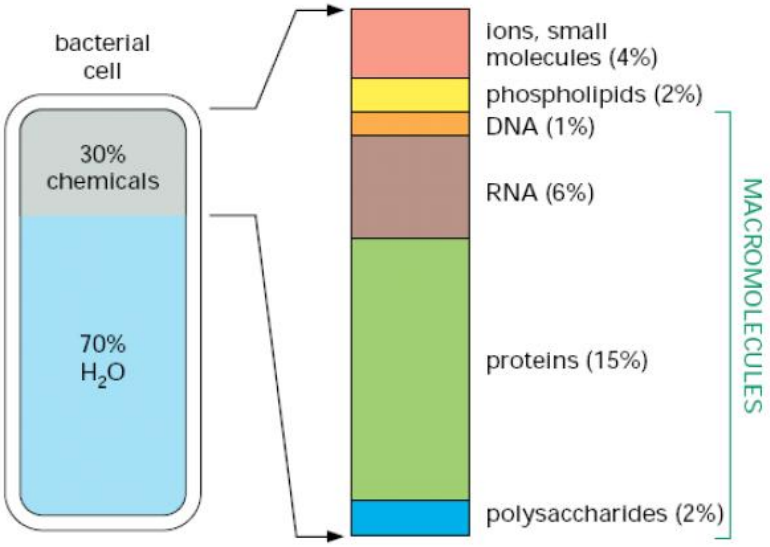
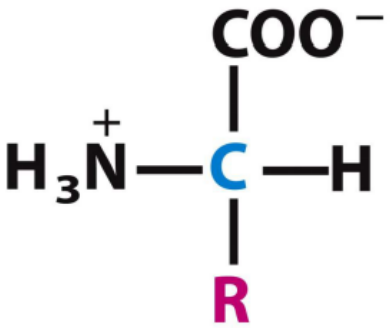
Biological Chemistry Notes

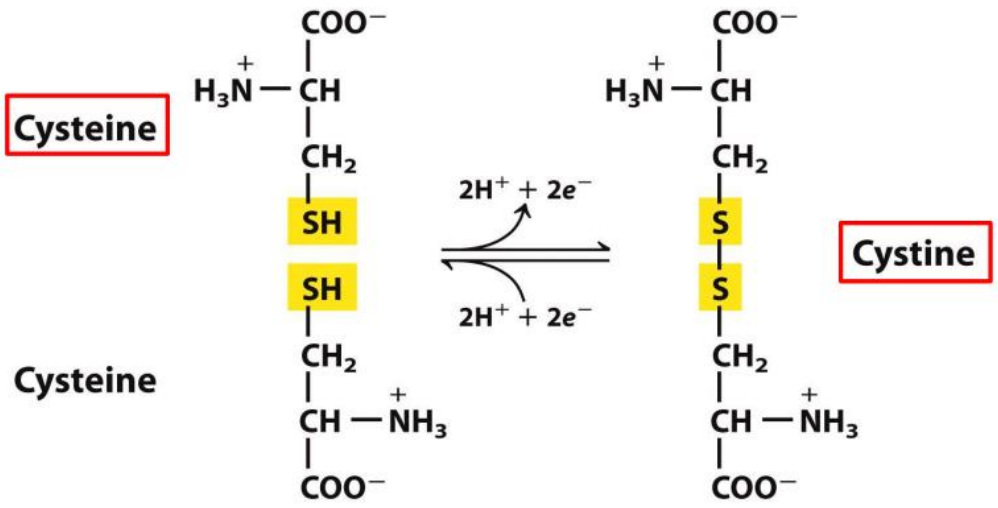
Proteins

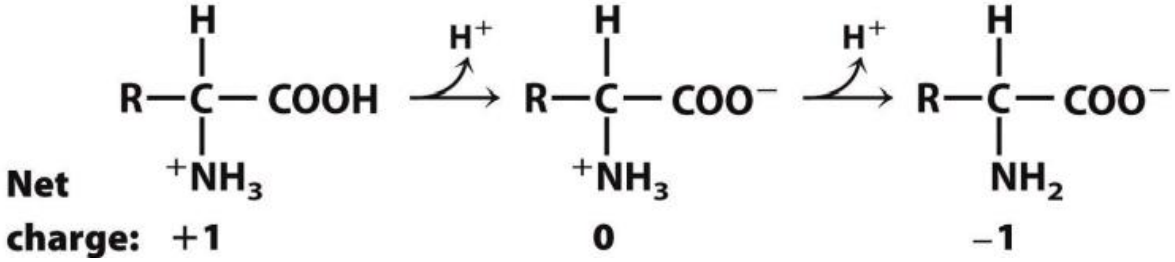
- Amino acids are zwitterions i.e. they are hybrid ions and can exist either as cations or as anions
- pI means isoelectric point, the pH at which an amino acid exists in zwitterionic form and will not move under an electric field
- Zwitterionic molecules are positively charged (cationic) below their pI values and negatively charged above them
- Peptides and proteins – named beginning from the amino terminal residue, which by convention is placed at the left
- The final pI of a polypeptide or protein is not a simple average of the pIs of individual amino acids. It typically depends on several factors as a polypeptide will have only one free α-amino group, one free α-carboxyl group, and a few ionisable R groups, which will determine its pI value
- Usually very small difference in ΔG between folded (functional) and unfolded (non-functional) states i.e. 20-65 kJ/mol. This means that proteins are only marginally stable in native state
- The peptide bond has partial double bond like character, which provides some degree of rigidity to the protein structure – it is rigid and planar
- Secondary structure describes the local spatial arrangement of its main-chain atoms, without regard to the conformation of its side chains or its relationship to other segments
- Alpha-helicies form most readily as they make optimum use of internal hydrogen bonding
- Alpha helixes have 3.6 residues per turn, with alanine forming helices most readily and glycine and proline least often
- Beta-turns typically involve 4 amino acid residues to connect the ends of two adjacent antiparallel β-sheets
- A motif is a recognisable folding pattern involving two or more elements of secondary structure and the connection(s) between them. A motif may or may not be independently stable
- Domain is part of a polypeptide chain that is independently stable or could undergo movements as a single entity with respect to the entire protein. Different domains often have distinct functions
- Proteins with multiple polypeptide subunits form quaternary structures
- Protomer: the repeating structural unit in a multimeric protein, whether a single subunit or a group of subunits
- Fibrous proteins have simple repeating elements of secondary structure and mainly serve the structural roles
- Globular proteins often have several types of secondary structures in the same polypeptide chain, thus having more complicated tertiary structures
- Chaperons are proteins that interact with partially folded or improperly folded polypeptides facilitating correct folding pathways or providing microenvironments in which folding can occur

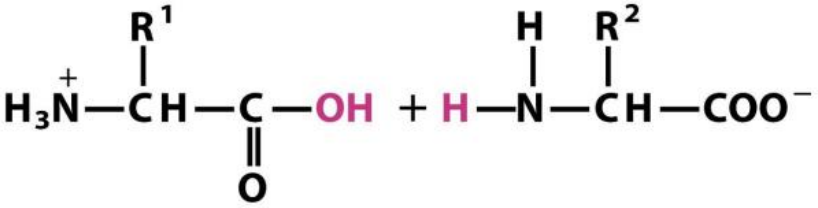




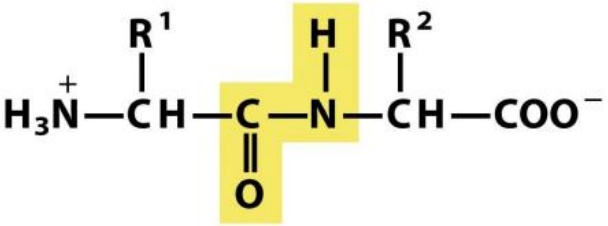
Amino acid	Abbreviation/ symbol	M_r*	pK_a values: pK_1 (—COOH)	pK_2 (—NH_3^+)	pK_R (R group)	pI	Hydropathy index†	Occurrence in proteins (%)‡
Nonpolar, aliphatic								
R groups								
Glycine	Gly G	75	2.34	9.60		5.97	−0.4	7.2
Alanine	Ala A	89	2.34	9.69		6.01	1.8	7.8
Proline	Pro P	115	1.99	10.96		6.48	1.6	5.2
Valine	Val V	117	2.32	9.62		5.97	4.2	6.6
Leucine	Leu L	131	2.36	9.60		5.98	3.8	9.1
Isoleucine	Ile I	131	2.36	9.68		6.02	4.5	5.3
Methionine	Met M	149	2.28	9.21		5.74	1.9	2.3
Aromatic								
R groups								
Phenylalanine	Phe F	165	1.83	9.13		5.48	2.8	3.9
Tyrosine	Tyr Y	181	2.20	9.11	10.07	5.66	−1.3	3.2
Tryptophan	Trp W	204	2.38	9.39		5.89	−0.9	1.4
Polar, uncharged								
R groups								
Serine	Ser S	105	2.21	9.15		5.68	−0.8	6.8
Threonine	Thr T	119	2.11	9.62		5.87	−0.7	5.9
Cysteine§	Cys C	121	1.96	10.28	8.18	5.07	2.5	1.9
Asparagine	Asn N	132	2.02	8.80		5.41	−3.5	4.3
Glutamine	Gln Q	146	2.17	9.13		5.65	−3.5	4.2
Positively charged								
R groups								
Lysine	Lys K	146	2.18	8.95	10.53	9.74	−3.9	5.9
Histidine	His H	155	1.82	9.17	6.00	7.59	−3.2	2.3
Arginine	Arg R	174	2.17	9.04	12.48	10.76	−4.5	5.1
Negatively charged								
R groups								
Aspartate	Asp D	133	1.88	9.60	3.65	2.77	−3.5	5.3
Glutamate	Glu E	147	2.19	9.67	4.25	3.22	−3.5	6.3

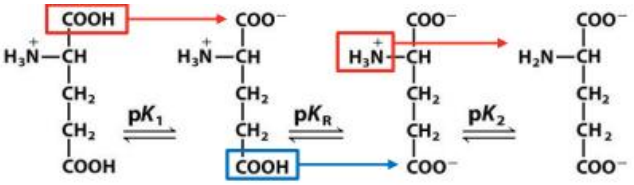

Cysteine
Cysteine
2H+ + 2e−
2H+ + 2e−
Cystine

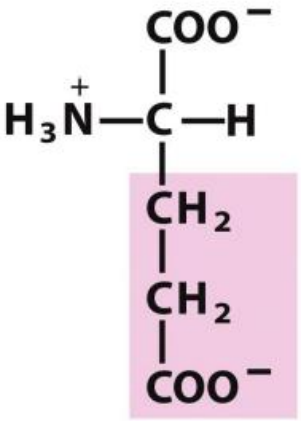

H+
H+
Net
charge: +1
0
−1

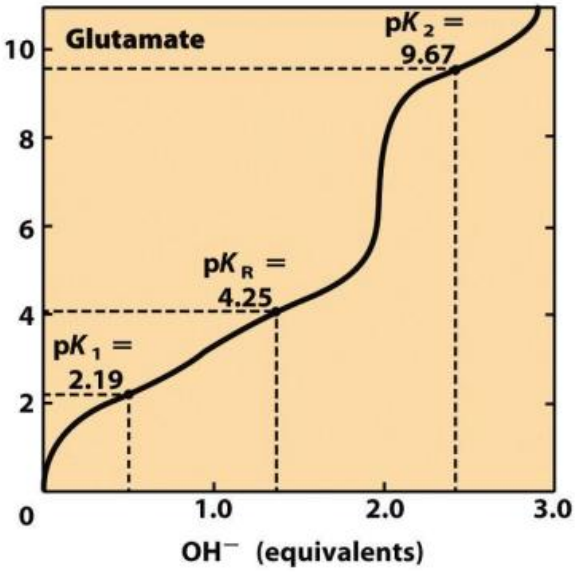



H2O
H2O
Condensation reaction







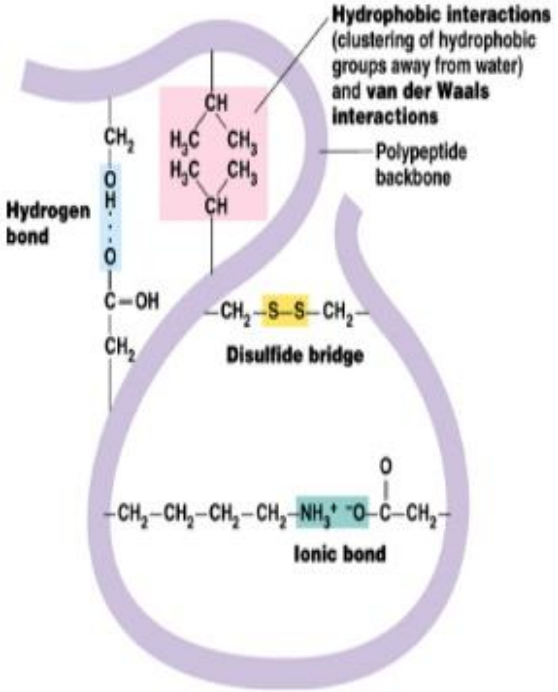


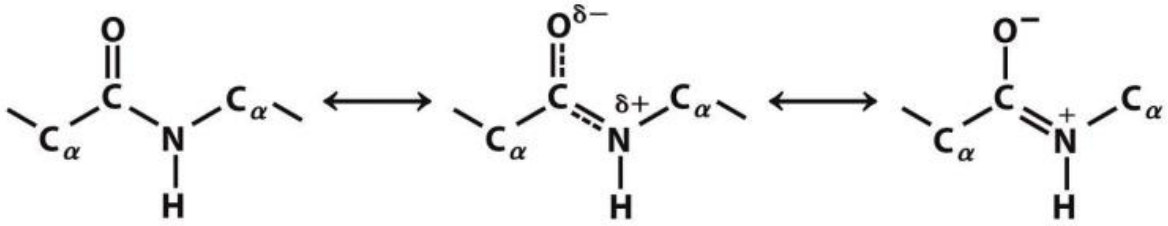
Tertiary structure is

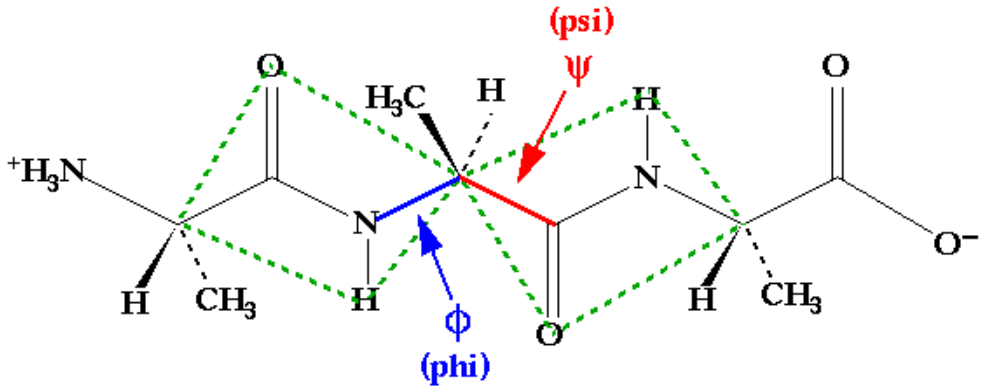
determined by a variety of interactions (bond formation) among R groups and between R groups and the polypeptide backbone.

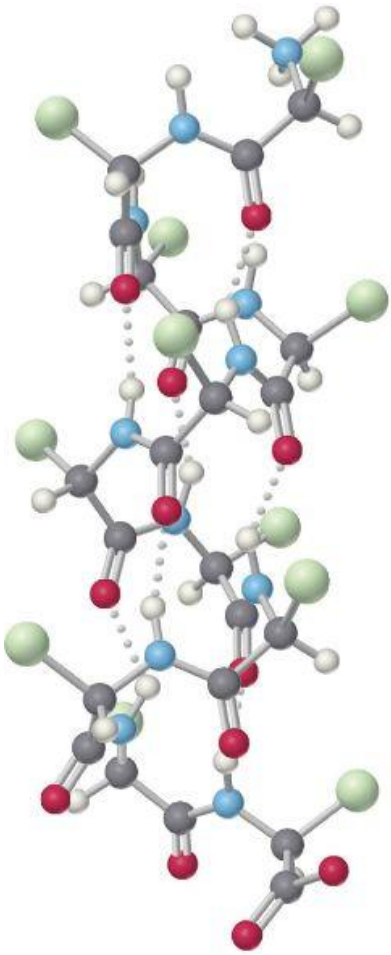
a. **The weak interactions** include:

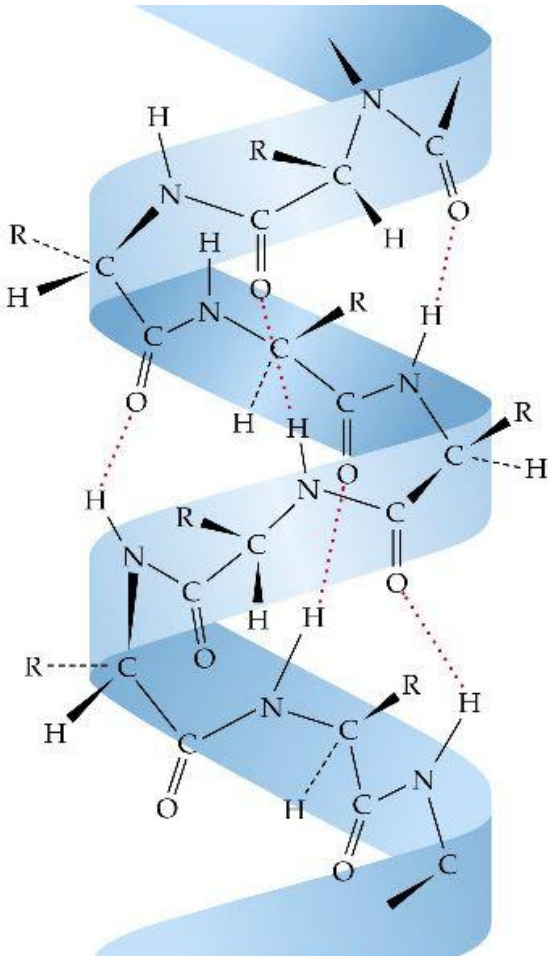
- **Hydrogen bonds** among polar side chains
- **Ionic bonds** between charged R groups (basic and acidic amino acids)
- **Hydrophobic interactions** among hydrophobic (non polar) R groups.



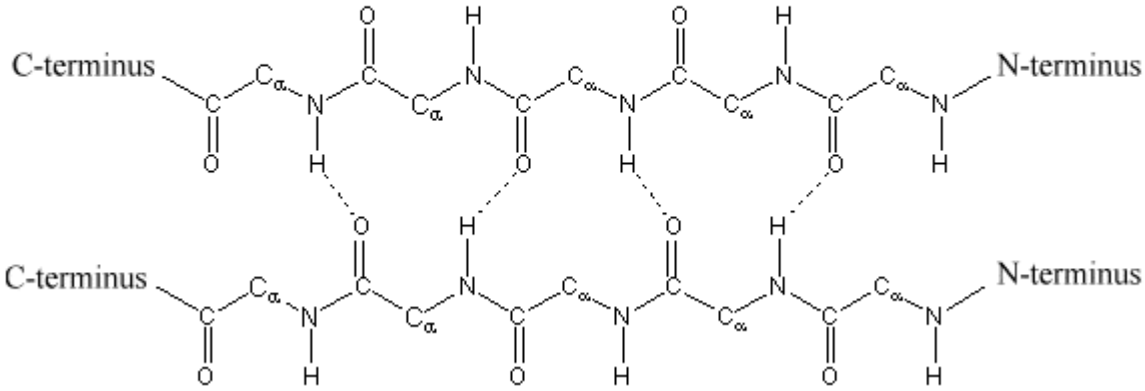



(psi)
ψ
(phi)
ϕ





Parallel β Sheet



Hemoglobin

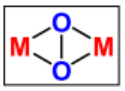
- Three known oxygen transport and storage systems:
  - Haemoglobin (Hg): function in all vertebrates and many invertebrates, plus myoglobin found in muscles
  - Hemocyanin (Hc): function in arthropods and molluscs
  - Hemerythrin (Hr): function in 4 phyla of marine invertebrates
- Hemoglobin exists as a tetramer, each polypeptide chain possessing a folded structure similar to Mb, with two identical α chains and two identical β chains
- The subunits exhibit cooperative binding, so the affinity increases as more subunits are bound. As oxygen ligates to the vacant position around the iron, the haem group flattens (into relaxed state), pulling up the proximal histidine, and hence causing a conformational change of the entire tetramer
- If porphyrin ring is not protected by the surrounding protein matrix, then irreversible oxidation occurs
- The Bohr effect helps to compensate for a fall in pH as oxygen is used and CO2 produced, by the equilibrium of the reaction CO2 + H2O <-> HCO3- + H+ shifting to the right
- Both CO and CN- bind to the Fe more strongly than O2, and thus will produce oxygen deprivation if allowed to accumulate in high concentrations (normally binding is limited by steric hindrance)

(10^{-3}M) Na > K > Mg > Ca > Fe > Zn > Cu > Mn > Mo > Co > Se (10^{-15}M)

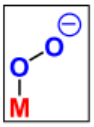
Those involved in oxygen activation Fe > Cu > (Zn) > Mn > Mo

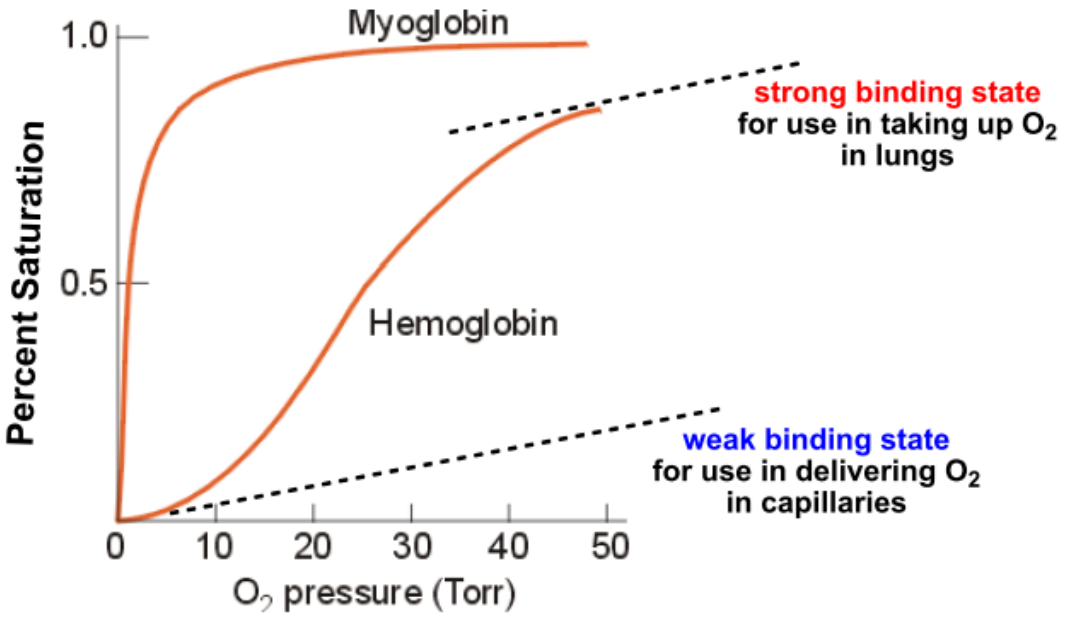
(Cu/Zn) Menkes disease, Wilsons disease, Alzheimers, ALS, CJD

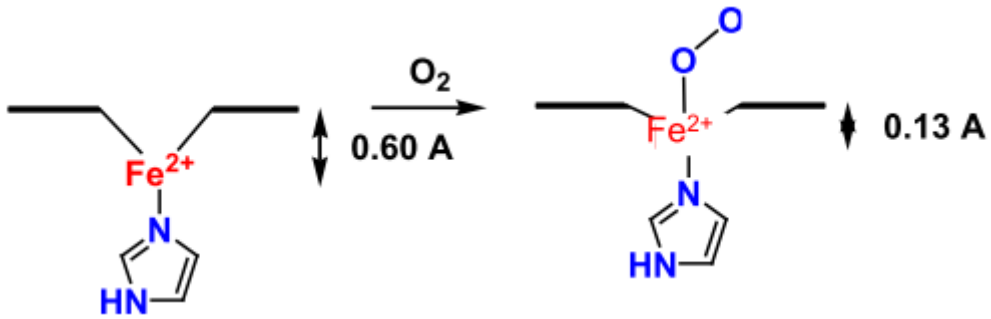
- In **Hr** and **Hc**, the O_2-binding reaction involves an actual reaction of O_2 with a bi metal center to form a peroxide group

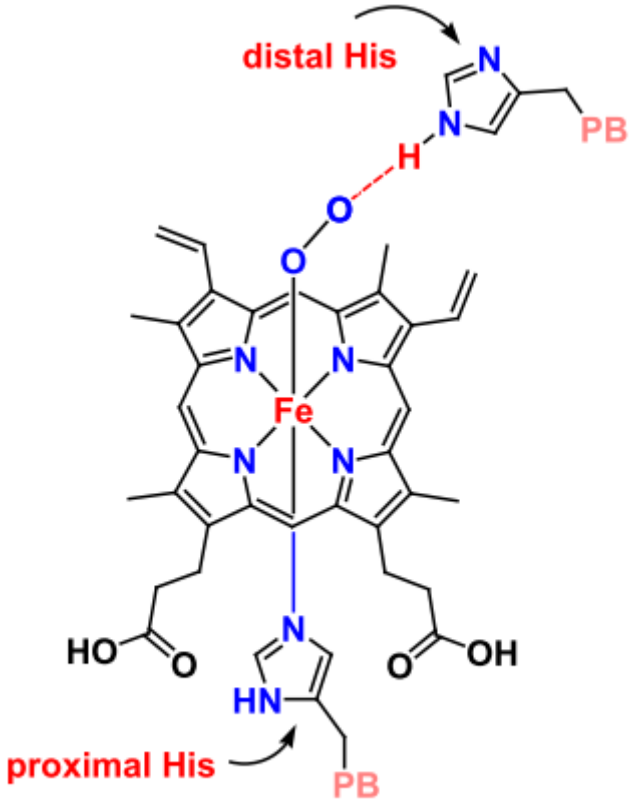


- In **Hemo**, O_2 binds end on to one metal centre, forms a 'superoxide' ion

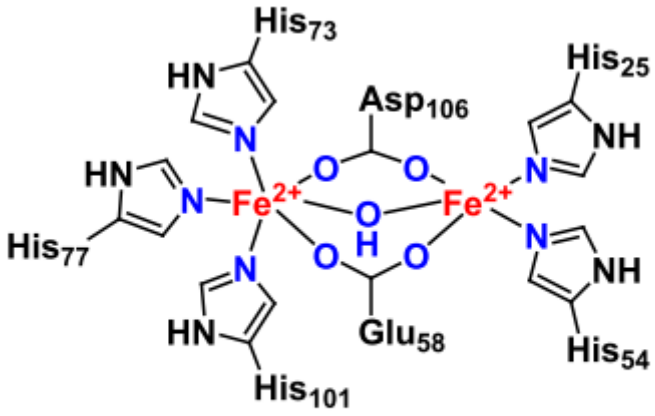



Myoglobin
1.0
0.5
Percent Saturation
strong binding state
for use in taking up O_2
in lungs
Hemoglobin
weak binding state
for use in delivering O_2
in capillaries
0
10
20
30
40
50
O_2 pressure (Torr)

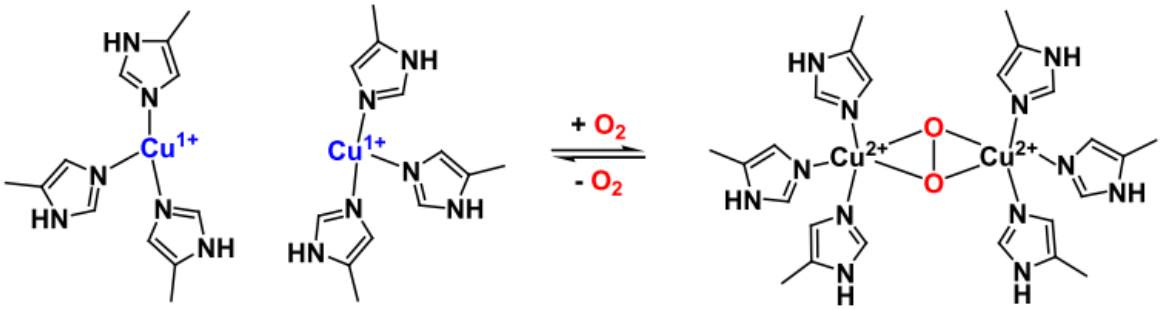

O_2
Fe^{2+}
0.60 A
Fe^{2+}
0.13 A
N
HN
O
O
N
HN


distal His
N
N
H
PB
O
O
N
N
Fe
N
N
HO
O
O
OH
N
HN
proximal His
PB

Active site



Active site

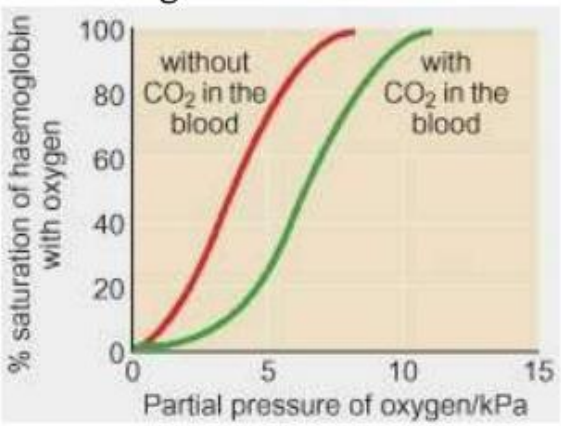


colourless
d^{10} metal centres

bright blue
(hence 'cyanin')
d^{9} metal centres
diamagnetic

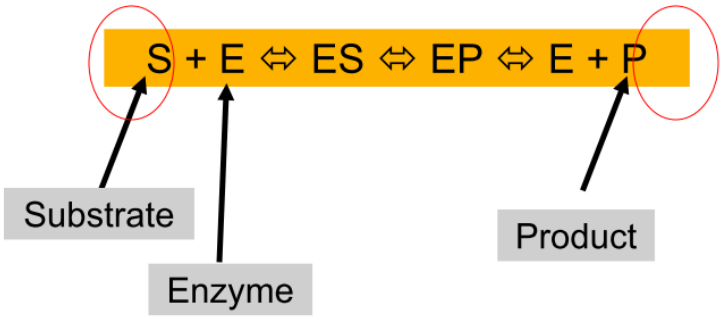
Bohr effect

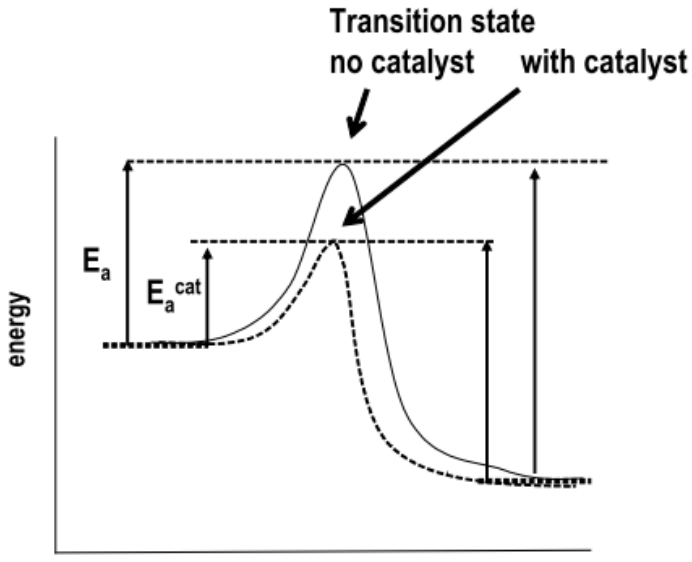
- Increased carbon dioxide levels lowers the pH of the blood
- This affects the ability of the haemoglobin subunits to transport oxygen
- A lower pH causes the Haemoglobin to release more oxygen
- A higher pH causes the Haemoglobin to hold onto more oxygen



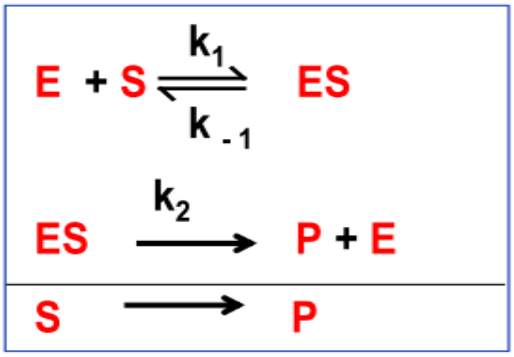
Enzymes

- The active site is the region that binds the substrates (and cofactors if any)
- It is a 3-dimensional cleft (excluding H2O) formed by groups that come from different parts of the amino acid sequence
- The active site takes up a relatively small part of the total volume of an enzyme. The rest being used for scaffolding, regulatory sites, interaction sites for other proteins, and channels
- The interaction of the enzyme and substrate at the active site promotes the formation of the transition state
- The catalyst provides an alternative mechanism for a reaction to occur via a transition state with lower energy
- Tightly bound cofactors are called prosthetic groups, more loosely attached ones are called coenzymes
- An apoenzyme is an inactive enzyme, activation of the enzyme occurs upon binding of an organic or inorganic cofactor. A holoenzyme is an apoenzyme together with its cofactor
- Km is a measure of the enzyme's affinity for the substrate
- Vmax is the maximum catalytic rate at full saturation
- Usually, the binding of the first S changes the rate at which the second S binds. If the binding rate of the second S is increased, it's called positive cooperativity, while if the binding rate of the second S is decreased, it's called negative cooperativity
- **Allosteric regulation** is the regulation of a protein by binding an effector molecule at a site other than the enzyme's active site
- Inhibitors suppress enzyme activity. Irreversible inhibitors are inevitably poisons





Cofactor	Enzyme
Coenzyme	
Thiamine pyrophosphate	Pyruvate dehydrogenase
Flavin adenine nucleotide	Monoamine oxidase
Nicotinamide adenine dinucleotide	Lactate dehydrogenase
Pyridoxal phosphate	Glycogen phosphorylase
Coenzyme A (CoA)	Acetyl CoA carboxylase
Biotin	Pyruvate carboxylase
5′-Deoxyadenosyl cobalamin	Methylmalonyl mutase
Tetrahydrofolate	Thymidylate synthase
Metal	
Zn^{2+}	Carbonic anhydrase
Zn^{2+}	Carboxypeptidase
Mg^{2+}	*Eco*RV
Mg^{2+}	Hexokinase
Ni^{2+}	Urease
Mo	Nitrate reductase
Se	Glutathione peroxidase
Mn^{2+}	Superoxide dismutase
K^{+}	Propionyl CoA carboxylase



Menten Kinetics

- when [S]= K_M, the equation reduces to

$$V = \frac{V_{max}[S]}{K_M + [S]} = \frac{V_{max}[S]}{[S] + [S]} = \frac{V_{max}}{2}$$

- when [S] >> K_M, the equation reduces to

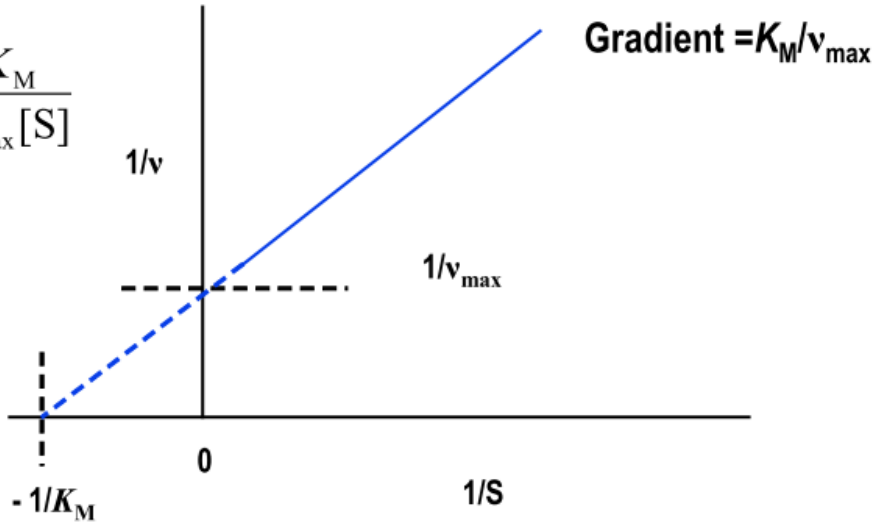
$$V = \frac{V_{max}[S]}{K_M + [S]} = \frac{V_{max}[S]}{[S]} = V_{max}$$

- when [S] << K_M, the equation reduces to

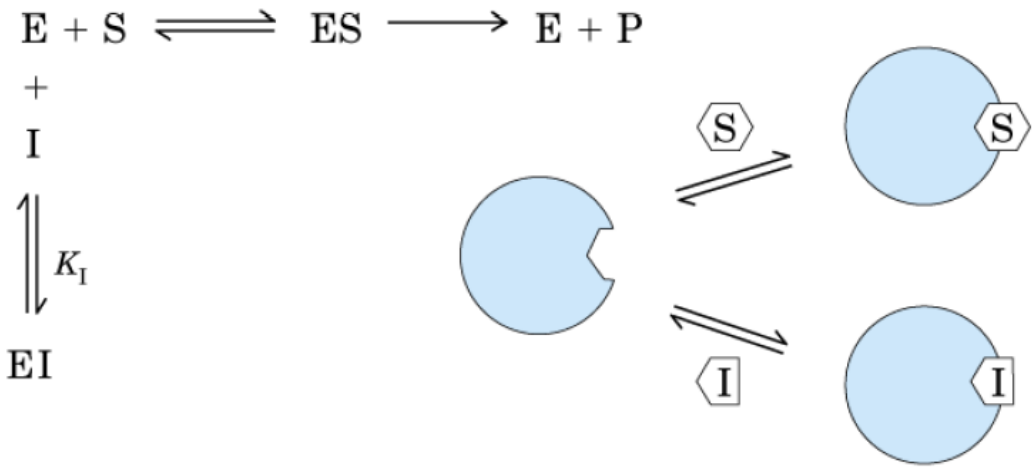
$$V = \frac{V_{max}[S]}{K_M + [S]} = \frac{V_{max}[S]}{K_M} = \frac{V_{max}}{K_M}[S]$$

Lineweaver-Burk plot

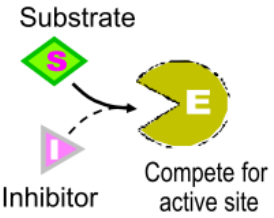
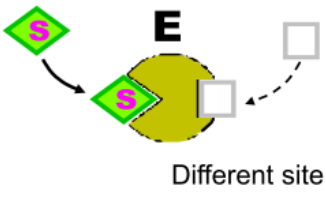
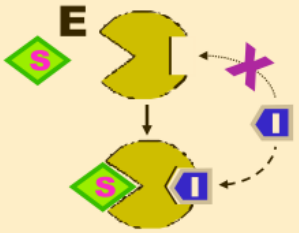
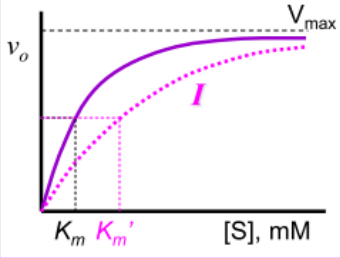
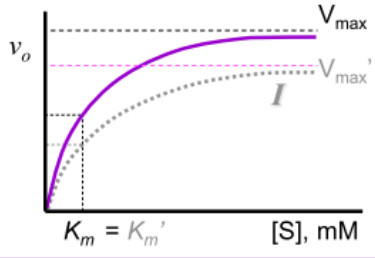
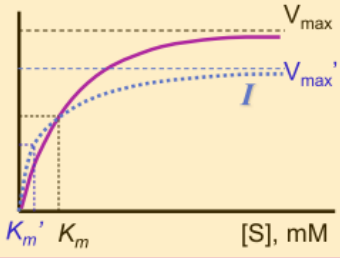
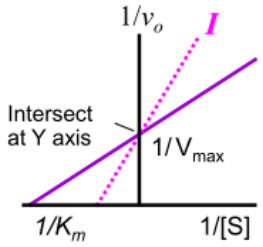
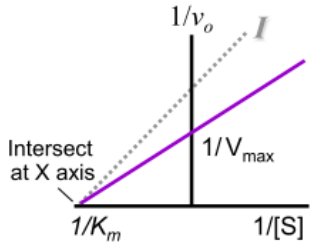
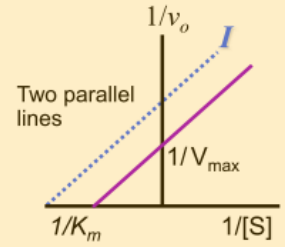
$$\frac{1}{v} = \frac{1}{v_{max}} + \frac{K_M}{v_{max}[S]}$$

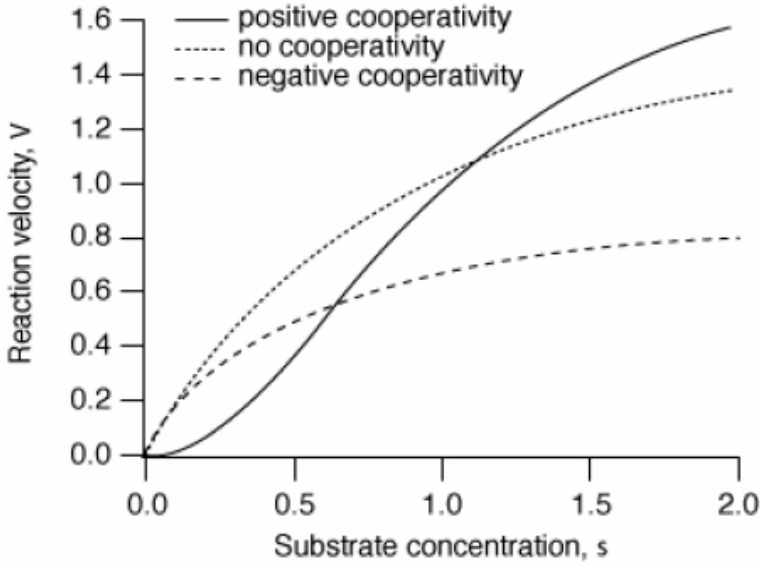


- The extrapolated intercept at 1/S = 0 is equal to $1/v_{max}$
- Use gradient plus intercept on y-axis or the intercept on x-axis to determine K_M.
- Disadvantage: plot dominated by points at low [S], high 1/[S]



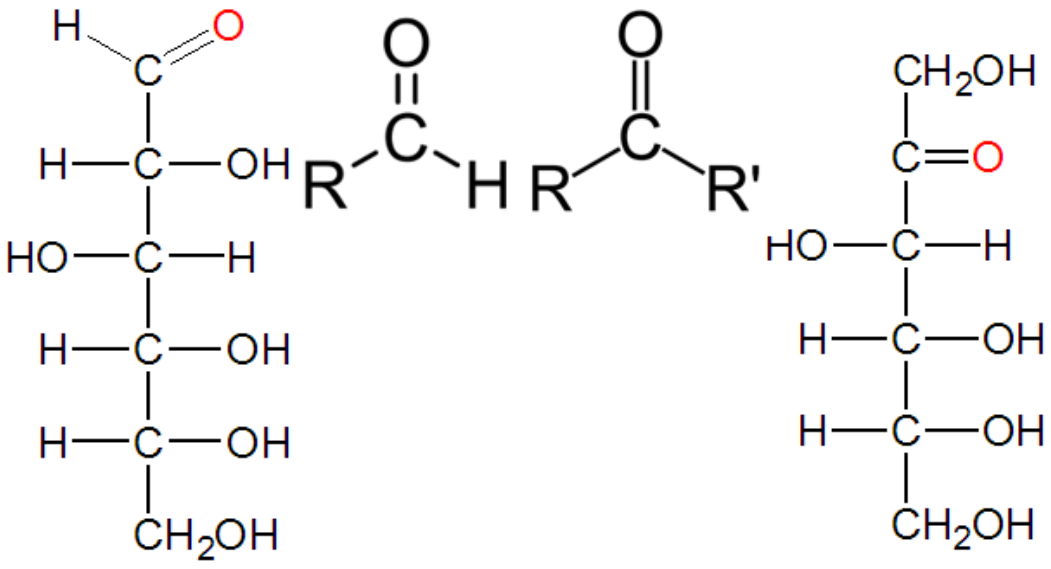
(a) Competitive inhibition

	Competitive	Non-competitive	Uncompetitive
Cartoon Guide			
Equation and Description	$E + S \rightleftarrows ES \rightarrow E + P$ $+$ I $\Updownarrow$ EI	$E + S \rightleftarrows ES \rightarrow E + P$ $+ \quad +$ $I \quad I$ $\Updownarrow \quad \downarrow \uparrow$ $EI + S \rightarrow EIS$	$E + S \rightleftarrows ES \rightarrow E + P$ $+$ I $\downarrow\uparrow$ EIS
	[*I*] binds to free [E] only, and competes with [S]; increasing [S] overcomes Inhibition by [*I*].	[*I*] binds to free [E] or [ES] complex; Increasing [S] can not overcome [*I*] inhibition.	[*I*] binds to [ES] complex only, increasing [S] favors the inhibition by [*I*].
Direct Plots			
	V_{max} unchanged K_m increased	V_{max} decreased K_m unchanged	Both V_{max} & K_m decreased
Double Reciprocal			



Carbohydrates

- Made from aldehyde or keytone groups with multiple hydroxyl groups
- Functions
    - Fuel, energy stores and metabolic intermediates (starch, glycogen)
    - Structural framework of DNA and RNA
    - Structural elements in cell walls of bacteria, plants and fungi as well as the exoskeletons of arthropods
    - Linked to many proteins and lipid
- Carbohydrates with three or more linked sugars include starches and fiber (found in legumes and wholemeal bread and pasta) are categorized as complex carbohydrates
- Plants store glucose as amylose or amylopectin, glucose polymers collectively called starch
- Monosacharides: Aldoses (e.g. glucose) have an aldehyde group at one end, Ketoses (e.g. fructose) have a keto group, usually at C2
- D and L designations are based on the configuration about the single asymmetric C in glyceraldehyde
- L-Sugars are the mirror images of the corresponding D sugars - the conformation at *all chiral carbons* is reversed
- An anomer is one of two stereoisomers of a cyclic saccharide that differs only in its configuration at the hemiacetal or hemiketal carbon, also called the anomeric carbon
- Pentoses and hexoses can cyclise as the ketone or aldehyde reacts with a distal OH. When an aldehyde reacts in this way it forms a hemiacetal, while a ketone forms a hemiketal
- Glucose forms an intra-molecular hemiacetal, as the C1 aldehyde & C5 OH react, to form a 6-member pyranose ring, named after pyran
- Fructose forms either a 6-member pyranose ring, by reaction of the C2 keto group with the OH on C6, or a 5-member furanose ring, by reaction of the C2 keto group with the OH on C5
- The highly branched structure of glycogen permits rapid glucose release from glycogen stores, e.g., in muscle during exercise. The ability to rapidly mobilize glucose is more essential to animals than to plants.

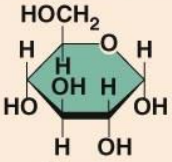


(a) Monosaccharides

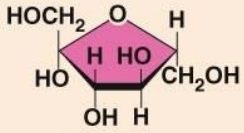
Monomers of carbohydrates

Example

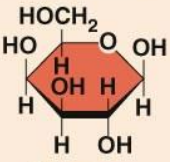
Hexose sugars (the hexoses shown here are isomers)



Glucose



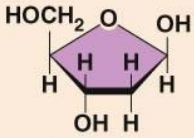
Fructose



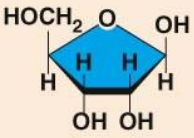
Galactose

Example

Pentose sugars



Deoxyribose



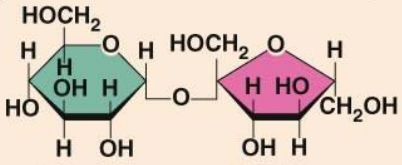
Ribose

(b) Disaccharides

Consist of two linked monosaccharides

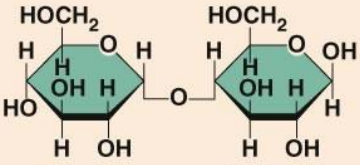
Example

Sucrose, maltose, and lactose
(these disaccharides are isomers)



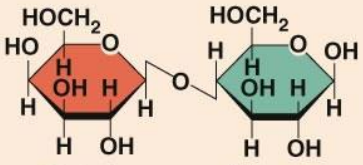
Glucose Fructose

Sucrose



Glucose Glucose

Maltose



Galactose Glucose

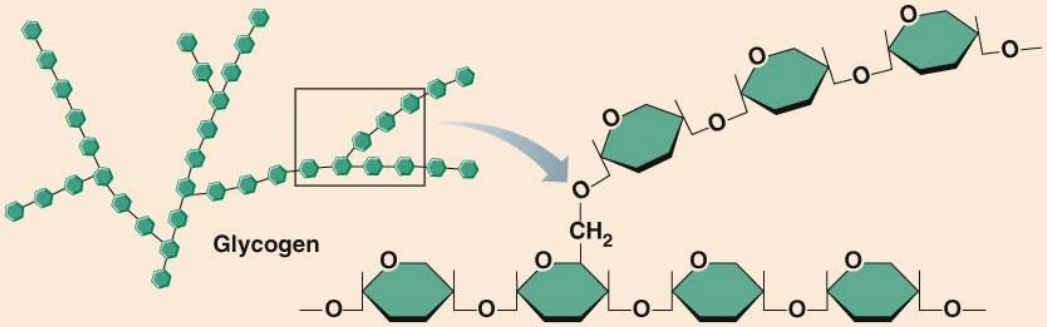
Lactose

(c) Polysaccharides

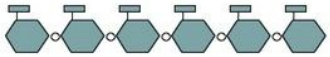
Long chains (polymers) of linked monosaccharides

Example

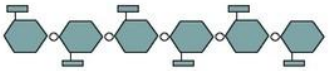
This polysaccharide is a simplified representation of
glycogen, a polysaccharide formed from glucose units.



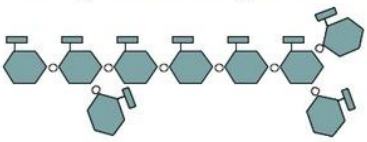
Starch
Unbranched chain of glucose molecules
all orientated in same direction

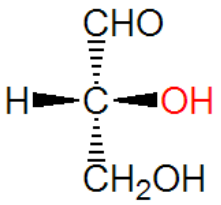


Cellulose
Unbranched chain of glucose molecules
in opposite orientations (repeating)

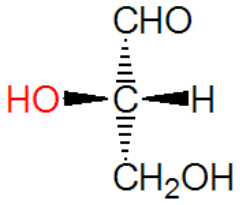


Glycogen
Branched chain of glucose molecules
resulting in a forked arrangement

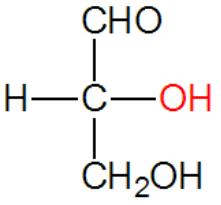




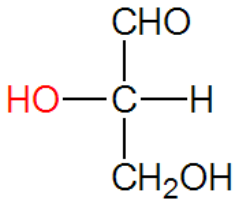
D-glyceraldehyde



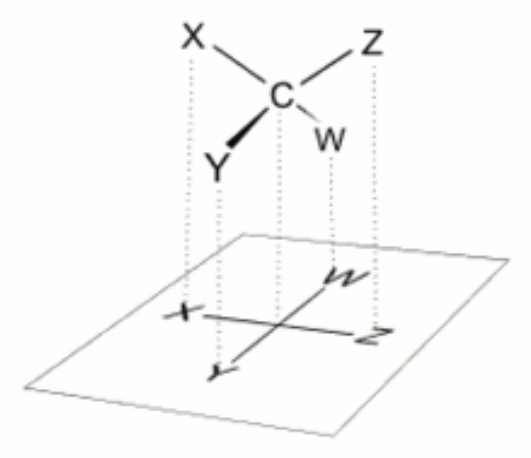
L-glyceraldehyde



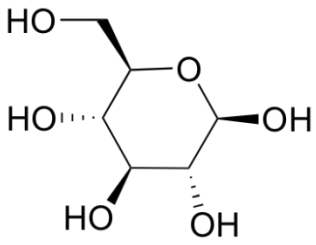
D-glyceraldehyde



L-glyceraldehyde



A:



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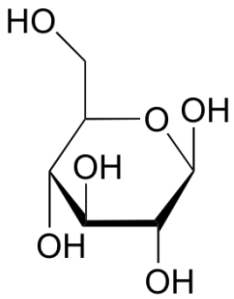
B:



Haworth projection

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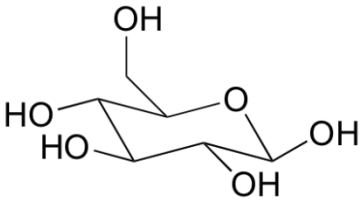
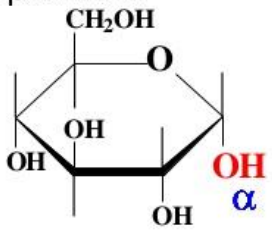
C:



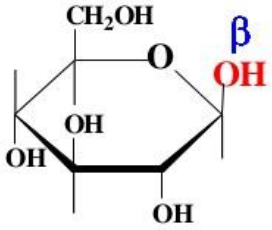
chair conformation

α and β Anomers for D-Glucose

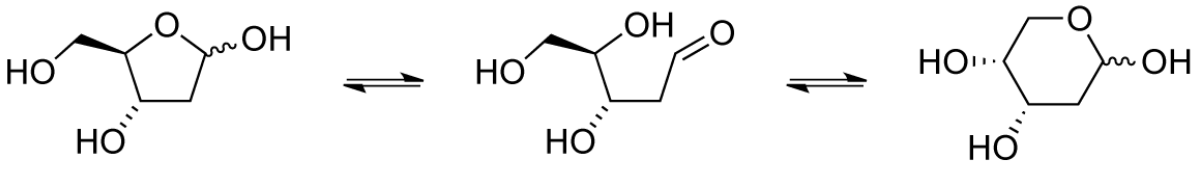
- Anomers are isomers which differ in placement of hydroxyl on C1
- The –OH is drawn down for the α-anomer, and up for the β-anomer



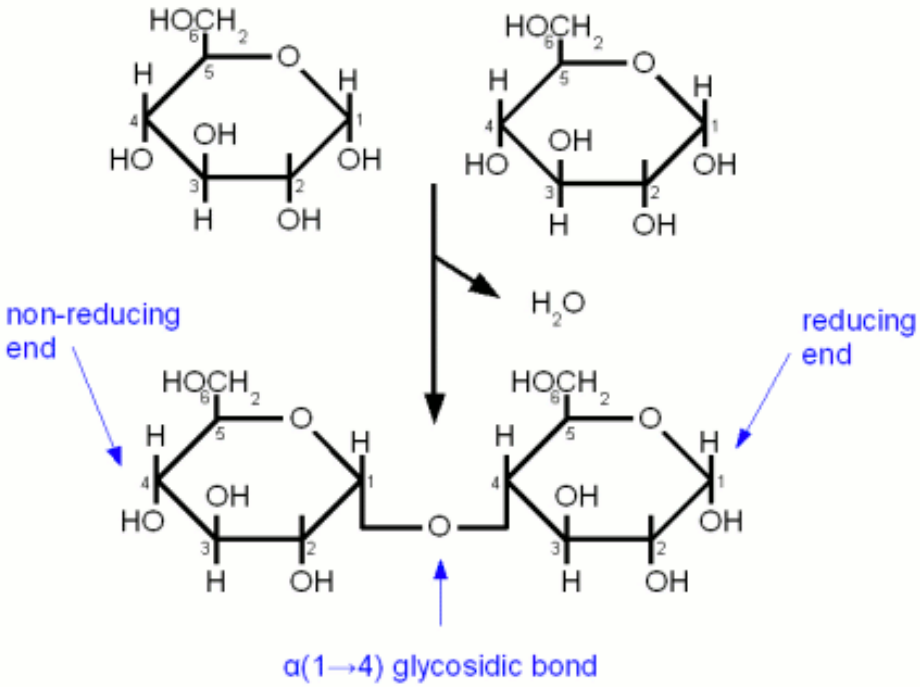
α-D-Glucose



β-D-Glucose

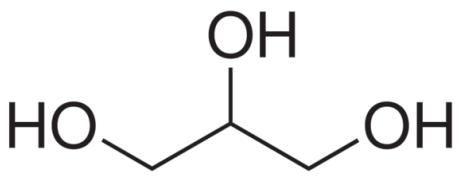


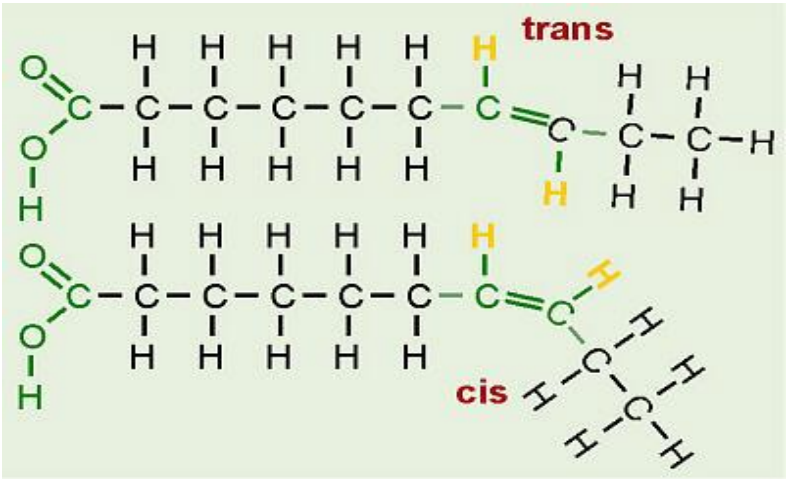
furanose acyclic pyranose



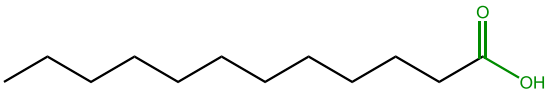
Lipids

- Main biological functions of lipids include energy storage, as structural components of cell membranes, and signalling molecules
- The complete oxidation of fatty acids provides high caloric content, about 9 kcal/g, compared with 4 kcal/g for the breakdown of carbohydrates and proteins. Since a gram of carbohydrate or protein has considerable water of hydration associated with it, it occupies more volume than a gram of fat, so that fat is an even more efficient storage form of energy
- Lateral diffusion of molecules in bilipid layers is common, but transverse movement (flip-flop) is rare
- Glycerolipids are composed mainly of mono-, di- and tri-substituted glycerols, the most well-known being the fatty acid esters of glycerol (triglycerides). They comprise the bulk of storage fat in mammalian tissues
- Glycerophospholipids, also referred to as phospholipids, are ubiquitous in nature and are key components of the lipid bilayer of cells, as well as being involved in metabolism and signalling
- Sphingolipids are a complex family of compounds that share a common structural feature, a sphingoid base backbone that is synthesized from serine and a long-chain fatty acyl-CoA, then converted into ceramides, phosphosphingolipids, glycosphingolipids, and other species
- Sterol lipids, such as cholesterol and its derivatives are an important component of membrane lipids. The steroids, which also contain the same fused four-ring core structure, have different biological roles as hormones and signalling molecules
- Saccharolipids describe compounds in which fatty acids are linked directly to a sugar backbone, forming structures that are compatible with membrane bilayer

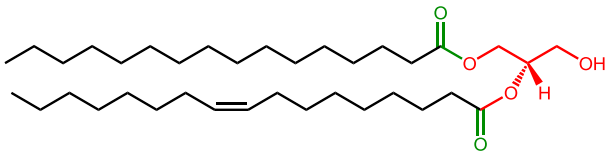




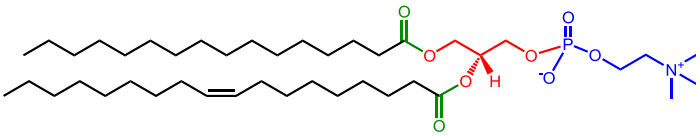
Fatty Acyls (FA)



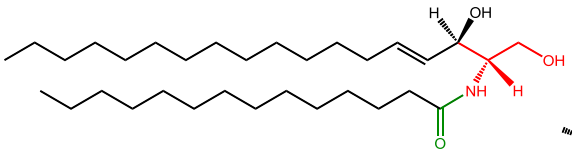
Glycerolipids (GL)



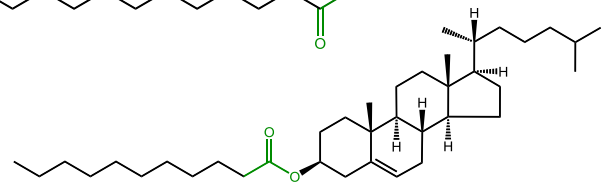
Glycerophospholipids (GP)



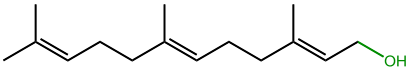
Sphingolipids (SP)



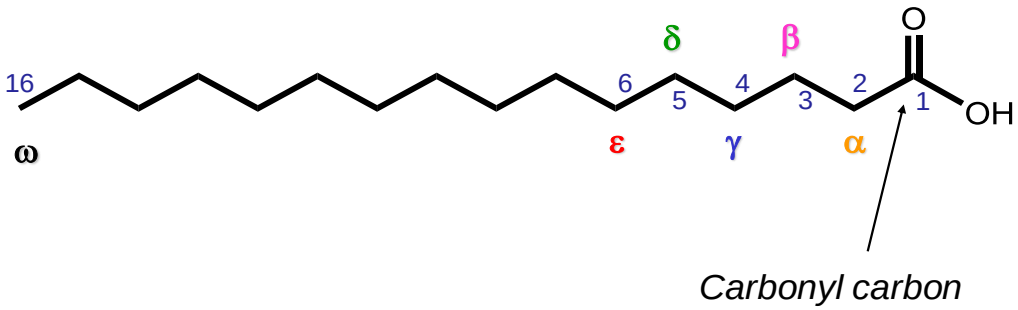
Sterol Lipids (ST)



Prenol Lipids (PR)

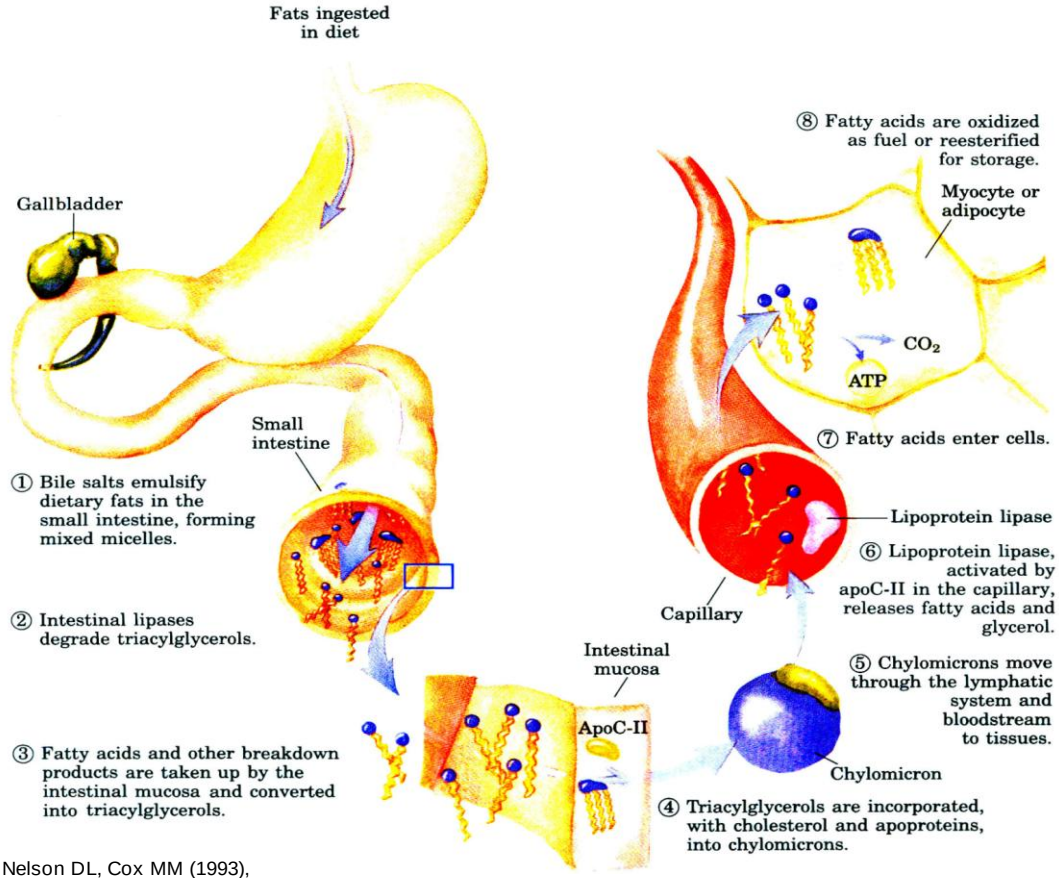


Naming Conventions: Palmitic Acid



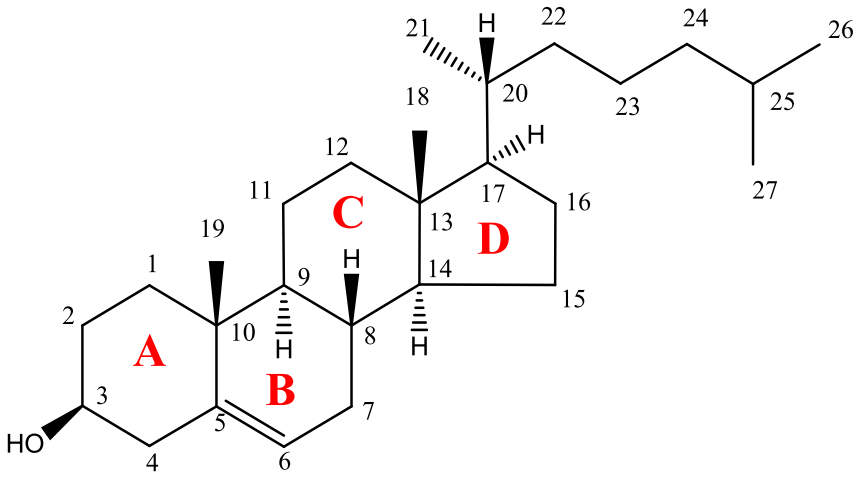
ω	omega, always the last alkyl carbon
ε	epsilon, fifth carbon after the carbonyl
δ	delta, fourth carbon after the carbonyl
γ	gamma, third carbon after the carbonyl
β	beta, second carbon after the carbonyl
α	alpha, first carbon after the carbonyl

Digestion of Fats

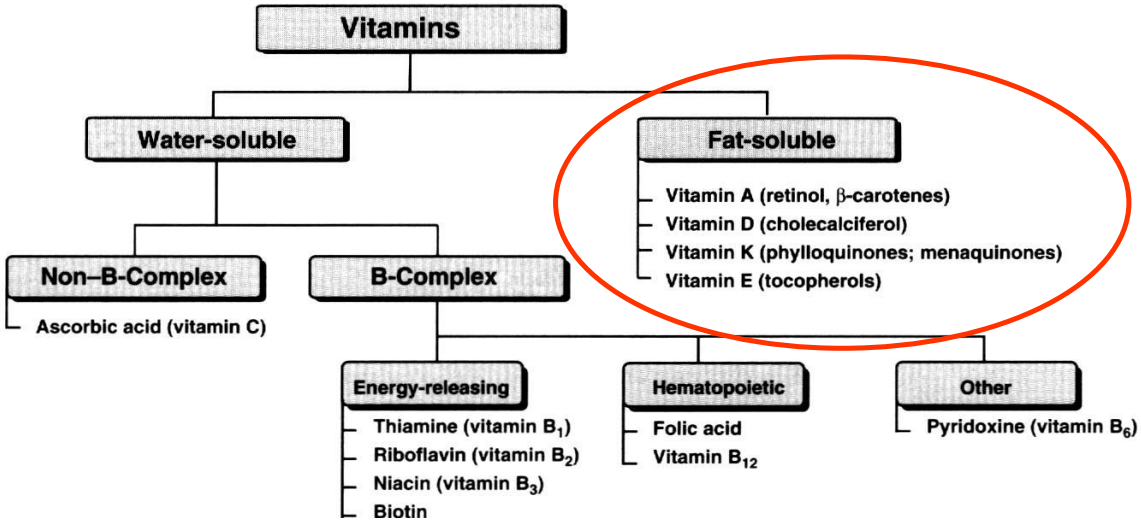


Nelson DL, Cox MM (1993),

Cholesterol Structure and Numbering



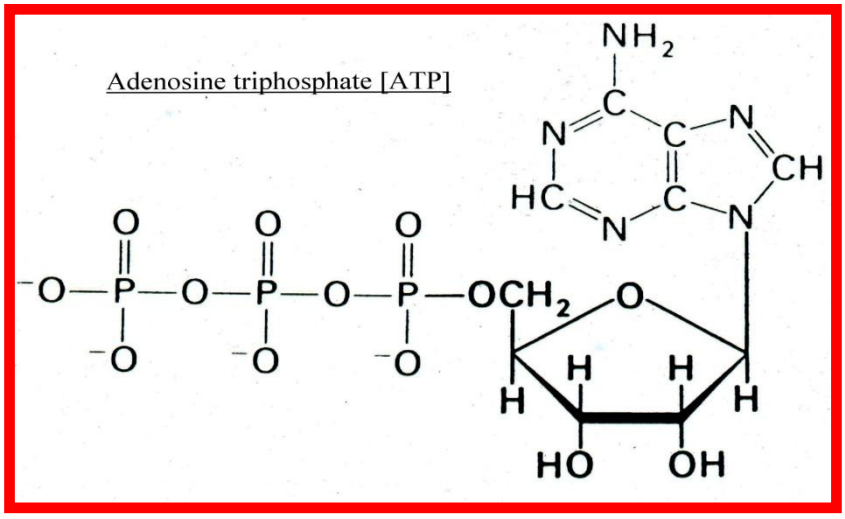
Vitamins: The Family Tree

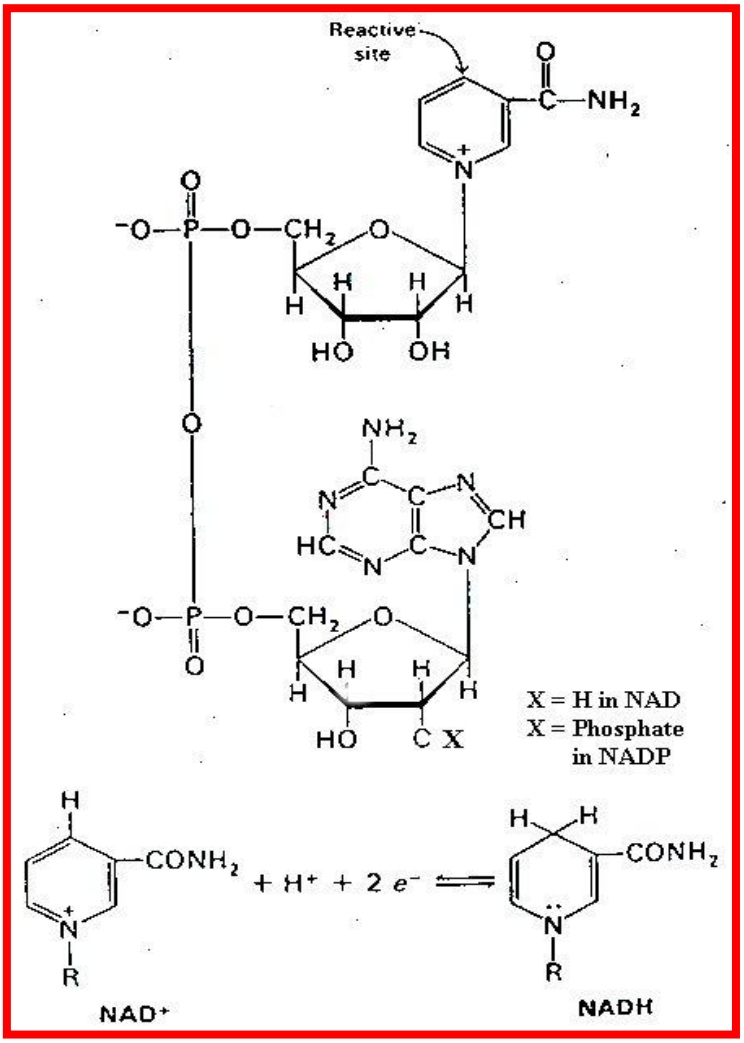


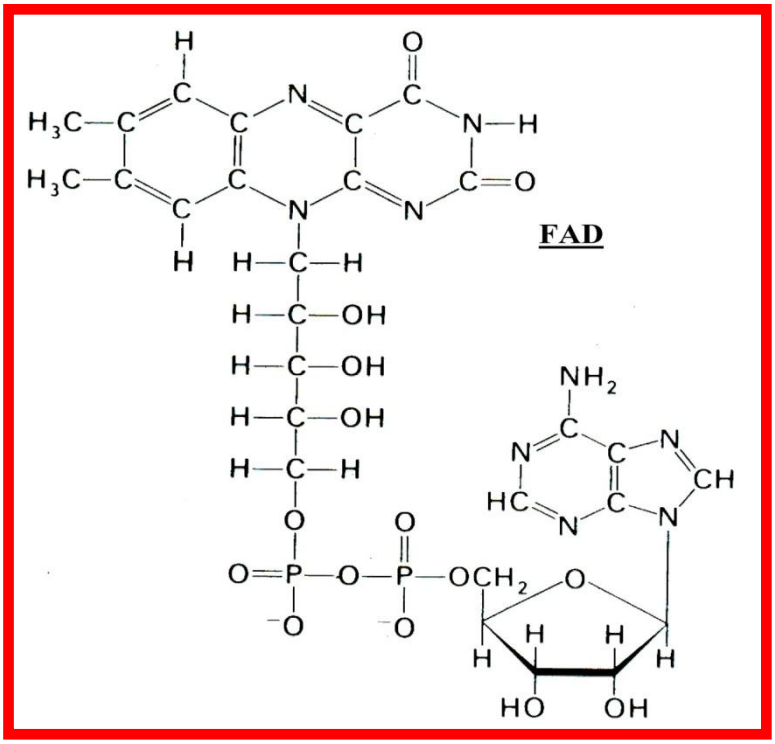
Metabolism

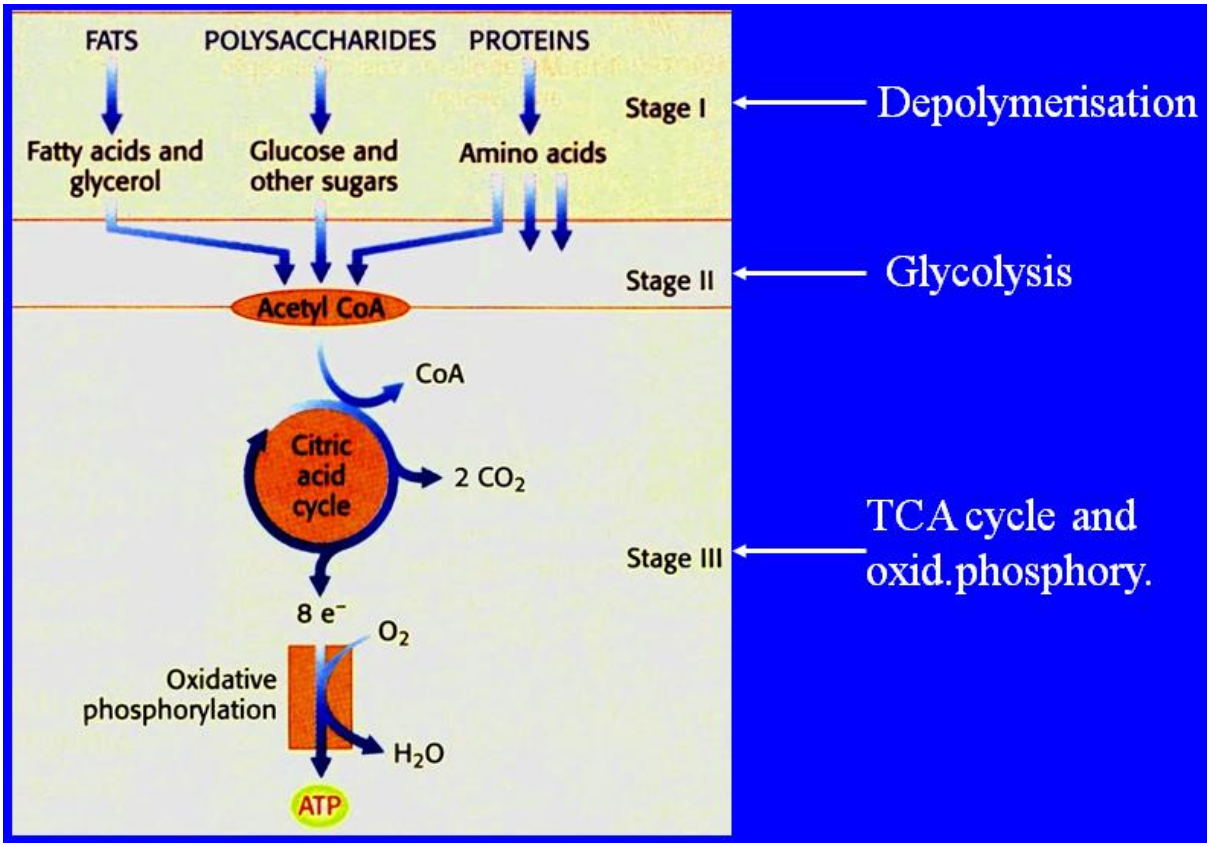
- ΔG^{o} = standard free energy change under the conditions when pH = 0, 1M concentrations and at 25° C.
- $\Delta G^{o'}$ = standard biological free energy change where ' signifies modified - pH 7.0, 1M concentrations and 25° C
- In cells, endergonic reactions are driven by coupling to exergonic reactions. An enzyme(s) needs to be present for coupling to occur
- Phosphate group transfer - in effect puts free energy into a compound which thus has more free energy for use in subsequent metabolism, not by simple hydrolysis of ATP
- ATP synthesis is a strongly endergonic reaction: ADP + Pi $\Rightarrow$ ATP + H_2O [$\Delta G^{o\prime}$ = +30 kJ mol^{-1}]
- When coupled to a metabolic exergonic reaction ATP synthesis is known as: substrate level phosphorylation
- Nicotinamide adenine dinucleotide is a specialised e- carrier cofactor (loosely bound to proten) of some enzymes
- Flavin adenine dinucleotide (FAD) acts as a prosthetic group and is tightly bound to its enzyme. It can accept 2 electrons and 2 protons and acts as a temporary store for electrons
- The reduced redox coenzymes may be oxidised by the electron transport system of the mitochondria liberating a large amount of free energy
- The complete oxidation of glucose to CO_2 + H_2O: $\Delta G^{o'}$ = -2860 kJ mol^{-1} whereas the oxidation of glucose to 2 x pyruvate: $\Delta G^{o'}$ = -146 kJ mol^{-1}, just ~ 5% of the total potential energy
- Much more ATP can be made under aerobic conditions by the re oxidation of the reduced coenzymes – NADH and $FADH_2$ using the cytochrome chain of the mitochondrial inner membrane.
- Enzymes catalysing irreversible reactions are potential control sites and there are three virtually irreversible enzymes in glycolysis: Hexokinase, PFK-1, and pyruvate kinase

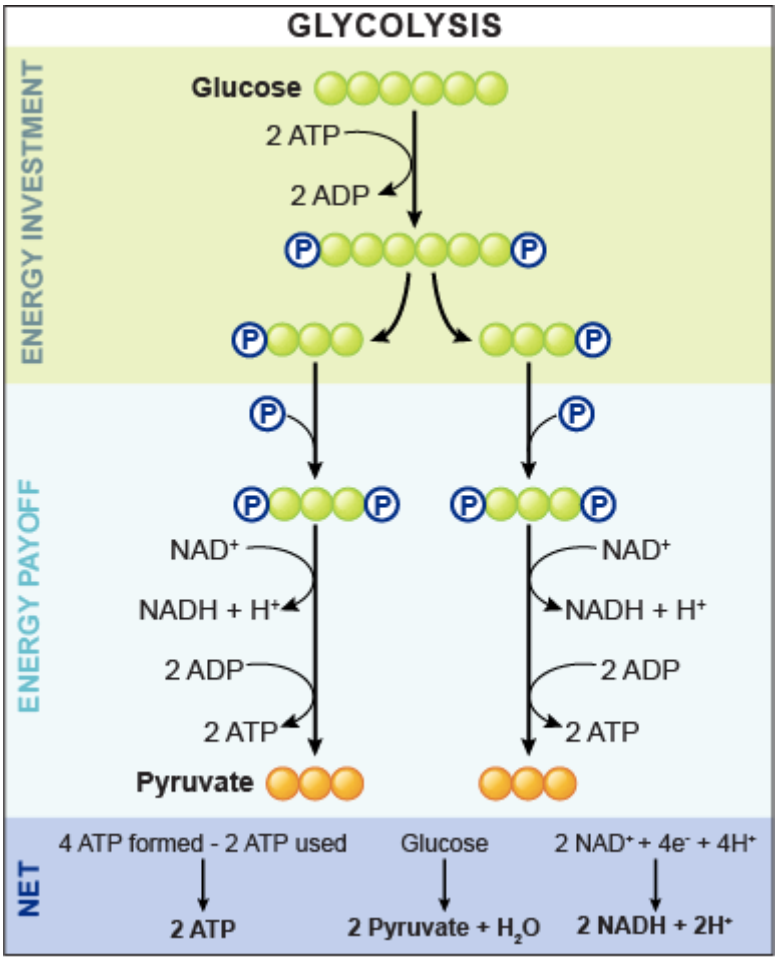
- Pyruvate dehydrogenase complex comprises five coenzymes - FAD / CoA-SH NAD^+ / TPP / Lipoate and three enzymes. It controls a key irreversible step in the TCA cycle and is subject to various forms of control: Pyruvate + NAD^+ + CoA => Acetyl CoA + NADH + CO_2
- Glycolysis generates 2 molecules of pyruvate that can enter the mitochondrion (via a transporter) and undergo reaction in the pyruvate pyruvate dehydrogenase complex to liberate acetyl CoA which undergoes the first reaction (a condensation) catalysed by citrate synthase
- If intermediates are drawn off for biosyntheses the TCA cycle will stop until they have been replenished e.g. succinyl CoA for haem biosynthesis would deplete mitochondrial OAA
- Triacylglycerols (TAGS) are very compact fuel reserves laid down in adipose tissue and can be mobilised by lipases. These enzymes hydrolyse TAGS to glycerol and fatty acid. Both of these products of TAG hydrolysis can feed into the glucose oxidation pathway
- Entry into the citric acid cycle is via acetyl CoA and occurs in mitochondria. There are four redox reactions which produce 3 NADH and 1 $FADH_2$
- The energy to drive this ATP synthesis comes from the re oxidation of NADH or $FADH_2$ by the respiratory (cytochrome) chain generating a pmf (Δp) which is composed of $\Delta\psi$ = [membrane potential] and ΔpH = [proton concentration gradient]
- Electron flow through the respiratory complexes present in the inner mitochondrial membrane results in protons being pumped into the intermembrane space (IMS)
- Protons are driven by the pmf from the IMS through the ATP synthase (they are unable to cross the impermeable inner membrane) to synthesise ATP in the matrix
- Electron transport from NADH to O_2 results in the transport of 10 H^+ from the matrix to the ims using NAD - dehydrogenase / cyt bc_1 and cytochrome c oxidase (6 H^+ are transported upon re oxidation of $FADH_2$ using just the bc_1 complex and cytochrome c oxidase). One ATP is produced for every four H+ ions moving through ATPase.
- Most ATP is synthesised in the mitochondrion but is used in the cytosol for biosyntheses. Newly synthesised ATP_{MITO} is exchanged for ADP_{CYTO} by a mitochondrial ATP/ADP translocase

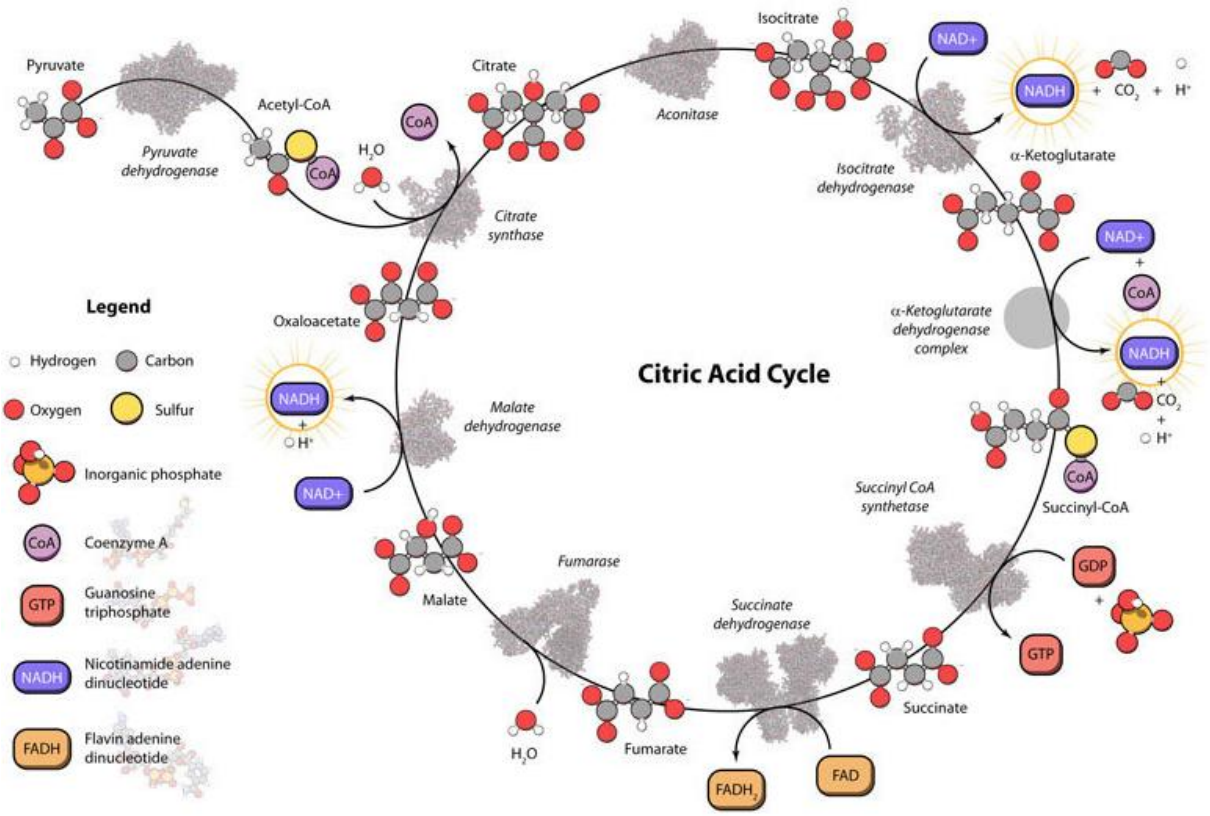


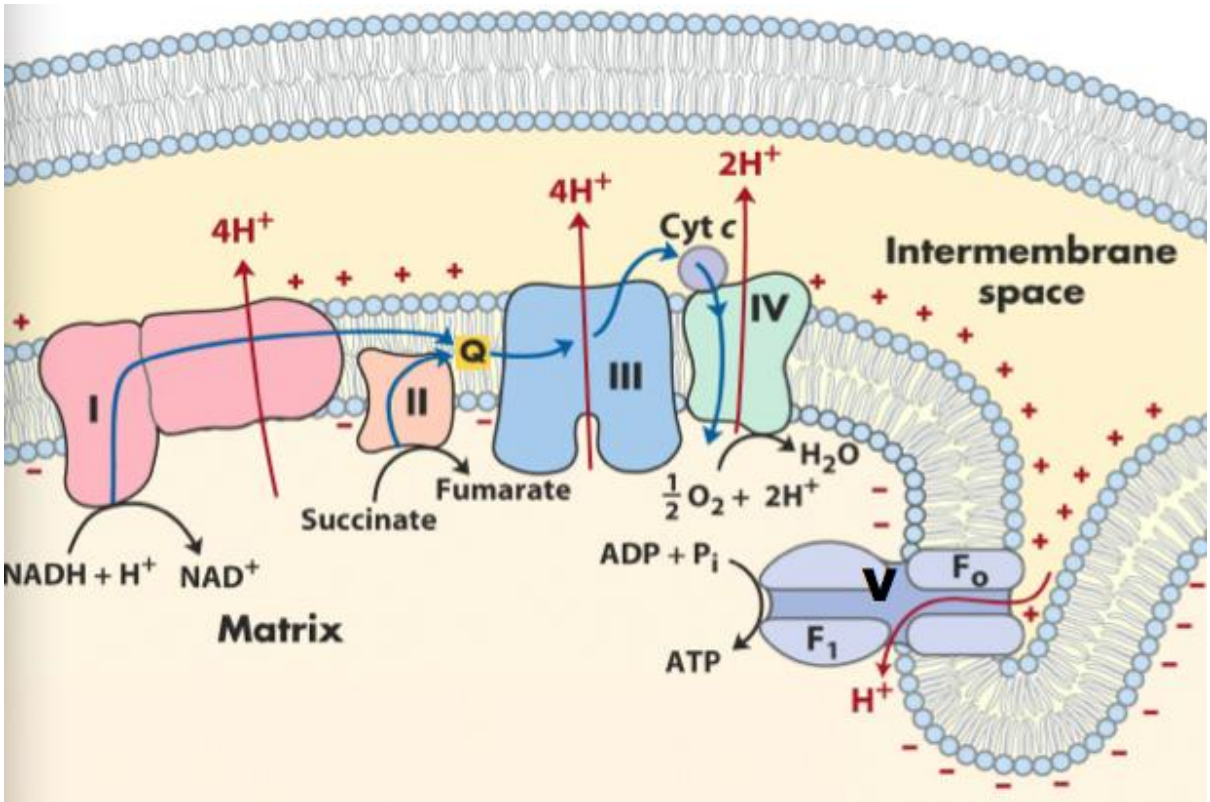

Reactive site
X = H in NAD
X = Phosphate in NADP
NAD+
NADH


FAD

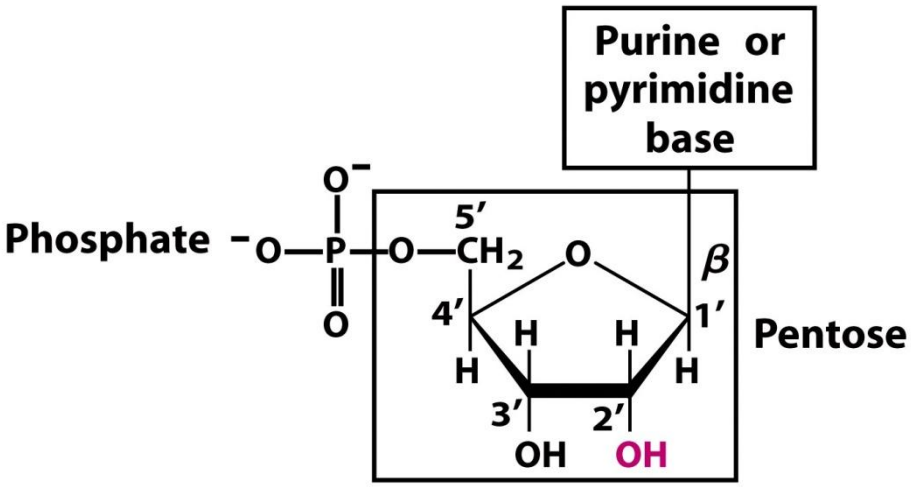

FATS
POLYSACCHARIDES
PROTEINS
Fatty acids and glycerol
Glucose and other sugars
Amino acids
Stage I
Depolymerisation
Stage II
Glycolysis
Acetyl CoA
CoA
Citric acid cycle
2 CO2
Stage III
TCA cycle and oxid.phosphory.
8 e⁻
O2
Oxidative phosphorylation
H2O
ATP

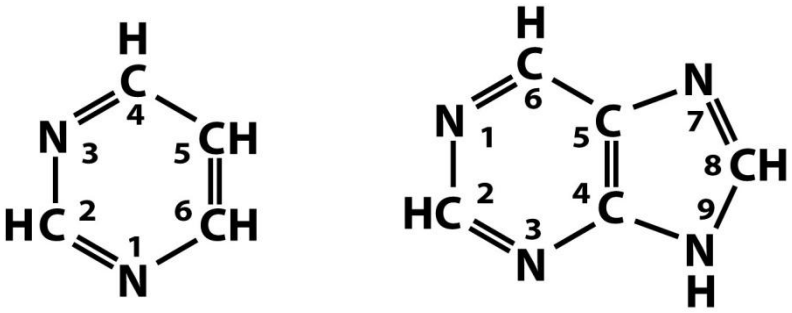

GLYCOLYSIS
ENERGY INVESTMENT
Glucose
2 ATP
2 ADP
ENERGY PAYOFF
NAD+
NADH + H+
2 ADP
2 ATP
Pyruvate
NET
4 ATP formed - 2 ATP used
2 ATP
Glucose
2 Pyruvate + H2O
2 NAD+ + 4e- + 4H+
2 NADH + 2H+


Citric Acid Cycle
Legend
Hydrogen
Carbon
Oxygen
Sulfur
Inorganic phosphate
CoA Coenzyme A
GTP Guanosine triphosphate
NADH Nicotinamide adenine dinucleotide
FADH Flavin adenine dinucleotide
Pyruvate
Pyruvate dehydrogenase
Acetyl-CoA
CoA
H_2O
Citrate
Citrate synthase
Aconitase
Isocitrate
Isocitrate dehydrogenase
NAD+
NADH
$+ CO_2 + H^+$
α-Ketoglutarate
α-Ketoglutarate dehydrogenase complex
Succinyl CoA synthetase
Succinyl-CoA
GDP
GTP
Succinate
Succinate dehydrogenase
FAD
$FADH_2$
Fumarate
Fumarase
H_2O
Malate
Malate dehydrogenase
Oxaloacetate

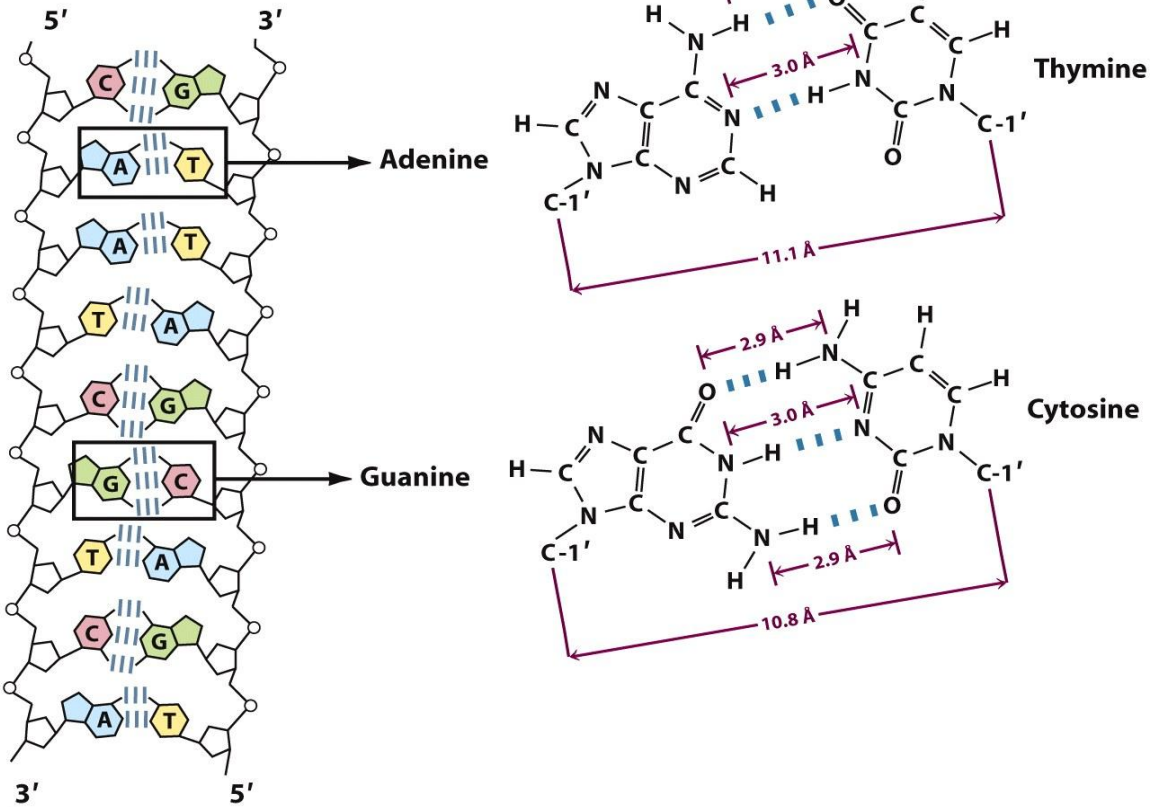

$4H^+$
$4H^+$
$2H^+$
Cyt c
Intermembrane space
I
II
Q
III
IV
H_2O
$\frac{1}{2} O_2 + 2H^+$
Fumarate
Succinate
$NADH + H^+$
NAD^+
Matrix
$ADP + P_i$
ATP
V
F_o
F_1
H^+

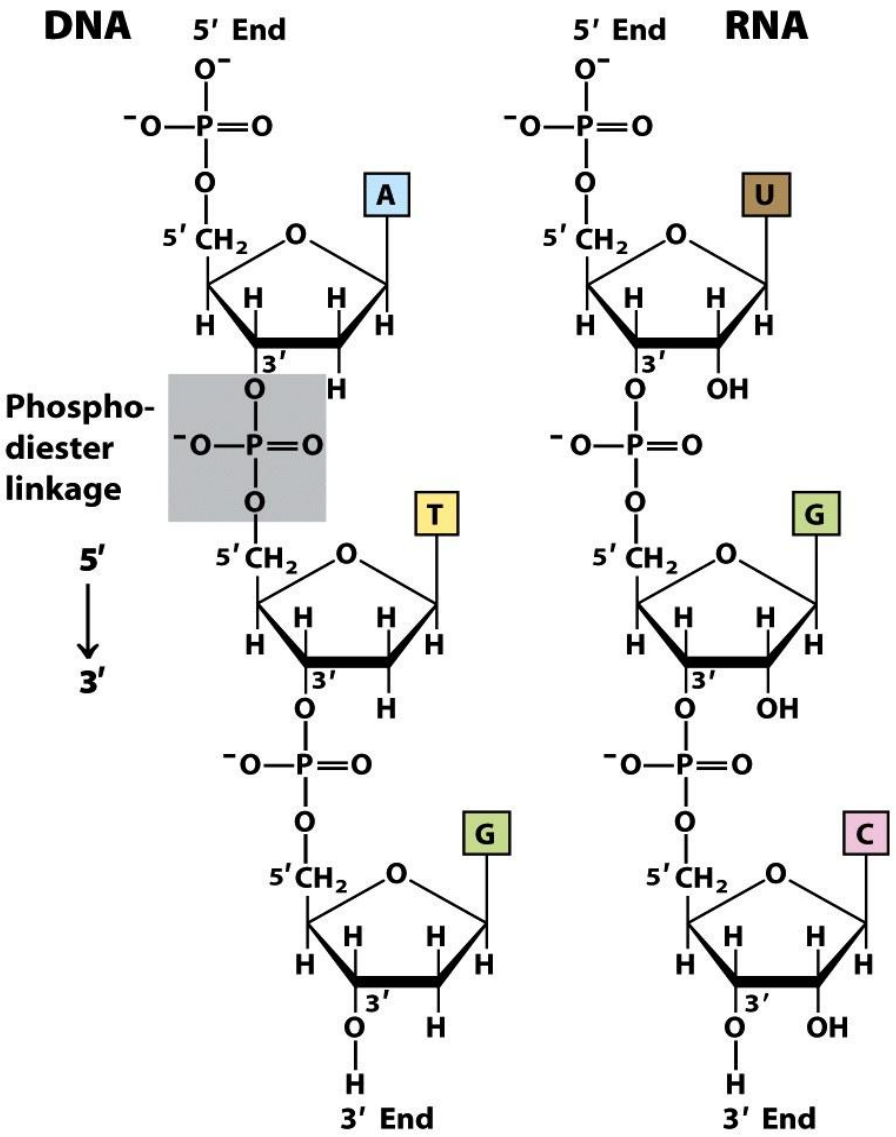
Nucleic Acids

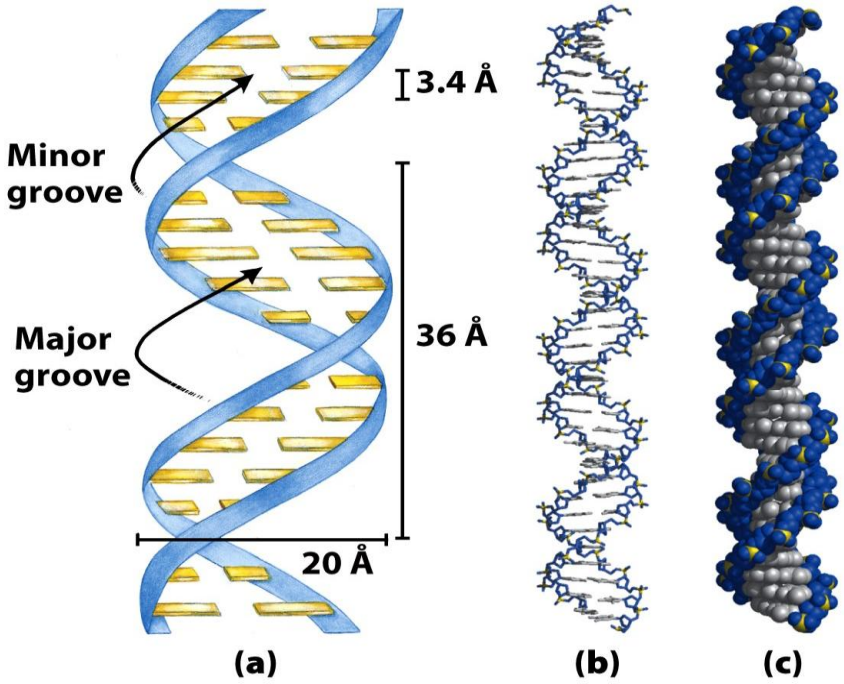




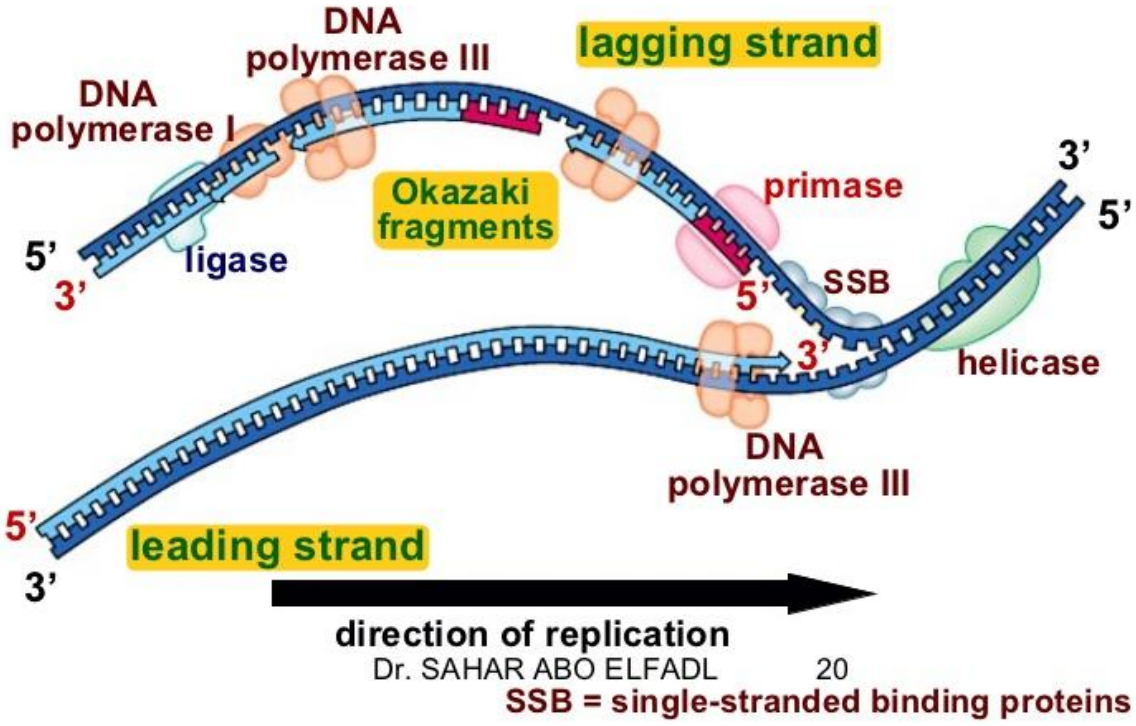
Pyrimidine Purine




DNA
5′ End
RNA
5′ End
A
U
T
G
G
C
Phospho-
diester
linkage
5′
3′
3′ End
3′ End


3.4 Å
Minor
groove
Major
groove
36 Å
20 Å
(a)
(b)
(c)

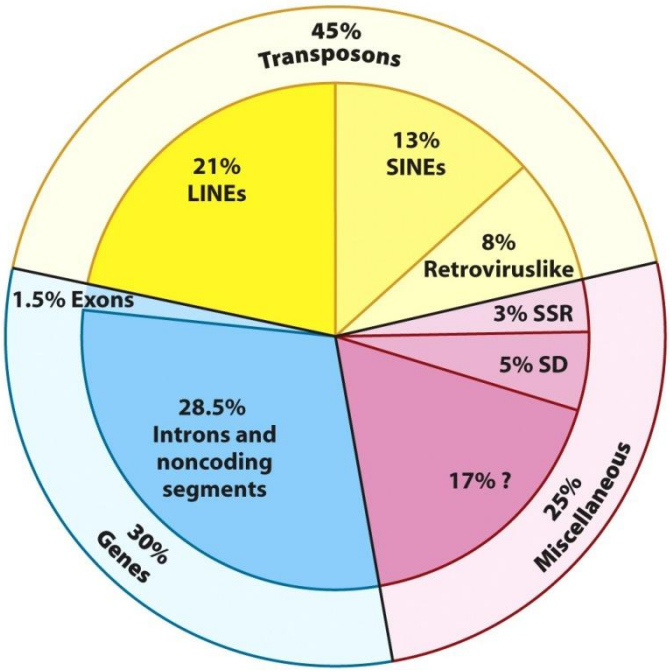
Replication fork

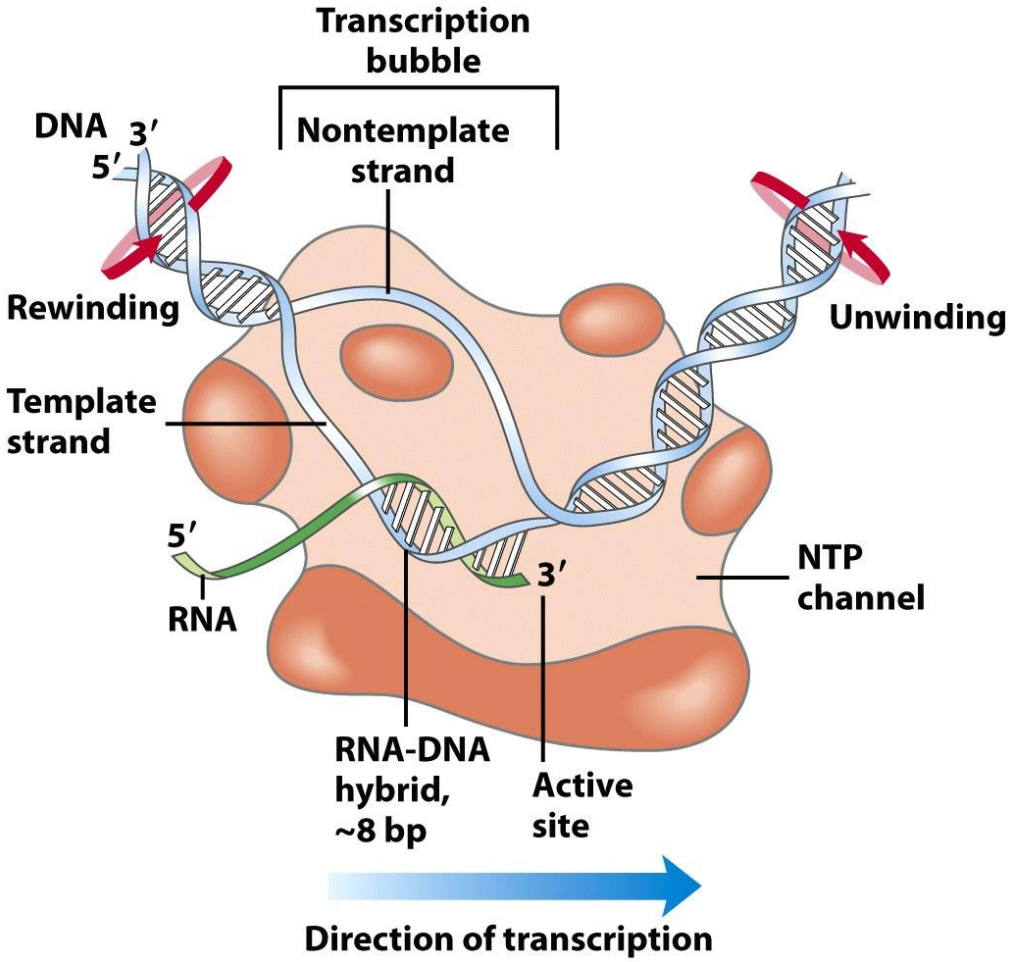


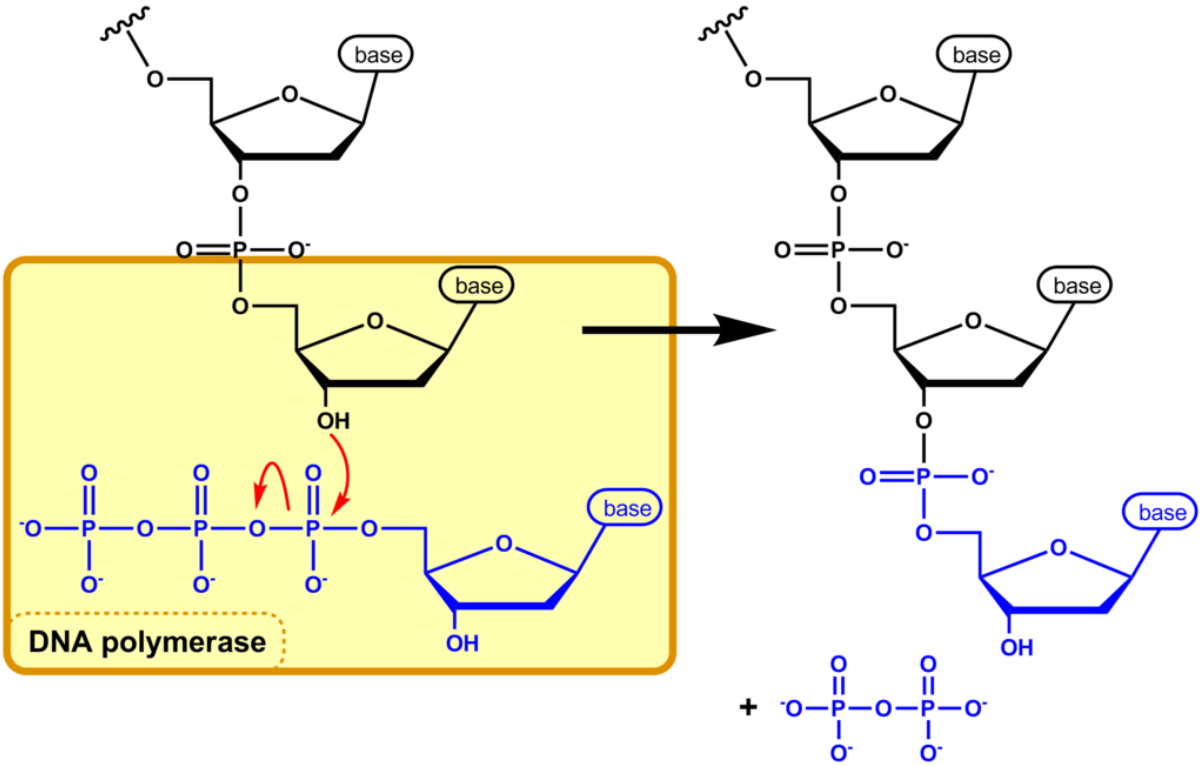
Dr. SAHAR ABO ELFADL 20

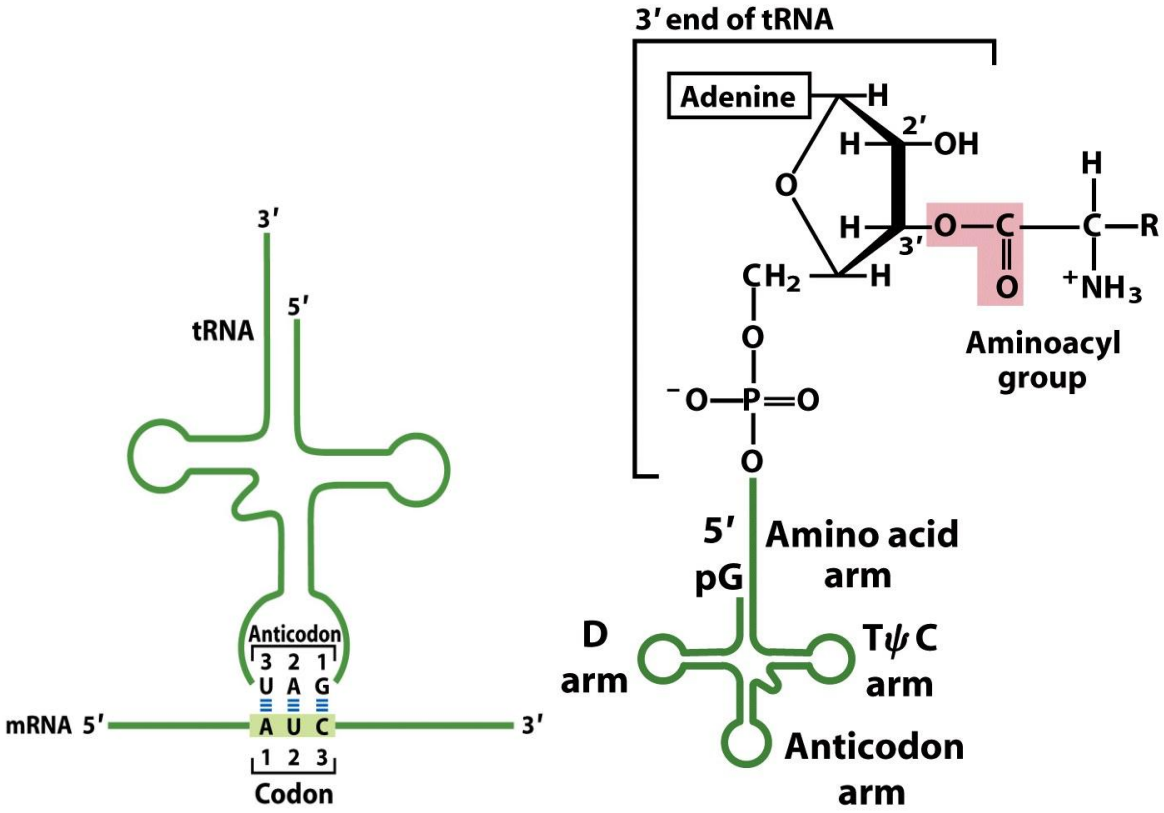
SSB = single-stranded binding proteins

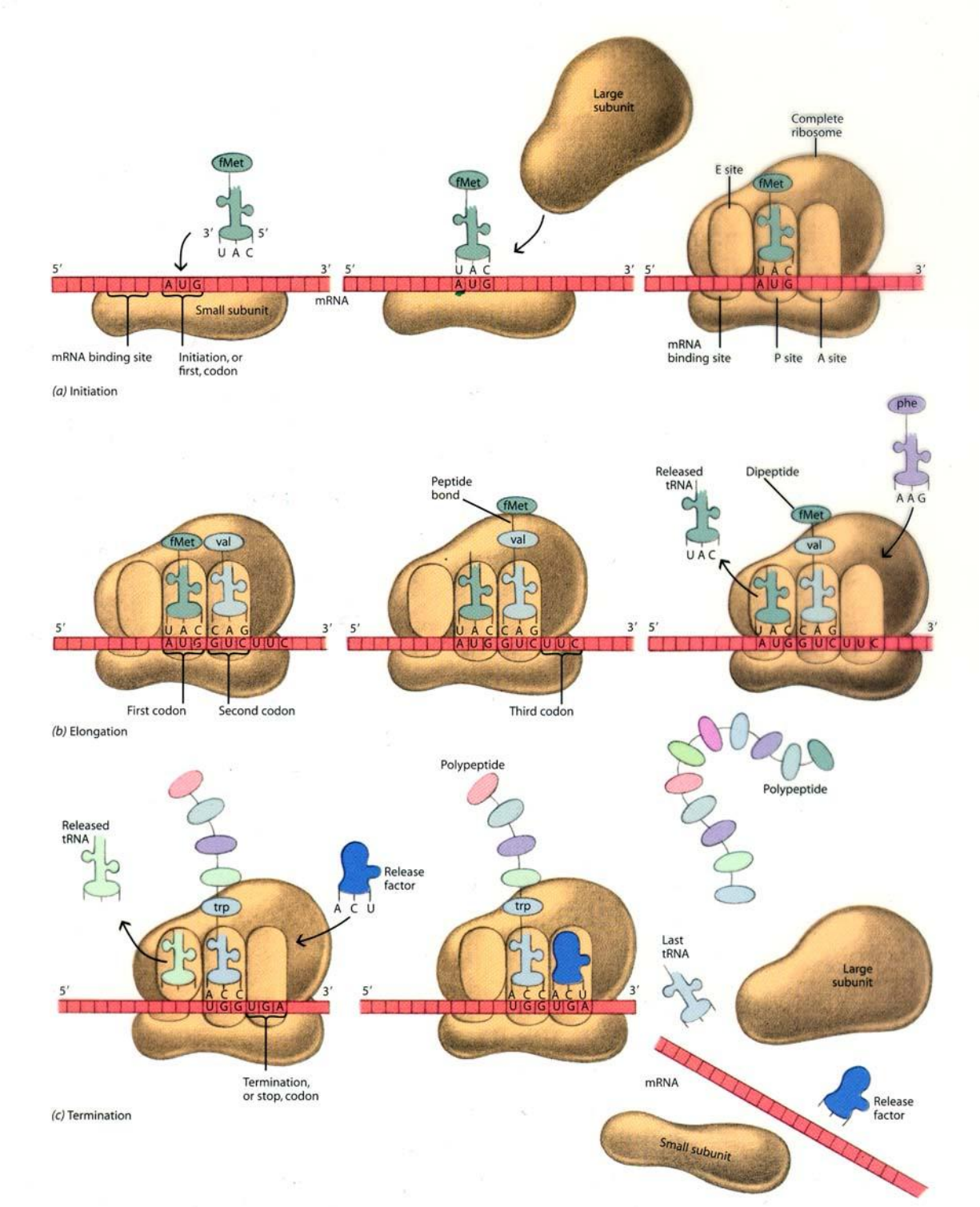
	A form	B form	Z form
Helical sense	Right handed	Right handed	Left handed
Diameter	~26 Å	~20 Å	~18 Å
Base pairs per helical turn	11	10.5	12
Helix rise per base pair	2.6 Å	3.4 Å	3.7 Å
Base tilt normal to the helix axis	20°	6°	7°
Sugar pucker conformation	C-3′ endo	C-2′ endo	C-2′ endo for pyrimidines; C-3′ endo for purines
Glycosyl bond conformation	Anti	Anti	Anti for pyrimidines; syn for purines

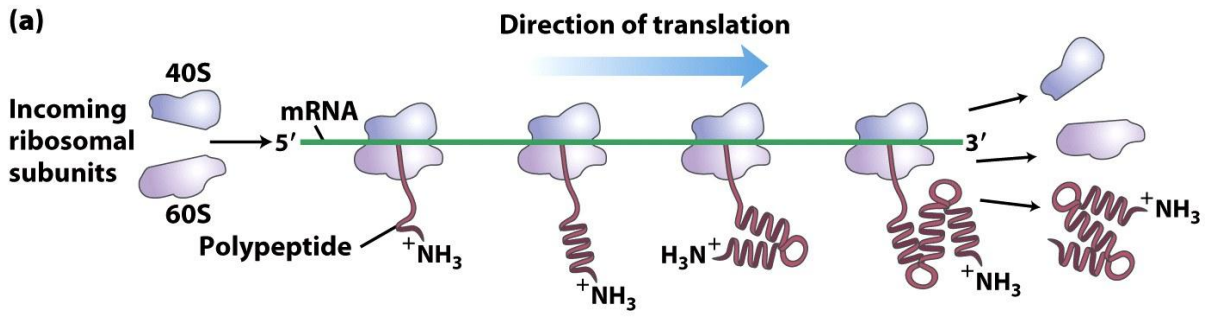

45%
Transposons
21%
LINEs
13%
SINEs
8%
Retroviruslike
3% SSR
5% SD
25%
Miscellaneous
17% ?
28.5%
Introns and
noncoding
segments
1.5% Exons
30%
Genes


Transcription
bubble
Nontemplate
strand
DNA 3′
5′
Rewinding
Unwinding
Template
strand
5′
RNA
3′
NTP
channel
RNA-DNA
hybrid,
~8 bp
Active
site
Direction of transcription


base
OH
DNA polymerase


3′ end of tRNA
Adenine
2′ OH
3′
Aminoacyl group
5′ pG
Amino acid arm
D arm
TψC arm
Anticodon arm
3′
5′
tRNA
Anticodon
3 2 1
U A G
mRNA 5′
A U C
3′
1 2 3
Codon


Large subunit
Complete ribosome
fMet
E site
Small subunit
mRNA
mRNA binding site
Initiation, or first, codon
P site
A site
(a) Initiation
phe
Peptide bond
Released tRNA
Dipeptide
val
First codon
Second codon
Third codon
(b) Elongation
Polypeptide
Released tRNA
Release factor
trp
Last tRNA
Termination, or stop, codon
(c) Termination


(a)
Direction of translation
40S
Incoming ribosomal subunits
60S
mRNA
5′
3′
Polypeptide
+NH3
H3N+