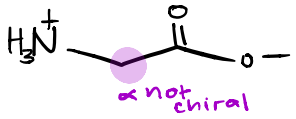
Proteins

amino acids = polymers
oligopeptides = small chain of amino acids
polypeptides = long chain of amino acids



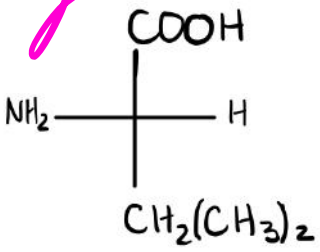
(glycine)

(valine)

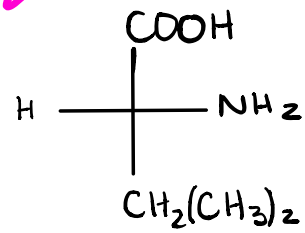
all amino acids are L configuration

Love
Amino
Acids

fischer progection



L-valine



D-valine

* AMINO ACIDS *

- hydrophilic vs phobic
- naming
- structure
- aromaticity
- charge

Examples of amino acids:

Catalytic triad (chymotrypsinogen)
- serine
- histidine
- aspartate

Hemoglobin
- histidine (proximal bound to Fe^{2+})

α keto acid
- glutamate

Releases urea
- argenine

Ionizable amino acids + pkas

* COOH ~ 2

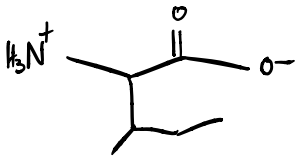
aspartate ~ 3
glutamate ~ 4
histidine ~ 6
cysteine ~ 8.18

* NH_3 ~ 9

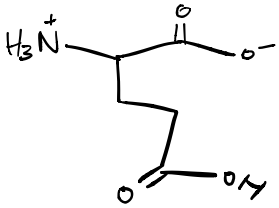
tyrosine ~ 10.07
lysine ~ 10.5
arginine ~ 12.48

Zwitter Ion

dipolar amino acid where charges cancel out.



isoleucine in zwitterion form



glutamate in zwitter ion form

* all amino acids without a charge are zwitter ions at physiological pH.

pH > pka	acids : − bases : 0
pH < pka	acids : 0 bases : +

Isoelectric point : where the molecule carries no charge. Or pKa = pH.

isoelectric point is similar to equivalence point.

~ Isoelectric point for amino acids

Neutral amino acids : take the average (pKa) of amine + carboxyl

$9-2 = 7/2 = 4.5$ ~ isoelectric point

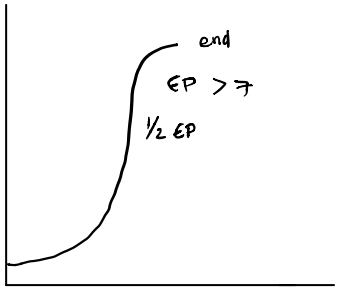
acidic amino acids : average of R group + carboxyl group

glutamate pKa = 4
cooh pKa = 2
> 3 ~ isoelectric point

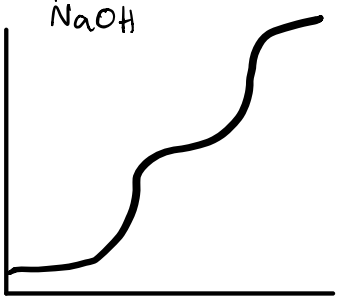
basic amino acids : average of R group + amine group

Lysine pKa = 10.07
amine pKa = 9
> 9.5 ~ isoelectric point

NaOH
+
Phenolalanine

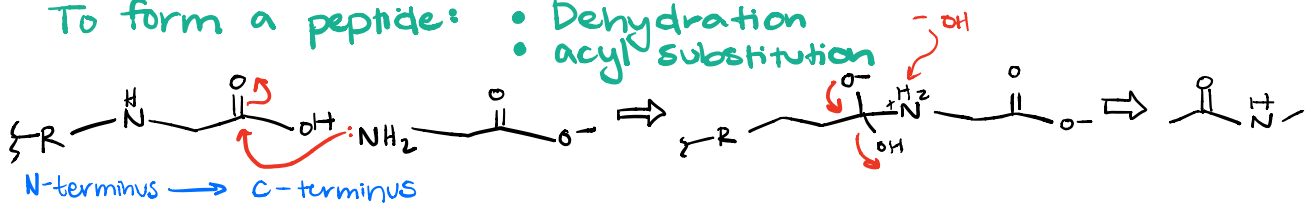


aspartic acid
+
NaOH



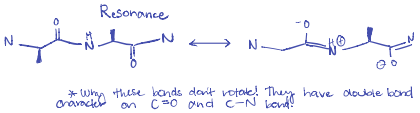
Amino Acid Rxn's

To form a peptide:
- Dehydration
- acyl substitution



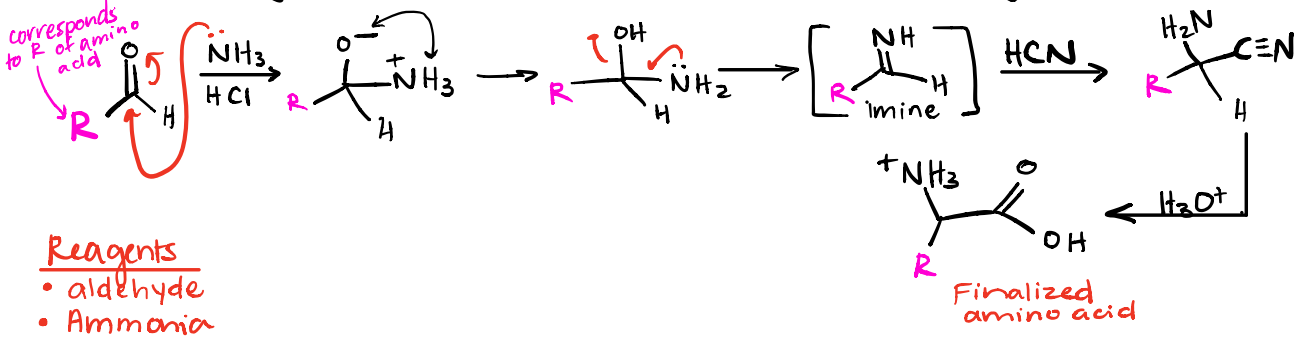
Protein Hydrolysis:
- Trypsin
- Chymotrypsin

→ *arginine, lysine
→ * phenylalanine, tryptophan, tyrosine



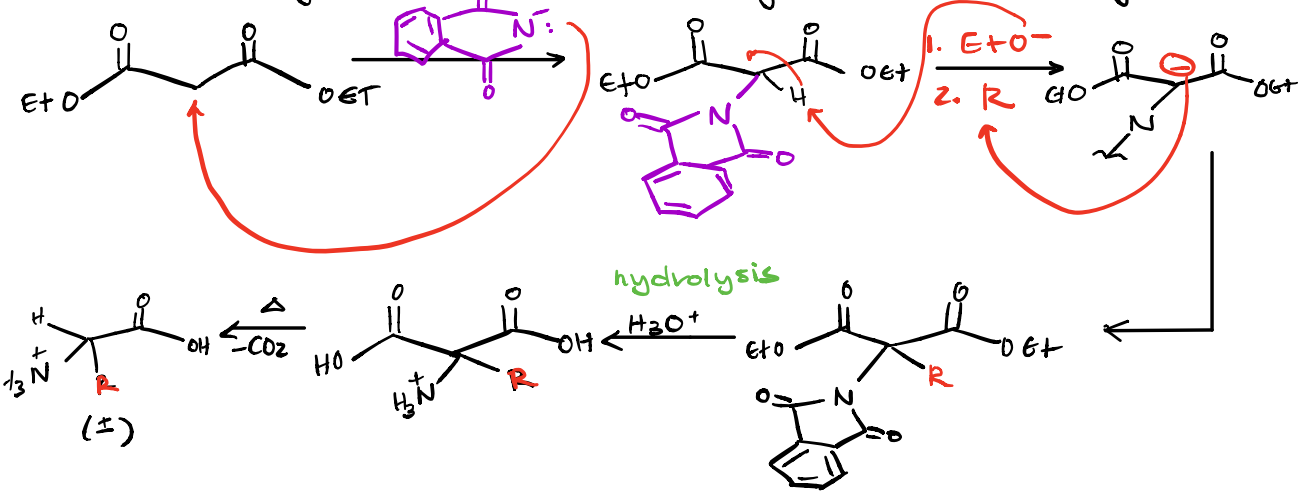
* Why these bonds don't rotate! They have double bond characted on C=O and C–N bond!

Strecker Synthesis: (how an aminoacid is synthesized)



Reagents
- aldehyde
- Ammonia
- HCN
- H_3O^+

Gabriel Synthesis: (amino acid synthesis from acyl halide)



Which method of amino acid synthesis results in an ophically active solution?

I. Strecker Synthesis
II. Gabriel Synthesis
III. Trypsin Synthesis

a. I only
b. II only
c. I, II, III
d. None of the above

Which method of amino acid synthesis results in an ophically active solution?

I. Strecker Synthesis
II. Gabriel Synthesis
III. Trypsin Synthesis

a. I only
b. II only
c. I, II, III
d. None of the above

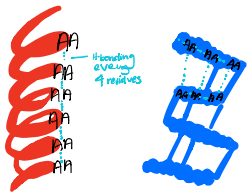
Both Strecker + Gabriel synthesis have planar intermediates which can have front and backside attacks. This results in a racemic mixture of enantiomers which is optically inactive. Trypsin synthesis = not a thing!

~ Protein Structure ~

1° amino acid sequence

– G – M – S – L – I – V – C – Q – W –
Glutamate, methionine, serine, leucine, isoleucine, valine, cysteine, Glutamine, tryptophan

2° 3-dimentional protein folding



ex: Keratin ex: Fibroin

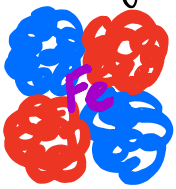
Proline = rarely in α-helix

3° Folded protein made of α-helices and Beta sheets

molecular interactions:
- h-bonding
- IMF (van der waals)
- covalent bonding
- ionic bonding (Na^+ bridges)
- disulfide bonds
- Proline turns

4° Multiple proteins come together

Hemoglobin



] subunit α
] subunit β

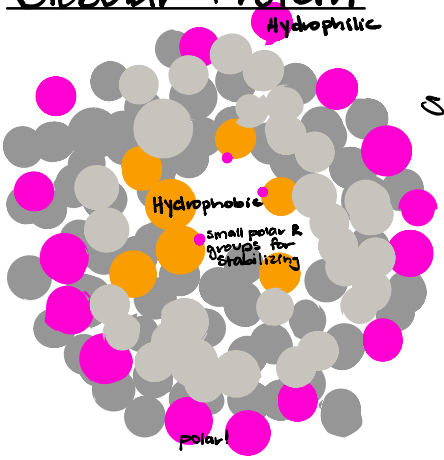
Positive cooperativity = ligand affinity increases with each ligand bound. I.e. first O_2 molecule to bind Hgb has relatively low affinity, but increases with O_2 #2, 3, and 4.

Globule: fully folded

Molten globule: partially folded

Molten: denatured protein

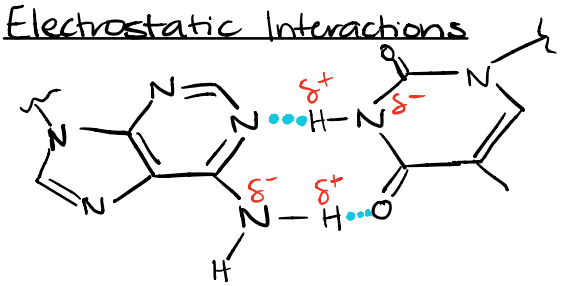
Globular Protein



Q: Are globular proteins soluble in water?

A: Yes, because the hydrophobic side groups are pointed inwards and hydrophillic are pointed outwards the globular proteins are water soluble.

Electrostatic Interactions

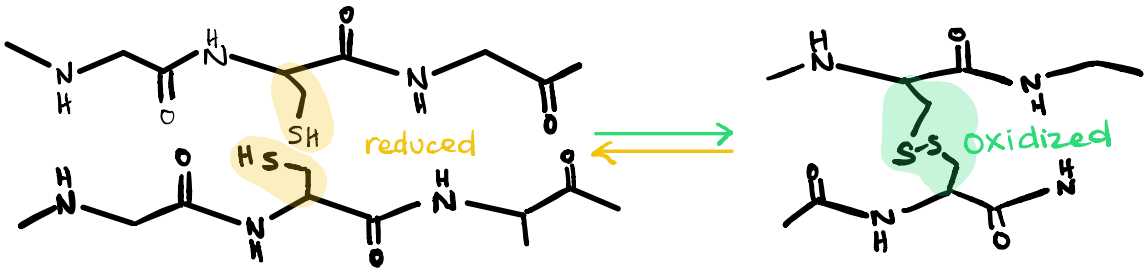


Q: Do electrostatic interactions improve or discourage protein folding?

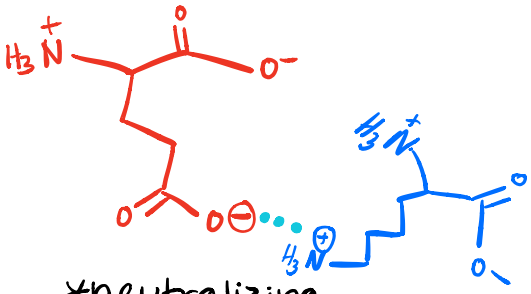
A: the electrostatic interactions improve protein folding and stabilize the protein itself!

• H-bonds are a form of electrostatic interaction

Disulfide Bridges



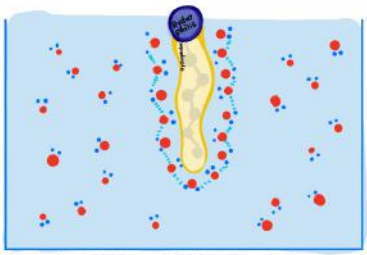
Salt Bridges



neutralizing acidic + basic R-groups

Q:

Solvation Layer



Hydration cage results in highly ordered H_2O molecules.

MCAT Question: If there were multiple hydrophobic molecules in solution, what would be the result of placing the molecules together?

a. an increase in entropy
b. an increase in enthalpy
c. weaker hydrophobic interactions
d. increased size in the water envelope

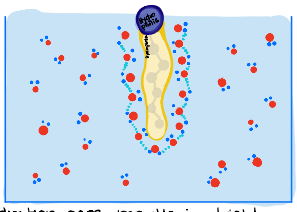
*** NOTE ***

Transitioning from solvation of non-polar regions to solvation of mostly polar globular proteins results in a net increase in entropy

↑ NET increase in entropy: Major contributor to overall conformational stability of a folded protein.

A:

Solvation Layer



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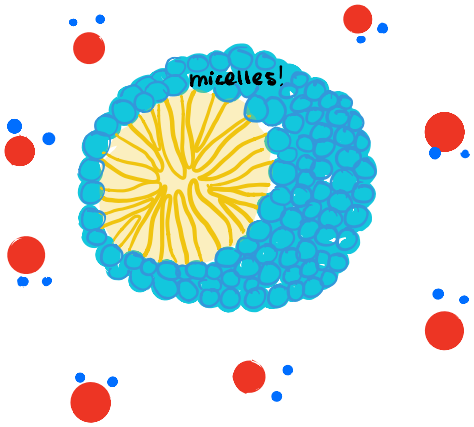


MCAT Question: If there were multiple hydrophobic molecules in solution, what would be the result of placing the molecules together?

a. an increase in entropy
b. an increase in enthalpy
↳ not applicable
c. weaker hydrophobic interactions
↳ stronger hydrophobic interactions
d. increased size in the water envelope
↳ decreased size in water envelope

* Multiple separated hydrophobic molecules would cause a serious decrease in entropy (due to decreased randomness of H_2O molecules.) If all the hydrophobic molecules were joined together we would increase entropy because there would only be one ordered H_2O layer. *

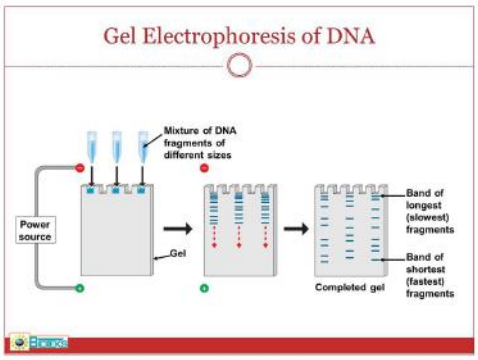
Denaturing Proteins

- acid
- Heat
- urea: H-bonds to (+) areas on proteins which disrupts 2° structure
- mercaptoethanol: reduces disulfide bonds irreversibly

Protein Separation

- isoelectric point: where protein has no net charge. pI = pH
- Electrophoresis

* coat proteins in universal negative charge (SDS-PAGE)

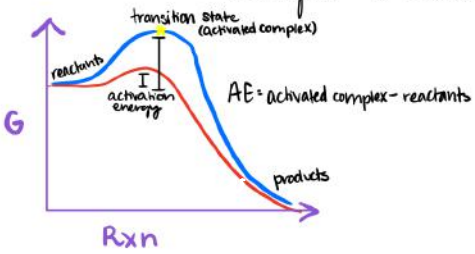


ENZYMES

Enzyme vs catalyst: both decrease activation energy of a reaction. Enzymes are organic. Neither are consumed during a reaction.

a. Enzymes...
a. ↑ rxn rate
b. ↓ energy of activation
c. do not change equilibrium or Keq
d. do not change % yield
e. ↑ yield. (Kind of, just faster)

↑ Enzyme = ↓ Ea (activation energy) = ↑ k (rate constant) = ↑ Rate



Enzymes don't:

- Change equilibrium or equilibrium constant ∆K.
- Change Gibbs Free Energy.
- Catalyst isn't used up as long as there is substrate present.

Classes:

Oxidoreductases: oxidize/reduce a species
- oxidase
- dehydrogenase
- hydroxylation

hydrolases: hydrolytically cleave substrate
- lipase
- amylase
- pepsin
- protease

transferases: move one group (methyl, phosphate) onto substrate.
- kinase
- phosphatase
- methylase

isomerase: change spacial orientation (make isomers)
- phosphohexose isomerase
- fumarase

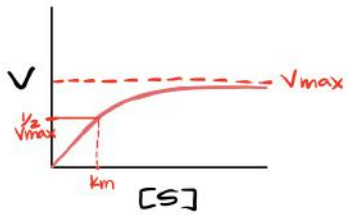
Lyase: Non-hydrolytic cleavage or removal.
- synthase

Ligase: Join substrates by condensation "addition reaction"
- synthetase

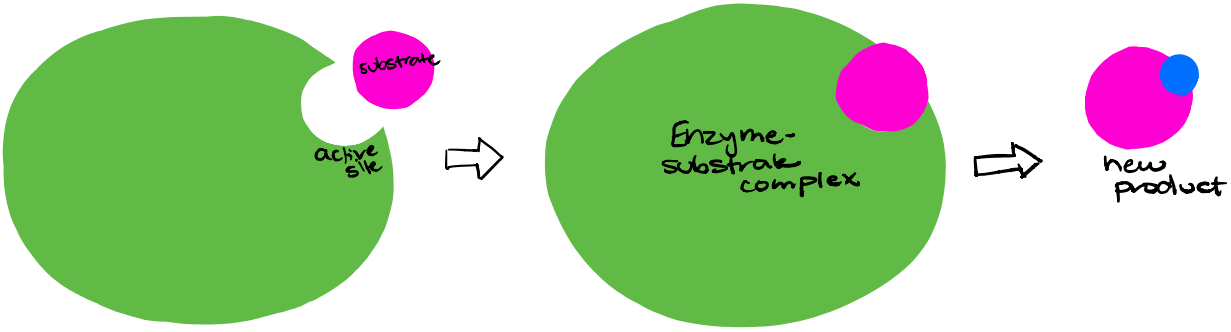
Kinetics:

Michaelis-Menten Plot

- V_{max} = max ability of enzyme at given [enzyme]
- K_m = M.M. constant is [substrate] at which ½ V_{max} happens



↑ Km = ↓ affinity (for substrate)



Enzyme Specificity Theories:

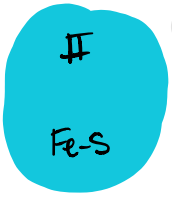
- Induced Fit * Favored
- Lock + Key * largely dismissed

Co Factors: Pyridoxal Phosphate (for Glycogen Phosphorylase)

Coenzymes: Coenzyme Q in ETC → carry electrons

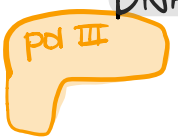
Prosthetic groups: Fe-S clusters in complex II of ETC

Hemoglobin = holoenzyme

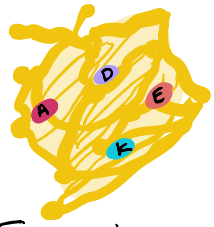


complex II : holoenzyme

DNA polymerase : apoenzyme



Vitamins → metabolism (organic)



Fat soluble

* Fat soluble vitamins are stored and more difficult to get rid of.

Q: What is NAD derived from?

A: a vitamin! Niacin specifically

all other vitamins

Water soluble

Minerals → Bone formation/ion gradients/O_2 transport (inorganic)

Michaelis-Menten Kinetics

$$V_0 = \frac{V_{max}[S]}{K_m + S}$$

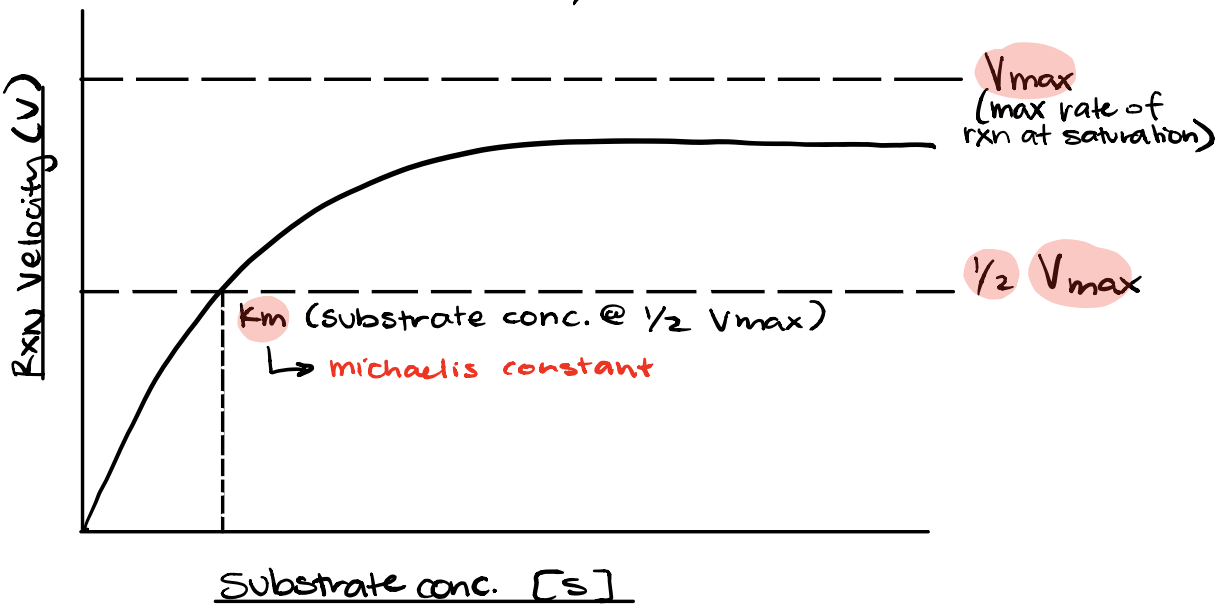
$$K_m + S = \frac{V_{max} S}{V_0}$$

$K_m = S_{1/2 V_{max}}$

$$K_m = \frac{K_2 + \frac{1}{K_1}}{K_1}$$

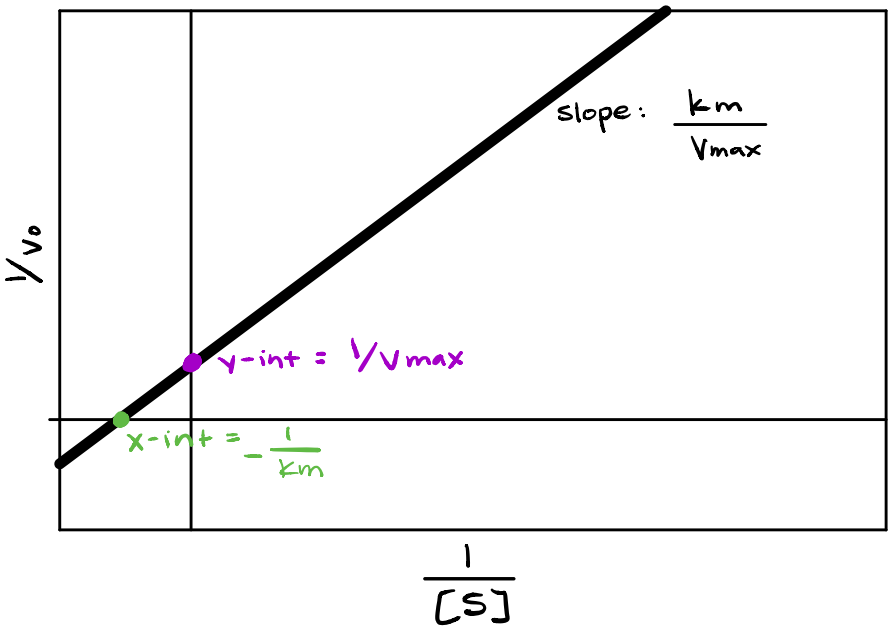
↓ K_m = ↑ binding affinity of an enzyme

K_m = [S] @ ½ V_{max}

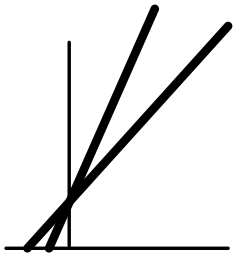


Line-Weaver Burke Plots

double reciprocal of michaelis-menten in order to linearize the data

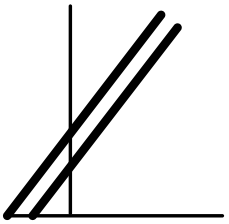


Types of Inhibitors



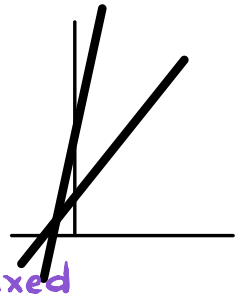
Competitive
substrate + inhibitor compete for enzyme catalytic site

Vmax: no change
Km: ↑



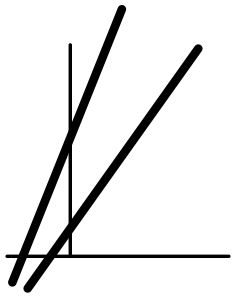
Uncompetitive
substrate binds first, then the inhibitor can bind

V-max: ↓
Km: ↓



mixed
either substrate or inhibitor may bind @ any time

Vmax: ↓
Km: ↑ or ↓

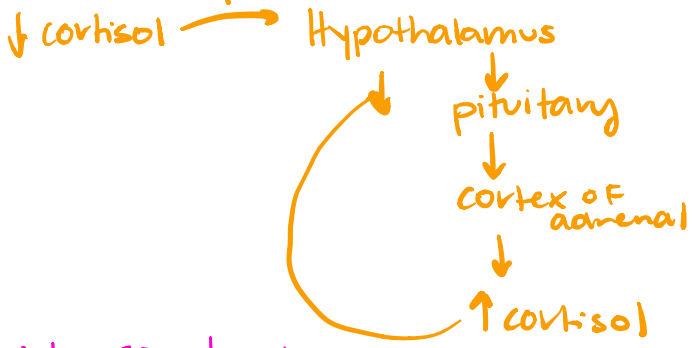


non-competitive
inhibitor always binds enzyme but NOT @ active site.

V-max: ↓
Km: no change

Feedback Inhibition

Negative Feedback: cortisol loop.



Positive Feedback: Amniotic sac breaks

↑ oxytocin for contractions

↑ contractions

↑ oxytocin

Zymogens: enzymes that are inactive until acted on

↑ chyme

↑ peptidase

↑ trypsin → trypsinogen

zymogen chymotrypsinogen

↑ chymotrypsin

↑ breakdown

Allosteric enzymes: change conformation upon binding

Hemoglobin! (as O_2 binds)

Mini Nomenclature break ☺

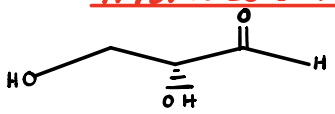
Monosaccharides : $(CH_2O)_n$

Polysaccharides: $C_n(H_2O)_x$

—ose = sugar
deoxy— = where an H replaced an —OH
Aldose = aldehyde
Ketose = ketone

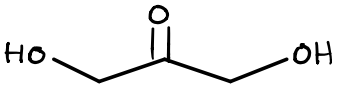
Sugars to know for the MCAT:

Monosaccharides



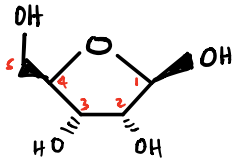
Glyceraldehyde

ex: glyceraldehyde-3-phosphate (glycolysis)



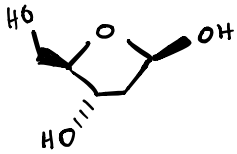
Dihydroxyacetone

ex: dihydroxyacetone phosphate (glycolysis)



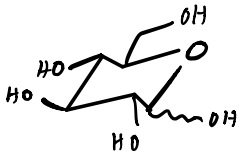
Ribose

ex: ribonucleic acid (RNA)



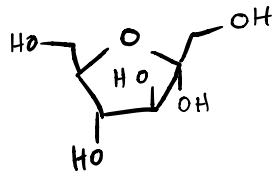
Deoxyribose

ex: deoxyribonucleic acid (DNA)



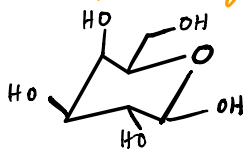
Glucose

ex: glucose ☺



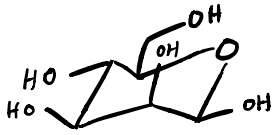
Fructose

ex: phosphofructo kinase



Galactose

ex: UDP-galactose



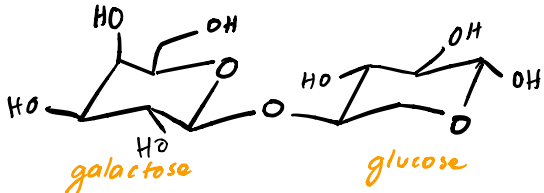
Mannose

ex: D-mannose

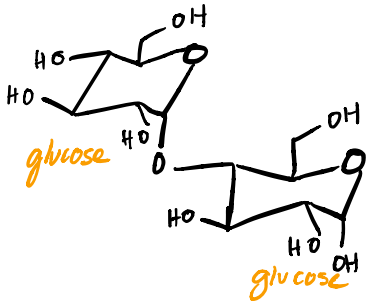
Epimers at C_2

Epimers at C_4

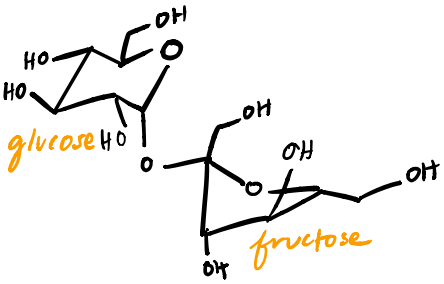
Disaccharides



Lactose



Maltose



Sucrose

Q: DSW is a 5% glucose solution used intravenously to treat patients with hyperkalemia. Which of the following disaccharides would be most likely used to create this solution?

I. Sucrose
II. Maltose
III. Lactose
IV. Galactose

a. I and III
b. II and IV
c. II only
d. I only

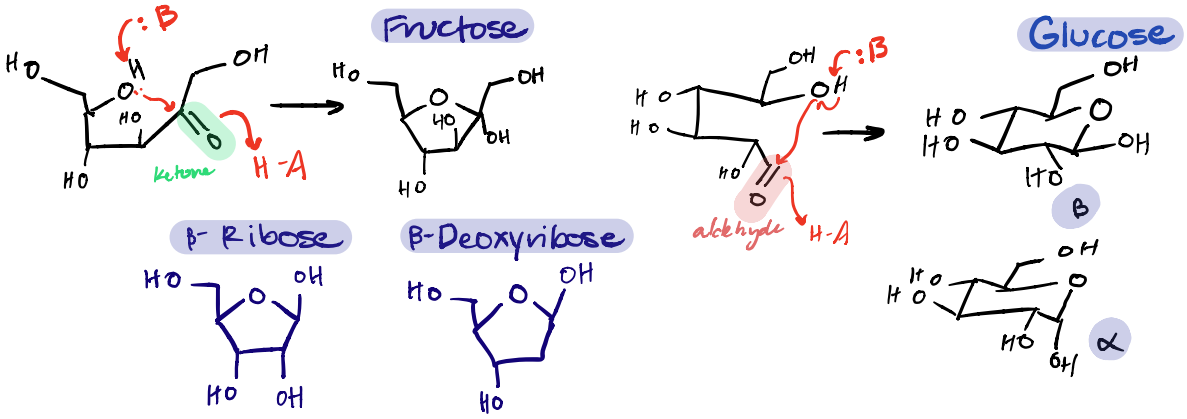
A: DSW is a 5% glucose solution used intravenously to treat patients with hyperkalemia. Which of the following disaccharides would be most likely used to create this solution?

I. Sucrose
II. Maltose
III. Lactose
IV. Galactose

a. I and III
b. II and IV
c. II only
d. I only

The only information we have is that DSW is glucose. Therefore it is most logical to assume from our options Maltose is used (which is glucose–glucose.) Sucrose is glucose–fructose and Lactose is glucose–galactose.

* all human sugars are "D" as opposed to all human amino acids which are "L" conformation *



Reducing sugar – not attached at anomeric carbon + an aldehyde

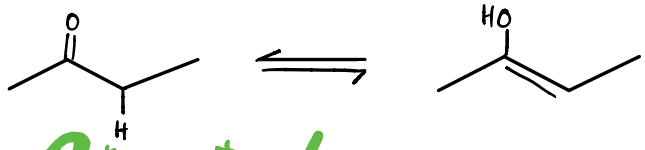
Non-reducing sugar – attached at anomeric carbon

Tautomerism: isomers of a compound that only differ in the position of protons and electrons.

- hydride shifts -

Keto-enol tautomerism: Acid/Base catalyzed

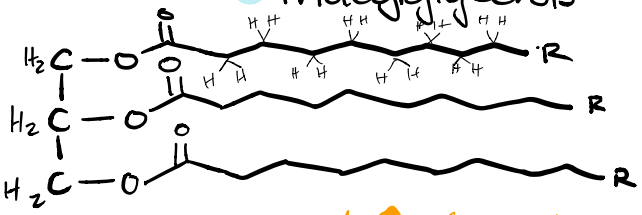
ie.



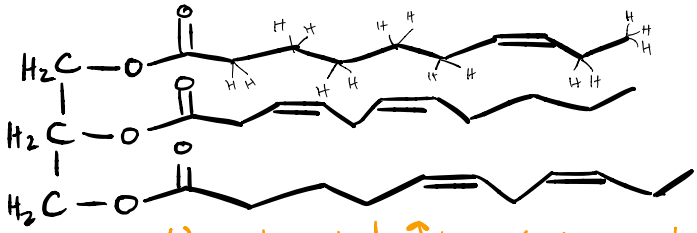
Lipids

1) Biomolecules
2) Hydrophobic

- Fatty acids – COOH Ampipathic
- Triacylglycerols – Esters Hydrophobic



Saturated: fully saturated with hydrogens, solid @ room temp. (Butter, oils)



Unsaturated: Not fully saturated with hydrogen. liquid @ room temp.

Healthier

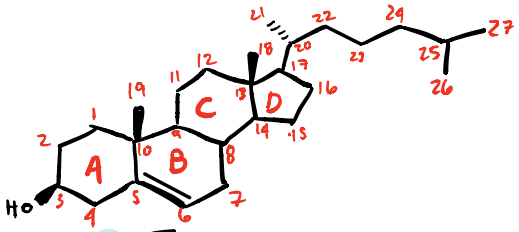
- Phospholipids – Esters Ampipathic

Saponification: Triglycerides react with KOH or NaOH

↓

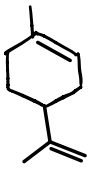
Soap + glycerol

- **Steroids** – 4 membered ring
  Hydrophobic



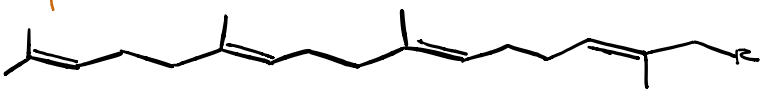
- **Terpenes** – $C_{10}H_{16}$ (unsaturated hydrocarbons)
  Hydrophobic

ex:



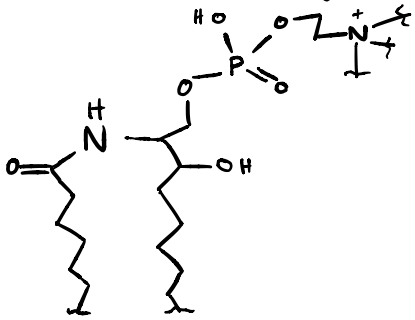
D-limonene

or

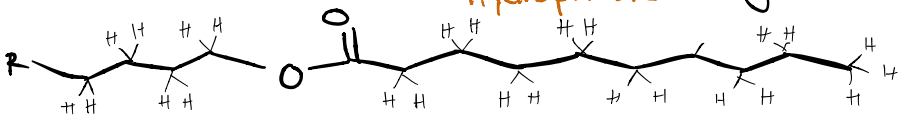


squalene

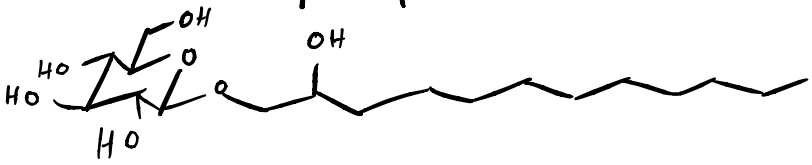
- **Spingolipids** (fatty acid derivatives of sphingosine.. found in brain + nervous tissue)
  Ampipathic



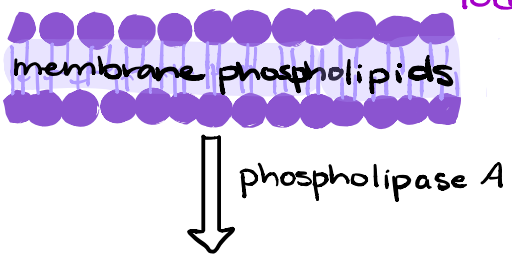
- **Waxes** – Ester + long chain alcohol + F.A.
  Hydrophobic



- **Glycolipid** Ampipathic



- **Prostaglandins** — lipid mediators that act like localized hormones



Aracadonic Acid

COX — NSAIDS — cyclooxygenase

↓

Prostaglandin G_2

↓ POX

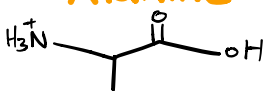
Prostaglandin H_2

→ prostaglandins
→ prostacyclin
→ Thromboxane

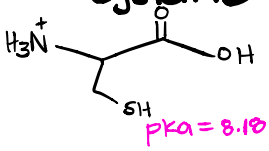
Hydrophobic (non-polar)	A, Y, W, V, I, L, M, F
Hydrophilic (polar)	Q, S, N, T
Negatively charged	D, E
Positively charged	K, H, R
ionizable	Y, C, H, E, R, K, D

Amino Acids

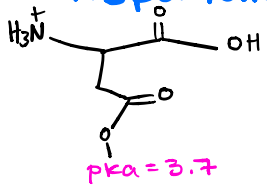
(A) Ala
Alanine



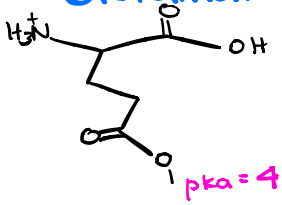
(C) Cys
• **Cysteine**



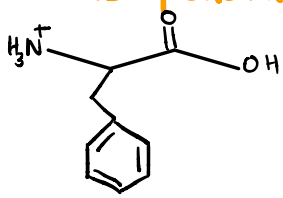
(D) Asp
• **Aspartate**



(E) Glu
• **Glutamate**

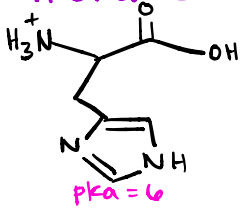


(F) Phe
Phenylalanine

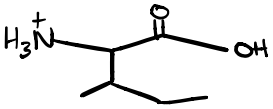


(G) Gly
Glycine

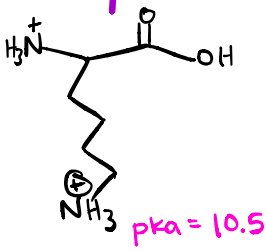
(H) His
• **Histidine**



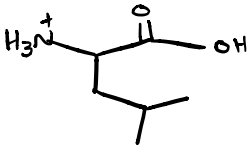
(I) Ile
Isoleucine



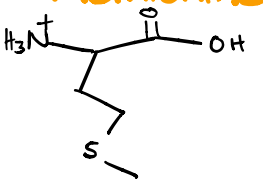
(K) Lys
• **Lysine**



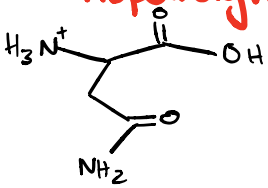
(L) Leu
Leucine



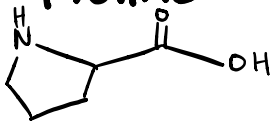
(M) Met
Methionine



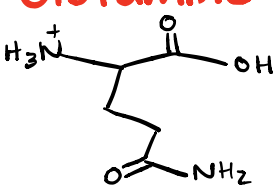
(N) Asp
Asparagine



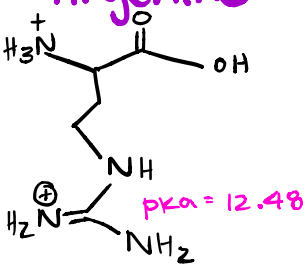
(P) Pro
Proline



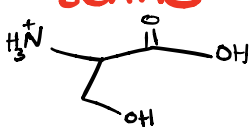
(Q) Gln
Glutamine



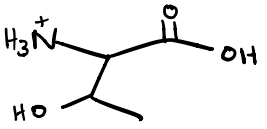
(R) Arg
• **Argenine**



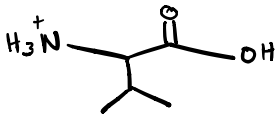
(S) Ser
Serine



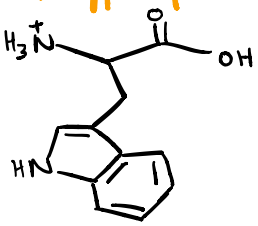
(T) Thr
Threonine



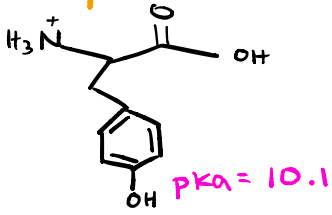
(V) Val
Valine



(W) Trp
Tryptophan



(Y) Tyr
• **Tyrosine**



Bioenergetics → thermodynamics of biological systems

$\Delta H - T\Delta S = \Delta G$

	+H	−H
+S	depends	−G spontaneous
−S	+G not spontaneous	depends

Living Systems maintain a non-equilibrium state

Several steps in glycolysis have ΔG's that are large and positive. How does the reaction still proceed forward?

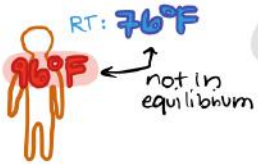
a. enzymes
b. nutrients
c. Reaction coupling

answer: c!
Reaction coupling drives glycolysis forward. Reactions rely on the products of previous steps.

Dynamic Steady State: (Homeostasis)

Living things maintain a constant steady internal environment.

↳ NOT in equilibrium with surroundings



Lowest possible entropy

EQUILIBRIUM ≠ STEADY STATE

Gibbs Free Energy

ΔG: no standard conditions
ΔG°: standard conditions
ΔG°': ~~physiological conditions~~ (pH = 7)

$$\Delta G = \Delta G^{\circ\prime} + RT \ln Q$$

reaction quotient

Temp

gas constant

variable — Fixed

& can be measured @ anytime during reaction.

True / False Q's

a) For Reaction X, $\Delta G = -30.78$ kJ. For Reaction Y, $\Delta G = 22.5$ kJ. It can be concluded that Reaction Y is closer to its equilibrium than is Reaction X,

b) At equilibrium, $\Delta G^{\circ\prime} = 0$

c) At equilibrium $\Delta G = 0$

d) For a given reaction at a given temperature, there are an infinite number of different $\Delta G^{\circ\prime}$ values associated with different ratios of products to reactants

e) For a given reaction at a given temperature, there are an infinite number of different ΔG values associated with different ratios of products to reactants

f) $\Delta G^{\circ\prime}$ represents the free energy change for a complete conversion of all reactants to products.

Answers

a. **True** : ΔG tells us which direction the rxn needs to proceed to reach equilibrium.

b. **False** $\Delta G^{\circ\prime} = -RT\ln K_{eq}$ at equilibrium.

c. **True** $\Delta G = 0$ at equilibrium

d. **False** $\Delta G^{\circ\prime}$ is a set value and independent of concentrations.

e. **True** ΔG can be calculated at any point

f. **False** $\Delta G^{\circ\prime}$ = free energy associated with proceeding from standard conditions to equilibrium.

$\Delta G^{\circ\prime}$ and K_{eq}

@ Equilibrium...
$Q = K_{eq}$
$\Delta G = 0$

$\Delta G^{\circ\prime} = -RT\ln K_{eq}$

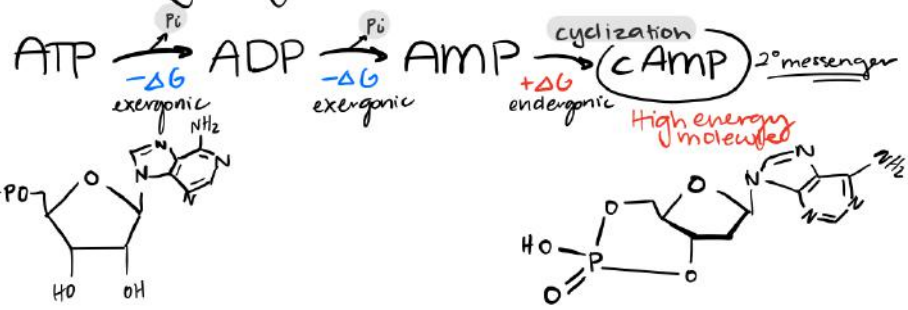
Endergonic = $+\Delta G$ = nonspontaneous

Exergonic = $-\Delta G$ = spontaneous

- if $K_{eq} = 1$ then $\Delta G^{\circ} = 0$
- if $K_{eq} = 6$
- if $Q = 1$, $\Delta G = \Delta G^{\circ}$
- if $K_{eq} > 1$ then $\Delta G^{\circ} = (-)$

ATP

Atp hydrolysis = $\Delta G'^{\circ} = -30.5$ kJ/mol $<< 0$



formation

Substrate level phosphorylation: ADP + ~P → ATP

Phosphate comes from another molecule

- cytosol (glycolysis) & mitochondrial matrix (GTP in CAC)

must be coupled to exergonic rxn

Oxidative Phosphorylation: ADP + P_i → ATP

phosphate comes from free organic phosphate

- exclusively in mitochondrial matrix.

ie: ATP formed by ATP synthase.

consumption

Hydrolysis: $ATP + H_2O \rightarrow ADP + P_i + energy$

(P_i: inorganic phosphate created)

almost always coupled to another reaction

ie: cocking myosin head

Phosphoryl Group Transfers: $ATP \rightarrow ADP + energy$

Phosphate gets transfered to another molecule.

ie: Glucose + ATP → G-6-P + ADP

Phosphorylation using ATP

• MAJOR HUMAN BODY REGULATORY MECHANISM •

↳ turns enzymes / proteins / signaling molecules "off" or "on".

Phosphorylation

ATP is phosphate donor

kinase → phosphorylates

Dephosphorylation

dephosphorylates → P_i

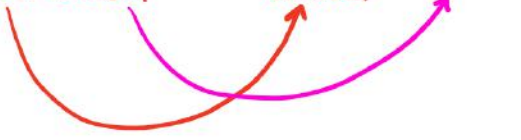
phosphatase

Biological Redox Reactions

step 6 (glycolysis)

$GADP + NAD^+ + P_i \rightarrow 1,3\text{-}BPG + NADH$

GADP: reduced; NAD^+: oxidized; 1,3-BPG: oxidized; NADH: reduced



½ reactions

$NAD^+ + H^+ + 2e^- \rightarrow NADH$

$+ \quad GADP + Pi \rightarrow 1,3BPG + 2e^- + H^+$

$NAD^+ + Pi + GADP \rightarrow NADH + 1,3\,BPG$

when you see...
- NADH/NAD+
- NADPH/NADP+
- $FADH_2$ / FAD
- $FMNH_2$ / FMN
- Semiquinone
- Ubiquinone
- Cytochrome

} think... REDOX

these are soluble electron carriers & there is always e- transfer as they pass from one to another

Carbohydrate metabolism...

the sum of all chemical reactions in the body

* Respiration

an organic compound serves as the final electron acceptor in order to generate ATP.

[anaerobic: O_2 is not final e- acceptor ← fermentation or lactic acid
aerobic: O_2 is final e- acceptor] ← • citric acid cycle • electron transport

humans do BOTH!

Obligate aerobes: organisms that can only use aerobic respiration

Obligate anaerobes: organisms that only use anaerobic respiration

Faculate aerobes: organisms that prefer aerobic respiration but can perform either aerobic or anaerobic. *humans*

Faculate anaerobes: organisms that prefer anaerobic respiration but can do either.

NET:
- 2 ATP
- 2 NADH
- 2 Pyruvate

Gluconeogenesis

• reverse glycolysis •

Liver

done during fasting to increase blood sugar.

Glucose
↓ H_2O, P_i — *Glucose-6-phosphatase*
G-6-P
↓ phosphoglucose isomerase
F-6-P
↓ P_i, H_2O — *fructose-1,6-bisphosphatase*
F-1,6-P
↓ aldolase
GAD-3-P + DHA-P (triose phosphate isomerase)
↓ P_i, NAD^+, $NADH$
1,3-BPG
↓ ADP, ATP (phosphoglycerate kinase)
3-Phosphoglycereate
↓ phosphoglycerate mutase
2-Phosphoglycerate
↓ H_2O (enolase)
Phosphoenol pyruvate
↓ GDP, GTP
oxaloacetate
↓ ADP, ATP — *phosphoenol pyruvate carboxy kinase*
pyruvate

~ New Gluconeogenesis enzymes catalyze irreversible steps ~

Pyruvate Dehydrogenase Complex

pyruvate → acetyl CoA

glycolysis —PDH→ Krebs

pyruvate

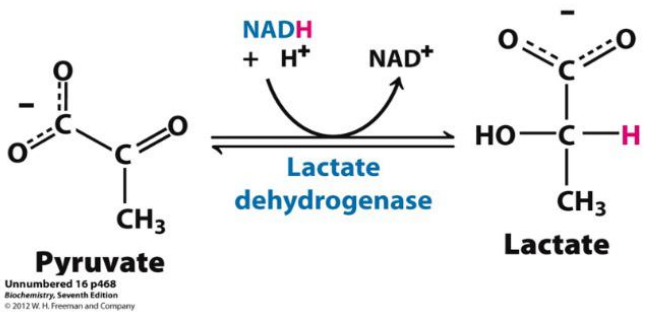
1. PDH complex → acetyl-CoA
2. lactate dehydrogenase → lactate
3. pyruvate carboxylase → oxaloacetate

fermentation

anaerobic glycolysis
- bacteria
- animals during exercise
- erythrocytes

Ethanol fermentation: yeast + bacteria
↳ ethanol is produced as is the final electron acceptor.

Lactic acid fermentation: animals
↳ lactate is produced and is the final electron acceptor.



*fermentation regenerates NAD^+ so glycolysis can continue *

Pentose Phosphate ... pathway ...

1) **NADPH** synthesis: "Reductive Biosynthesis" (fatty acids) & production of Glutathione (radical O_2 antioxidant).

2) **Ribulose-5-phosphate**: synthesizes nucleotides

Oxidative Phase
Glucose-6-P → 6-Phosphogluconate → Ribulose-5-P
*coupled w/ $NADP^+$ → NADPH

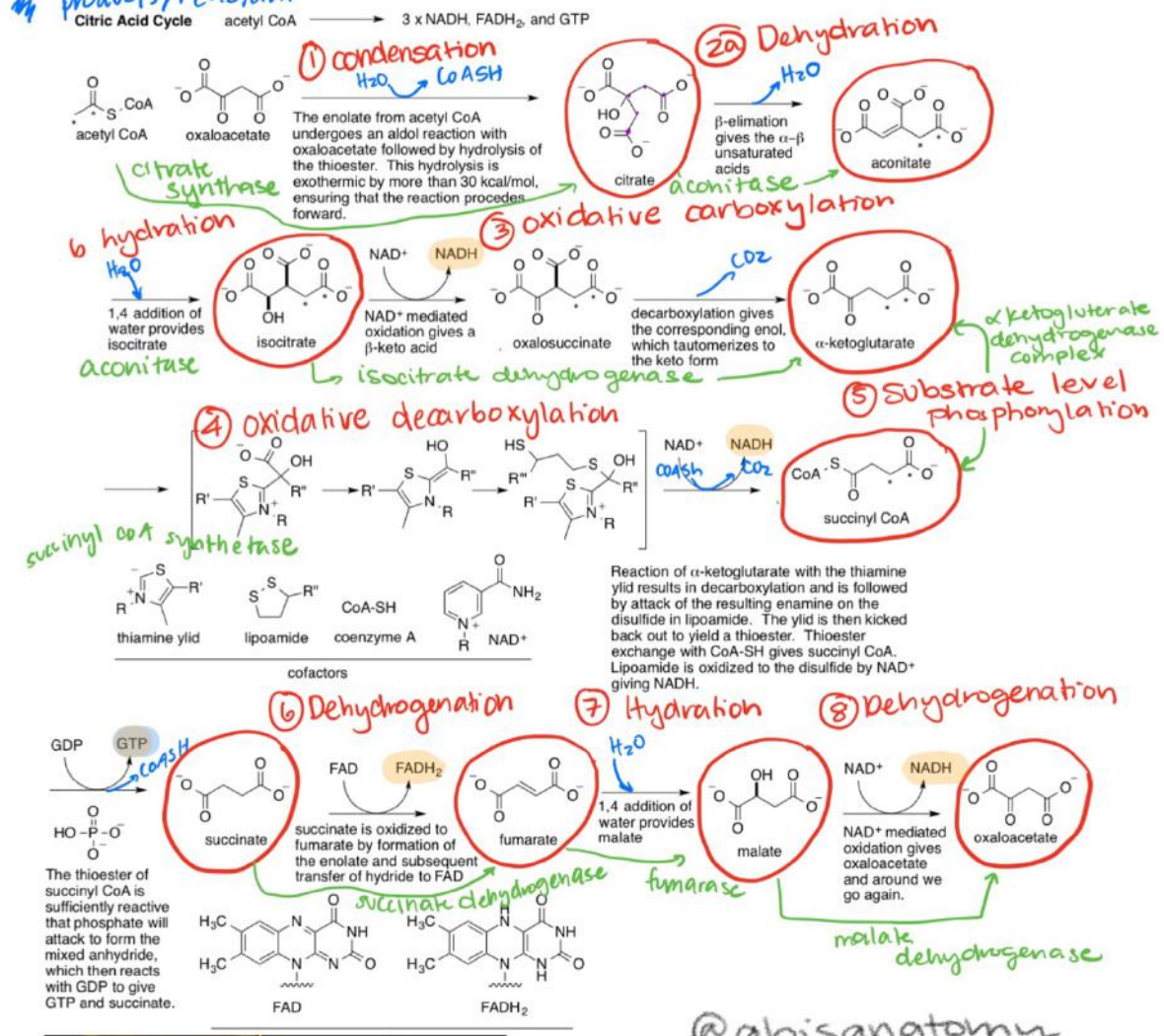
Non-oxidative Phase
Ribulose 5-P → R5P ↔ Sugar Pool ↔ Glucose-6-P
output
Transketolase
Transaldolase

1 glucose = 2 NADPH = 4 glutathiones

The Citric Acid Cycle

*substrate level phosphorylation

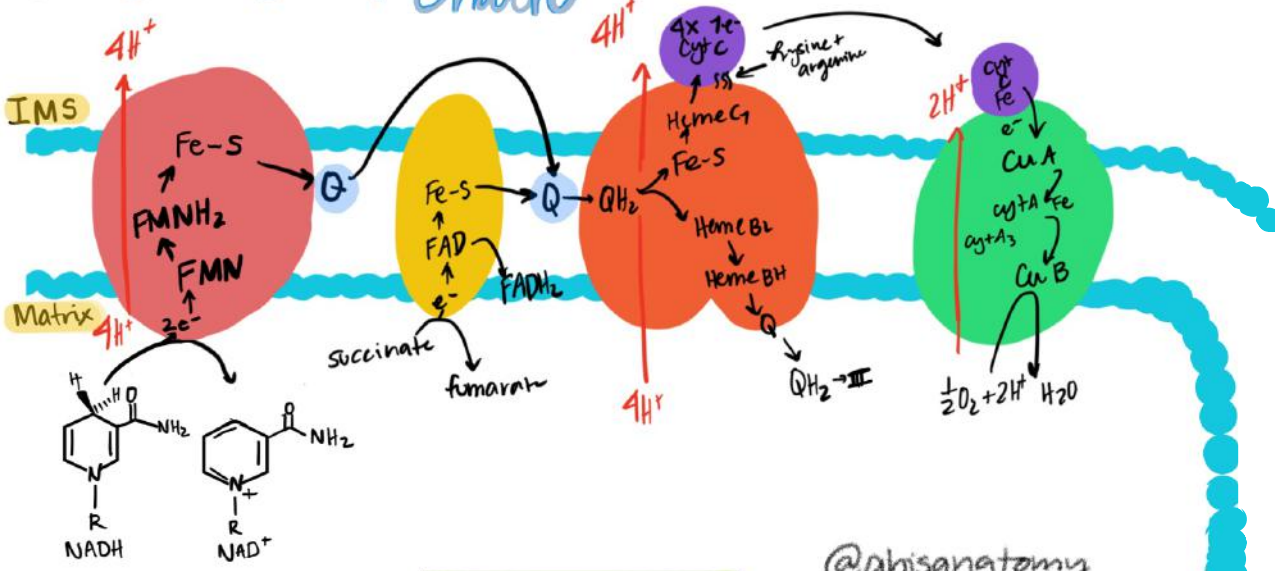
intermediate
enzyme
products/reactants



@abisanatomy

NET:
- 6 NADH
- 2 $FADH_2$
- 4 CO_2
- 2 ATP

Electron transport chain



@abisanatomy

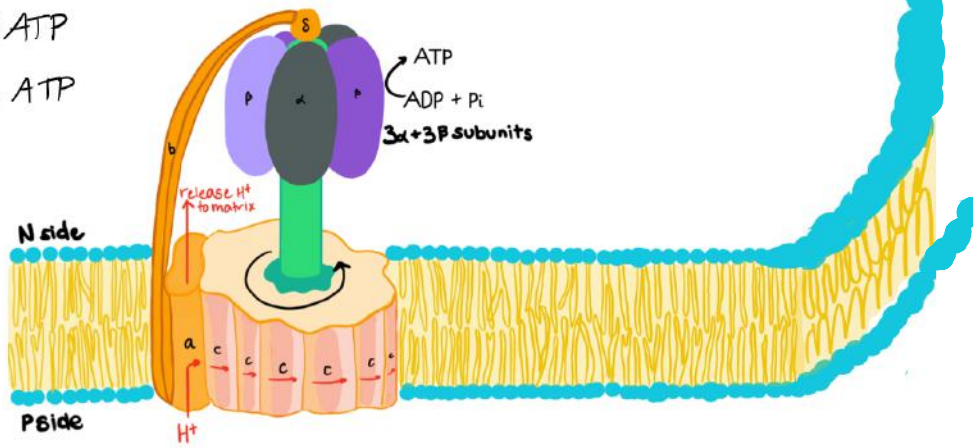
ATP Synthase

* Oxidative phosphorylation

Each NADH = 10 H^+, 3 ATP

Each $FADH_2$ = 6 H^+, 2 ATP

(FADH2 by passes complex 1)



Total

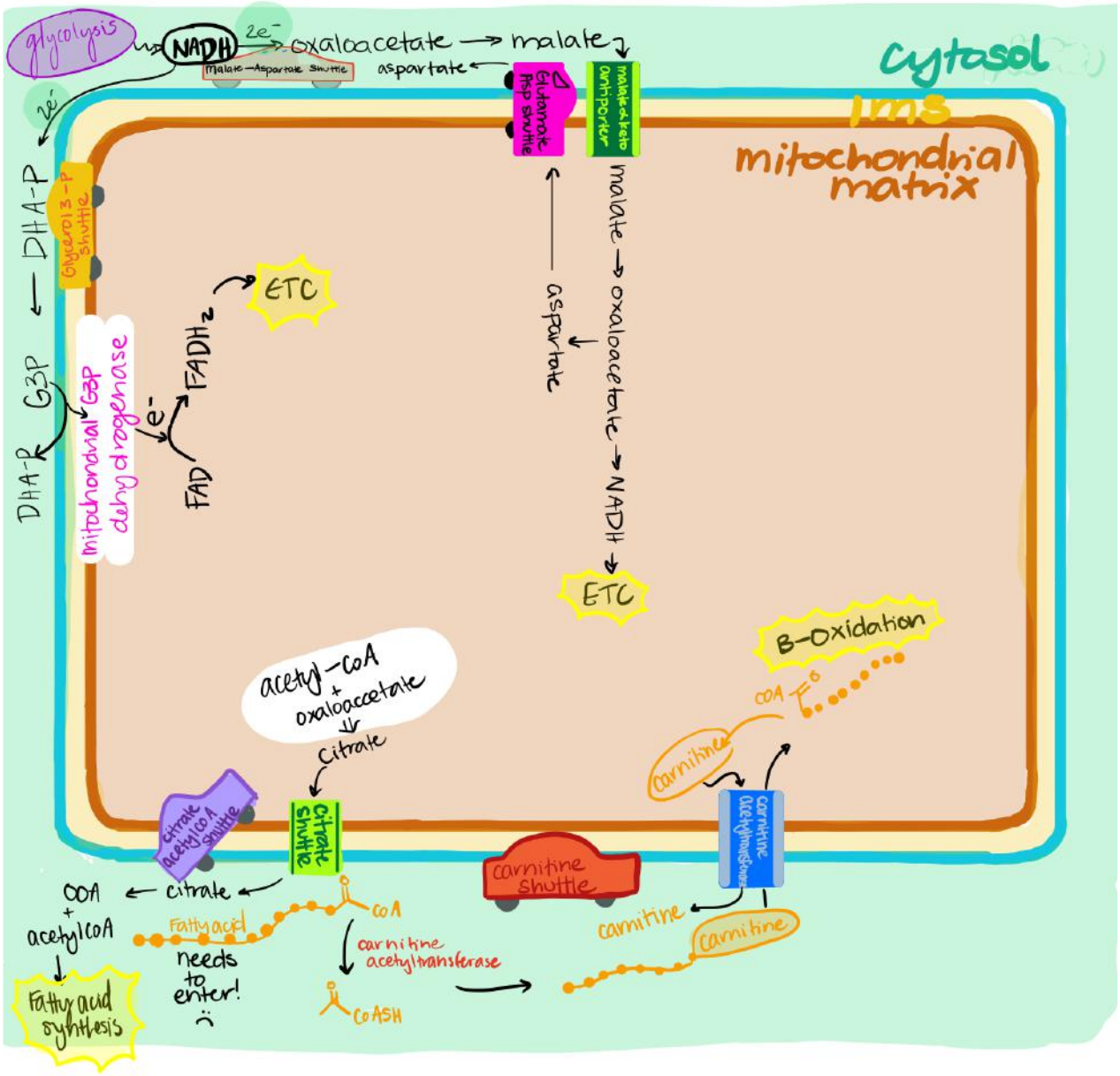
NADH = 3 ATP
↳ in glycolysis = 2 ATP
$FADH_2$ = 2 ATP

	NADH	$FADH_2$	ATP
Glycolysis	2 (2 ATP)	0	2
Citric Acid cycle	8 (24 ATP)	2 (4 ATP)	2 (GTP)
total	10 (28 ATP)	2 (4 ATP)	4

= 36 ATP

Biochemical Shuttles

transport molecules across impermeable membranes

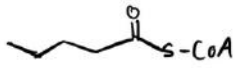


β-Oxidation

4 Basic Steps of β-oxidation

Input
- FAD
- H_2O
- NAD^+
- CoASH

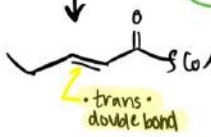
1 – OXIDATION BY FAD



acyl-CoA

FAD → $FADH_2$

2 – HYDRATION

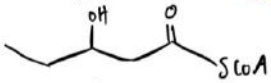


"trans" double bond

cis-FA in natural diet

trans-FA [hydrogenated oils] (partial hydrogenation of peanut butter)

$+ H_2O$ — Enoyl-CoA hydratase — enoyl-CoA

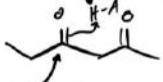


β-hydroxy acyl CoA

3 – OXIDATION BY NAD^+

oxidation

NAD^+ → NADH — β-hydroxyacyl-CoA dehydrogenase



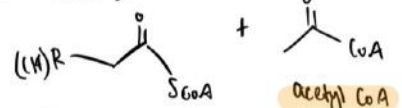
β-ketoacyl-CoA

4 – THIOLYSIS BY CoA

in matrix

$CoA-SH$ (sets up possible continuation of β-oxidation)

thiolase



CH acyl CoA + Acetyl CoA

Output
- $FADH_2$ → 2 ATP
- NADH → 3 ATP
- Acetyl CoA → 12 ATP

* Note rules for odd vs even & saturated vs unsaturated

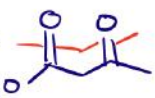
Ketone Bodies

a family the liver will generate but cannot use when you watch your weight. [Fast]

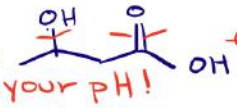
↓ blood pH (ketoacidosis)

acetone: is all alone — no energy

acetoacetate: has a mate — energy for ♥ & Not



3-hydroxybutyrate: OH! OH! we decrease your pH! — energy for ♥ & NOT

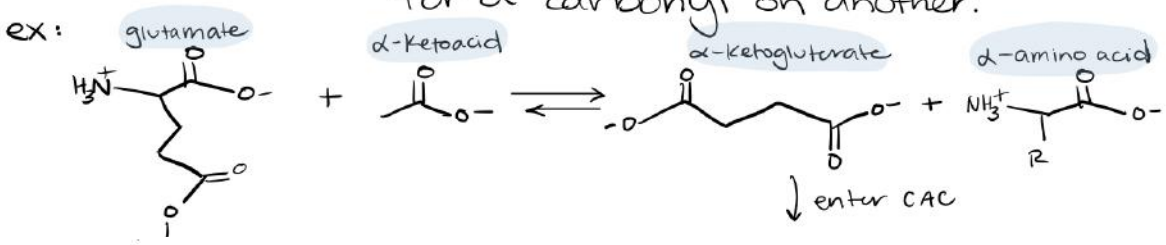


Protein Metabolism

amino acids can be broken down by pyruvate or acetyl-coA and fed into citric acid cycle.

transamination: exchange of an amine group on one molecule for a carbonyl on another.

ex:



Suppose the following biomolecules were radioactively labeled... where would we see them in the greatest abundance?

a. pyruvate	the cytosol
b. oxaloacetate	the mitochondrial matrix
c. phosphofructokinase-1	the cytosol
d. PDH complex	the mitochondrial matrix
e. phosphoenolpyruvate	the cytosol
f. glycogen synthase	the cytosol
g. pyruvate carboxylase	the mitochondrial matrix
h. α-ketoglutarate	the mitochondrial matrix
i. succinate dehydrogenase	Inner mitochondrial membrane
j. ATP synthase	Inner mitochondrial membrane
K. Fatty acids in β-oxidation	mitochondrial matrix
l. citrate	mitochondrial matrix
m. Ketolysis	mitochondrial matrix but NOT of liver cells

Regulation of metabolism

organism level

well-fed state (Postprandial) = hours after eating

↑ insulin levels ↓ glucagon levels

↑ anabolism (vs catabolism)

↑ glycogen synthesis (glycogenesis)

↑ fatty acid synthesis

Fasting state (Post-absorptive)

↑ glucagon levels ↓ insulin levels

↑ catabolism (vs anabolism)

immediate glycogenolysis delayed gluconeogenesis

Starvation

↑↑ glucagon

↑↑ epinephrine

↑↑ gluconeogenesis

↑ fatty acid oxidation = ketoacidosis

tissue level

↑ glucose in well-fed state
↑ fatty acids when fasting
No ketones

↑ glucose in well-fed state
↑ glucose when fasting
↑ ketones if starving

↑ glucose during well-fed state
↑ fatty acids when fasting

↑ Glucose in all states via anaerobic glycolysis

muscles

↑ fatty acids in well-fed state
↑ Fatty acids & ketones during fasting

↑ glucose during well-fed state
↑ fatty acids & ketone during fasting.

fatty acid synthesis

★ Occurs in the cytosol of liver cells.
★ Constructs 16-carbon palmitic acid.