Proteins

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Classification

- Function
- Structure
- Connecting peptide parts

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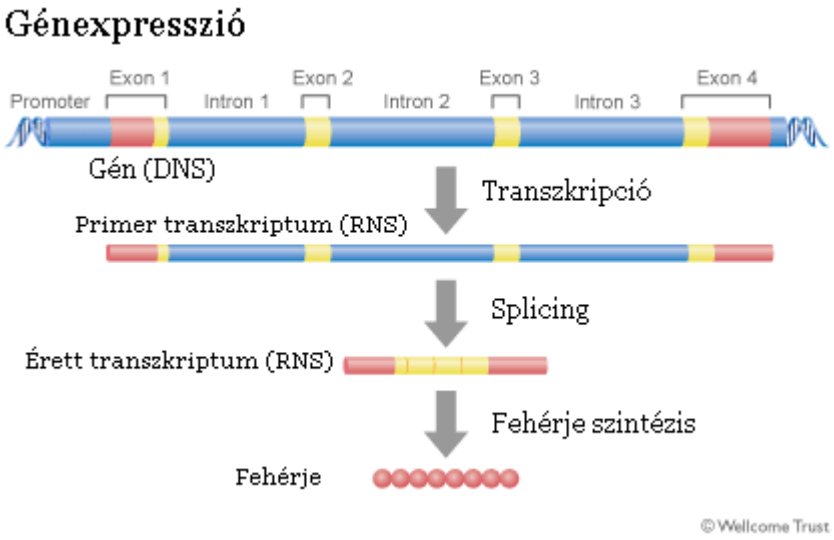
Synthesis

- Transcription - nucleus
- Translation - cytoplasma
- Posttranslation changes (folding)
  - endoplasmatic reticulum



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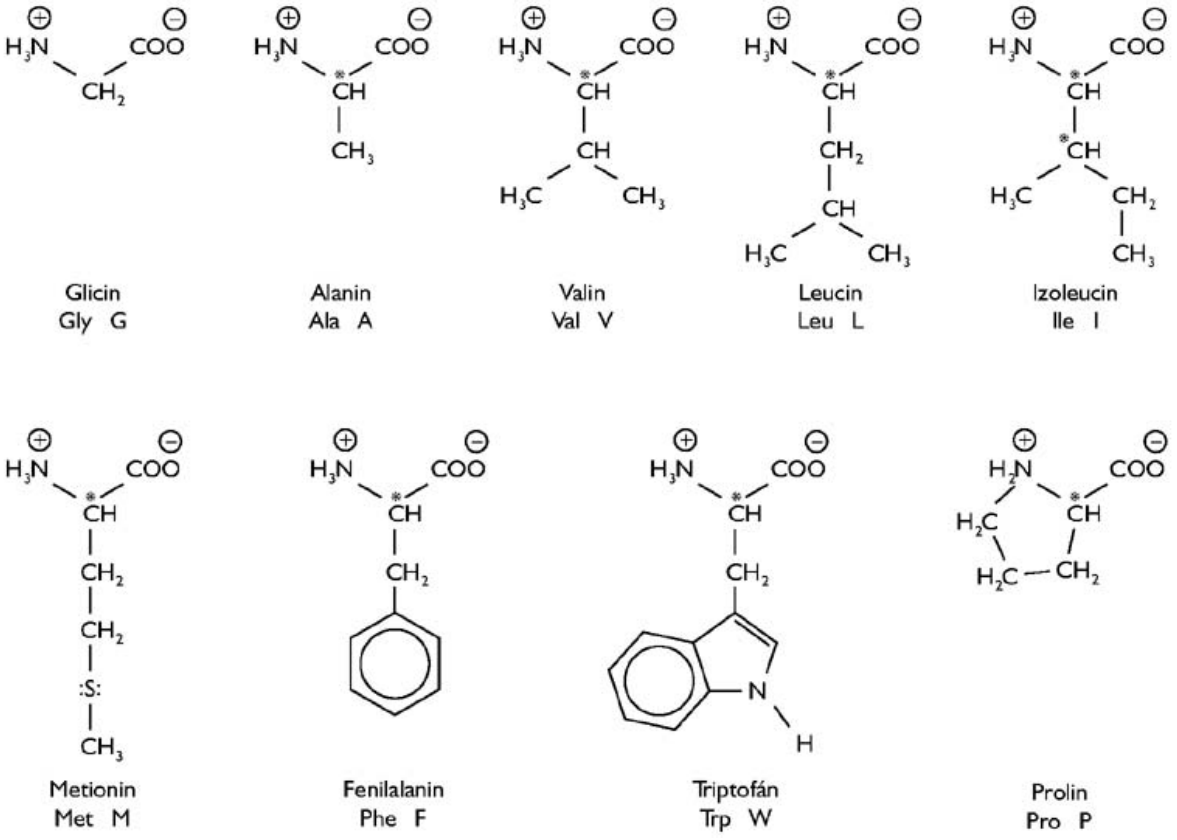
Amino acids

Apoláris oldalláncúak



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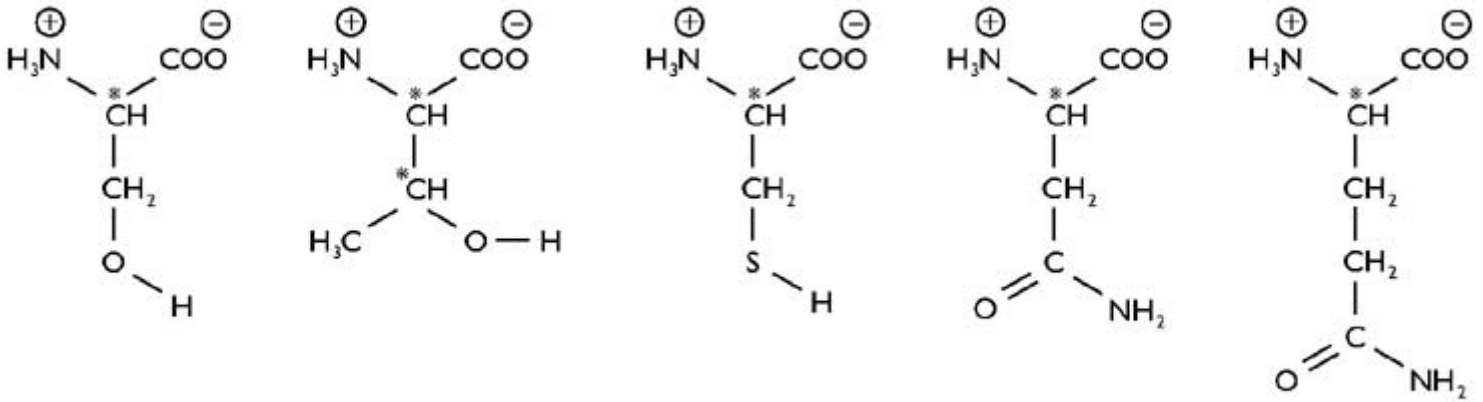
Amino acids

Poláris, semleges oldalláncúak



Szerin
Ser S

Treonin
Thr T

Cisztein
Cys C

Aszparagin
Asn N

Glutamin
Gln Q

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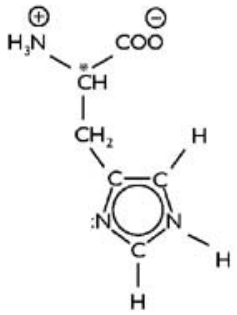
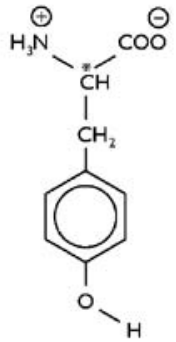
Amino acids

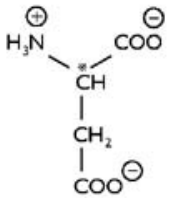
Poláris, savas, ill. bázisos oldalláncúak



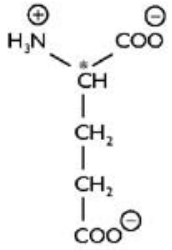
Hisztidin
His H



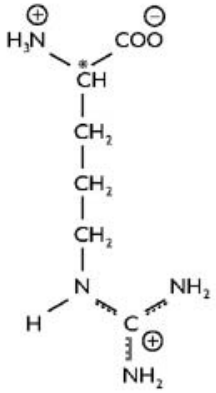
Tirozin
Tyr Y



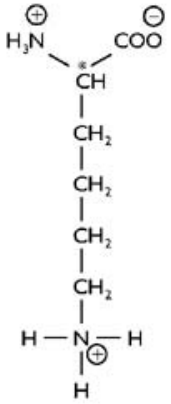
Aszparaginsav
Asp D



Glutaminsav
Glu E



Arginin
Arg R



Lizin
Lys K

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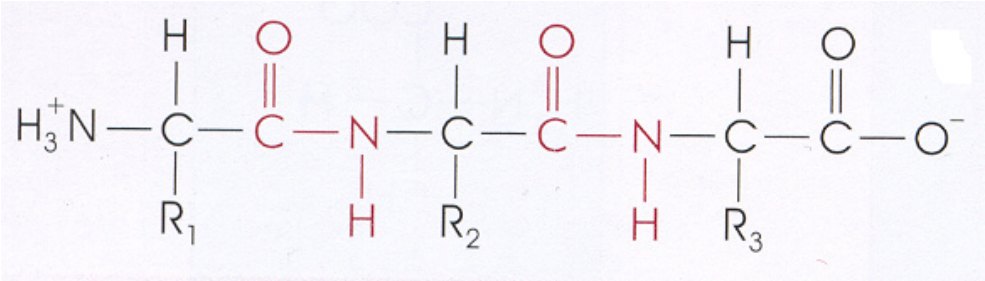
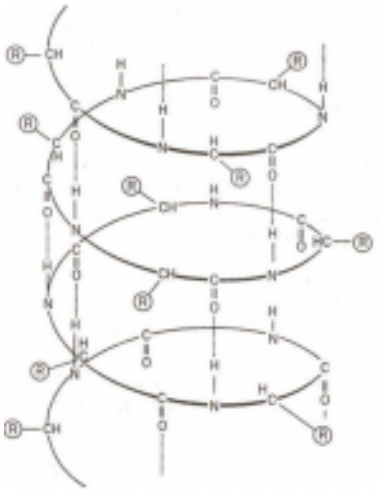
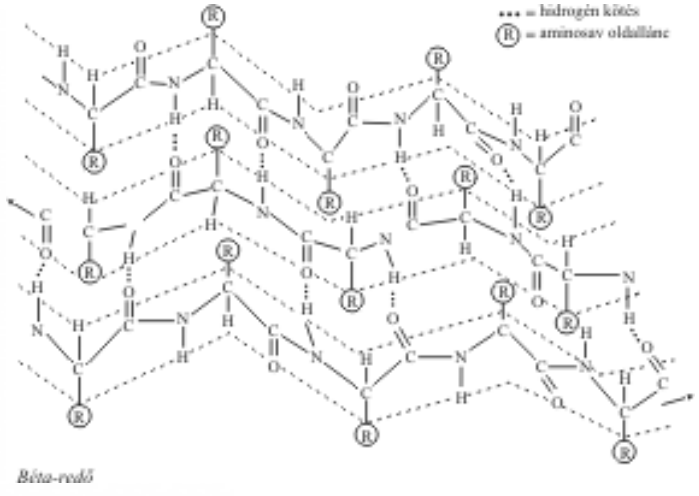
Structure

- Primer= order of the aminoacids



- Secunder= the conformation of the peptide chain alfa-helix, beta-sheet, beta-turn, random coil





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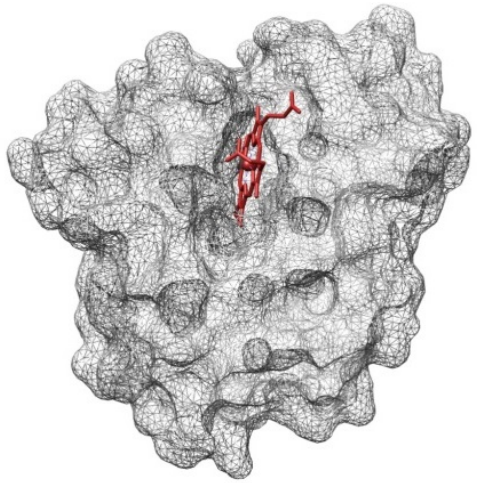
Structure

- Suprasecunder: the location of the domains inside the tertier structure

- Tertier= shape of the peptide chain globular, fibrillar



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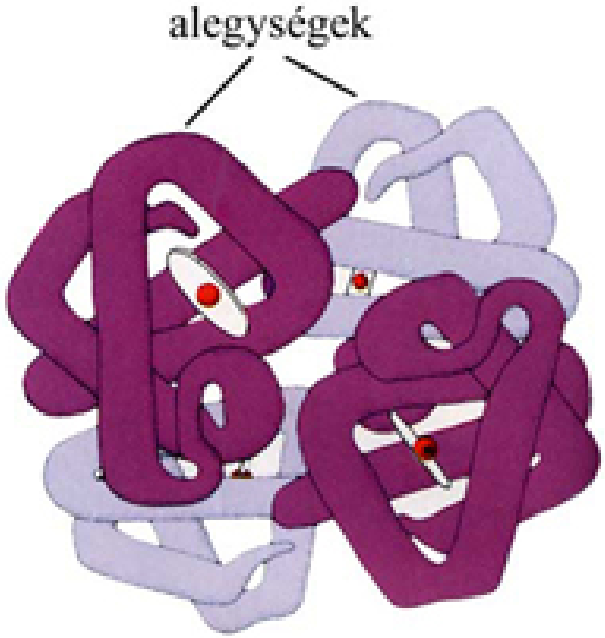
Structure

- Quaterner= location of the subunits (peptide chains)



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Folding, Denaturation

- Protein folding: formation of the native conformation
  - chaperons' features and roles

- Denaturation: loss of native structure
  - reasons
  - reversible (tertier, quaterner structure)
  - irreversible (secunder)

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Bioenergetics

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Termodynamics

- Isolated system
- Closed system
- **Open system:** material-, energy- and informationtransport, if the entropy level is low
  - Energy source: C-atom (oxidation)

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- Free entalpy-change

$A + B \longleftrightarrow C + D$

$\Delta G = \Delta Go + RT \ln ([C] [D] / [A] [B]) = \Delta Go + RT \ln K$

- $\Delta G = \Sigma$ Gproducts - Σ Gstarting materials
  +: endergon; 0: balance; -: exergon

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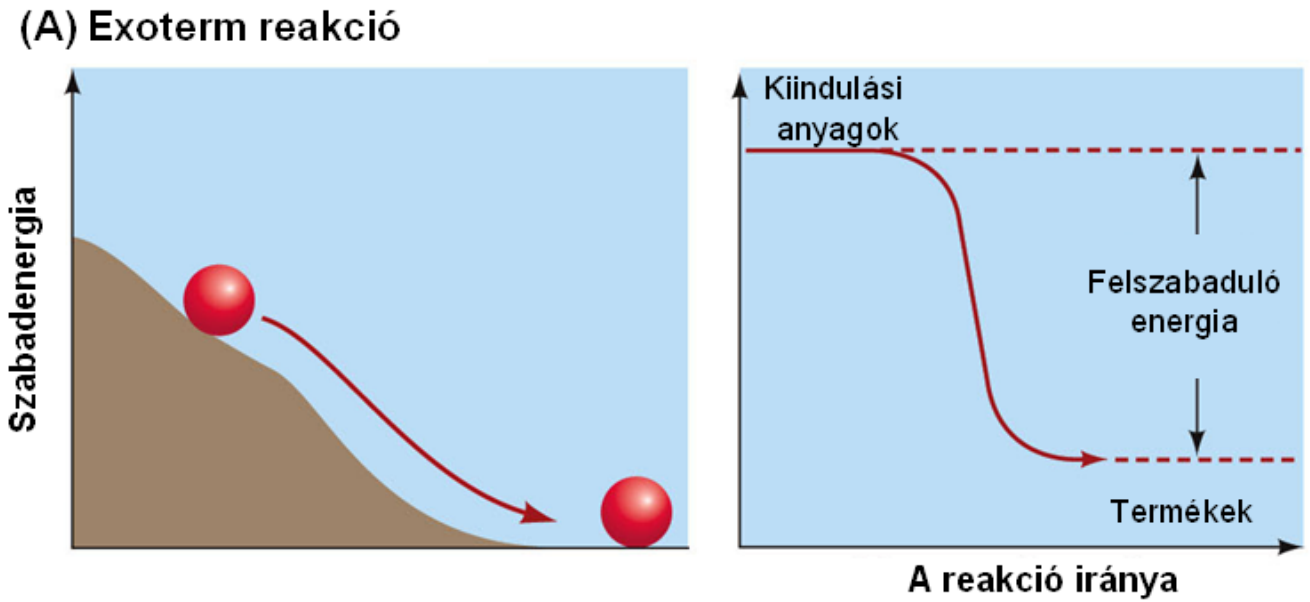

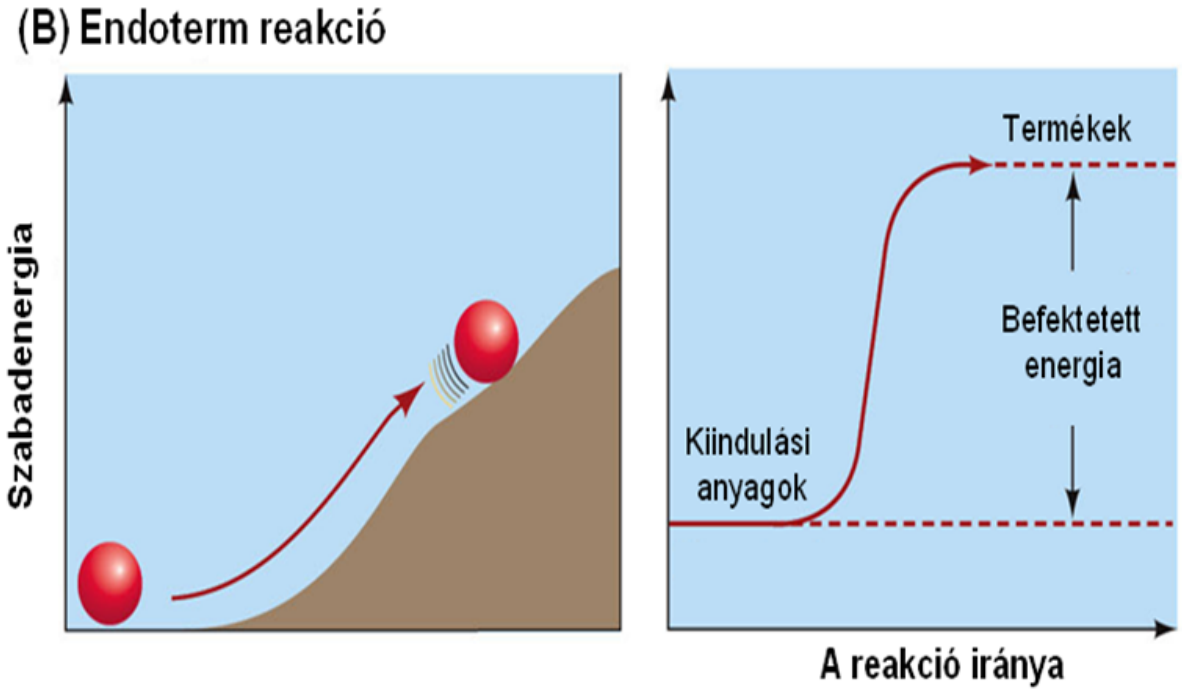

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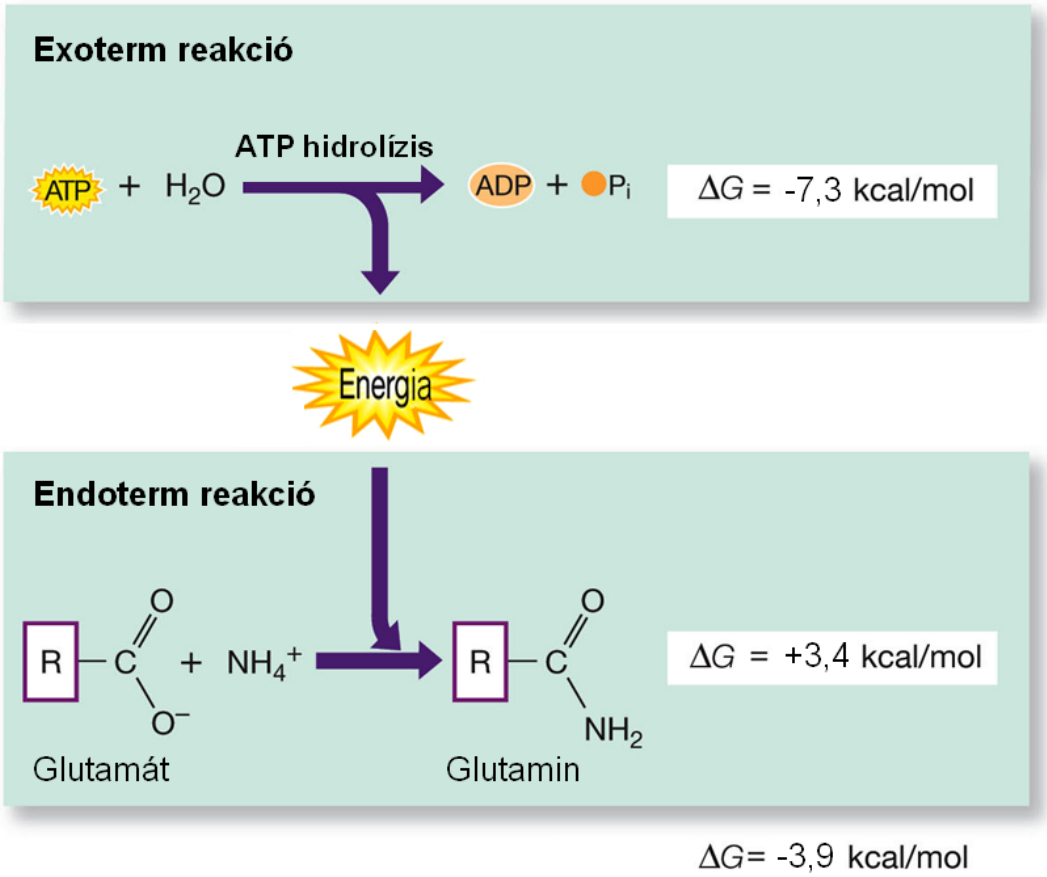
Linked reactions



***LIFE 8e*, Figure 6.7**

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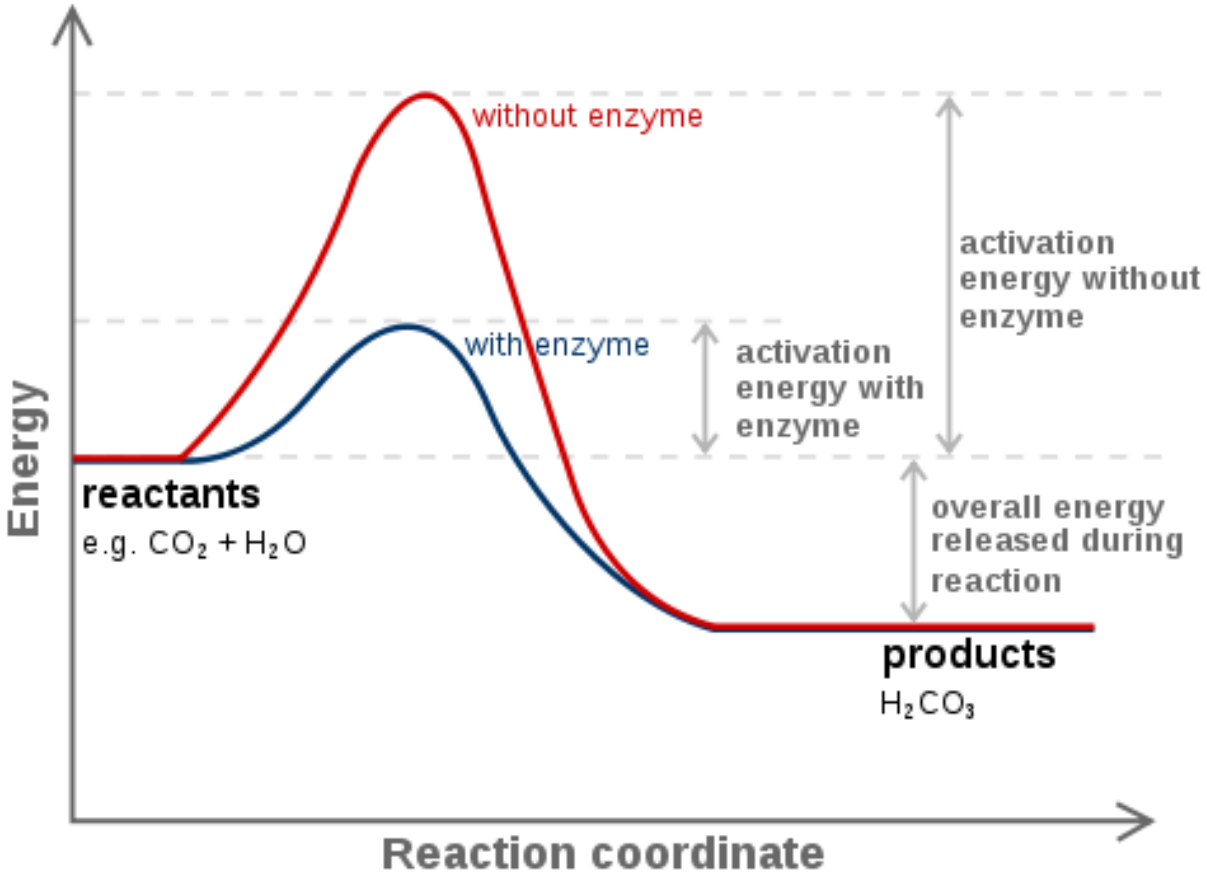
Role of the enzymes: the decrease of the activation energy



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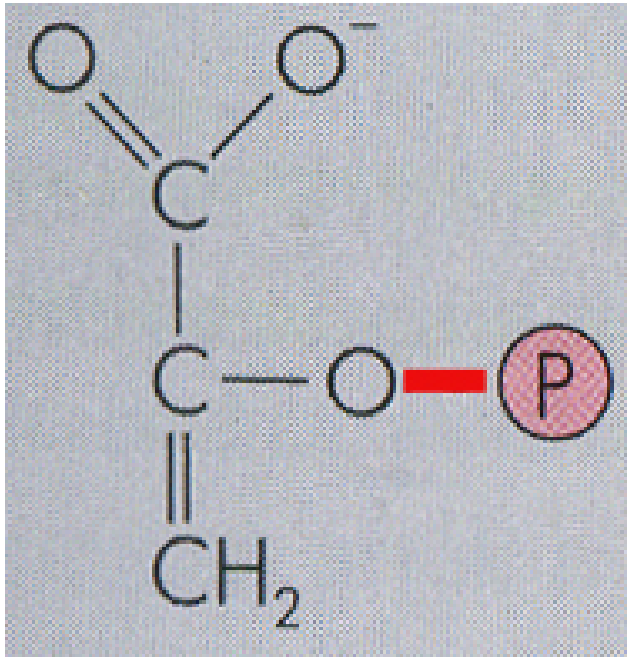
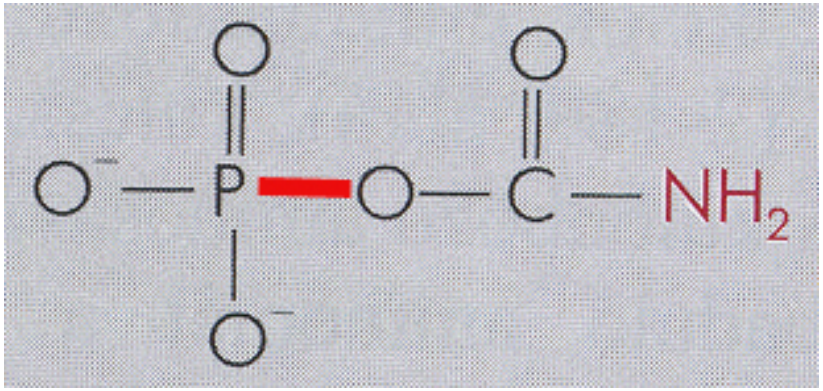
Macroerg compounds

- Macroerg binding (>30kJ) containing molecules



phosphoenol-piruvate



Carbamil-phosphate

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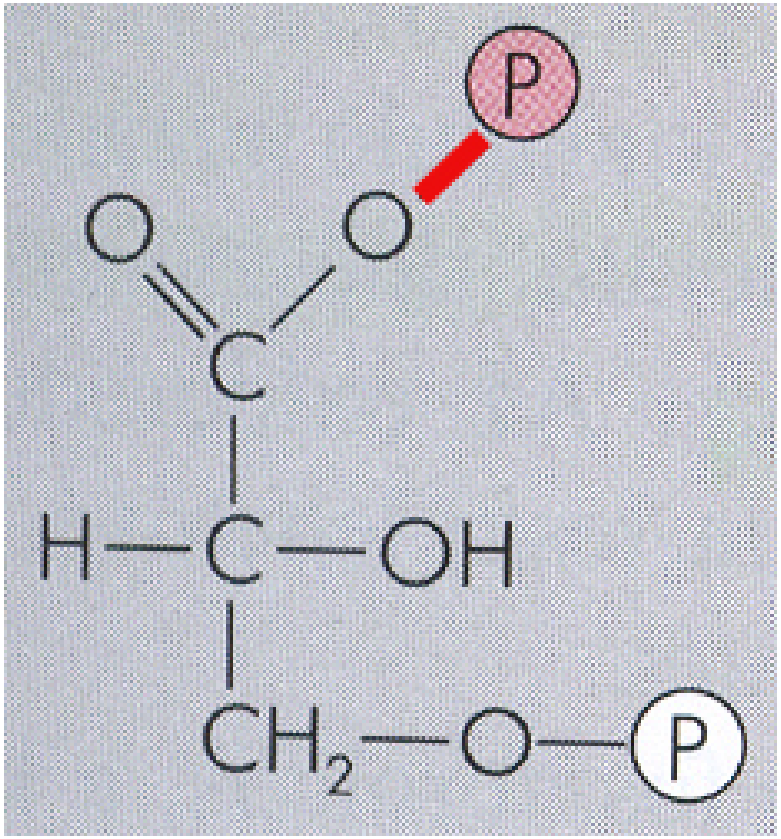
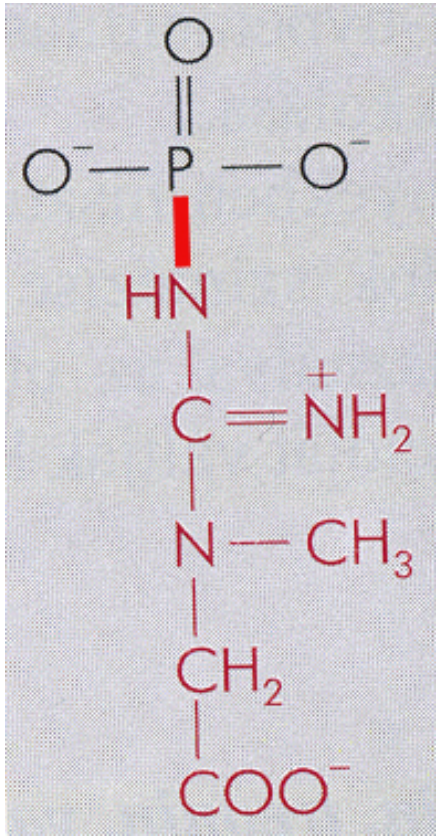
Macroerg compounds



1,3-bifosphoglycerate



Creatine-phosphate

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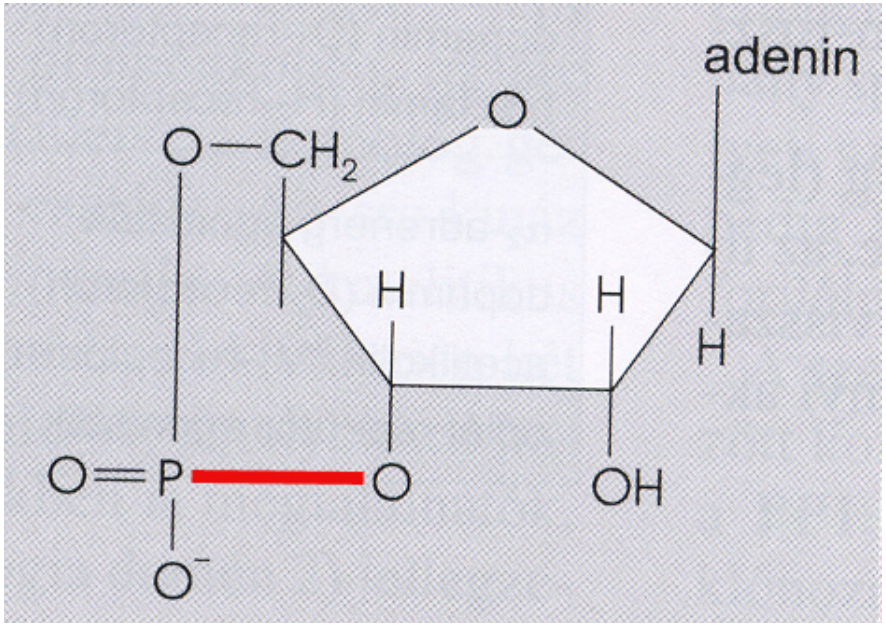
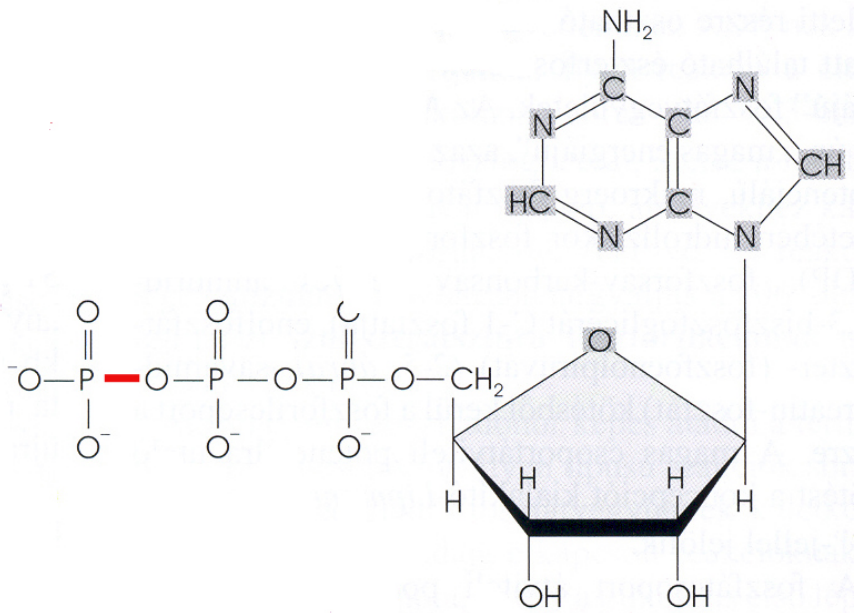
Macroerg compounds



Cyclic adenosine-monophosphate



Adenosine-triphosphate

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Enzymes

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General features

- Biocatalisator
- Definers of velocity, specificity, direction of the reaction
- Conditions of the optimal work: temperature, pH, ions

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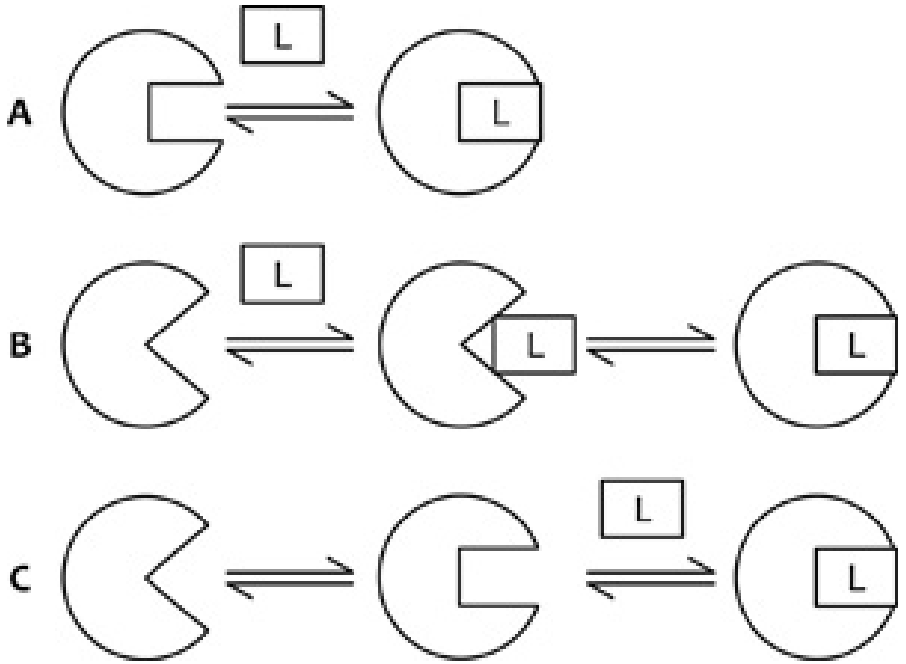
Models of substrate binding

- A: Lock and key model
- B: Induced fit
- C: Fluktuation



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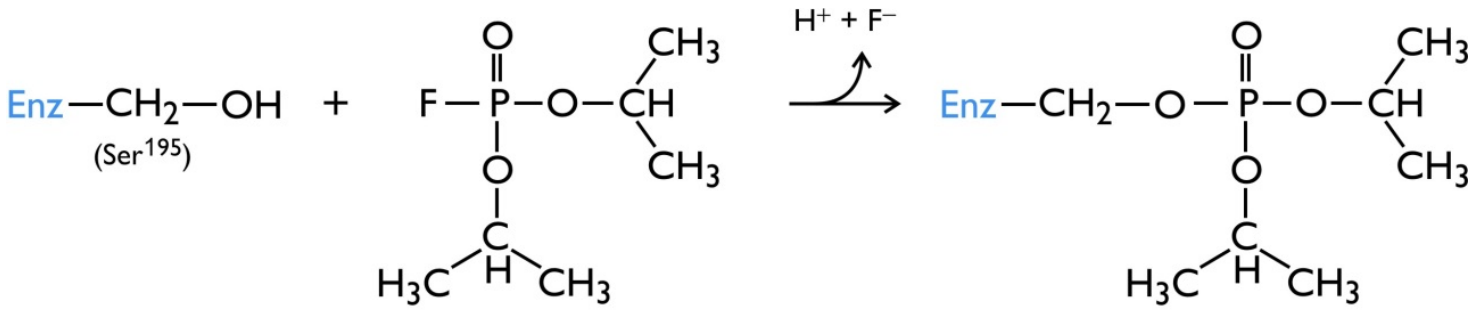
Types of enzyme catalysis

- Kovalent catalysis
  - temporary kovalent binding (side chains)→instabile intermedier
  - eg.: trypsin, etc.



DFP

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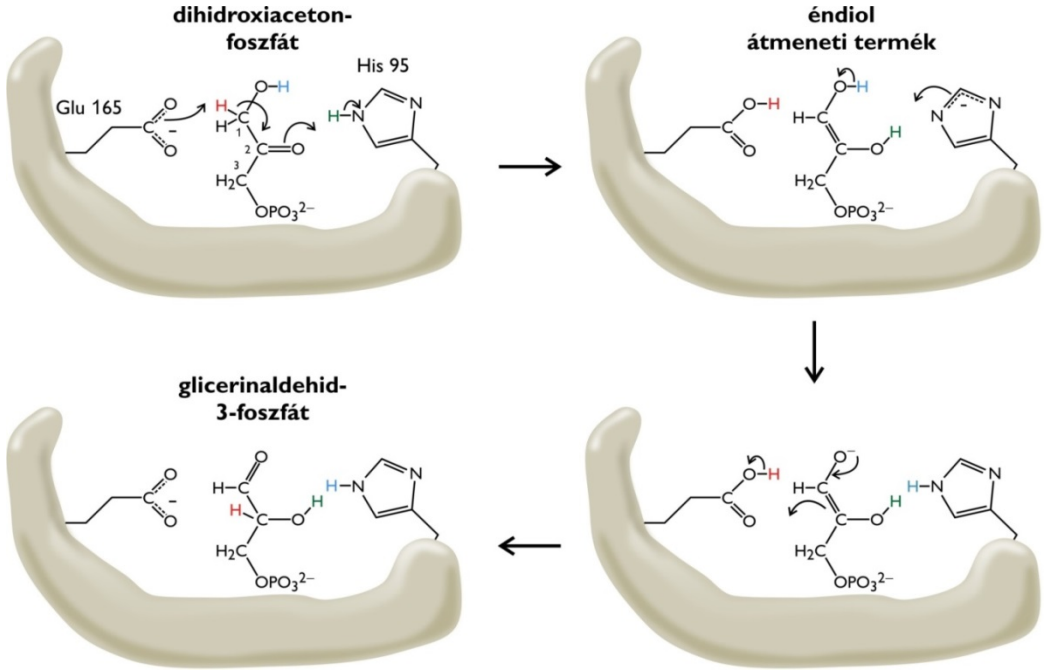
Types of enzyme catalysis

- Acid-basis
  - H+ absorbation/adsorbation (acidic and basical side chains)
  - eg.: ribonuclease



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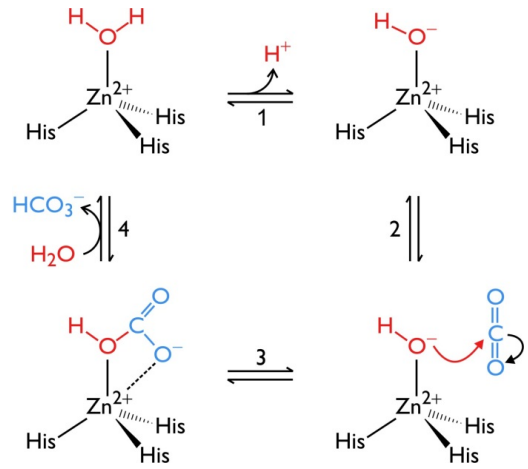
Types of enzymecatalysis

- Metal ione-catalysis
  - temporary binding to a metal ion deformation, tension of the binding
  - carbonic acid-anhydrase



- Entropy-effect
  - temporary decrease of the entropy→the chance of the proper collision is elevated

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Enzyme classes

- Nomenclature: **1**. class - **2**. subclass - **3**. group - **4**. concrete enzyme

- 1.: Oxydoreductases
  - oxidases, oxigenases, reductases, etc.
  - eg.:glycerine aldehide-3-phosphate-dehydrogenase

- 2.: Transferases
  - kinases, transaldolases, transketolases, transferases
  - eg.: hexokinase, glucokinase

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Enzyme classes

- Hidrolases
  - phosphatases, esterases, etc.
  - eg.: glucose-6-phoszphatase

- Liases
  - C-C, C-O, C-N, C-S, C-O liases, subtypes
  - eg.: aldolase

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Enzyme classes

- Isomerases
  - cis-trans isomerases, intramolecular isomerases, etc.
  - eg.: triose phosphate-isomerase
- Ligases
  - C-O, C-S, C-N, C-C, P-ester, N-Me binding producers
  - eg.: piruvate-carboxylase

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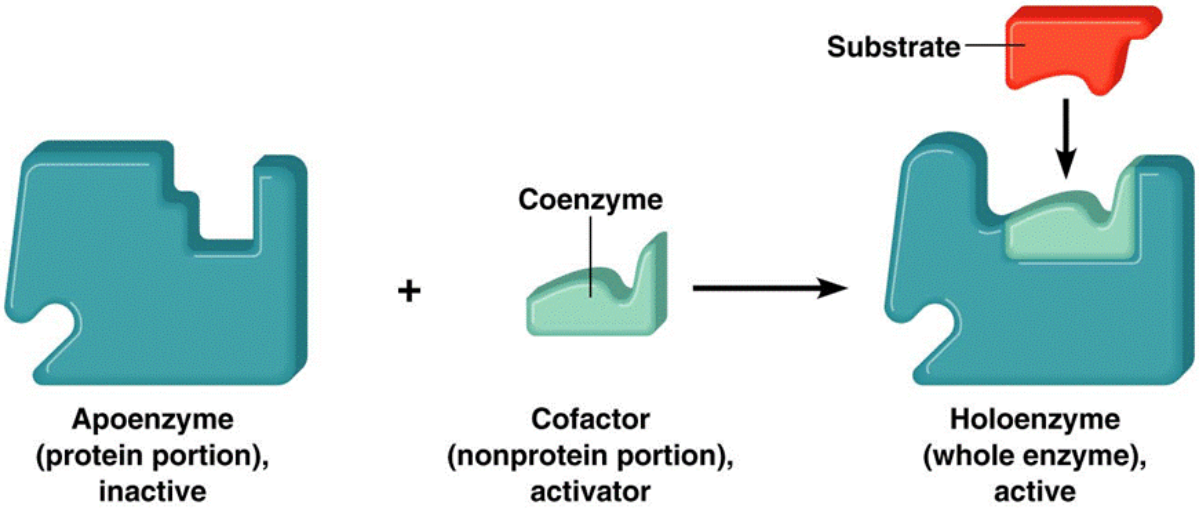
Coenzymes

- Necessary for the enzyme's work, but not protein
- Role: energytransfer, chargetransfer, acil-group transfer
- Prostetic group



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Nutritients with coenzyme-function

- Metal ions and atoms
  - eg.: Fe2+ - cytocrome-oxydase, Mg2+ - glucokinase, Se – glutatione-peroxydase

- Vitamins
  - eg.:
  B1-vitamine (tiamin) – tiamin-pirophosphate – aldehids – piruvate acid-dehydrogenase
  Folic acid (B9) - tetrahidrofolate (THF) – one C atomic groups – timidilate synthase

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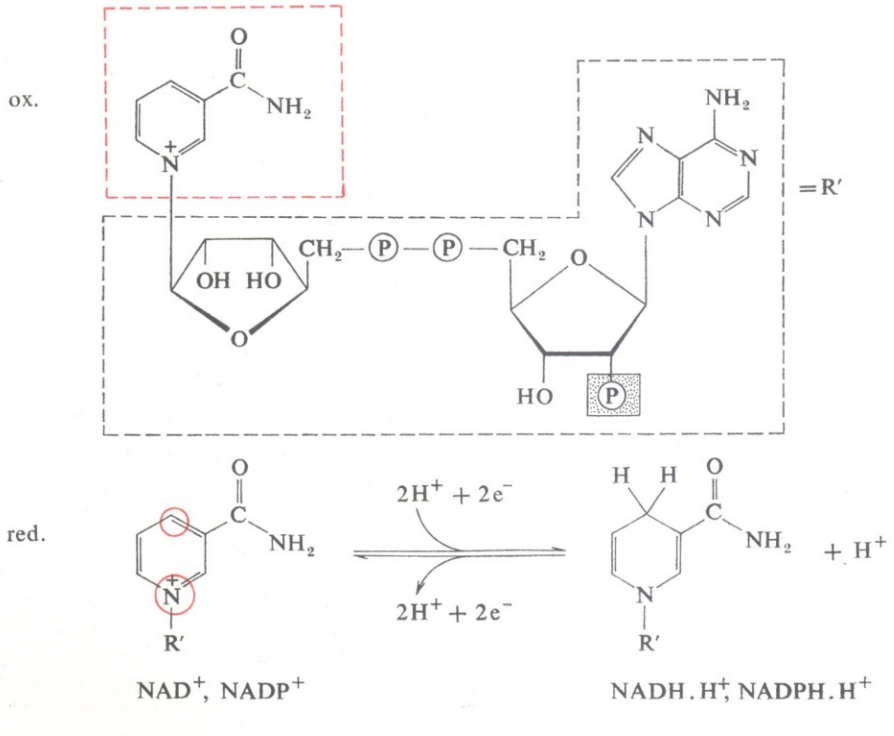
Coenzymes of oxydoreductases

1. Nicotinamide-adenin-dinucleotide (-phosphate; NAD^+ & $NADP^+$; vitamine B_3, niacin)



eg.
-alcohol dehydrogenase
-lactate dehydrogenase

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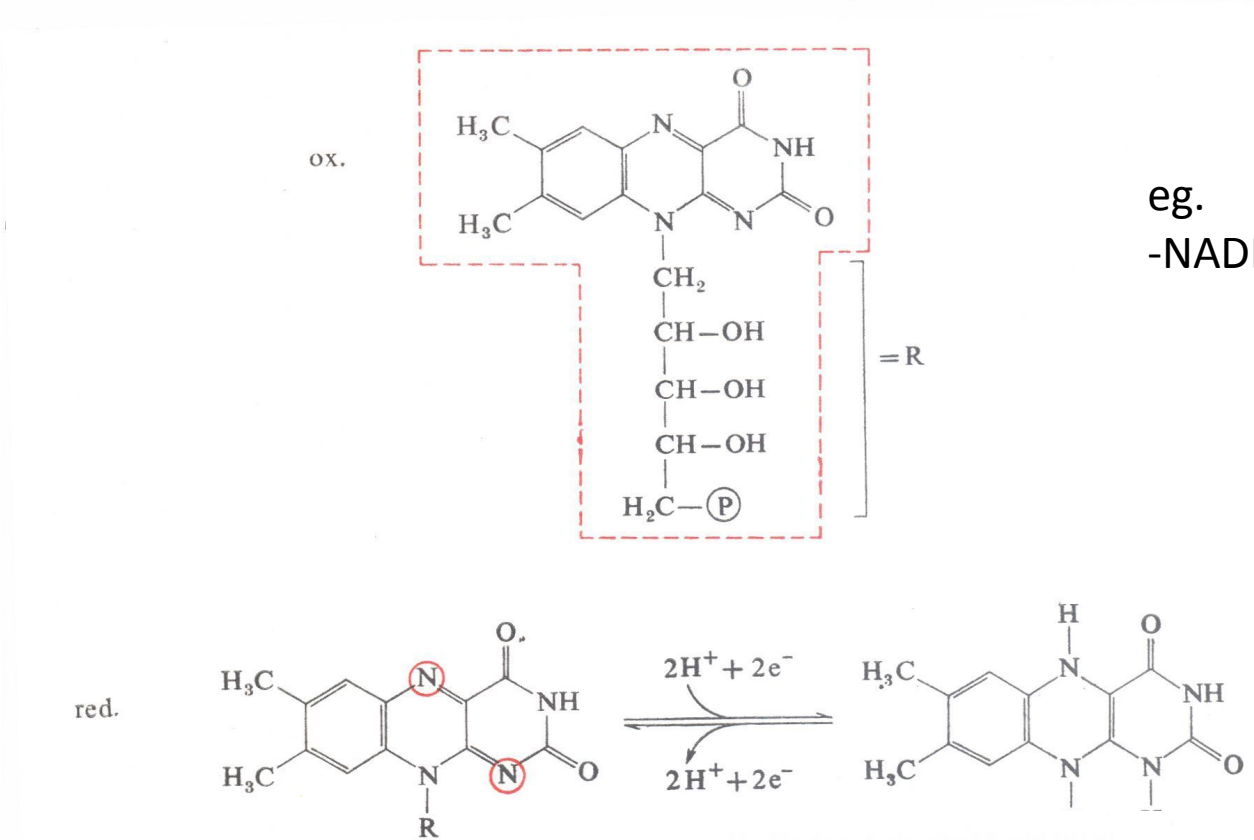
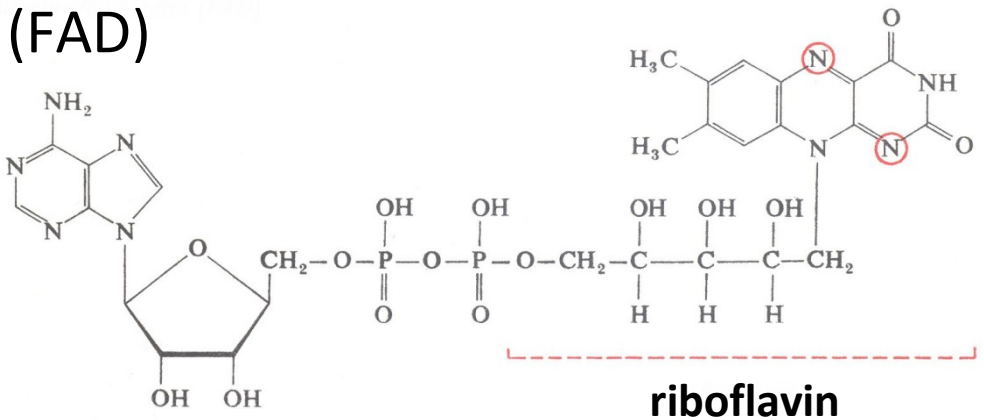
2. a) Flavin-mononucleotide (FMN; vitamine B_2, riboflavin)



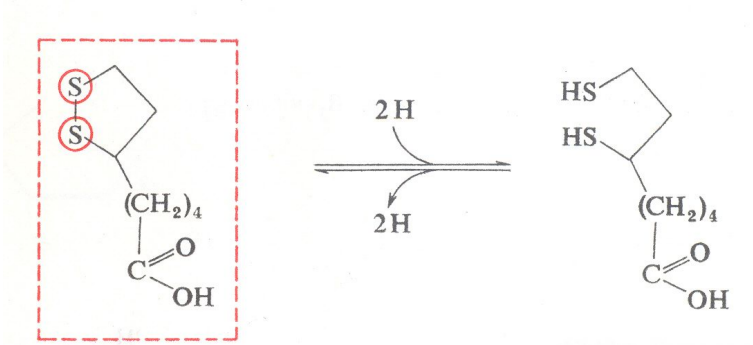
eg.
-NADH dehydrogenase

2. b) Flavin-adenin-dinucleotide (FAD)

eg.
-succinate dehydrogenase
-acyl-CoA-dehydrogenase



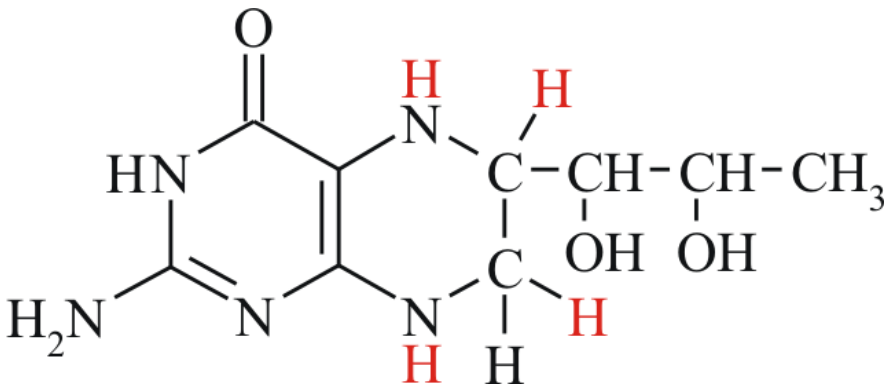
3. Lipoic acid (dithio octanic acid)



Dihydro lipoic acid

eg.
-pyruvate dehydrogenase

4. Tetrahydrobiopteryn (THB, BH_4)



eg.
-tyrosine hydroxylase
-nitrogen monoxide synthase

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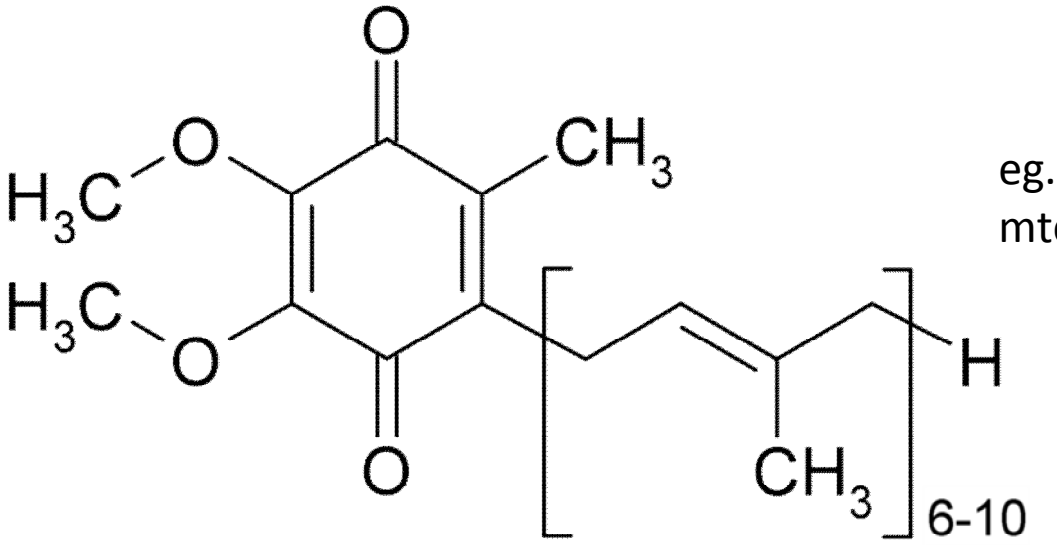
5. Coenzyme Q (Q9 or Q10 coenzyme, ubiquinone)



eg.
mtchrial respiratory chain Complex I & II

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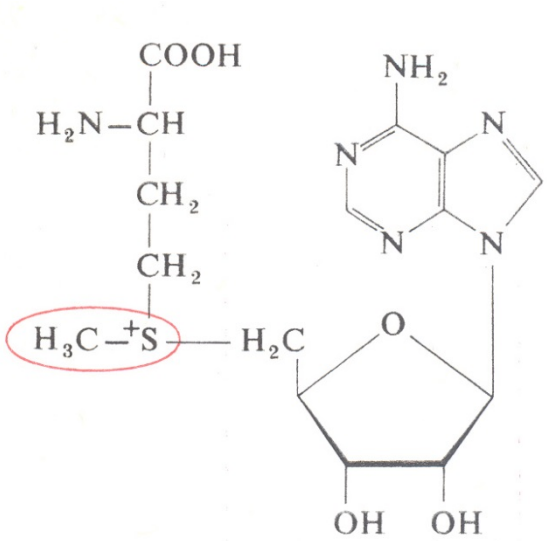
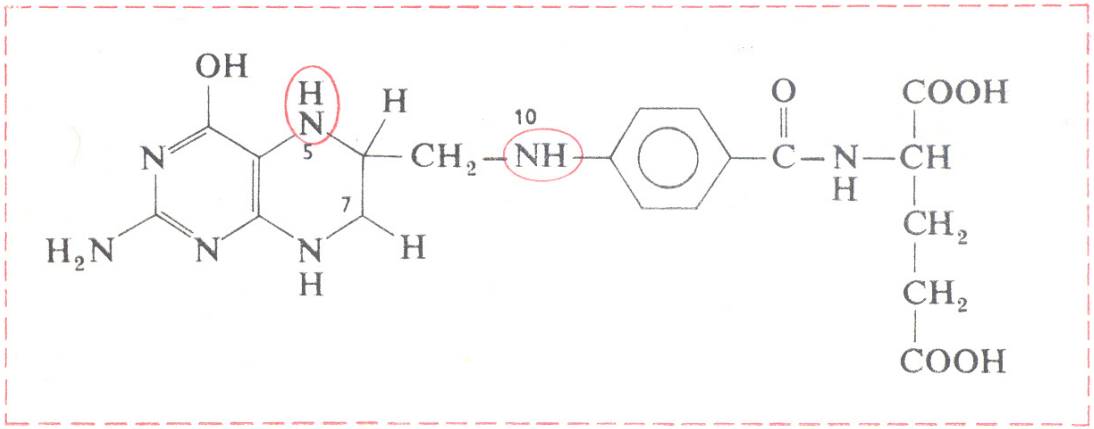
Coenzymes for transferases

1. S-adenosyl-methionine (SAM)



eg.
-choline acetyl transferase

2. Tetrahydrofolate (THF, FH_4; folate, pteroylglutamate, vitamine B_9)



methyl-
methylene-
methenyl-
formyl-
formimino-
} THF

Eg.: thymidilate synthase
-purine nucleotide synthesis

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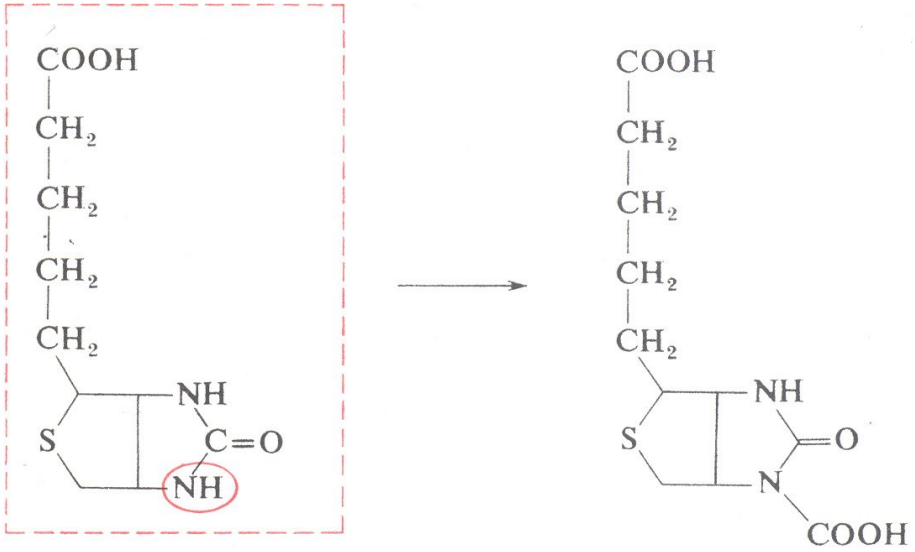
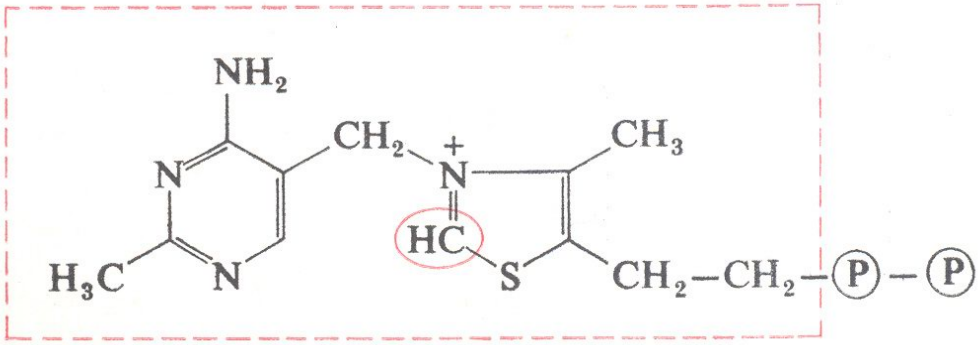
3. biotin (vitamine H)



eg.
-pyruvate carboxylase
-acetyl-CoA carboxylase
-propionyl-CoA carboxylase

4. Thiamine pirophosphate (TPP; thiamine, vitamine B_1)



eg.
-Pyruvate dehydrogenase

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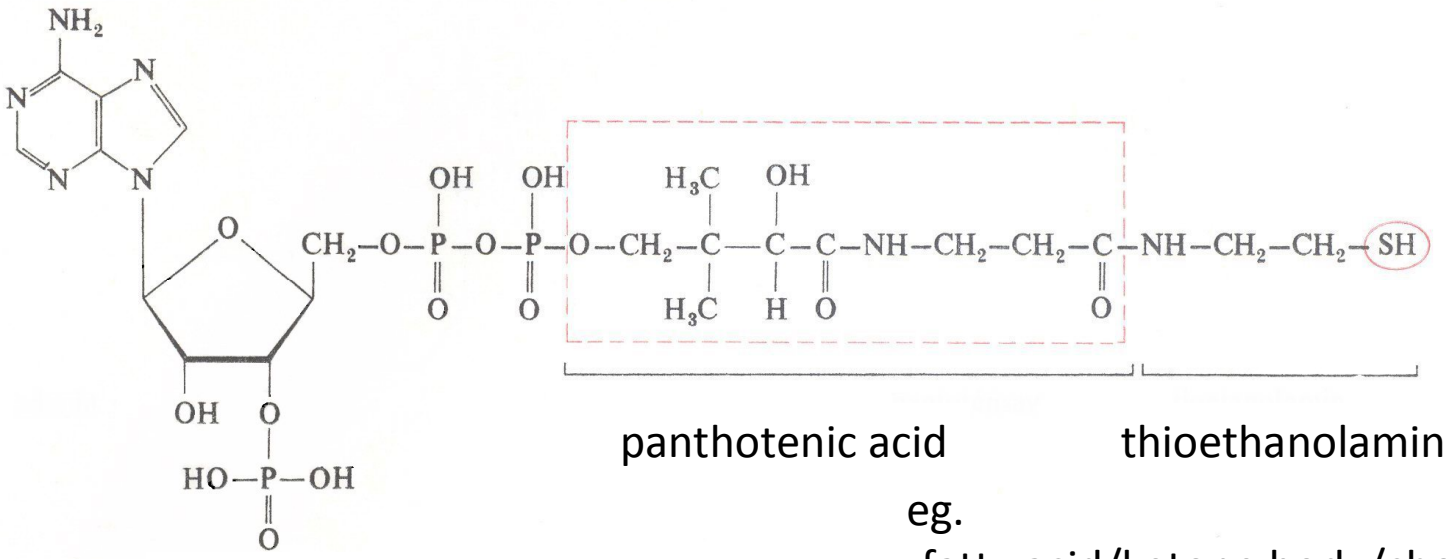
5. Coenzyme A (CoA; panthotenic acid, vitamine B_5)



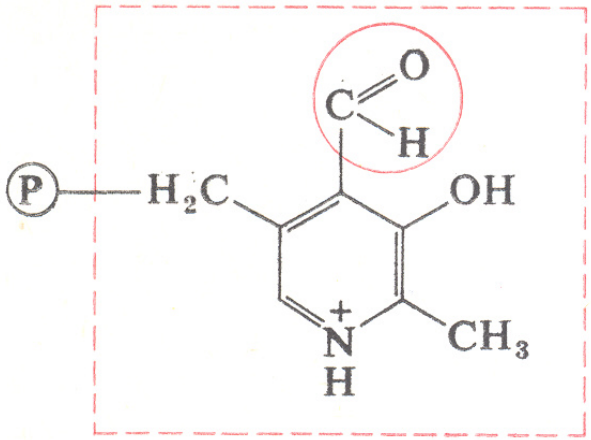
adenosine

panthotenic acid

thioethanolamine

eg.
-fatty acid/ketone body/cholesterol synthesis
-pyruvate dehydrogenase

6. Pyridoxal phosphate (PLP; adermine, vitamine B_6)



eg.
-transaminase reactions:
- Alanine aminotransferase (ALT)
- Aspartate aminotransferase (AST)

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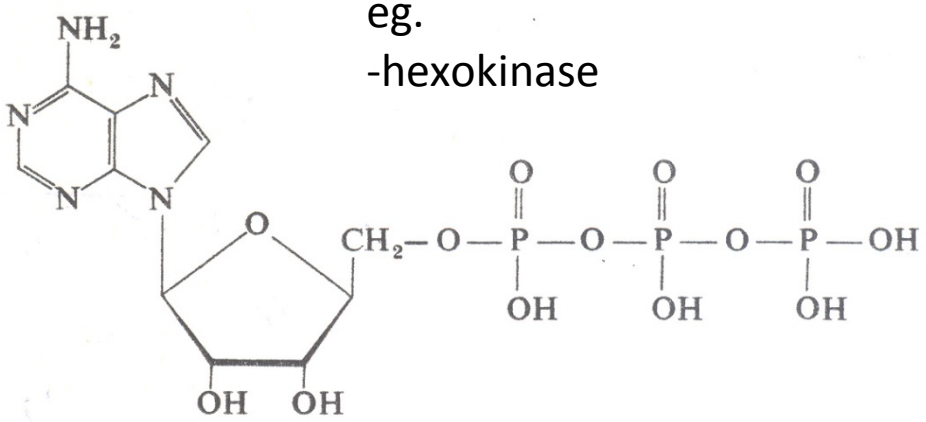
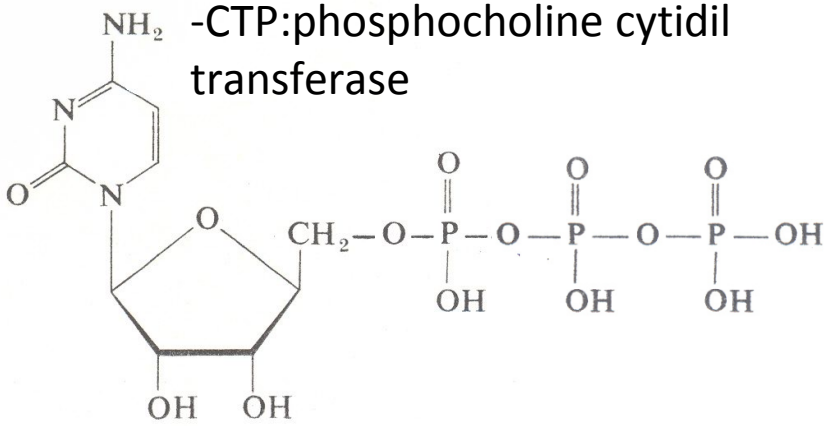
7. adenosine-triphosphate (ATP)

eg.
-hexokinase

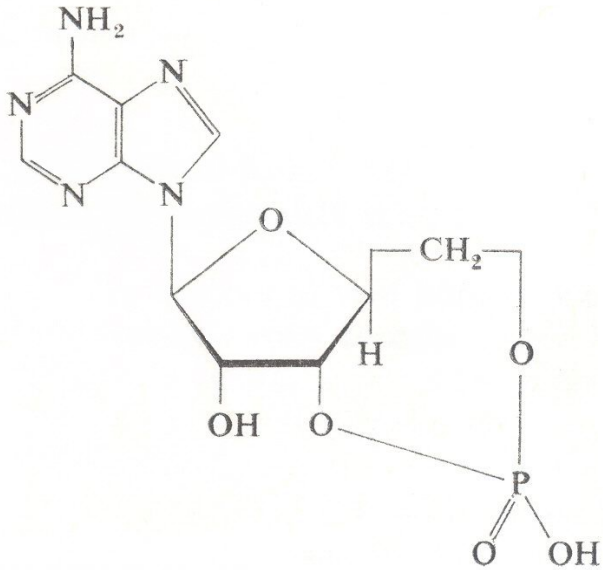


9. cytidine triphosphate (CTP)

eg.
-CTP:phosphocholine cytidil transferase

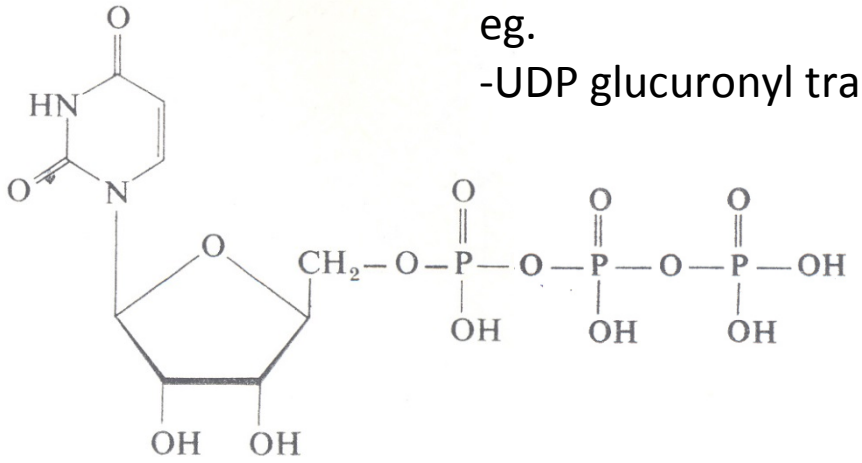


8. cyclic adenosine monophosphate (cAMP)



10. uridine triphosphate (UTP)

eg.
-UDP glucuronyl transferase



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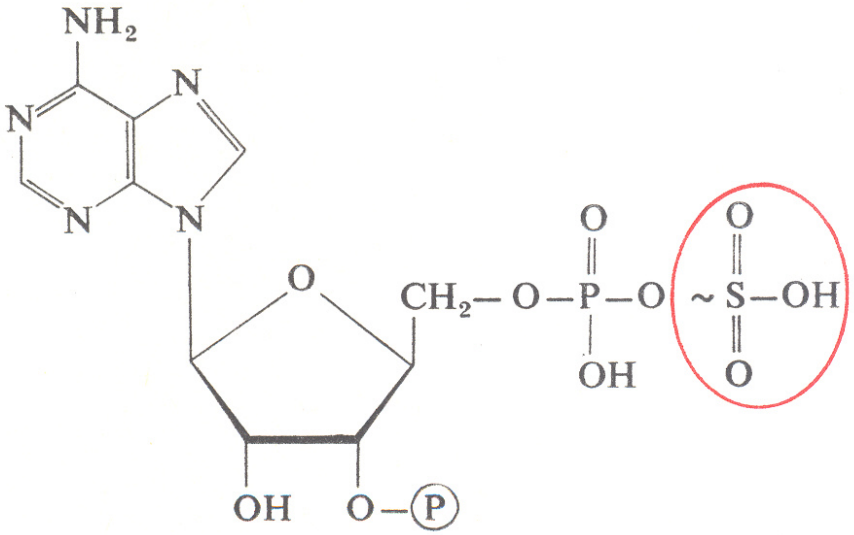
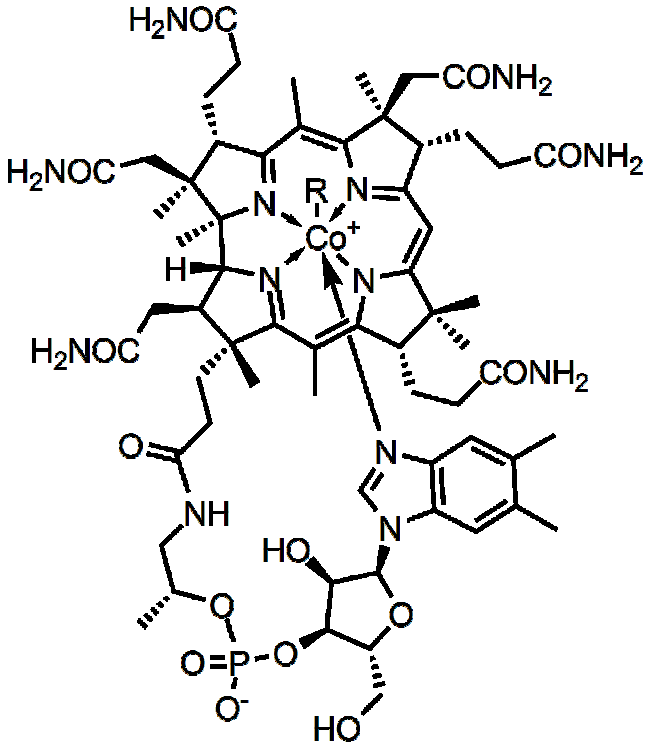
11. 3’-phosphoadenosine-5’-phosphosulfate (PAPS; active sulfate)



eg.
-sulfotransferases

12. Cobalamine (vitamine B_{12})



R = 5'-deoxyadenosyl, Me, OH, CN

eg.
-methyl malonyl CoA mutase
-homocystein methyl transferase

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Coenzymes for lyases

1. thiamine PP
2. pyridoxal P
3. biotin

} (see at transferases)

Coenzymes for isomerases

1. NADH (see at oxidoreductases)
2. cobalamine (see at transferases)
3. pyridoxal phosphate (see at transferases)

Coenzymes for ligases

1. Nucleoside triphosphates (ATP, GTP, UTP, CTP; see at transferases)
2. NADH (see at oxidoreductases)

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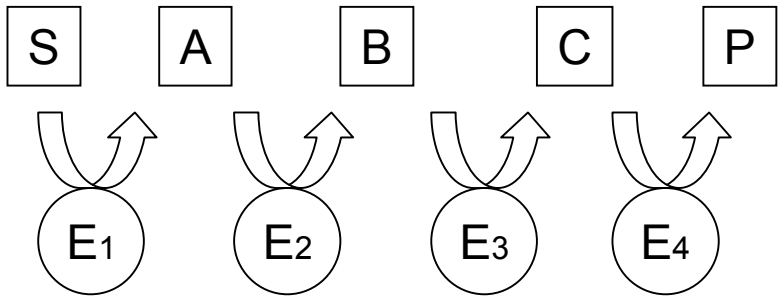
Multienzyme system

- Meaning:
  Entirety of closely working enzymes that catalyses different steps of the same reaction chain.
- Closely placed in the space
- eg.: fatty acid synthase



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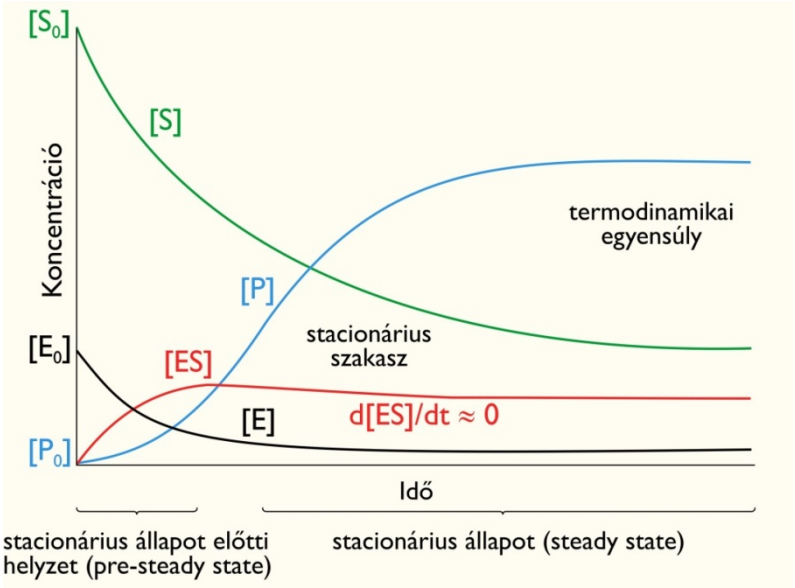
Kinetics of the enzyme reaction

- 0 order: the velocity of the reaction is not affected by the concentration
- 1st order: the velocity affected by the starting concentration
- 2nd order: the velocity is affected by the concentration of two materials



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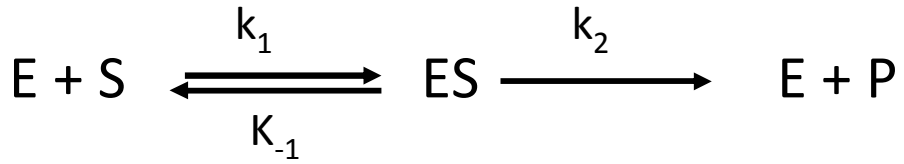
The kinetics of the enzyme reaction

- **<u>Michaelis-Menten model:</u>** the velocity of the reaction depends on the S concentration
  - saturation curve



- Conditions:
  - . At the beginning the [P] is small, thus velocity (v) of the backforming is minimal, k_2 process occurs irreversible
  - [S]>>[E]
  - free [S] = initial [S] (for the initial [S] to [P] is minimal)

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The kinetics of the enzyme reaction

v of ES production

V of ES elimination

$$k_1[E][S] = k_{-1}[ES] + k_2[ES]$$

$$k_1[E][S] = (k_{-1} + k_2)[ES]$$

$$[E][S] = \frac{(k_{-1} + k_2)[ES]}{k_1}$$

$K_M = [S]$, where the v is the half of v_{max}

Briggs-Halden formula: $v = v_{max} \frac{[S]}{[S] + K_M}$

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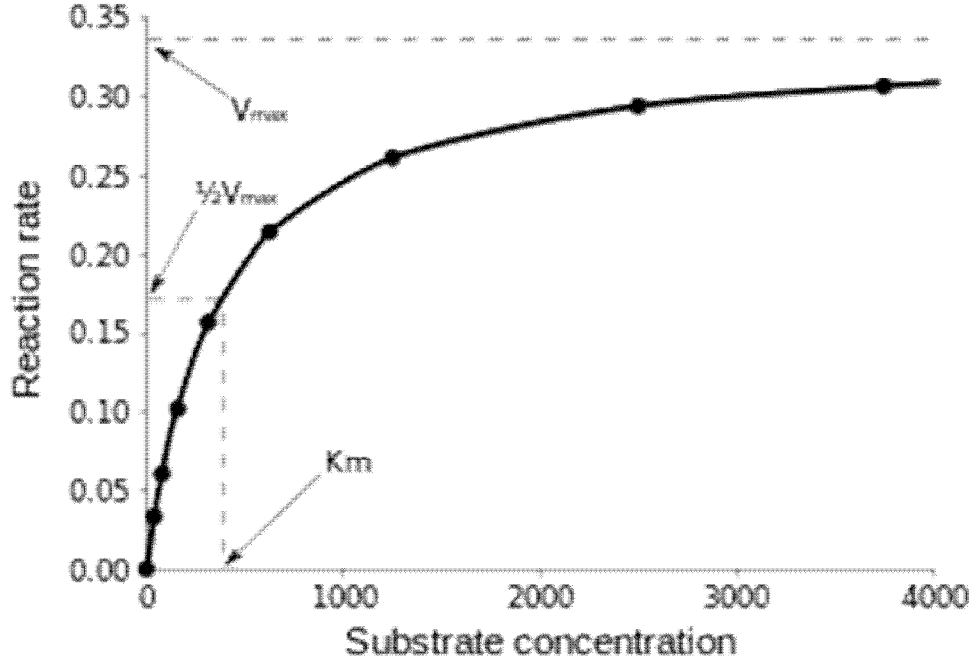
The kinetics of the enzyme reaction- the direct linearisation



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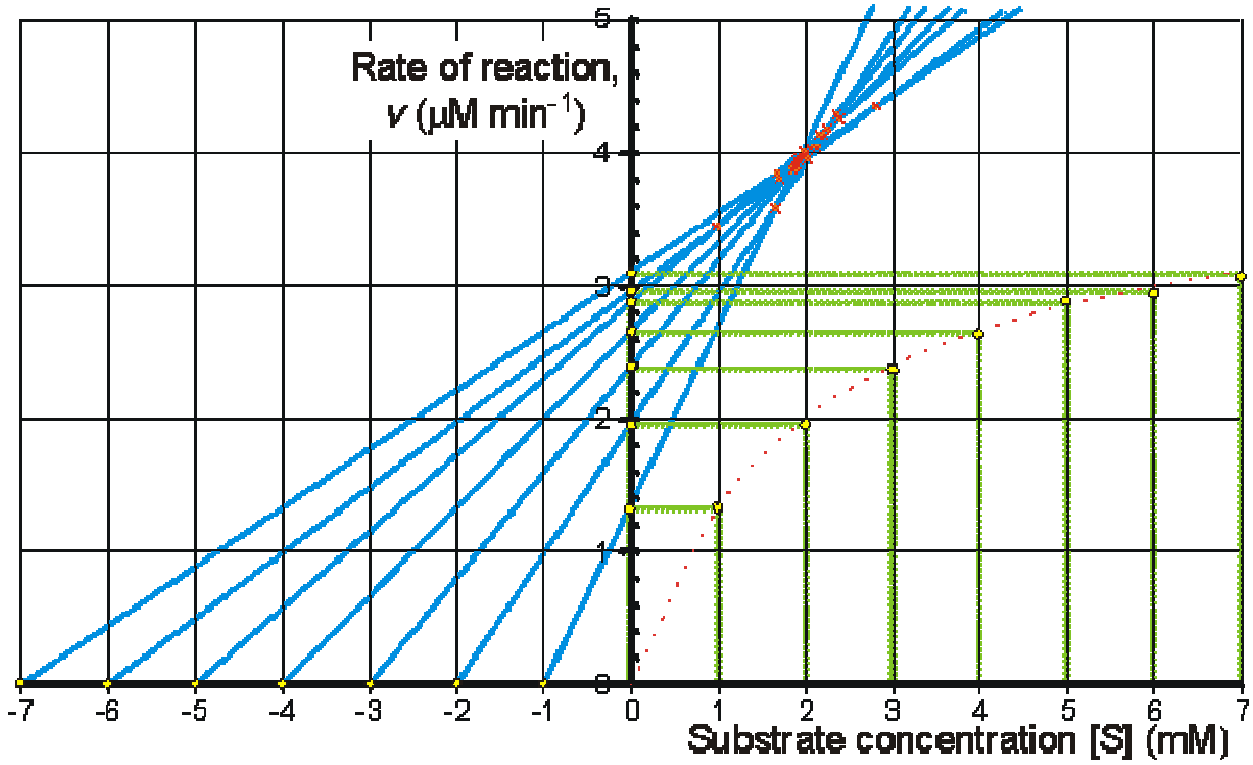
The kinetics of the enzyme reaction – Linewaver-Burk form

- Take the reciproke

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



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Regulation of the enzyme-function

- Kovalens modification
- Limited proteolysis
- Gene induction
- Allosterical regulation
- Compartmentalisation
- Inhibition

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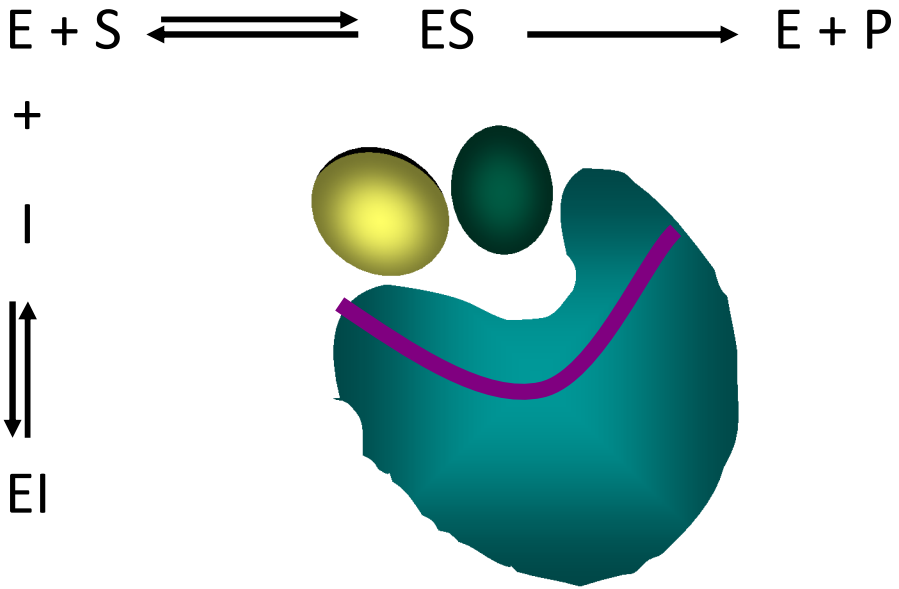
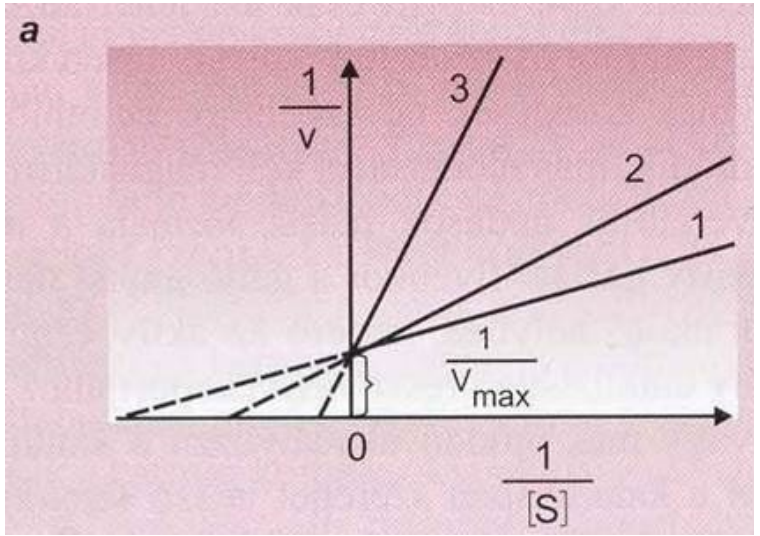
Modulation of the enzyme activity – Competitive

- substrate (S) & inhibitor (I) contest for **the same site**
- **K_M ↑, v_{max} ø**
- pl.: phrosphofructokinase – ATP





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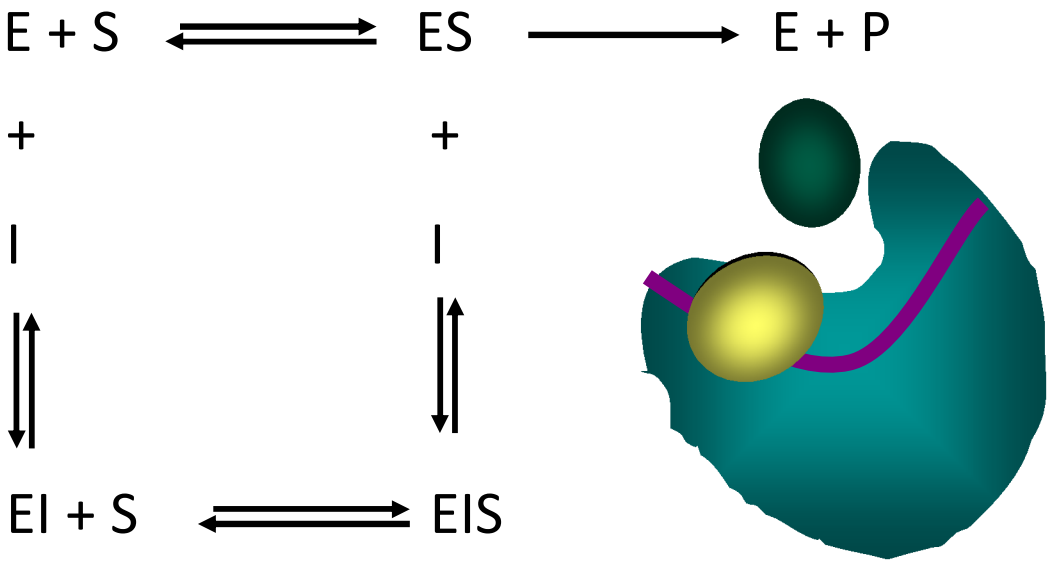
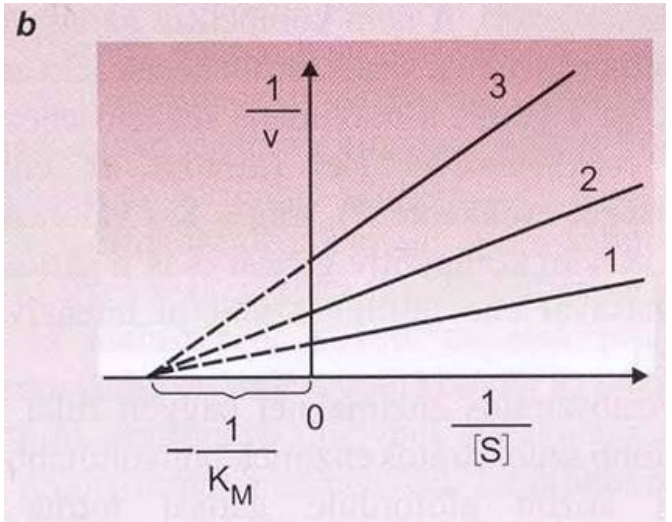
Modulation of the enzyme activity – nonkompetitive

- inhibitor inhibits the catalysis by binding to another site
- **KM ø, vmax ↓**
- eg.: metal ions (Zn^{2+} carbonic acid anhydrase)





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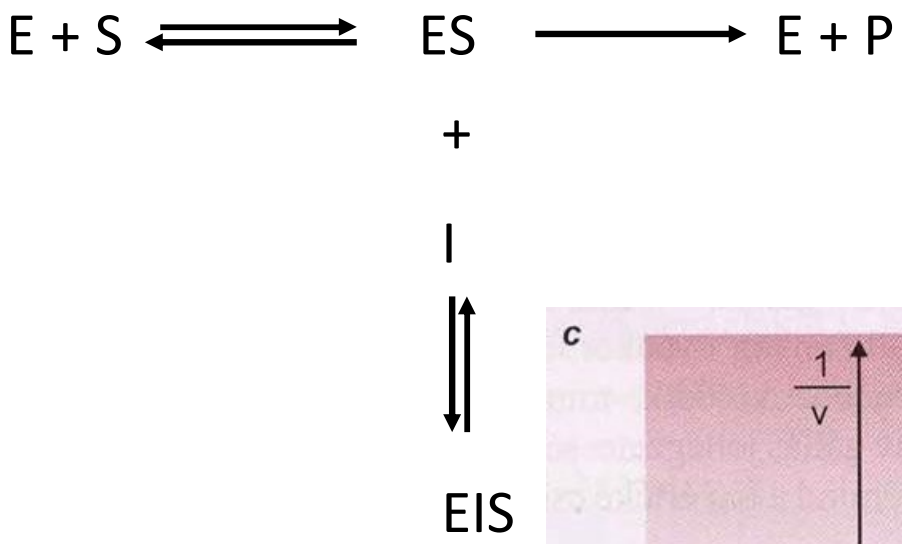
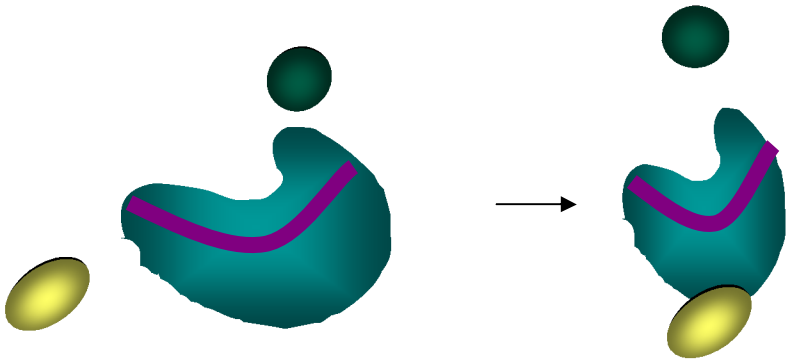
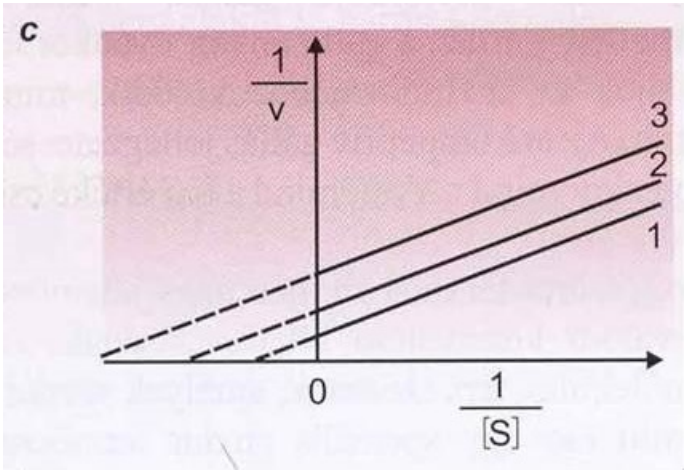
Modulation of the enzyme activity – uncompetitive

- inhibitor binds to an alternative form of the enzyme
- **KM ↓, vmax ↓**







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