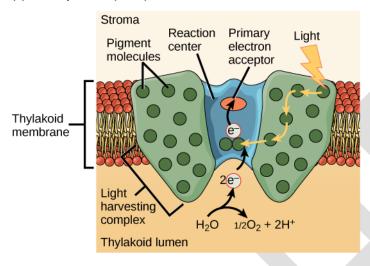
The two stages of photosynthesis: Photosynthesis takes place in two stages: light-dependent reactions and the Calvin cycle (light-independent reactions). Light-dependent reactions, which take place in the thylakoid membrane, use light energy to make ATP and NADPH. The Calvin cycle, which takes place in the stroma, uses energy derived from these compounds to make GA3P from CO2.

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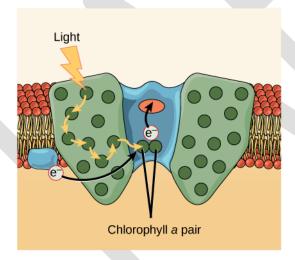
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Photosystems

(a) Photosystem II (P680)



(b) Photosystem I (P700)



Photosystems I & II: As explained above, the photosystems manipulate electrons with energy harvested from light.

The process that converts light energy into chemical energy takes place in a multi-protein complex called a photosystem. Two types of photosystems are embedded in the thylakoid membrane:

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photosystem II (PSII) and photosystem I (PSI). Each photosystem plays a key role in capturing the energy from sunlight by exciting electrons. These energized electrons are transported by "energy carrier" molecules, which power the light-independent reactions.

Photosystems consist of a light-harvesting complex and a reaction center. Pigments in the light-harvesting complex pass light energy to two special chlorophyll a molecules in the reaction center. The light excites an electron from the chlorophyll a pair, which passes to the primary electron acceptor. The excited electron must then be replaced. In photosystem II, the electron comes from the splitting of water, which releases oxygen as a waste product. In photosystem I, the electron comes from the chloroplast electron transport chain.

The two photosystems oxidize different sources of the low-energy electron supply, deliver their energized electrons to different places, and respond to different wavelengths of light.

Light-Independent Reactions

In the light-independent reactions or Calvin cycle, the energized electrons from the light-dependent reactions provide the energy to form carbohydrates from carbon dioxide molecules. The light-independent reactions are sometimes called the Calvin cycle because of the cyclical nature of the process.

Although the light-independent reactions do not use light as a reactant (and as a result can take place at day or night), they require the products of the light-dependent reactions to function. The light-independent molecules depend on the energy carrier molecules, ATP and NADPH, to drive the construction of new carbohydrate molecules. After the energy is transferred, the energy carrier molecules return to the light-dependent reactions to obtain more energized electrons. In addition, several enzymes of the light-independent reactions are activated by light.

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UNIT IV

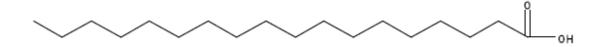
Lipids : Structure and functions –Classification, nomenclature and properties of fatty acids, essential fatty acids. Phospholipids, sphingolipids, glycolipids, cerebrosides, gangliosides, Prostaglandins, Cholesterol. β-oxidation of fatty acids.

Lipids

Lipids

Biomolecules that have the common property of being soluble in organic (nonpolar) solvents, but not in water.

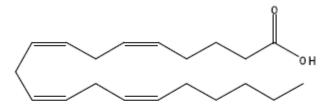
Fatty Acids – most lipids contain fatty acids (the simplest type of lipids) in their structures. They are carboxylic acids with an even number of carbon atoms, usually between 10 and 20 (memorize their common names).



Prostaglandins are formed from arachidonic acid (*all-cis-5*,8,11,14-eicosatetraenoic acid), which is an unsaturated fatty acid with 20 carbons. These hormone like substances increase or lower the blood pressure, inflammation and pain when tissues are injured. Prostaglandins are potent but have a short half-life before being inactivated and excreted. Therefore, they exert only a paracrine (locally active) or autocrine (acting on the same cell from which it is synthesized) function.

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- *Lipids* are naturally occurring molecules from plants or animals that are soluble in nonpolar organic solvents.
- Lipid molecules contain large hydrocarbon portion and not many polar functional group, which accounts for their solubility behavior.

FATTY ACIDS (FAs)

two major physiological roles:

- (i) building blocks of phospholipids and glycolipids in biological membranes
- (ii) fuel molecules

CLASSIFICATION OF FAS

- According to the chain length
- short-chain fatty acid SCFA < 6 carbon atoms
- medium-chain fatty acid MCFA 6-12 carbon atoms
- long-chain fatty acid LCFA 14-20 carbon atoms
- very-long chain fatty acid VLCFA > 20 carbon atoms
- According to the degree of saturation (presence or absence of double bonds)
- saturated
- unsaturated cis/trans isomers

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Name	Туре	Number of carbon atoms	Number of double bonds	Symbol
Palmitic acid	Saturated	16	0	16:0
Stearic acid	Saturated	18	0	18:0
Oleic acid	Monounsaturated	18	1	18:1n-9
α-linolenic acid (ALA)	ω-3 polyunsaturated	18	3	18:3n-3
Eicosapentaenoic acid (EPA)	ω-3 polyunsaturated	20	5	20:5n-3
Docosapentaenoic acid (DPA) n-3	ω-3 polyunsaturated	22	5	22:5n-3
Docosahexaenoic acid (DHA)	ω-3 polyunsaturated	22	6	22:6n-3
Linoleic acid (LNA)	ω-6 polyunsaturated	18	2	18:2n-6
DPA n-6	ω-6 polyunsaturated	22	5	22:5n-6
Arachidonic acid (ARA)	ω-6 polyunsaturated	20	4	20:4n-6

UNSATURATED: with one double bond: + *enoic*

e.g. C18: Octadecenoic acid

• with two double bonds: + *dienoic*

e.g.C18: Octadecadienoic acid

• with three double bonds: + *trienoic*

e.g. C18: Octadecatrienoic acid

Most common in animal and plant fats

Less easily digestible

Common name Systematic name Formula

C14:0 Myristic acid Tetradecanoic acid CH3(CH2)12COOH

C16:0 Palmitic acid Hexadecanoic acid CH3(CH2)14COOH

C18:0 Stearic acid Octadecanoic acid CH3(CH2)16COOH

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C20:0 Arachidic acid Eicosanoic acid CH3(CH2)18COOH

MONOUNSATURATED FAs

16:1(9) Palmitooleic a. cis-9-Hexadecenoic acid

18:1(9) Oleic a. cis-9-Octadecenoic acid

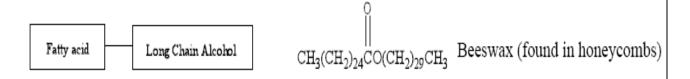
18:1(9) Elaidic a. trans-9-Octadecenoic acid

22:1(13) Erucic a. cis-13-Docosenoic acid

Classification of Lipids

Lipids are classified as follows:

- 1. Simple lipids: Esters of fatty acids with various alcohols.
- (a) Fats: Esters of fatty acids with glycerol. Oils are fats in the liquid state.
- (b) Waxes: are carboxylic acid esters where both R groups are long straight hydrocarbon chain. Performs external protective functions.



- The leaves and fruits of many plants have waxy coatings, which may protect them from dehydration and small predators. The feathers of birds and the fur of some animals have similar coatings which serve as a water repellent.
- Waxes are also used in wax polishes for furniture and other wood products, footwear and vehicles, as mold release agents in mold making, as a coating for Edam and Gouda cheeses, and to waterproof leather and fabric.
- 2. Complex lipids: Esters of fatty acids containing groups in addition to an alcohol and a fatty acid.

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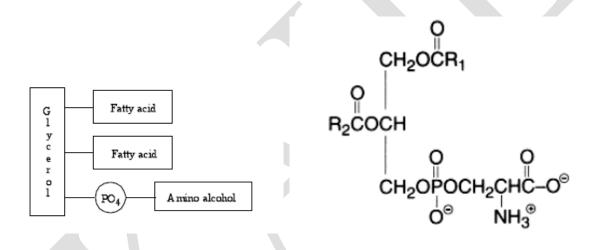
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• *Triacylglycerol* – are carboxylic acid triesters of glycerols. They are a major source of biochemical energy.

• *Glycerophopholipids* - triesters of glycerols that contain charged phosphate diesters. They help to control the flow of molecules into and out of cells.

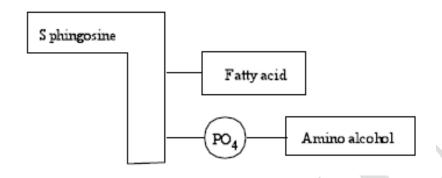
Glycerophospholipids (or phospholipids) are a family of lipids similar to TAG's except that one hydroxyl group of glycerol is replaced by the ester of phosphoric acid and an amino alcohol, bonded through a phosphodiester bond. Depending on the amino alcohol, these can be **Lecithins** (containing choline) or **Cephalines** (containing ethanolamine or serine). These are the most abundant lipids in cell membranes.



• *Sphingomyelins* – amides derived from an amino alcohol, also contain charged phosphate diester groups. They are essential to the structure of cell membranes.

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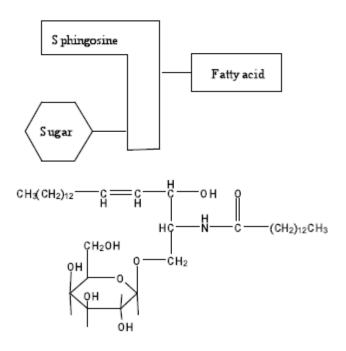


• *Glycolipids* – amides derived from sphingosine, contain polar carbohydrate groups. On the cell surface, they connect with by intracellular messengers.

Glycosphingolipids. **Cerebrosides** contain a monosaccharide and **Gangliosides** are similar, but they contain two or more monosaccharides.

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3. Precursor and derived lipids: These include fatty acids, glycerol, steroids, other alcohols, fatty aldehydes, and ketone bodies, hydrocarbons, lipidsoluble vitamins, and hormones. Because they are uncharged, acylglycerols (glycerides), cholesterol, and cholesteryl esters are termed neutral lipids.

Lipids that are not esters or amides:

Steroids – They performs various functions such as hormones and contributes to the structure of cell membranes.

Eicosanoids – They are carboxylic acids that are a special type of intracellular chemical messengers.

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This is one of the most important and abundant steroids in the body.

Fatty Acids

Fatty acids can be said to be carboxylic acids, and come in two major varieties.

□ Saturated fatty acids do not have any double bonds. A fatty acid is saturated when every carbon atom in the hydrocarbon chain is bonded to as many hydrogen atoms as possible (the carbon atoms are saturated with hydrogen). Saturated fatty acids are solids at room temperature. Animal fats are a source of saturated fatty acids. In addition, fatty acids pack easily and form rigid structures (e.g., fatty acids are found in membranes).

Unsaturated fatty acids can have one or more double bonds along its hydrocarbon chain. A fatty acid with one double bond is called monounsaturated. If it contains two or more double bonds, we say that the fatty acid is polyunsaturated. The melting point of a fatty acid is influenced by the number of double bonds that the molecule contains and by the length of the hydrocarbon tail. The more double bonds it contains, the lower the melting point. As the length of the tail increases, the melting point increases. Plants are the source of unsaturated fatty acids

$$-CH = CH - CH = CH -$$

Unsaturated fatty acid chain

Saturated fatty acid chain

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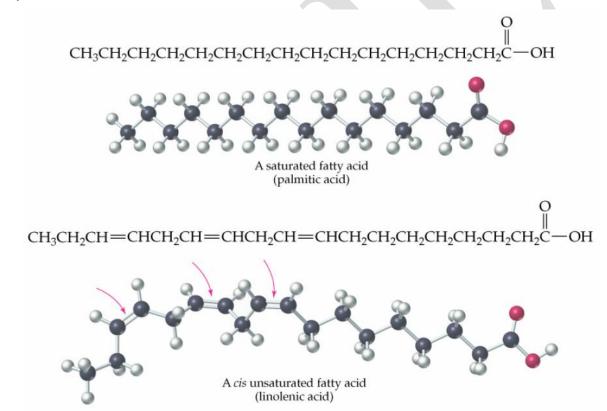
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Aliphatic chain showing structure of unsaturated fatty acid chain with double bonds and saturated fatty acid chain with single bonds.

Properties of Fats and Oils

Oils: A mixture of triglycerols that is liquid because it contains a high proportions of unsaturated fatty acids.

Fats: A mixture of triglycerols that is solid because it contains a high proportions of saturated fatty acids.



Properties of triglycerols in natural fats and oils:

- Nonpolar and hydrophobic
- No ionic charges
- Solid triglycerols (Fats) high proportions of saturated fatty acids.

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• Liquid triglycerols (Oils) - high proportions of unsaturated fatty acids.

Chemical Reactions of Triglycerols

Hydrogenation: The carbon-carbon double bonds in unsaturated fatty acids can be hydrogenated by reacting with hydrogen to produce saturated fatty acids. For example, margarine is produced when two thirds of the double bonds present in vegetable oil is hydrogenated.

Hydrolysis of triglycerols: Triglycerols like any other esters react with water to form their carboxylic acid and alcohol – a process known as hydrolysis. - In body, this hydrolysis is catalyzed by the enzyme hydrolase and is the first step in the digestion of dietary fats and oils.

- In the laboratory and commercial production of soap, hydrolysis of fats and oils is usually carried out by strong aqueous bases such as

NaOH and KOH and is called saponification.

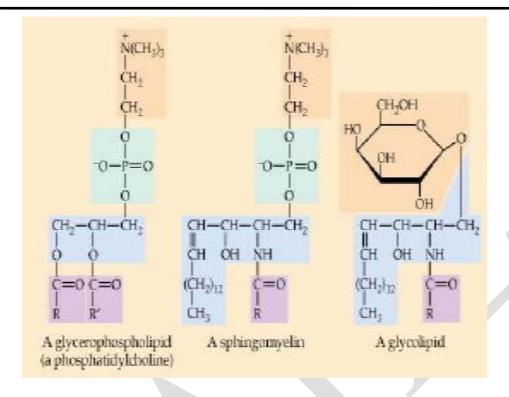
Cell Membrane Lipids:

Phosphilipids and Glycolipids

- Cell membranes establish a hydrophobic barrier between the watery environment in the cell and outside the cell. Lipids are ideal for this function.
- The three major kinds of cell membrane lipids in animals are *phospholipids*, *glycolipids*, and *cholesterol*.

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- Phosphoilipids contain an ester link between a phosphoric acid and an alcohol. The
 alcohol is either a glycerol to give a glycerophopholipid or a sphingosine to give
 sphingomyelins.
- Glycolipids: Glycolipids are derived from sphingosine. They differ from sphingomyelins by having a carbohydrate group at C1 instead of a phosphate bonded to a choline.

Cell Membrane Lipids:

Cholesterol

Animal cell membranes contain significant amount of cholesterol.

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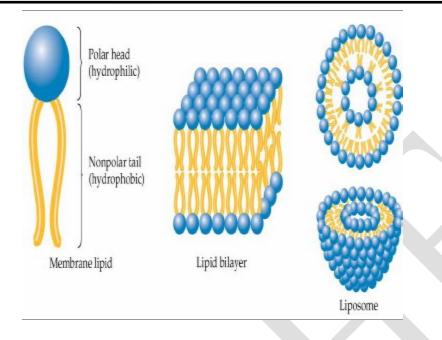
- Cholesterol is a steroid, a member of the class of lipids that all contain the same four ring system.
- Cholesterol serves two important purposes: as a component of cell membranes and as a starting materials for the synthesis of all other steroids.

Structure of Cell Membranes

The basic structural unit of cell membrane is lipid bilayer which is composed of two parallel sheets of membrane lipid molecules arranged tail to tail. Bilayers are highly ordered and stable, but still flexible.

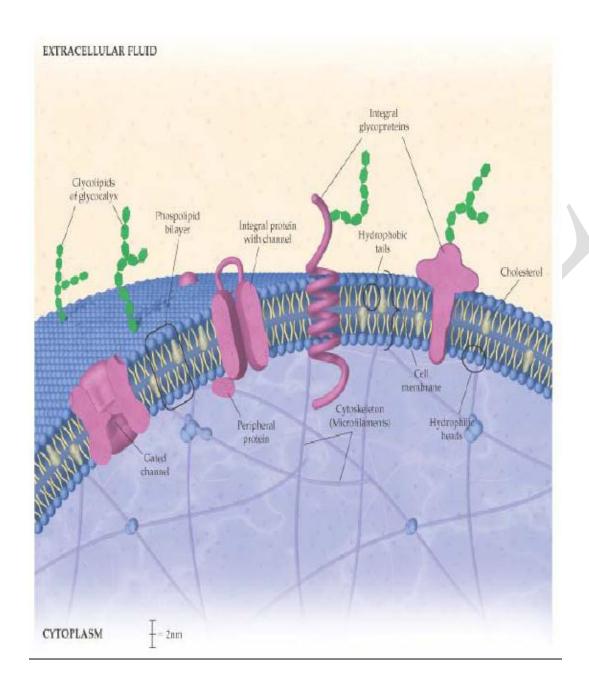
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When phospholipids are shaken vigorously with water, they spontaneously form liposome – small spherical vesicle with lipid bilayer surrounding an aqueous center. Water soluble substances can be trapped in the center of the liposome, and lipid-soluble substances can be incorporated into the bilayer.

Transport Across Cell Membranes

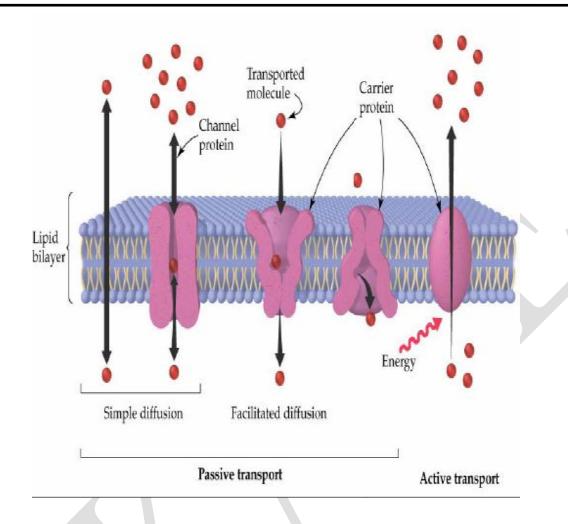
The cell membranes allow the passage of molecules and ions into and out of a cell by two modes; passive transportation and active transportation.

• *Passive transport* – substances move across the cell membrane freely by diffusion from regions of higher concentration to regions of lower concentration. Glucose is transported into many cells in this way.



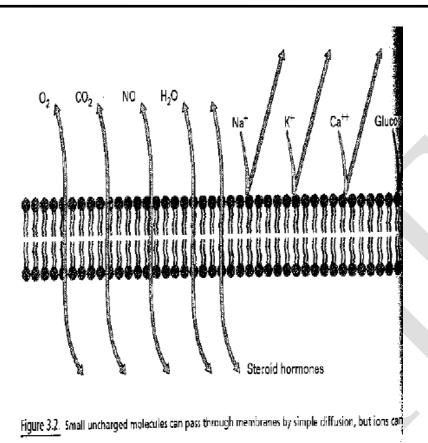
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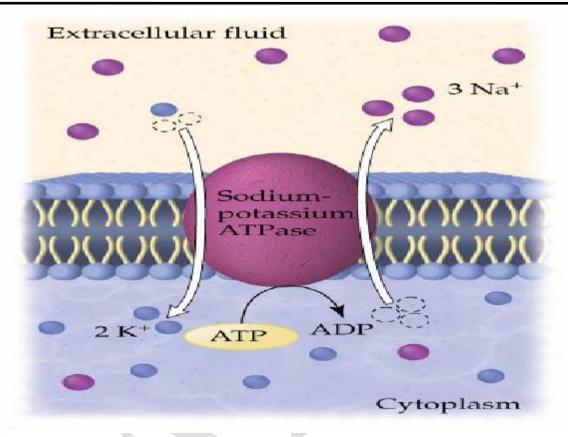
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Active transport - substances move across the cell membrane only when energy is supplied because they must go in the reverse direction from regions of lower to regions of higher concentration. Only by this method, cells maintain lower Na+ concentration within cells and higher Na+ concentration in extracellular fluids, with the opposite concentration ratio for K+.

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Properties of cell membranes:

- Cell membranes are composed of a fluid like phospholipid bilayer.
- The bilayer incorporates cholesterol, proteins, and glycolipids.
- Small nonpolar molecules cross by diffusion through the lipid bilayer.
- Small ions and polar molecules diffuse through the aqueous media in protein pores.
- Glucose and certain other substances cross with the aid of proteins without energy input.
- Na+, K+, and other substances that maintain concentration gradients inside and outside the cell cross with expenditure of energy and the aid of proteins.

OXIDATION OF FATTY ACIDS

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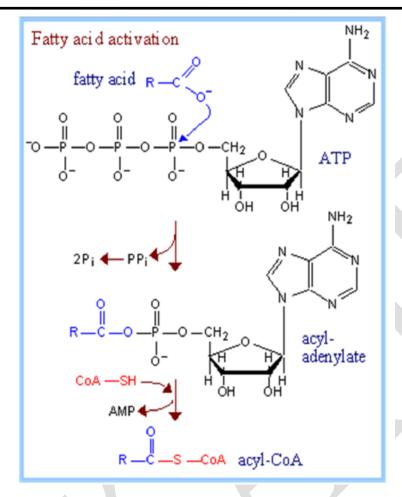
Although fatty acids are both oxidized to acetyl-CoA and synthesized from acetyl-CoA, fatty acid oxidation is not the simple reverse of fatty acid biosynthesis but an entirely different process taking place in a separate compartment of the cell. The separation of fatty acid oxidation in mitochondria from biosynthesis in the cytosol allows each process to be individually controlled and integrated with tissue requirements. Each step in fatty acid oxidation involves acyl-CoA derivatives catalyzed by separate enzymes, utilizes NAD+ and FAD as coenzymes, and generates ATP. It is an aerobic process, requiring the presence of oxygen.

OXIDATION OF FATTY ACIDS OCCURS IN MITOCHONDRIA

Fatty acids must first be converted to an active intermediate before they can be catabolized. This is the only step in the complete degradation of a fatty acid that requires energy from ATP. In the presence of ATP and coenzyme A, the enzyme **acyl-CoA synthetase** (**thiokinase**) catalyzes the conversion of a fatty acid (or free fatty acid) to an "active fatty acid" or acyl-CoA, which uses one high-energy phosphate with the formation of AMP and Ppi

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Long-Chain Fatty Acids Penetrate the Inner Mitochondrial Membrane as Carnitine Derivatives

Carnitine is widely distributed and is particularly abundant in muscle. Long-chain acyl-CoA (or FFA) will not penetrate the inner membrane of mitochondria. However, **carnitine palmitoyltransferase-I**, present in the outer mitochondrial membrane, converts long-chain acyl-CoA to acylcarnitine, which is able to penetrate the inner membrane and gain access to the β -oxidation system of enzymes (Figure 22–1). **Carnitine-acylcarnitine translocase** acts as an inner membrane exchange transporter. Acylcarnitine is transported in, coupled with the transport out of one molecule of carnitine. The acylcarnitine then reacts with CoA, catalyzed by **carnitine palmitoyltransferase-II**, located on the inside of the inner membrane. Acyl-CoA is reformed

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in the mitochondrial matrix, and carnitine is liberated.

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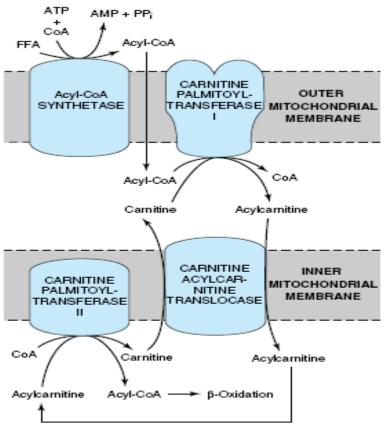


Figure 22-1. Role of carnitine in the transport of long-chain fatty acids through the inner mitochondrial membrane. Long-chain acyl-CoA cannot pass through the inner mitochondrial membrane, but its metabolic product, acylcarnitine, can.

β-OXIDATION OF FATTY ACIDS INVOLVES SUCCESSIVE CLEAVAGE WITH RELEASE OF ACETYL-CoA

In β -oxidation (Figure 22–2), two carbons at a time are cleaved from acyl-CoA molecules, starting at the carboxyl end. The chain is broken between the $\alpha(2)$ - and $\beta(3)$ -carbon atoms—hence the name β -oxidation. The two-carbon units formed are acetyl-CoA; thus, palmitoyl- CoA forms eight acetyl-CoA molecules.

The Cyclic Reaction Sequence Generates FADH2 & NADH

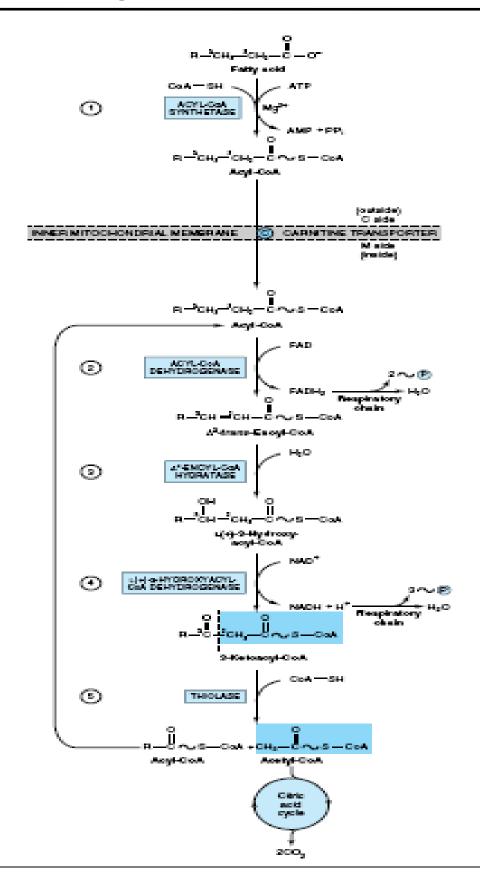
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- Several enzymes, known collectively as "fatty acid oxidase," are found in the mitochondrial matrix or inner membrane adjacent to the respiratory chain. These catalyze the oxidation of acyl-CoA to acetyl-CoA, the system being coupled with the phosphorylation of ADP to ATP (Figure 22–3).
- The first step is the removal of two hydrogen atoms from the $2(\alpha)$ and $3(\beta)$ -carbon atoms, catalyzed by **acyl-CoA dehydrogenase** and requiring FAD. This results in the formation of $\Delta 2$ -trans-enoyl-CoA and FADH2. The reoxidation of FADH2 by the respiratory chain requires the mediation of another flavoprotein, termed **electron-transferring flavoprotein.**
- Water is added to saturate the double bond and form 3-hydroxyacyl-CoA, catalyzed by _2-enoyl-CoA hydratase. The 3-hydroxy derivative undergoes further dehydrogenation on the 3-carbon catalyzed by L(+)-3- hydroxyacyl-CoA dehydrogenase to form the corresponding 3-ketoacyl-CoA compound. In this case, NAD+ is the coenzyme involved.
- Finally, 3-ketoacyl- CoA is split at the 2,3- position by **thiolase** (3-ketoacyl- CoAthiolase), forming acetyl-CoA and a new acyl- CoA two carbons shorter than the original acyl-CoA molecule. The acyl-CoA formed in the cleavage reaction reenters the oxidative pathway at reaction 2 (Figure 22–3).
- In this way, a long-chain fatty acid may be degraded completely to acetyl-CoA (C2 units). Since acetyl-CoA can be oxidized to CO2 and water via the citric acid cycle (which is also found within the mitochondria), the complete oxidation of fatty acids is achieved.

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Beta - oxidation of fatty acids

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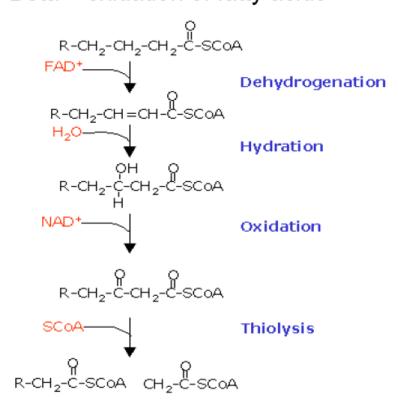
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Beta – oxidation of fatty acids

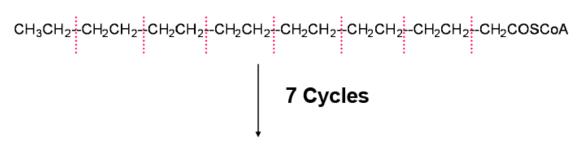
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Beta – oxidation of fatty acids



Complete Beta Oxidation of Palmitoyl CoA



8 CH₃COSCoA + 7 FADH₂ + 7 NADH + 7 H⁺

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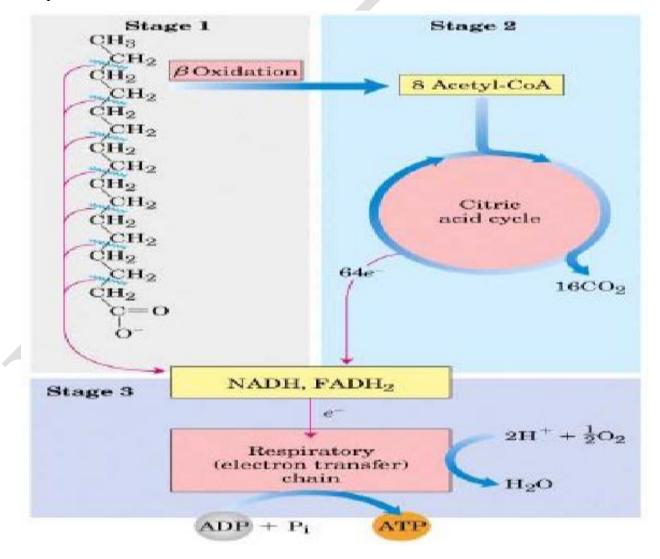
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For example for a 16 carbon fatty acid, Palmityl-CoA, it will take 7

cycle of β-oxidation to generate 8 acetyl-CoA.

Thus there will be production of 7 FADH2, 7 NADH molecules during the β -oxidation cycles.

Oxidation of 8 acetyl-CoA in TCA cycle will produce 8 ATPs, 8 FADH2, 24 NADH



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Though it produces more energy, it does not directly produce ATP during the oxidation steps(no substrate level phosphorylation)

β-Oxidation yields Acetyl CoA,NADH & FADH,requiring TCA cycle and Respiratory chain for further metabolism

TCA cycle and Respiratory chain requires O2

So Fatty acid cannot be used as an energy source in the absence of O2

Oxidation of a Fatty Acid With an Odd Number of Carbon Atoms Yields Acetyl- CoA Plus a Molecule of Propionyl-CoA

Fatty acids with an odd number of carbon atoms are oxidized by the pathway of β -oxidation, producing acetyl- CoA, until a three-carbon (propionyl-CoA) residue remains.

This compound is converted to succinyl-CoA, a constituent of the citric acid cycle. Hence, the propionyl residue from an odd-chain fatty acid is the only part of a fatty acid that is glucogenic.

Oxidation of Fatty Acids Produces a Large Quantity of ATP

Transport in the respiratory chain of electrons from FADH2 and NADH will lead to the synthesis of five high-energy phosphates for each of the first seven acetyl-CoA molecules formed by β -oxidation of palmitate (7 . 5 = 35).

A total of 8 mol of acetyl- CoA is formed, and each will give rise to 12 mol of ATP on oxidation in the citric acid cycle, making $8 \cdot 12 = 96$ mol.

Two must be subtracted for the initial activation of the fatty acid, yielding a net gain of 129 mol of ATP per mole of palmitate, or 129 . 51.6* = 6656 kJ. This represents 68% of the free energy of combustion of palmitic acid.

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Energy yield from palmitic acid

 From palmitoyl CoA to acetyl CoA: 					
Acyl CoA dehydrogenase 7 FADH2	14				
Beta-OH dehydrogenase 7 NADH	21				
From 8 acetyl CoA	96				
 Total energy yield 	131				
ATP are used for activation of FA	-2				
Hence net gain of ATP	129				



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UNIT : V (Nucleic acids)

UNIT V

Nucleic acids: Structure and functions: Physical & chemical properties of Nucleic acids, Nucleosides & Nucleotides, purines & pyrimidines, Biologically important nucleotides, Double helical model of DNA structure, A, B & Z – DNA, denaturation and renaturation of DNA.

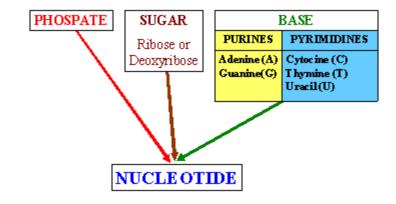
Nucleic acids:

Nucleic acids consist of nucleotides that have a sugar, nitrogen base, and phosphate. Two types of nucleic acid are found.

- Deoxyribonucleic acid (DNA)
- Ribonucleic acid (RNA)

Physical & chemical properties of Nucleic acids

- Polymers of four nucleotides
- Linked by alternating sugar-phosphate bonds
- RNA: ribose and A, G, C, U
- DNA: deoxyribose and A,G,C,T
- Nucleic acids are polynucleotides
- Their building blocks are nucleotides



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Structure of purines and pyrimidines:

Purines:

- A purine is a heterocyclic aromatic organic compound, consisting of a pyrimidine ring fused to an imidazole ring.
- Adenine = 6-amino purine
- Guanine = 2-amino-6-oxy purine
- Hypoxanthine = 6-oxy purine
- Xanthine = 2,6-dioxy purine

- Adenine and guanine are found in both DNA and RNA.
- Hypoxanthine and xanthine are not incorporated into the nucleic acids as they are being synthesized but are important intermediates in the synthesis and degradation of the purine nucleotides.

Pyrimidines:

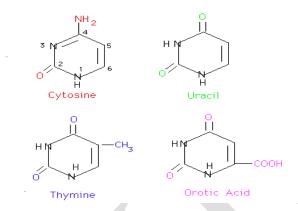
- Uracil = 2,4-dioxy pyrimidine
- Thymine = 2,4-dioxy-5-methyl pyrimidine

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• Cytosine = 2-oxy-4-amino pyrimidine

• Orotic acid = 2,4-dioxy-6-carboxy pyrimidine



- Cytosine is found in both DNA and RNA.
- Uracil is found only in RNA.
- Thymine is normally found in DNA.
- Sometimes tRNA will contain some thymine as well as uracil.

Nucleosides:

- If a sugar, either ribose or 2-deoxyribose, is added to a nitrogen base, the resulting compound is called a nucleoside.
- Carbon 1 of the sugar is attached to nitrogen 9 of a purine base or to nitrogen 1 of a pyrimidine base.
- The names of purine nucleosides end in -osine and the names of pyrimidine nucleosides end in -idine.
- The convention is to number the ring atoms of the base normally and to use l', etc. to distinguish the ring atoms of the sugar.
- Unless otherwise specified, the sugar is assumed to be ribose.
- To indicate that the sugar is 2'-deoxyribose, a d- is placed before the name.
 - Adenosine

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Guanosine

➤ Inosine - the base in inosine is hypoxanthine

Uridine

> Thymidine

> Cytidine

Nucleotides:

- Adding one or more phosphates to the sugar portion of a nucleoside results in a nucleotide.
- Generally, the phosphate is in ester linkage to carbon 5' of the sugar.
- If more than one phosphate is present, they are generally in acid anhydride linkages to each other.
- If such is the case, no position designation in the name is required.
- If the phosphate is in any other position, however, the position must be designated.
- For example, 3'-5' cAMP indicates that a phosphate is in ester linkage to both the 3' and 5' hydroxyl groups of an adenosine molecule and forms a cyclic structure.
- 2'-GMP would indicate that a phosphate is in ester linkage to the 2' hydroxyl group of a guanosine. Some representative names are:
 - ➤ AMP = adenosine monophosphate = adenylic acid
 - > CDP = cytidine diphosphate

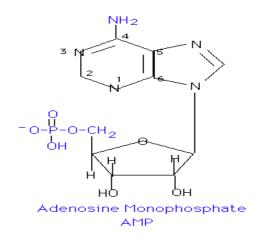
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➤ dGTP = deoxy guanosine triphosphate

➤ dTTP = deoxy thymidine triphosphate (more commonly designated TTP)

 \triangleright cAMP = 3'-5' cyclic adenosine monophosphate



DNA

- DNA is a polymer of deoxyribonucleotides (or simply deoxynucleotides).
- It is composed of monomeric units namely deoxyadenylate (dAMP), eoxyguanylate (dGMP), deoxycytidylate(dCMP) and deoxythymidylate(d TMP) (It may be noted here that some authors prefer to use TMP for deoxythymidylate, since it is found only in DNA).
- The details of the nucleotide structure are given above.

DNA double helix:

• The double helical structure of DNA was proposed by lames Watson and Francis Crick in 1953 (Nobel Prize, 1962).

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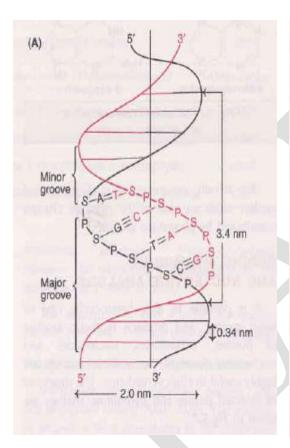
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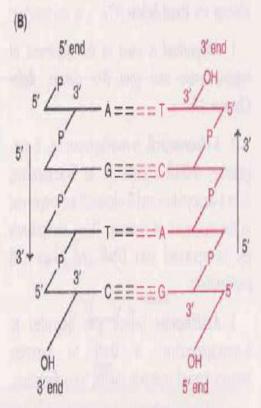
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• The elucidation of DNA structure is considered as a milestone in the era of modern biology.

• The structure of DNA double helix is comparable to a twisted ladder.

 The salient features of Watson - Crick Model of DNA (now known as B-DNA) are described next.

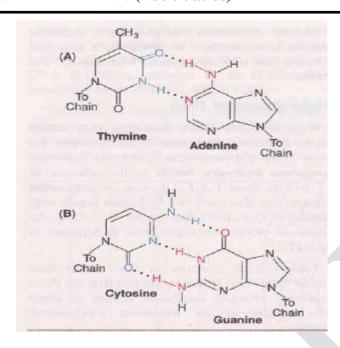




(A) Watson-Crick model of DNA helix (B) Complementary base pairing in DNA helix.

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Complementary base paring in DNA

- (A) Thymine pairs with adenine by 2 hydrogen bonds
- (B) Cytosine pairs with guanine by 3 hydrogenbonds. The DNA is a right handed double helix.
 - It consists of two polydeoxyribonucleotide chains (strands) twisted around each other on a common axis.
 - The two strands are antiparallel, i.e., one strand runs in the 5' to 3' direction while the other in 3'to 5'direction. This is comparable to two parallel adjacent roads carrying traffic in opposite direction.
 - The width (or diameter) of a double helix is 20 A° (2 nm).
 - Each turn (pitch) of the helix is 34 A" (3.4 nm) with 10 pairs of nucleotides each pair placed at a distance of about 3.4 A°.

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• Each strand of DNA has a hydrophilic deoxyribose phosphate backbone (3'-5' phosphor diester bonds) on the outside (periphery) of the molecule while the hydrophobic bases are stacked inside (core).

- The two polynucleotide chains are not identical but complementary to each other due to base pairing.
- The two strands are held together by hydrogen bonds formed by complementary base pairs.
- The A-T pair has 2 hydrogen bonds while G-C pair has 3 hydrogen bonds. The G = C is stronger by about 50% than A=T.
- The hydrogen bonds are formed between a purine and a pyrimidine only.
- If two purines face each other, they would not fit into the allowable space. And two pyrimidines would be too far to form hydrogen bonds.
- The only base arrangement possible in DNA structure, from spatial considerations is A-T, T-A, G-C and C-C.
- The complementary base pairing in DNA helix proves Chargaffs rule.
- The content of adenine equals to that of thymine (A = T) and guanine equals to that of cytosine (G = C). 10.
- The genetic information resides on one of the two strands known as template strand or sense strand.
- The opposite strand is antisense strand.
- The double helix has (wide) major grooves and (narrow) minor grooves along the phosphodiester backbone.
- Proteins interact with DNA at these grooves, without disrupting the base pairs and double helix.

Forms of DNA

B-Form, A-Form, Z-Form of DNA

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Three major forms of DNA are double stranded and connected by interactions between complementary base pairs. These are terms A-form, B-form, and Z-form DNA.

B-form DNA

The information from the base composition of DNA, the knowledge of dinucleotide structure, and the insight that the X-ray crystallography suggested a helical periodicity were combined by Watson and Crick in 1953 in their proposed model for a double helical structure for DNA. They proposed two strands of DNA -- each in a right-hand helix -- wound around the same axis. The two strands are held together by H-bonding between the bases (in anti conformation) as shown in Fig. 2.13.

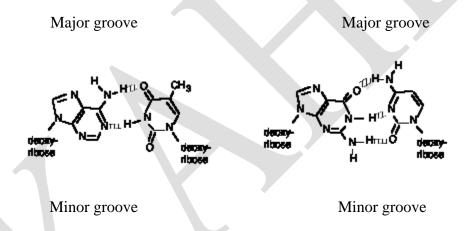


Figure 5.1. (left) An A:T base pair and (right) a G:C base pair

Bases fit in the double helical model if pyrimidine on one strand is always paired with purine on the other. From **Chargaff's rules**, the two strands will pair A with T and G with C. This pairs a keto base with an amino base, a purine with a pyrimidine. Two H-bonds can form between A and T, and three can form between G and C. This third H-bond in the G:C base pair is between the additional exocyclic amino group on G and the C2 keto group on C. The pyrimidine C2 keto group is not involved in hydrogen bonding in the A:T base pair.

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These are the complementary base pairs. The base-pairing scheme immediately suggests a way to replicate and copy the the genetic information.

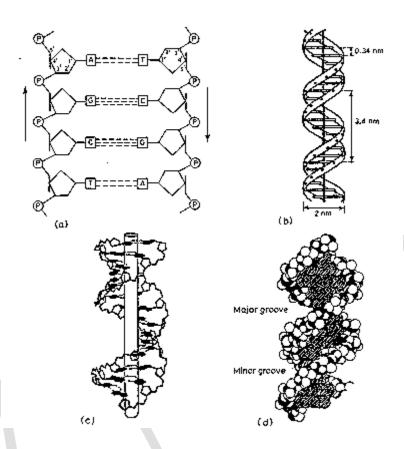


Figure 5.2 Antiparallel (a), plectonemically coiled (b, c, d) DNA strands. The arrows in a are pointed 3' to 5', but they illustrate the antiparallel nature of the duplex. The two strands of the duplex are antiparallel and plectonemically coiled. The nucleotides arrayed in a 5' to 3' orientation on one strand align with complementary nucleotides in the the 3' to 5' orientation of the opposite strand.

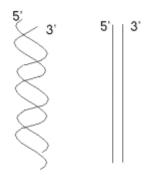
The two strands are not in a simple side-by-side arrangement, which would be called a paranemic joint (Fig. 2.15). (This will be encountered during recombination in Chapter 8.) Rather the two strands are coiled around the same helical axis and are intertwined with themselves (which is referred to as a plectonemic coil). One consequence of this intertwining is

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that the two strands cannot be separated without the DNA rotating, one turn of the DNA for every "untwisting" of the two strands.



In a plectonemic coil, the two strands wrap around each other. In a paranemic joint, the two strands align side-by-side.

Figure 5.3. Duplex DNA has the two strands wrapped around each other in a plectonemic coil (left), not a paranemic duplex (right).

Dimensions of B-form (the most common) of DNA

- 0.34 nm between bp, 3.4 nm per turn, about 10 bp per turn
- 1.9 nm (about 2.0 nm or 20 Angstroms) in diameter

Major and minor groove

The major groove is wider than the minor groove in DNA (Fig. 2.14d), and many sequence specific proteins interact in the major groove. The N7 and C6 groups of purines and the C4 and C5 groups of pyrimidines face into the major groove, thus they can make specific contacts with amino acids in DNA-binding proteins. Thus specific amino acids serve as H-bond donors and acceptors to form H-bonds with specific nucleotides in the DNA. H-bond donors and acceptors are also in the minor groove, and indeed some proteins bind specifically in the minor groove. Base pairs stack, with some rotation between them.

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A-form nucleic acids and Z-DNA

Three different forms of duplex nucleic acid have been described. The most common form, present in most DNA at neutral pH and physiological salt concentrations, is B-form. That is the classic, right-handed double helical structure we have been discussing. A thicker right-handed duplex with a shorter distance between the base pairs has been described for RNA-DNA duplexes and RNA-RNA duplexes. This is called A-form nucleic acid.

A third form of duplex DNA has a strikingly different, left-handed helical structure. This Z DNA is formed by stretches of alternating purines and pyrimidines, e.g. GCGCGC, especially in negatively supercoiled DNA. A small amount of the DNA in a cell exists in the Z form. It has been tantalizing to propose that this different structure is involved in some way in regulation of some cellular function, such as transcription or regulation, but conclusive evidence for or against this proposal is not available yet.

Differences between A-form and B-form nucleic acid

The major difference between A-form and B-form nucleic acid is in the conformation of the deoxyribose sugar ring. It is in the C2' endoconformation for B-form, whereas it is in the C3' endoconformation in A-form. As shown in Fig. 2.16, if you consider the plane defined by the C4'-O-C1' atoms of the deoxyribose, in the C2' endoconformation, the C2' atom is above the plane, whereas the C3' atom is above the plane in the C3' endoconformation. The latter conformation brings the 5' and 3' hydroxyls (both esterified to the phosphates linking to the next nucleotides) closer together than is seen in the C2' endoconfromation (Fig. 2.16). Thus the distance between adjacent nucleotides is reduced by about 1 Angstrom in A-form relative to B-form nucleic acid (Fig. 2.17).

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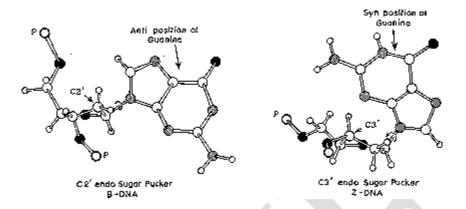


Figure 5.4 .Syn and anti conformations of the base relative to the sugar in nucleotides.

A second major difference between A-form and B-form nucleic acid is the placement of base-pairs within the duplex. In B-form, the base-pairs are almost centered over the helical axis (Fig. 2.15), but in A-form, they are displaced away from the central axis and closer to the major groove. The result is a ribbon-like helix with a more open cylindrical core in A-form.

Z-form DNA

Z-DNA is a radically different duplex structure, with the two strands coiling in left-handed helices and a pronounced zig-zag (hence the name) pattern in the phosphodiester backbone. As previously mentioned, Z-DNA can form when the DNA is in an alternating purine-pyrimidine sequence such as GCGCGC, and indeed the G and C nucleotides are in different conformations, leading to the zig-zag pattern. The big difference is at the G nucleotide. It has the sugar in the C3' endoconformation (like A-form nucleic acid, and in contrast to B-form DNA) and the guanine base is in the synconformation. This places the guanine back over the sugar ring, in contrast to the usual anticonformation seen in A- and B-form nucleic acid. Note that having the base in the anticonformation places it in the position where it can readily form H-bonds with the complementary base on the opposite strand. The duplex in Z-DNA has to accommodate the distortion of this G nucleotide in the synconformation. The cytosine in the adjacent nucleotide of Z-DNA is in the "normal" C2' endo, anticonformation.

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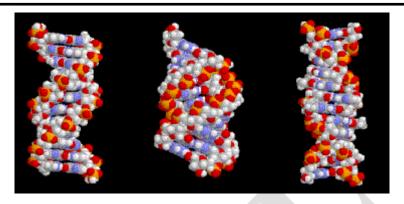


Figure 5.6. B-form (left), A-form (middle) and Z-DNA (right).

Comparisons of B-form, A-form and Z-DNA

	В	A	Z
helix sense	RH	RH	LH
bp per turn	10	11	12
vertical rise per bp	3.4	2.56	3.7 Angstroms
rotation per bp	+36	+33	-30 degrees
helical diameter	19	23	18 Angstroms

Even classic B-DNA is not completely uniform in its structure. X-ray diffraction analysis of crystals of duplex oligonucleotides shows that a given sequence will adopt a distinctive structure. These variations in B-DNA may differ in the propeller twist (between bases within a pair) to optimize base stacking, or in the 3 ways that 2 successive base pairs can move relative to each other: twist, roll, or slide.

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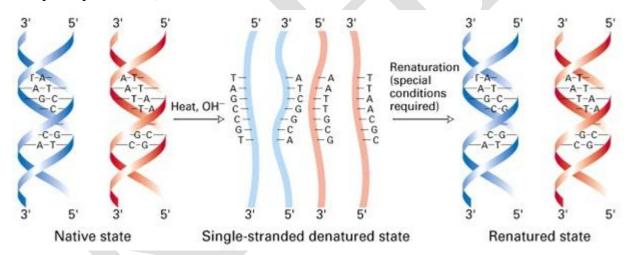
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Denaturation of DNA strands:

• The two strands of DNA helix are held together by hydrogen bonds.

- Disruption of hydrogen bonds (by change in pH or increase in temperature) results in the separation of polynucleotide strands.
- This phenomenon of loss of helical structure of DNA is known as denaturation.
- The phosphodiester bonds are not broken by denaturation.
- Loss of helical structure can be measured by increase in absorbance at 260 nm (in a spectrophotometer).



Denaturation and renaturation of DNA.

- Melting temperature (Tm) is defined as the temperature at which half of the helical structure of DNA is lost.
- Since C-C base pairs are more stable (due to 3 hydrogen bonds) than A-T base pairs (2 hydrogen bonds), the Tm is greater for DNAs with higher C-C content.

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• Thus, the Tm is 65°C for 35% G-C content while it is 70°C for 50% G-C content.

- Formamide destabilizes hydrogen bonds of base pairs and, therefore, lowers Tm.
- This chemical compound is effectively used in recombinant DNA experiments.

Renaturation:

- Renaturation or reannealing is the process in which the separated complementary DNA strands can form a double helix.
- It is effected by cooling
- It involves reannealing or formation of hydrogen bond between complimentary base pairs.
- Upon renaturation viscocity increases
- The rate renaturation is directly proporotional to the concentration of complementary strands.

Application of denaturation and renaturation

- To understand genome size and complexity
- To understand Genetic relatedness
- To understand Relative proportion of single copy and repetitive sequence

Questions	A	В	С	D	Answer
UNIT I	Α	D .	C	D .	Allswei
UNIII				Having both polar and non-	
What are amphiphilic molecules?	Highly polar	Highly non-polar	Neutral	polar groups	Having both polar and non-polar groups
The shape of a water molecule is	0 7 1	<i>U</i> , 1	Tetrahedron	Distorted Tetrahedron	Distorted Tetrahedron
In taxonomy, classifications of organisms are on the basis	Linear	Trigonal	Tetraneuron	Distorted Tetrahedron	Distorted Tetrahedron
of	Overall morphology	Proteomics	Genomics	Evolution	Overall morphology
In phylogeny, classifications of organisms are on the basis of	Overall morphology	Proteomics	Genomics	Evolution	Evolution
How many H-bond a water molecule can make with neighboring water molecules?	1	2	3	4	4
What is osmosis?	Movement of solvent molecules across a semipermeable membrane.	Movement of solute molecules across a semipermeable membrane.	Movement of both solvent and solute molecules across a semipermeable membrane.	None of the above.	Movement of solvent molecules across a semipermeable membrane.
What is dialysis?	Movement of solvent molecules across a semipermeable membrane.	Movement of solute molecules across a semipermeable membrane.	Movement of both solvent and solute molecules across a semipermeable membrane.	None of the above.	Movement of solute molecules across a semipermeable membrane.
Buffers are	Mixture of weak acid and its conjugate base	Mixture of weak acid and weak base	Mixture of strong acid and its conjugate base.	Mixture of strong acid and strong base.	Mixture of weak acid and its conjugate base
At Acidosis condition, the blood pH is	7.3	< 7.2	7.4	> 7.4	7.3
At Alkalosis condition, the blood pH is	< 7.4	7.4	7.5	> 7.4	> 7.6
Physiological pH of the blood is	< 7.0	7	> 7.0	7.4	7.4
The blood pH is mainly maintained by the following	\ 1.U	/	/ 1.0	7.7	7.64
components.	O ₂ and CO ₂	CO ₂ and HCO ₃	O ₂ and CO	CO and CO ₂	CO ₂ and HCO ₃
Hyperventilation may cause	Acidosis	Alkalosis	Both the acidosis and alkalosis Both the acidosis	None of the above.	Alkalosis
Closed ventilation may cause	Acidosis	Alkalosis	and alkalosis	None of the above.	Acidosis
	Acidosis				
All living things contain the element in some form	Iodine	Phosphorous	Carbon	All the above.	Carbon
The primary element of all biological macromolecules is	Iodine	Phosphorous	Carbon	All the above.	Carbon
Molecular self-assembly is directed through	Covalent interaction	Non-covalent interaction	Both covalent and non-covalent interaction	All the above.	Non-covalent interaction

Amyloid fibers are due to	Molecular self-assembly of correctly folded proteins	Molecular self-assembly of incorrectly folded proteins	Molecular self- assembly of lipids	Molecualr self-assembly of lipids and proteins.	Molecular self-assembly of incorrectly folded proteins
			Either	Neither endogenous nor	
			endogenous or	exogenous	
Biomolecules are	Endogenous	Exogenous	exogenous	CAOGCHOUS	Either endogenous or exogenous
An atom is made up of central containing	nucleus	molecule	nucleolus	shells	nucleus
positively charged protons					
The number of electrons that can be present in the L shell	12	8	18	17	8
is					
The simplest atom consisting of positively charged proton	oxygen	hydrogen	nitrogen	sulphur	hydrogen
and an single negatively charged electron orbit is					
The mass of a proton or neutron is called	amu	aum	anm	aun	aum
The number of protons on an atom is called the of	atomic number	mass number	molecular number	proton number	atomic number
the atom.					
	gaseous potential	ionization potential	molecular	proton potential	gaseous potential
The amount of energy required to remove loosely held		_	potential		
electron from a normal gaseous atom is called					
A chemical bond that involves the sharing of electron	covalent	coordinate	electrovalent	non covalent	covalent
pairs between atoms is called					
Chemical bond formed between two atoms due to	coordinate	electrovalent	noncovalent	covalent	electrovalent
transfer of electron(s) from one atom to the other, atom is					
called .					
of an atom is a measure of its power to attract	electronegativity	electronaffinity	electropositivity	electroavidity	electroavidity
electrons that it is sharing in a covalent bond.	, and a significant	, , , , , ,	1		
The distance between two atomic nuclei in a covalent	Bond angle	Bond circle	Bond distance	Bond area	Bond distance
molecule is called .					
Cytochrome oxidase is	a3	aa3	a	none of the above	aa3
Ionization of water can be described by an	molecular	ionization	equilibrium	ionizable	ionization
constant.			1		
The number of H+ ions present in a solution is a measure	Alkalinity	basicity	acidity	avidity	acidity
of of the solution.					
The of a solution is dependent upon the number for	basicity	acidity	alkalinity	neutrality	alkalinity
hydroxyl ions present.			,		
is defined as the negative logarithm of	pH	[-H]	[-OH]	H+	рН
hydrogen ion concentration.	*		'		<i>E</i>
The pH of pure water at 25°C is	6	8	7	10	7
A condition called occurs when pH of the blood is	acidosis	alkalosis	basidosis	avidosis	alkalosis
higher than normal.				-	
A is defined as a substance that has a greater	strong acid	weak acid	strong base	weak base	strong acid
tendency to lose its proton and completely dissociates.					
A compound which can accept a pair of electrons from a	electrophile	nucleophile	extremophile	acidophile	electrophile
base is called .	r	. · · · ·	r	T.	* '
is used to determine the amount of an acid in a	centrifugation	separation	titration	neutralization	titration
given solution.		•			
	l .	I	1	I .	

resists changes in pH on the addition of acid or	buffer	pH paper	acidohile	electrophile	buffer
base.		F F-F			
The pK _a of the weak acid is given by a simple expression	Lowry-Bronsted	Lowry-Hasselbach	Henderson-	Hasselbach	Henderson-Hasselbach
called equation.			Hasselbach		
The principal buffer for erythrocytes is	bicarbonate	phosphate	protein	hemoglobin	hemoglobin
The pH of blood is maintained at .	7.8	7.4	6.4	7.1	7.4
is the number of isomers of glucose.	4	8	12	16	16
The human heart muscle contains	D- Arabinose	Galactose	D- Lyxose	D- Xylose	D- Lyxose
Epimers of Glucose	Fructose	Galactose	Ribose	Deoxyribose	Galactose
Cellulose is made up of the molecules of	α- Glucose	β-Glucose	Mannose	non of the above	β-Glucose
Glucose absorption may be decreased in	Oedema	Nephritis	Rickets	Osteomyelitis	Oedema
Fructose 1, 6- bisphosphate is activated by?	ATP	AMP	UTP	ADP	ATP
Glucose -6 - phosphate is absent from	Adipose tissue	Kidney	Intestine	Heart	Adipose tissue
The number of high energy phosphates contained by ATP is	1	3	5	2	2
The synthesis of adenylate cyclase is increased by.	parathyroid	pituitary	thyroid	insulin	thyroid
The toxicity of oxygen is due to its conversion to	metaloxide	superoxide	hyperoxide	hypooxide	superoxide
Keratin the protein of hair is synthesized from the aminoacid	glycine	Serine	Proline	Methionine	Methionine
Most aminoacids are substrates for transamination	Alanine	Threonine	Serine	Valine	Threonine
	Alainne	Tiffeofffie	Sernie	vanne	Tiffeoinne
In the liver Glyceroldehyde 3 phosphate is converted	Glycol	Formaldehyde	Formic acid	Glycerol	Glycerol
into	Glycor	Tormandenyde	1 offine deld	Glyceror	difector
Cytochrome Oxidase is poisoned by	cyanide	sulphide	sulphite	sulphate	cvanide
The respiratory chain is folded in to	2	4	3	1	2
oxidation/reduction loops in the membrane.					
Glutamic dehydrogenase is a	monomer	Tetramer	Dimer	Non of the above	monomer
The energy released in the formation of noncovalent bond is	0 kcal/mol.	1-5 kcal/mol	6-9 kcal/mol	0.1-0.5 kcal/mol	1-5 kcal/mol
An example for hydrophobic molecule is	water	heat	rosewater	oils	oils
bond is considered to be a very weak bond.	ionic	covalent	hydrophobic	vanderwaals	vanderwaals
Primary atomic bond is bonds.	covalent	hydrogen	vanderwaals	all	all
Secondary atomic bond is bonds.	Covalent	ionic	metallic	hydrogen	hydrogen
The bond formed between atoms or groups carrying	covalent	electrostatic	hydrogen	metallic	electrostatic
opposite charges is known as					
Ionic bond is otherwise known as bond.	covalent	metallic	hydrogen	electrovalent	electrovalent
Increasing salt concentration the strength of ionic bonding.	increases	stabilizes	regulates	reduces	reduces
pH of hydrochloric acid secreted by stomach lining is	6	7	3	1	1
Grape fruit is in the pH of	6	7	3	1	1
is a substance which produces hydrogen	Base	water	liquid	acid	acid
ions(H ⁺) by dissociation.			1		
The pH scale ranges between	0 & 14	-114	-115	0 & 15	0 & 14
THE PIT SCARE PARISES DELWEER	U CC 1 T	117	113	0 & 13	V GL 17

An axid dissociation constant is denoted by	Ka	V	Kb	a & b	K _a
An acid dissociation constant is denoted by	$\kappa_{\rm a}$	K_{da}	KU	a & 0	$\mathbf{A}_{\mathbf{a}}$
The bicarbonate ion is the conjugate base of	2 carbon atom	Carbonic acid	Carbamides	Carbondioxide	Carbonic acid
Retinol exists as an ester with higher fatty acids in the	Liver	Kidney	Lung	All the above	All the above
Carotenes are transported with the	Protein	Lipoprotein	Minerals	Lipids	Lipoprotein
The percentage of Vitamin A in the form of esters is stored in the liver	80	85	90	95	95
a pH indicator composed of a solution of	pH indicator	Acid indicator	Alkali indicator	Universal indicator	Universal indicator
several compounds that exhibits several smooth colour changes over a pH value range from 1-14 to indicate the acidity or alkalinity of solutions.					
pKa value of phenol is	1.99	1.99	8.99	10	10
Amphetamine has pK _A of	1.8	2.28	3.38	9.9	9.9
		_		_	
UNIT II	A	В	С	D	Answer
The pI of 'Lysine' can be calculated by using the formula	$pI = (pK_2 + pK_R)/2$	$pI = (pK_1 + pK_R)/2$	$pI = (pK_1 + pK_2)/2$	$pI = (pK_1 + pK_2 + pK_R)/3$	$pI = (pK_2 + pK_R)/2$
The pI of 'glutamic acid' can be calculated by using the formula	$pI = (pK_2 + pK_R)/2$	$pI = (pK_1 + pK_R)/2$	$pI = (pK_1 + pK_2)/2$	$pI = (pK_1 + pK_2 + pK_R)/3$	$pI = (pK_1 + pK_R)/2$
The pI of 'alanine' can be calculated by using the formula	$pI = (pK_2 + pK_R)/2$	$pI = (pK_1 + pK_R)/2$	$pI = (pK_1 + pK_2)/2$	$pI = (pK_1 + pK_2 + pK_R)/3$	$\mathbf{pI} = (\mathbf{pK}_1 + \mathbf{pK}_2)/2$
The axial ratio of globular proteins is	> 10	< 10	> 20	< 20	< 10
The axial ratio of fibrous proteins is	> 10	< 10	> 20	< 20	> 10
Supercoiled DNA molecules have	W > 0	W < 0	W = 0	None of the above.	W > 0
Negatively supercoiled DNA molecules have	W > 0	W < 0	W = 0	None of the above.	W < 0
The sugar puckering effect in A-DNA is	C3' endo	C3' exo	C2' endo	C2' exo	C3' endo
The sugar puckering effect in B-DNA is	C3' endo	C3' exo	C2' endo	C2' exo	C2' endo
Reducing sugars have following structural and chemical			Reduce Tollen's		
features	Hemiacetal configuration	Exhibit mutarotation	reagent	All the above.	All the above.
Non-reducing sugars have following structural and		E 1212	Reduce Tollen's	A 11 d	A . 1 . 6"
chemical features	Acetal configuration β-D-Glucose	Exhibit mutarotation α-D-Glucose	reagent	All the above. B-L-Glucose	Acetal configuration
The monomeric unit of 'starch' is	,		α-L-Glucose		α-D-Glucose
The monomeric unit of 'cellulose' is	β-D-Glucose	α-D-Glucose	α-L-Glucose	β-L-Glucose	β-D-Glucose
Triglycerides are composed of	Monohydric alcohols and fatty acids	Dihydric alcohols and fatty acids	Trihydric alcohols and fatty acids	None of the above.	Trihydric alcohols and fatty acids
Waxes are composed of	Monohydric alcohols and fatty acids	Dihydric alcohols and fatty acids	Trihydric alcohols and fatty acids	None of the above.	Monohydric alcohols and fatty acids
Phospholipids are	Simple lipids	Compound lipids	Derived lipids	All the above.	Compound lipids
Phosphosphingosides are	Simple lipids	Compound lipids	Derived lipids	All the above	Compound lipids
'Drying oils' exhibit	Low Iodine value	High Iodine value	Low acid number	High acid number	High Iodine value
Glycosides are found in many	drugs	vitamins	minerals	nucleoproteins	drugs

Iodine solution produces no colour with	cellulose	glycogen	starch	dextrin	cellulose
The distinguishing test between monosaccharides and	barfoed's test	seliwanoff's test	fehling's test	benedict's test	barfoed's test
dissacharides is	barroed s test	Senwanon s test	remmig 5 test	benearer 5 test	barroed 5 test
Barfoed's solution is not reduced by .	glucose	mannose	sucrose	ribose	sucrose
The non-protein part of rhodopsin is	Retinal	Retinol	Carotene	Repsin	Retinal
Heparin has a molecula weight of	14000	14500	17000	17500	17000
The component of cartilage and cornea is	dermatosulphate	keratosulphate	hyaluronic acid	chondroitin sulphate.	keratosulphate
In place of glucuronic acid chondroitin sulphate B	gluconic acid	gulonic acid	iduronic acid	sulphonic acid	iduronic acid
contains .	6			T	
UDPG is essential for the synthesis of	Lactose	galactose	ribose	deoxtribose	Lactose
Cellulose is made up of molecules of	a glucose	b-glucose	d- glucose	g- glucose	b-glucose
Continued intake of excesive amounts of vitamin A	Irritability	Anorexia	Headache	All of the above	All of the above
especailly in children produces					
Each branch of amylopectin is at an interval of glucose units.	14-20	24-30	34-40	44-50	24-30
Hexokinase has high affinity for glucose than	Fructokinase	Glucokinase	Galactokinase	All the above	Glucokinase
Glucose is removed from the blood following a meal by	hexokinase	glucokinase	heparinkinase	phosphokinase	hexokinase
Cyclic AMP is formed from ATP by the enzyme adenylate cyclase which is activated by the hormone.	insulin	epinephrine	glucagons	progesterone	epinephrine
The absorption of glucose is interfered by the deficiency of	vitamin A	thiamine	riboflavin	pyridoxine	thiamine
The branching enzyme acts on the glycogen chain between glucose units of	1 and 6	2 and 7	3 and 9	6 and 11	6 and 11
The synthesis of adenylate cyclase is increased by	thyroid hormones	growth hormones	ACTH	FTH	thyroid hormones
Inulin is a .	glucosan	fucosan	fructosan	pyranosan	fructosan
Glucose on treatment with strong mineral acids produces	levulinic acid	levunyl acid	gluconic acid	glucuronic acid	levulinic acid
Heparin is used as an	anticoagulant	coagulant	depressent	antidepressent	anticoagulant
Each turn of the helix amylose consists of glucose units.	2	4	6	7	6
The method of formation of glucose and glycogen from non-carbohydrate sources is called as	glycogenesis	glucogenesis	Gluconeogenesis	Glycolysis	glucogenesis
Enzymes are destroyed by	formaldehyde	sucrose	dextrose	fructose	formaldehyde
The enzyme splits fructose 1,6 diphosphate in to two triose phosphate.	enolase	glucokinase	aldolase	hexokinase	aldolase
Pyruvate dehydrogenase is inhibited by	fluoride	sulphide	arsenite	sulphate	arsenite
Hypoglycemia occurs due to the inhibition of phosphoglucomutase by	fructose -1 phosphate	glucose-6 phosphate	fructose	glucose 1,6 phosphate	fructose -1 phosphate
The approximate number of mols of pyruvate dehydrogenase in pyruvate dehydrogenase complex is	19	29	34	24	29
The carrier of citric acid cycle is	succinate	fumarate	malate	oxaloacetate	oxaloacetate

When equal amounts of dextro and levo rotatory isomers are present in a mixture it is said to be	isomeric	epimeic	racemic	enantiomeric	racemic
Cis-trans isomerism occurs in compounds with bonds.	single	double	sugar	phosphate	sugar
Fructokinase is present in	intestine	adipose tissue	heart	brain	intestine
Pyruvate is accumulated by the dietary deficiency of .	folic acid	B6	b12	thiamine	thiamine
The glycogen content of is more than in muscle.	liver	brain	kidney	intestine	liver
In galactosemic individual UDP galactose is formed by epimerization from	glucose	UDP glucose	CDP glucose	ITP glucose	UDP glucose
In the liver glyceraldehyde –3 phosphate is converted to	glycol	formaldehyde	formic acid	glycerol	glycerol
The reaction involving the conversion of succinyl CoA to succinate requires	CDP	GDP	ADP	ATP	ADP
The heptose ketose sugar formed as a result of chemical reactionin HMP shunt is	glucoheptose	galactoheptose	sedoheptulose	manooheptose	sedoheptulose
On boiling benedict's solution is not reduced by	sucrose	lactose	maltose	fructose	sucrose
The general formula for polysaccharide is	$(C_6H_{10}O_5)n$	$(C_6H_{12}O_6)n$	$(C_6H_{12}O_5)n$	1(C ₆ H ₁₀ O ₆)n	$(C_6H_{10}O_5)n$
Human heart muscle contains	D-Arabinose	D-Ribose	D-Lyxose	D-Xylose	D-Lyxose
The intermediate n hexose monophosphate shunt is	D-Ribulose	D-Arabinose	D-Lyxose	D-Xylose	D-Ribulose
Honey contains the hydrolytic product of	Lactose	Maltose	Inulin	Starch	Inulin
Iodine solution produces no colour with	Cellulose	Starch	Dextrin	Glycogen	Cellulose
Amylose contains glucose units	100-200	200-300	300-400	500-600	300-400
Blood group substances consist of	Lactose	Maltose	Fucose	Mucose	Fucose
Salivary amylase is activated by	Na ⁺	K ⁺	HCO ₃	Cl	CI
Glucose absorption may be decreased in	Oedema	Nephritis	Rickets	Osteomyelitis	Oedema
Sugars forming five-membered rings are called	Epimerases	Furanoses	Racemases	Hydrolases	Furanoses
A method for synthesis of monosaccharides was first proposed by	Michaelis Menton	Firoz	Kiliani	Persoz	Kiliani
Galactose on reduction yields	Dulcitol	Mannitol	Sorbitol	Aldol	Dulcitol
Sucrose is refered as	Sugar	Simple sugar	Fructosan	Invert sugar	Invert sugar
Starch is formed bychain	α-glucosidic	β- glucosidic	γ- glucosidic	All	α-glucosidic
Gluconeogenesis is a reversal of	Krebs cycle	HMP shunt	PMP	Glycolysis	Glycolysis
cannot be synthesized in man.	Lactic acid	HCl	Protein	Ascorbic acid	Ascorbic acid
Insulin is destroyed by	Lyases	Ligases	Aldolases	Peptidase	Peptidase
are antagonists to insulin.	Pyruvic acid	Glucokinase	Glycogenin	Glucagon	Glucagon
In Juvenile Diabetes, the of pancreas are exhausted.	α-cells	β-cells	γ-cells	All	β-cells
The key enzyme of TCA cycle is	Citrate synthase	Isocitrate dehydrogenase	α -ketoglutarate	All	All

UNIT III	A	В	С	D	Answer
Enzymes are classified into	4 major classes	5 major classes	6 major classes	7 major classes	6 major classes
Enzyme activity is influenced by	pH	Temperature	Concentration	All the above	All the above
When the velocity of an enzymatic reaction is half		•			
maximal	Km > [Substrate]	Km = [Substrate]	Km < [Substrate]	All the above.	Km = [Substrate]
			without		
Apoenzymes are the enzymes	holoenzymes	with coenzymes	coenzymes	isoenzymes	without coenzymes
	_		without		
Holoenzymes are the enzymes	apoenzymes	with coenzymes	coenzymes	isoenzymes	with coenzymes
				G.S.	
Isoenzymes are the enzymes	Depicting similar functions	Depicting similar structures	Coenzymes	Cofactors	Depicting similar functions
The "Michaelis – Menten plot" is	ν vs. [S]	1/v vs. 1[S]	ν vs. 1/[S]	1/v vs. [S].	v vs. [S]
According to the 'Lock and Key' model, the active site of			depending on	depending on experimental	
an enzyme is	pre-defined	not predefined	substrate	conditions	pre-defined
According to the 'Induced-fit' model, the active site of an			depending on	depending on experimental	
enzyme is	pre-defined	not predefined	substrate	conditions	depending on substrate
The 'Lock and Key' model was proposed by Fischer in					
	1874	188-	1894	1904	1894
				1973	
The 'Induced-fit' model was proposed by Kushland in	1943	195:	3 1963	1973	1963
The 'Lock and Key' model was proposed by	Fisher in 1894	Fisher in 1963	Kushland in 1894	Kushland 1963	Kushland in 1894
The 'Induced-fit' model was proposed by	Fisher in 1894	Fisher in 1963	Kushland in 1894	Kushland 1963	Fisher in 1963
In diabetic individuals, Sorbitol level is in eye	Decreased	Increased	Moderate	Highly decreased	Increased
lens.					
Fats are solids at	10° C	20° C		40° C	20° C
Lecithin contains a nitrogenous base named as	ethanolamine	choline	inositol	phospholipids	ethanolamine
Postaglandins increase intestinal motility and	Constipation	Loose motion	Diarrhoea	Dysentery	Loose motion
cause					
Esters of fatty acids with higher alcohols other than	waxes	fats	both of the above	lipoprotein	waxes
glycerol are said to be					
Gangliosides are the glycolipids occurring in	liver	brain	kidney	muscle	brain
The prostaglandins are synthesized from	arachidonic acid	oleic acid	linoleic acid	linolenic acid	arachidonic acid
The essential fatty acids retard	atherosclerosis	diabetes mellitus	nephritis	edema	atherosclerosis
Eicasonoids are formed from	arachidonate	palmitate	stearate	butyrate	arachidonate
The principal organ for cholesterol synthesis is	brain	thyroid	liver	lungs	liver B
LDL contains the apoprotein	C-I	C-II	C-III	B Chalantanal	D
Fats are esters of with glycerol	fatty acids	waxes	Phospholipids	Cholesterol	fatty acids
PG3 and TX3 inhibit the release of	oleic acid	palmitoleic acid		arachidonic acid	arachidonic acid
Serum LDL has been found to be increased in	obstructive jaundice	hepatic jaundice	hemolytic	septicemia	obstructive jaundice
	1 .	1'	jaundice		1
Sulpholipids have been isolated from	heart	liver	brain	intestine	brain
Lecithins are soluble in ordinary fat solvents except	benzene	ethylalcohol	methylalcohol	acetone	acetone
Cardiolipin found in mitochondria is formed from	lipositol	phosphatidyl ethanolamine	phosphadityl glycerol	inositol	phosphadityl glycerol

	T	ı		I	
w- oxidation takes place by the hydrolysis in microsomes involving	cytochrome b	cytochrome c	cytochrome p-450	cytochrome a3	cytochrome p-450
Prostaglandins are liberated in the circulation by the stimulation of	posterior pituitary	anterior pituitary	adrenal gland	thyroid	adrenal gland
The great majority of absorbed fat appears in the form of	HDL	chylomicrons	VLDL	LDL	chylomicrons
The fatty acids containing even and odd numbers of carbon atoms and also unsaturated fatty acids are oxidized by	a- Oxidation	b - Oxidation	w- Oxidation	g- Oxidation	b - Oxidation
Long chain fatty acids are first activated to acyl- CoA in the	cytosol	mitochondria	microsomes	lysosomes	cytosol
Phospholipids help the oxidation of	glycerol	fatty acids	glycerophosphate s	glycophosphates	fatty acids
Cyclooxygenase is termed as	inhibiting enzyme	suicide enzyme	oxidizing enzyme	reducing enzyme	suicide enzyme
The synthesis of prostaglandins is inhibited by	aspirin	arsenite	fluoride	cyanide	aspirin
Faty acids synthesis takes place in the presence of the coenzyme	NAD+	reduced F+	reduced NAD	reduced NADP	reduced NADP
The concentration of sphingomyelins are inceased in	Gaucher's disease	Fabry's disease	Febrile disease	Niemann pick disease	Niemann pick disease
The protein moiety of lipoproteins is known as	apoprotein	preprotein	post protein	pseudoprotein	apoprotein
In adipose tissue prostaglandins decrease	lipogenesis	ketogenesis	lipolysis	ketolysis	lipogenesis
The beta lipoprotein fraction increases in severe	diabetes mellitus	uremia	.nephritis	muscular dystrophy	diabetes mellitus
An example of cardiac glycoside is	digitoxin	strobanthin		digitalis	strobanthin
Acyl-CoA dehydrogenase converts acyl-CoA to a, b-	NAD+	NADP	ATP	FAD+	FAD+
unsaturated acyl-CoA in the presence of the coenzyme					
Before the action of lipase the fat is emulsified by	lipoproteins	phospholipids	ergosterols	digitoxin	phospholipids
Leukotrienes are not formed in	leukocytes	mastocytoma	platelets	brain cells	brain cells
Leukotriene C4 is formed by the addition of	ascorbic acid	glutathione	glutamate	1aspartate	glutathione
The blood cholesterol level is increased in the deficiency of	vitamin D	vitamin B2	pyridoxine	aspartate	pyridoxine
Phosphadityl inositol is found in	cabbages	soyabeans	cauliflower	apples	sovabeans
Ketone bodis are utilized in	mitochondria	extrahepatic tissues	nuclei	chromosomes	extrahepatic tissues
Carboxylation of acetyl coA to malonyl CoA takes place bin the presence of	FAD+	biotin	NAD+	NADP+	biotin
Hydrolysis of fat by alkali is known as	Saponification number	Saponification	Both	None of the above	Saponification
The concentration of sphingomyelins are increased in disease.	Gauchers	Fabrys	Febrile	Niemann-Picks	Niemann-Picks
Lignouric acid present in peanut oil contain carbon atom.	18	20	22	24	24
Arachidonic acid contain number of double bond.	2	3	4	5	4
The shape of arachidonic acid is	L	M	U	V	U
Waxes contains higher alcohols known as	Methyl	Ethyl	Phytyl	Cetyl	Cetyl
	t	1		G	
The synthesis of prostaglandins is inhibited by	Aspirin	Arsenite	Fluoride	Cyanide	Aspirin

Prostaglandins increase Cyclic AMP in	Thyroid	Corpus luteum	Platelets	All the above	All the above
Sterilized milk is devoid of	vitamin A	Vitamin B2	Vitamin D	Vitamin C	Vitamin C
The example of saponin is	Oxygenin	Deoxygenin	Digitonin	a & b	Digitonin
is essential for cholesterol absorption.	Bile	Fattyacids	Protein	Carbohydrates	Bile
Physical exercise the serum cholesterol level.	Increase	Decrease	Stimulates	Regulates	Decrease
Tay Sachs disease is characterized by increased accumulation of in brain and spleen.	GM ₁ Ganglioside	GM ₂ Ganglioside	GM ₃ Ganglioside	GM ₄ Ganglioside	GM ₂ Ganglioside
Krabbes disease is due to the deficiency of	Lipase	Permease	Transacetylase	B-galactosidase	B-galactosidase
Butyryl -Co A is the primer molecule in	Liver	Pancreas	Gall bladder	Mammary gland	Mammary gland
Alcoholism leads to	Liver cirrhosis	Splenomegaly	Kidney stone	b & c	Liver cirrhosis
in the dosage of ½ to 1 gm thrice daily lowers cholesterol.	Streptomycin	Niacin	Gentamicin	Kanamycin	Niacin
Sunflower oil contains a high proportion of fattyacids.	Monounsaturated	Polyunsaturated	Monosaturated	Polysaturated	Polyunsaturated
UNIT IV	A	В	C	D	Answer
is the poor source of vitamin D.	Egg	Butter	Milk	Liver	Milk
are found both inside and outside of	Streptokinases	Thiokinases	Lipokinases	Thyrokinases	Thiokinases
mitochondria.					
Out of 200 different aminoacids found in nature the	20	23	22	24	20
number of aminoacids present in protein is					
Enzyme catalyzed hydrolysis of proteins produces	D-	DL-	LD	L-	L-
aminoacids of the form	10.5	10.6	10.0	11	40.0
The ph of arginine is	10.5	10.6	10.8	11	10.8
The neutral aminoacid is	leucine alanine	lysine isoleucine	proline	Histidine	leucine
The aminoacid containing hydroxyl group is The basic aminoacid is		Histidine	arginine proline	threonine serine	threonine Histidine
All aminoacids are optically active except	glycine glycine	serine	threonine	tryptophan	glycine
The aminoacid which synthesizes many hormones is	valine	phenylalanine	alanine	Histidine	phenylalanine
The ammoacid which synthesizes many normones is	vanne	phenyiaianine	alailille	riistidille	рпенугаганше
Aminoacids are insoluble in .	acetic acid	chloroform	ethanol	benzene	benzene
The sulphur containing aminoacid is	glycine	methionine	valine	homoserine	methionine
The melting point of aminoacids is above	100° C	180° C	200° C	220° C	200° C
From two aminoacids peptide bond formation involves the removal of one molecule of	ammonia	water	carbondioxide	carboxylic acid	water
Normal daily output of urea through urine in grams is	10 to 20	15 to 25	20 to 30	25 to 35	20 to 30
An example of globulin is	leucosin	tuberin	oryzenin	legunelin	tuberin
An example of scleroprotein is	glutenin	gliadin	salmine	elastin	elastin
An example of metalloprotein is	elastin	siderophilin	mucin	glutenin	siderophilin
Many globular proteins are stable in water solution	hydrogen bond	covalent bond	salt bonds	disulphide bonds	disulphide bonds
although they lack in					
Each turn of a-helix consists of aminoacids.	3.2	3	2.8	3.6	3.6
The distance traveled per turn of a-helix is	0.34 nm	0.44nm	0.54nm	0.64nm	0.54nm

a-helix is stabilized by bonds.	hydrogen	disulphide	nonpolar	polar	hvdrogen
The milk protein in the stomach of infants is digested by	pepsin	trypsin	chymotrypsin	rennin	rennin
The half life of antibody proteins is	4 weeks	2 weeks	3 weks	1 week	2 weeks
Carboxy peptidase B in the small intestine hydrolyses peptides containing	Leucine	Isoleucine	Arginine	Cysteine	Arginine
Protein anabolism is stimulated by	ACTH	Testosterone	Glucagons	Epinephrine	Testosterone
The metabolism of protein is integrated with that of carbohydrate and fat through	Oxaloacetate	Citrate	Isocitrate	Malate	Oxaloacetate
In the small intestine trypsin hydrolyzes peptide linkages containing	Arginine	Histidine	Serine	Aspartate	Arginine
Chymotrypsin in the small intestine hydrolyzes peptide linkages containing	Phenylalanine	Alanine	Methionine	Valine	Phenylalanine
The building up and breakdown of protoplasm are concerned with the metabolism of	Carbohydrates	Fats	Protein	Minerals	Protein
Aminoacids provide the nitrogen for the synthesis of	the bases of the Phospholipids	uric acid	glycolipids	chondroitin sulphates	the bases of the Phospholipids
The end product of aminoacid nitrogen metabolism in uricotelic organisms is	bilirubin	urea	uric acid	biliverdin	uric acid
Oxidative conversion of many aminoacids to their corresponding a-keto acids occurs in mammalian	liver and kidney	adipose tissue	pancreas	intestine	liver and kidney
Synthesis of glutamine is accompanied by the hydrolysis of	ATP	ADP	TPP	creatinine phosphate	ATP
The biosynthesis of urea occurs mainly in the liver	cytosol	mitochondria	microsomes	nuclei	mitochondria
One molecule of urea is synthesized at the expense of number of ATP.	1	2	4	3	3
The symptom of ammonia intoxication includes	blurring of vision	constipation	mental confusion	diarrhea	blurring of vision
The pH at which the aminoacid has no net charge and does not move in the electric field is called as	Isobarric	piezoelectric	isoelectric	isothermic	isoelectric
The only ketogenic amino acid is	leucine	isoleucine	alanine	glycine	leucine
In severe acidosis, the output of urea is	Decreased	Slightly decreased	Highly increased	Moderately increased	Decreased
Glutathione is a	dipeptide	tripeptide	polypeptide	pentapeptide	tripeptide
The transaminase activity requires the coenzyme	ATP	B6-PO ₄	NAD+	FAD+	B6-PO ₄
Polymers of more than 100 aminoacids are termed as	Proteins	Polypeptides	Aminoacids	Glucoprotein	Proteins
The example of Phosphoprotein is	Mucin	Ovovitellin	Ovomucoid	Tendomucoid	Ovovitellin
Each hydrogen bond is quite	Strong	Weak	Non of the above	Both of the above	Weak
Glutamic dehydrigenase is a	Monomer	Tetramer	Dimer	Polymer	Tetramer
Aldolase molecule is a	Monomer	Tetramer	Trimer	Dimer	Trimer
Foetal haemoglobin contains	Two α and two γ chains	Two α and two β chains	Two α and two α chains	Two β and two β chains	Two α and two γ chains

D-41	Alonina	Sussimul Co A	Mathianina	Valine	C
Both valine and isoleucine on catabolism produce	Alanine	Succinyl-CoA	Methionine	vanne	Succinyl-CoA
By overheating, the nutritional value of cereal protein is	Increased	Lowered	Unchanged	Changed	Lowered
Transamination is a process.	Irreversible	Reversible	Inhibition	a & c	Reversible
Most aminoacid are substrates for transamination except	Alanine	Threonine	Serine	Valine	Threonine
In brain, the mechanism for the removal of ammonia is the formation of	Glutamate	Aspartate	Asparagine	Glutamine	Glutamine
The Competitive inhibitor of arginine is	Citrulline	Malate	Lysine	Serine	Lysine
Uremia occurs in	Cirrhosis	Nephritis	Diabetes	Thrombosis	Nephritis
Cysteine is formed from	Serine	Valine	Glutamine	Methionine	Methionine
on metabilism vields acetoacetate and acetyl -	Serine	Leucine	Valine	Glutamine	Leucine
CoA					
mg of tryptophan produce I mg of niacin.	20	40	80	60	60
UNIT V	A	В	C	D	Answer
	A	В	C	В	
The net numbers of ATP production of glycolysis under	2	4	8	24	24
aerobic condition is The net numbers of ATP production of glycolysis under	2	4	0	24	8
	2	4	0	24	8
anaerobic condition is	2	4	8	24	
The net numbers of ATP production in a TCA cycle is	2	4	8	24	24
			excessive		
Polyuria is	excessive thirst	excessive appetite	excretion of urine	glucose in urine	excessive excretion of urine
			excessive		
Polydipsia is	excessive thirst	excessive appetite	excretion of urine	glucose in urine	excessive thirst
Polyphagia is	excessive thirst	excessive appetite	excessive excretion of urine	glucose in urine	excessive appetite
			excessive		
Glucosuria is	excessive thirst	excessive appetite	excretion of urine	glucose in urine	glucose in urine
How may irreversible steps occur in glycolysis	1	2	3	4	3
The important reducing power produced in HMP shunt					
pathway is	NADH	FADH	NADPH	FADH2	NADPH
Lactate is converted into glucose in	Liver	Muscle	Kidney	Lung	Liver
Which of the following enzyme links glycolysis and TCA			Phosphoenol		
cycle	Pyruvate carboxylase	Pyruvate kinase	pyruvate kinase	Pyruvate dehydrogenase	Pyruvate dehydrogenase
	,		Phosphoenol		
Pyruvate is converted to oxaloacetate by	Pyruvate carboxylase	Pyruvate kinase		Pyruvate dehydrogenase	Pyruvate dehydrogenase
			Phosphoenol	, , ,	
Oxaloacetate is converted to phosphoenolpyruvate by	Pyruvate carboxylase	Pyruvate kinase	*	Pyruvate dehydrogenase	Phosphoenol pyruvate kinase

			Cl 6	T	
Cl	Character for an almost an	Classes for an assessed	Glycogen from	Classes for an expense.	Cl f
Glucagon stimulates synthesizing of	Glucose from glycogen	Glucose from pyruvate	glucose	Glycogen from pyruvate	Glucose from glycogen
E-i		CI C	Glycogen from	CI C	Cl f
Epinephrine stimulates synthesizing of	Glucose from glycogen	Glucose from pyruvate	glucose	Glycogen from pyruvate	Glucose from glycogen
highly concentrated in muscle and brain	Carnosine	Ornithine	Ergothionine	Kynurenine	Carnosine
tissues	3.6'11	NT: 1 1:	NT'.	G . 1	N74. 17
test is positive for the aminoacid Cysteine.	Millon	Ninhydrin	Nitroprusside	Catalase	Nitroprusside
The Protein act as the defense against infection by	Protein antigen	Protein antibodies	Amyloprotein	Glucoprotein	Protein antibodies
The first incoming NTP binds at the start	DNApolymerase I	polymerases	DNA polymerase	RNA polymerase	RNA polymerase
point of initiation	Divipolymerase i	polymerases	Divir polymerase	Kivi polymerase	Ki (11 polymerase
The word enzyme is derived from the Greek meaning in	Bacteria	Microbes	Yeast	Fungi	Yeast
The word emigrate is derived from the order medianing in					
The term enzyme was first used by in 1878.	Watson	Alan Ferst	Kuhne	Stevens	Kuhne
Non-protein chemical compound that is required for the	Coenzyme	Cofactor	Isomerases	Synthetases	Cofactor
protein's biological activity				-	
The 40S subunit contains 18S rRNA and about	10	20	40	30	30
aboutpolypeptide chains.					
The reactions in which two molecules are joined at the	Ligases	Isomerases	Transferases	Hydrolases	Ligases
expense of an energy source are catalyzed by					
Michaelis-Menton equation is	$v = V \max [S]/[S] + K m$	v = [S]+Km/Vmax[S]	$v = V \max$	v = Km/Vmax	$v = V \max[S]/[S] + K m$
			[S]+Km/[S]	[S]+[S]	
Retinal is reduced to retinol by retinene reductase in	NAD+	NADP+	NADH+H+	NADPH+H+	NADH+H+
presence of the coenzyme The unit of genetic information is the or	Comom	Codon	Gene	Anticodon	Gene
The unit of genetic information is the or cistron.	Genom	Codon	Gene	Anticodon	Gene
Chromatin consists of a long double stranded	RNA	DNA	Subunit	tDNA	DNA
molecules	KVA	DNA	Subunit	DIVA	DNA
The mammalian ribosome contains the number of major	1		4	5	
nucleoprotein subunits.		2			2
Each transfer RNA molecule contains the number of	J.B.Sumner	Koshland	Menten	Fisher	J.B.Sumner
nucleotides					
Gene is a segment of the DNA molecule containing base	300	400	500	600	600
pairs about					
The sequences recognized by RNA polymerase are called	Terminator	Promoter	Both of the above	Non of the above	Promoter
Optimum temperature for an enzyme-catalyzed	30°C-40°C	25°C-40°C	35°C-45°C	85°C-90°C	25°C-40°C
reaction is		_			
DNA is refered as	Transforming factor	Range constants	Transplantation	Heterogenous factor	Transforming factor
M DNA 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	15000 +- 20000	20000 4- 25000	factor	20000 4- 50000	20000 4 70000
Messenger RNA has a molecuar weight of	15000 to 30000	20000 to 35000	25000 to 40000	30000 to 50000	30000 to 50000
The COC and and the section for a DNA a focus DNA	190	30S	28S	40S	288
The 60S subunit contains 5s rRNA a 5.8S;rRNA and	18S	303	200	405	285
DNA is denotured by	Acid	Alkali	Heat	All the above	All the above
DNA is denatured by	Aciu	Alkali	rieat	All the above	All the above

A chemical bond formed between two molecules when the	Hydrophobic interaction	Hydrophilic interaction	Disulphide bonds	Peptide bonds	Peptide bonds
carboxyl group of one molecule reacts with the amino			_		•
group of the other molecule, releasing a molecule of water					
(H2O)					
cGMP is antagonistic to	cAMP	CTP	Non of the above	All the above	cAMP
Michaelis-Menten model describes	Enzyme stability	Enzyme specificity		None of the above	Enzyme kinetics
cGMP is formed fromby the enzyme adenyl	ATP	GDP	CTP	CDP	ATP
cyclase					
An example for a semipermeable membrane is	Plasma membrane	Cell membrane	Dialysis membrane	All the above	All the above
a procedure to remove waste products and	Osmosis	Reverse osmosis	Electrophoresis	Dialysis	Dialysis
excess fluid from the blood when the kidneys stop					
working properly					
is a functional group consisting of the formula RN=C=NR.	Gluteraldehyde	Carbodiimides	Carbondioxide	Glycoside	Carbodiimides
The lactam form is the predominant tautomer of	Uracil	Cytosine	Adenine	Xanthine	Uracil
The chemical name 2-amino-6-oxypurine is said to	Adenine	Xanthine	Guanine	Hypoxinthine	Guanine
be	racinic	runume	Guannie	Турохинише	Guillie
All catalysts are enzymes, but not all enzymes are	TRUE	FALSE	Non of the above	both of the above	TRUE
catalysts.					
is an important molecule in metabolism, used	Pyruvate	Carboxide	Acetyl Co A	Acetamide	Acetyl Co A
in many biochemical reactions			-		
An important antioxidant in plants, animals, fungi, and	Gluteraldehyde	Glutamate	Glycerol	Glutathione	Glutathione
some bacteria and archaea, preventing damage to					
important cellular components caused by reactive oxygen					
species such as free radicals, peroxides, lipid peroxides					
and heavy metals					
A dicarboxylic acid with structure	Succinic acid	Malonic acid	Pyruvic acid	Formic acid	Malonic acid
CH ₂ (COOH) ₂	En	T-t-1 F	C1	Dun dan at	m 4 1E
In Vmax, [Et] denotes	Enzyme at time t	Total Enzyme	Substrate 5 th	Product 4 th	Total Enzyme
Lyases belongs to class in the major classes of	314	2"4	5"	4"	4"
Enzymes. The is a molecule upon which an enzyme acts	Substrate utilized	Substrate involved	Substrate	Substrate recovered	Substrate oxidized
			oxidized		
The initiation of DNA synthesis requires priming by a	RNA	DNA	Hydroxyl group	Alkyl group	RNA
short length of	C.		77 . 1	27 .	CT.
International system of units is	SI	Anson	Katal	Newton	SI
A biochemically active compound formed by the	Apoenzyme	Isoenzyme	Holoenzyme	Heyteroenzyme	Holoenzyme
combination of an enzyme with a					
Coenzyme Engymes can be precipitated by	Ammonium Sulphate	Ammonium Oxalate	Ammonium	Ammonium oxide	Ammonium Sylphoto
Enzymes can be precipitated by	Animomum Surphate	Animolium Oxalate	Chloride	Animolium oxide	Ammonium Sulphate
is the inorganic chemical component that is required for enzyme activity	Coenzyme	Protein	Aminoacids	Cofactor	Cofactor

In the international union of Biochemistrty	1923		1941	1963	
	1923		1941	1963	
gave the classification and naming system of enzymes on					
the basis of overall reaction catalysed.		1961			1961
An active group of cysteine is	Alcoholic	Imidazole	Sulfhydryl	Phenolic	Sulfhydryl
Induced Fit Mechanism was proposed by	Fisher	Michael		Koshland	Koshland
induced Fit Mechanism was proposed by	risilei	Michael	Kunne	Kosmand	Kosmanu
The Substrate is specific towards of the	Active site	Allosteric group	Hydroxyl group	Inactive group	Active site
enzyme.					
For entrapping enzymes instead of cellulose acetate fibres	Calcium Chloride	Calcium oxalate	Calcium alginate	Cellulose oxide	Calcium alginate
is used					
DNA gyrases act to relieve the stress generated	Gyrases	Helicases	polymerases	All the above	Helicases
by					
The enzyme involved in hydrolysis is	Reductases	Lyases		Hydrolases	Hydrolases
IUPAC is	International Unit of Pure and	International Union of Pure		Indian Union of Pure and	International Union of Pure and Applied Chemistry
	Applied Chemistry	and Applied Chemistry	Pure and Applied	Applied Chemistry	
			Chemistry		
Fifth class enzyme is	Oxidoreductase	Lyases	Hydrolases	Isomerases	Lyases
Last digit number of E.C.Number represents the	Register number	Code number	Serial number	Account number	Serial number
of enzyme within the subsub class					
Systematic code number is otherwise known as	Enzyme cofactor number	Enzyme coenzyme number	Enzyme	Enzyme Commission	Enzyme Commission number
			coordinate	number	
			coordinate	number	
			number	number	
An example for yeast enzymes having E.C.number	Invertase	Raffinase	number	Lipase	Lactase
An example for yeast enzymes having E.C.number 3.2.1.23 is E.C.number of a-amylase is	Invertase 3.2.1.1	Raffinase 3.2.1.3	number Lactase		Lactase 3.2.1.1
3.2.1.23 is E.C.number of α-amylase is			number Lactase	Lipase 3.2.1.2	3.2.1.1
3.2.1.23 is	3.2.1.1	3.2.1.3 toxic	number Lactase 1.1.3.4 heterogenous	Lipase 3.2.1.2 extracellular	
3.2.1.23 is E.C.number of α-amylase is β-amylase is an enzyme.	3.2.1.1 intracellular	3.2.1.3	number Lactase 1.1.3.4 heterogenous Lipase	Lipase 3.2.1.2	3.2.1.1 extracellular
3.2.1.23 is E.C.number of α-amylase is β-amylase is an enzyme. An example for intracellular enzyme is	3.2.1.1 intracellular Pectinase	3.2.1.3 toxic Aminoacylase	number Lactase 1.1.3.4 heterogenous Lipase 3.2.1.15	Lipase 3.2.1.2 extracellular Papain	3.2.1.1 extracellular Aminoacylase
3.2.1.23 is E.C.number of α-amylase is β-amylase is an enzyme. An example for intracellular enzyme is E.C number of Raffinase is An example for extracellular enzyme is	3.2.1.1 intracellular Pectinase 3.2.1.23 Aminoacylase	3.2.1.3 toxic Aminoacylase 3.2.1.22 Lipase	number Lactase 1.1.3.4 heterogenous Lipase 3.2.1.15 Raffinase	Lipase 3.2.1.2 extracellular Papain 3.2.1.1 Catalase	3.2.1.1 extracellular Aminoacylase 3.2.1.22 Lipase
S.2.1.23 is E.C.number of α-amylase is β-amylase is an enzyme. An example for intracellular enzyme is E.C number of Raffinase is An example for extracellular enzyme is E.C.number of α-amylase is	3.2.1.1 intracellular Pectinase 3.2.1.23 Aminoacylase 3.2.1.1	3.2.1.3 toxic Aminoacylase 3.2.1.22 Lipase 3.2.1.3	number Lactase 1.1.3.4 heterogenous Lipase 3.2.1.15 Raffinase 1.1.3.4	Lipase 3.2.1.2 extracellular Papain 3.2.1.1 Catalase 3.2.1.2	3.2.1.1 extracellular Aminoacylase 3.2.1.22 Lipase 3.2.1.1
E.C.number of α-amylase is β-amylase is an enzyme. An example for intracellular enzyme is E.C number of Raffinase is An example for extracellular enzyme is E.C.number of α-amylase is An example for a animal enzyme is	3.2.1.1 intracellular Pectinase 3.2.1.23 Aminoacylase 3.2.1.1 Rennet	3.2.1.3 toxic Aminoacylase 3.2.1.22 Lipase 3.2.1.3 α-amylase	number Lactase 1.1.3.4 heterogenous Lipase 3.2.1.15 Raffinase 1.1.3.4 Pullulanase	Lipase 3.2.1.2 extracellular Papain 3.2.1.1 Catalase 3.2.1.2 Raffinase	3.2.1.1 extracellular Aminoacylase 3.2.1.22 Lipase 3.2.1.1 Rennet
S.2.1.23 is E.C.number of α-amylase is β-amylase is an enzyme. An example for intracellular enzyme is E.C number of Raffinase is An example for extracellular enzyme is E.C.number of α-amylase is	3.2.1.1 intracellular Pectinase 3.2.1.23 Aminoacylase 3.2.1.1	3.2.1.3 toxic Aminoacylase 3.2.1.22 Lipase 3.2.1.3	number Lactase 1.1.3.4 heterogenous Lipase 3.2.1.15 Raffinase 1.1.3.4 Pullulanase Lipase	Lipase 3.2.1.2 extracellular Papain 3.2.1.1 Catalase 3.2.1.2	3.2.1.1 extracellular Aminoacylase 3.2.1.22 Lipase 3.2.1.1