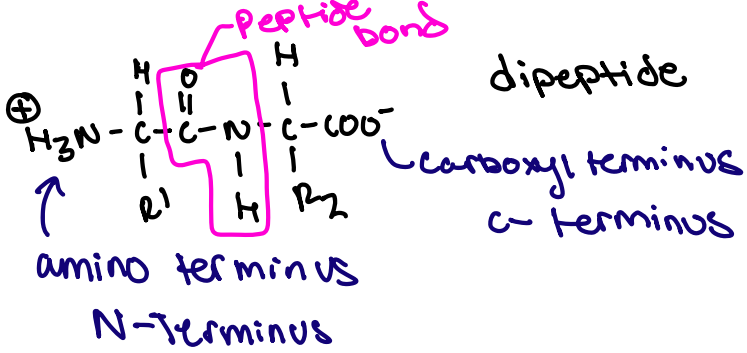


Aug ≥ methianine

Methianine is the amino acid that starts all proteins

III. B.4

Levels of protein structure

a. (1°) Primary Structure - a.a. sequence

- comes from DNA sequence
- involves covalent bonding
- all proteins have primary structure (1°)

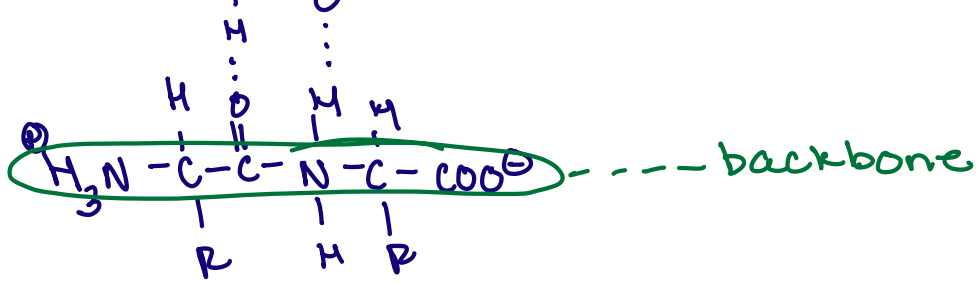
Oxytocin Smallest protein

"love hormone" Stimulates - milk letdown
- Uterine contractions during parturition

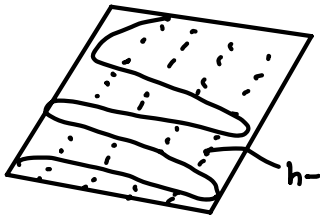
disulfide
Cysteine - covalent bond "Perms"

b. Secondary (2°)

- localized three-dimensional structures based on interactions among our R groups but mediated by hydrogen bonding between the carbonyl carbon (C=O) and amino N in peptide backbone.



III B. 4b. 2° three possible 2° structure



- sheet (β-pleated sheet)
- Helix (α-helix)

some R groups don't permit this conformation

- loop / random coil

neither one of the two choices → Misc. category

↑ not a helix

- Hydrogen bond mediate 2° structure
- All proteins have secondary structure

Leptin - 2° loop + helixes

Prolactin - peptide hormone acts on outside of cell sheets

↑ yellow marker covalent disulfide bridge

III B 4.c. Tertiary structure (3°)

-overall three-dimensional shape of a protein from interactions among 2° structures

Get rid of H-bonding - egg cooking

- heat
- Δ PH
- mediated by covalent (S-S), ionic interactions,

H-bonds van der Waal's, hydrophobic)

Can bond types!

- most proteins have

Disrupt 2° or 3° structure or remove structure artificially

ligand ~ lipid molecule binds – diffuse to everywhere in the body

Synthetic activator

Physical prop of a.a. hydrophobic tendency — Phenylalanine

III B.4.d. Quaternary Structure 4°

- Interactions of multiple protein sub-units to form an active protein complex
- can involve all bond types
- relatively few proteins have this

ex/: hemoglobin – in the blood – 2 α-globin proteins
2 β-globin proteins
+4 heme
+4 Fe^{++}

Enzymes!

But first remember thermodynamics

ΔG	rxn go? – spontaneously?
+	no
–	yes → but we need to overcome activation energy barrier ← done by enzymes
~0	maybe... depends on other factors, mostly concentration ⇌

I. Fundamentals... Enzymes are catalysts that speed up the rate of a reaction.

A. Characteristics of enzymes

Enzymes: - are usually a big protein (most are between 20-160 kDa avg: ~50 kDa

Fatty acid synthase: 272 kDa

- Usually have a very small active site - where catalysis occurs (a few a.a.)
- are specific to a (only 1) rxn
- are not the substrate (S) or the product (P) of the rxn
- Interact non-covalently with the substrate (S) and the product (P)
- Are not modified by the rxn (enzymes are the same before and after rxn)

B. Nomenclature

- Usually enzymes ends with suffix -ase
  - except our digestive proteases - end w/ "-in" Pepsin Trypsin
- Usually include the rxn type
- Usually include the name of S or P

Common exception

Kinase - add a phosphate (PO_4^-) to something
(hydroxyl amino acids accept)

) enzyme that causes something to go from potential to kinetic energy

↳ activates stuff turns things on/off

↳ Sometimes called phosphorylases

Opposite rxn is usually catalyzed by phosphatases

↗ Takes phosphate off of glucose in liver

C. Isoenzymes - Different enzymes that catalyze the same reaction

- usually differ in tissue expression + kinetics (behavior)

- glucokinase → both adds phosphate to glucose at the 6th carbon
- hexokinase → everywhere but the liver and acts at low concentrations of glucose (very)

* Glucokinase is expressed in the liver but works at much higher concentrations of glucose

D. Enzyme Cofactors.

- non covalently associated prosthetic groups or minerals that help the enzyme do its job. (hemoglobin)

(usually necessary)

- usually act to stabelize the enzyme structure of help w/ substrate binding.

Ex|| Minerals - Fe^{++}, Zn^{++}, Mn^{++}, Mg^{++}

Often the organic prostetic groups are derived from vitamins.

Ex|| Vit: B_7 Biotin - important for carboxylases (adds CO_2)

Vit: B_3 Niacin (critical to vitality, most have amine groups)

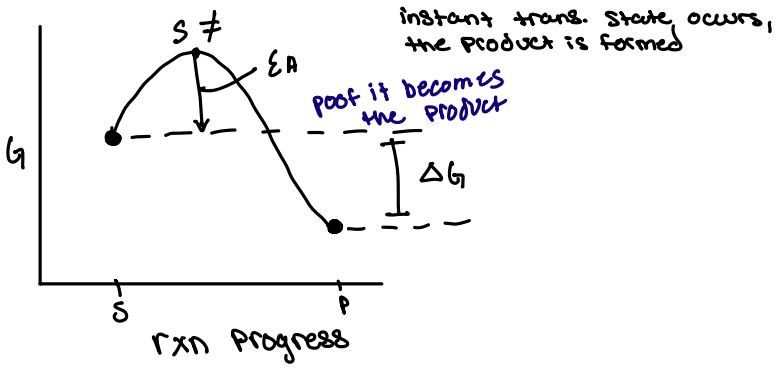
Subset of cofactors that get modified by rxn = coenzymes

ex|| : NAD^+ accepts hydrogens in dehydrogenation rxns

p - Niacin
p - adenine (google this) tiny compared to enzyme

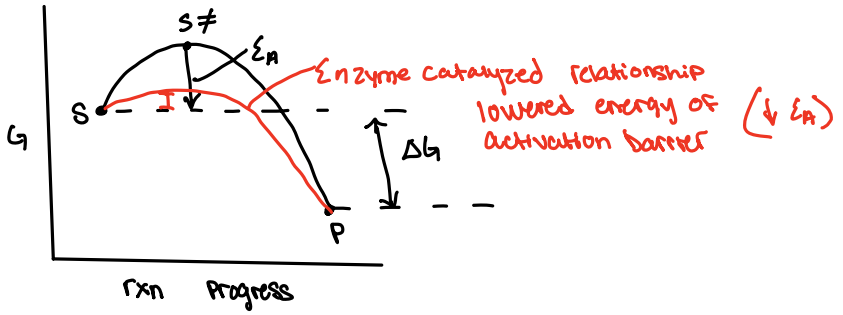
II Enzyme catalysis + kinetics

A. general principle of enzyme catalysis – enzymes bind (S) and strain S to form S ≠, Product is instantly formed. Enzyme releases P.



Affinity = tendency of two things to interact (attraction)

II A...



A. Enzyme has affinity for substrate

Enz. has higher affinity for transition state

Enz. Strains S into S ≠

P is immediately formed from the trans. state

Enz. releases the product due to a low affinity for it

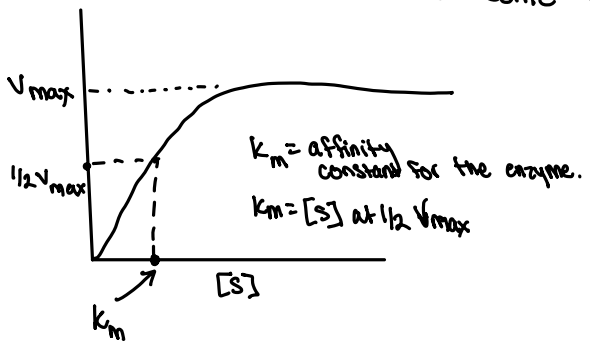
II.B. Describing enzyme kinetics (rxn rates and behaviors)

1913 German Confusion

1. Michaelis-Menton kinetics (of enzymes)

- described the relationship between reaction velocity (V) (Product formed / time per unit) and substrate concentration [S]

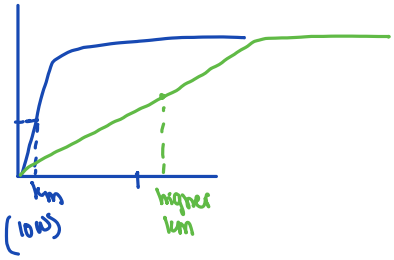
at some Fixed [enz]



Michaelis, Menton Equation: $V = V_{max} \cdot \frac{[S]}{K_m + [S]}$ (now instantaneous; the line)

more sub. needed
high km means low affinity

low km means high affinity



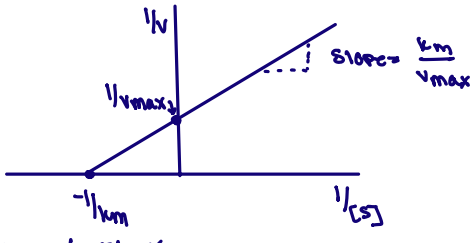
II B.2

Lineweaver and Burke (1936)

"Double reciprocal" plot = lineweaver Burke plot

$\frac{1}{V} = \frac{K_m}{V_{max}} \cdot \frac{1}{[S]} + \frac{1}{V_{max}}$

$y = m \quad x + b$ straight line



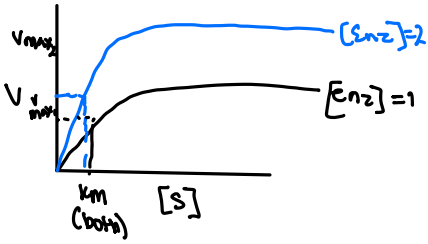
way easier to est. K_{max}

III Factors affecting enzyme kinetics

A. Concentration of a substrate (did that w/ graphs)

B. Changing the concentration of an enzyme – increase V_{max} but (don't affect K_m)

- longer) - term adjustment in cell



C. Post translational modification of enz.

most common form in nature

hydroxyl ← only ones can be phosphorylated
-OH a.a

1. Phosphorylation / dephosphorylation of enz.
kinase / phosphatase
phosphorylase

Enzyme ⇌ enz-(P) (kinase / phosphatase)

Enzymes are being turned on and off

active ⇌ inactive
or
inactive ⇌ active

(acute fast short-term on/off switch)

III C. proteolytic cleavage of an enzyme precursor to its active form

inactive precursor (zymogen) — irreversible activation

Irreversible activation (one way street to activate)

- most common w/ digestive proteases
- catalysis to activate often pH (changes 3° protein structure), autocatalysis (changes lid) or both

D. Environment conditions (pH, temp)

pH relevance? - digestive tract

temperature relevance? -
reproduction? - descended testes (testicles)
- fever

III. D. Environment (pH, temp)

pH...

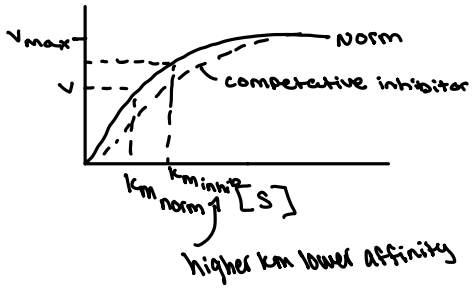
Temp... poikilotherms

E. Exogenous agents - inhibitors

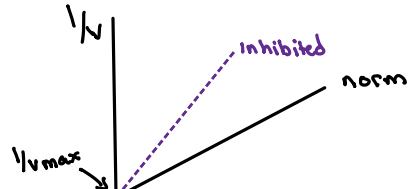
Competitive inhibitors - compete to bind @ active site

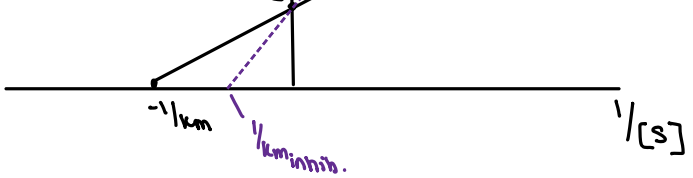
binds enz @ active site - affects ability of S to bind

alter apparent K_m but not apparent V_{max}



higher K_m lower affinity

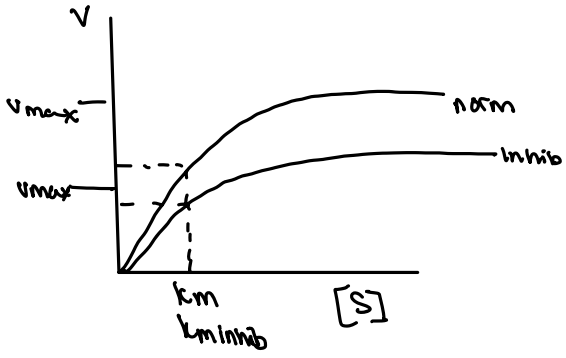


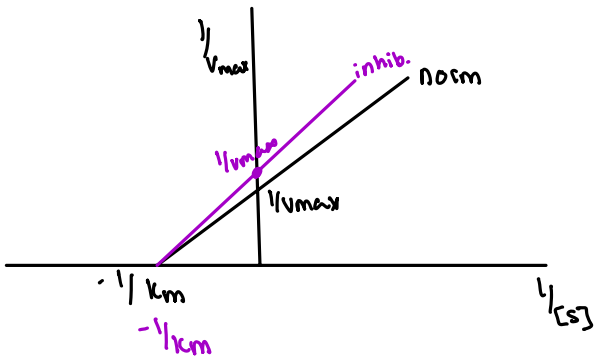


III E.2 Non Competative inhibitors

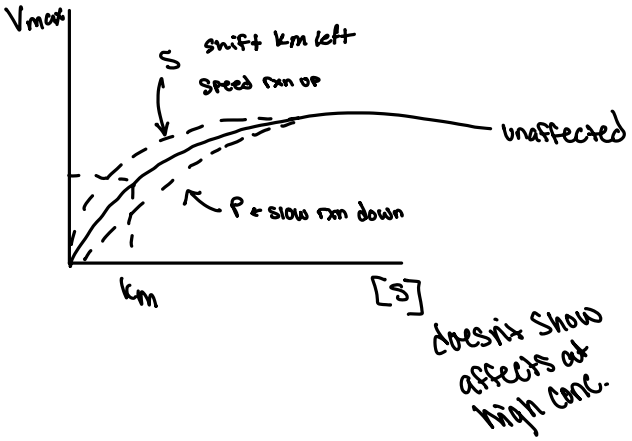
interact w/ enzyme somewhere other than the active site and impeds catalysis

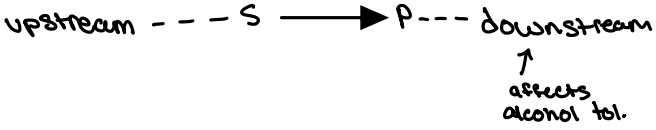
V_{max} reduced, no change in apparent km





III F. Allosteric effectors usually (S) or (P)roduct or some up or down stream metabolite that shift enzyme kinetics - usually affecting km (increase / decrease).





Digestive Physiology Review

I. Functional Summary

A. Digestion: Big molecules $\xrightarrow{\text{Enzymes}}$ Small molecules

(Polymers) (monomers)

2. Types:

Autoenzymatic - digestion with endogenous enzymes
↳ Saliva (little)
Stomach (some)
Pancreas (S.I) (lots)

Alloenzymatic digestion

by enzymes from symbiont microbes

- rumen, cecum large intestine | colon