

Chapter 16 - Citric Acid Cycle

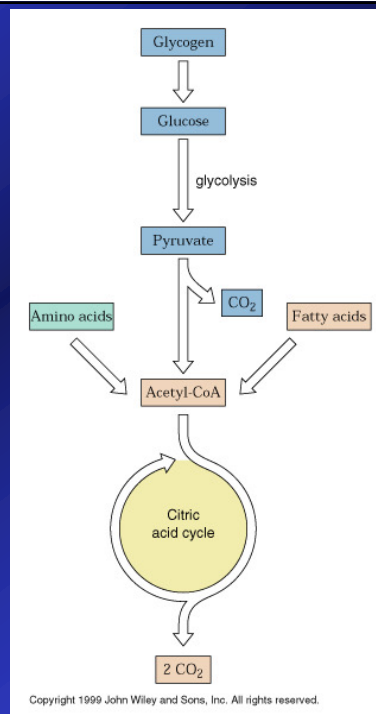
TCA (tricarboxylic acid cycle)
 Citric acid cycle and Krebs cycle
 Named after Sir Hans Krebs,
 Nobel Laureate. He worked as
 an assistant professor for Otto
 Warburg (Nobel Prize 1931) and
 his position terminated 1933 and
 at, Sir Fredrick Gowland Hopkin's
 (Nobel prize 1929) request he left
 Germany to hold a Rockefeller
 Studentship at the School of
 Biochemistry, Cambridge. In 1953
 he earned the Nobel Laureate in
 Medicine for his discovery of the
 citric acid cycle



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The Krebs cycle is a central
 pathway for recovering energy
 from three major metabolites:
 carbohydrates, fatty acids, and
 amino acids.

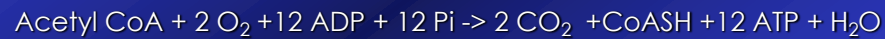
Most enter the cycle through
 Acetyl-CoA. The two carbons
 entered at this step are lost as
 CO_2 (the reason you breath out
 CO_2). The carbon atoms that
 enter by A-CoA leave after the
 second turn of the cycle.



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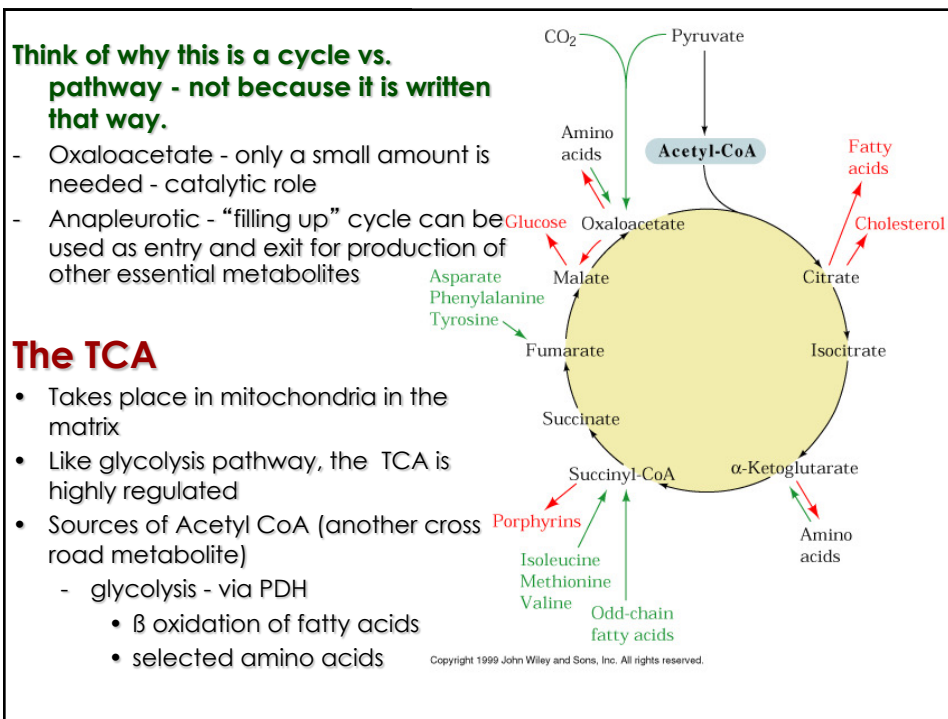
Synthesis of the TCA

- Reactions take place in mitochondria - thus transport of reactants and products are important
- Overall reaction involves the entry of a 2 carbon compound (acetyl CoA) into the cycle with the loss of 2 CO₂ and formation of 3 NADH, FADH₂ and GTP or ATP.



- No net change in the concentration of the 4 carbon compound oxaloacetate.
- The carbons lost as CO₂ are from previous A-CoAs not from the reactant A-Co

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Free energy considerations of the Citric Acid Cycle

TABLE 17-2 Standard Free Energy Changes (ΔG°) and Physiological Free Energy Changes (ΔG) of Citric Acid Cycle Reactions

Reaction	Enzyme	ΔG° (kJ · mol ⁻¹)	ΔG (kJ · mol ⁻¹)
1	Citrate synthase	-31.5	Negative
2	Aconitase	~5	~0
3	Isocitrate dehydrogenase	-21	Negative
4	α -Ketoglutarate dehydrogenase	-33	Negative
5	Succinyl-CoA synthetase	-2.1	~0
6	Succinate dehydrogenase	+6	~0
7	Fumarase	-3.4	~0
8	Malate dehydrogenase	+29.7	~0

Table 17-2
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The rxns with $-\Delta G$ directionally drive the pathway.
As these rxns are thermodynamically favorable, they
MUST be regulated.

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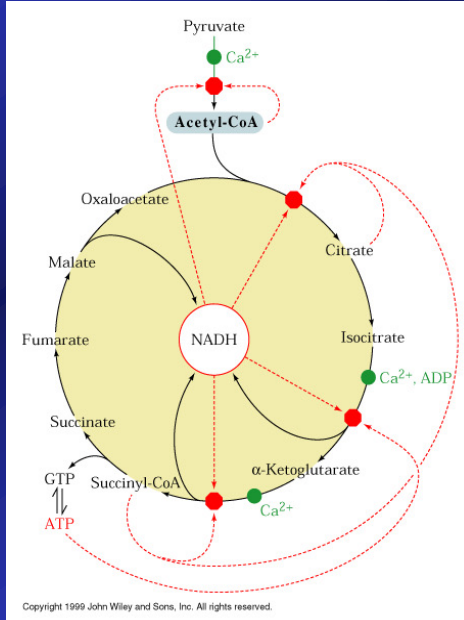
Regulation of the Citric Acid Cycle

Cycle enzymes

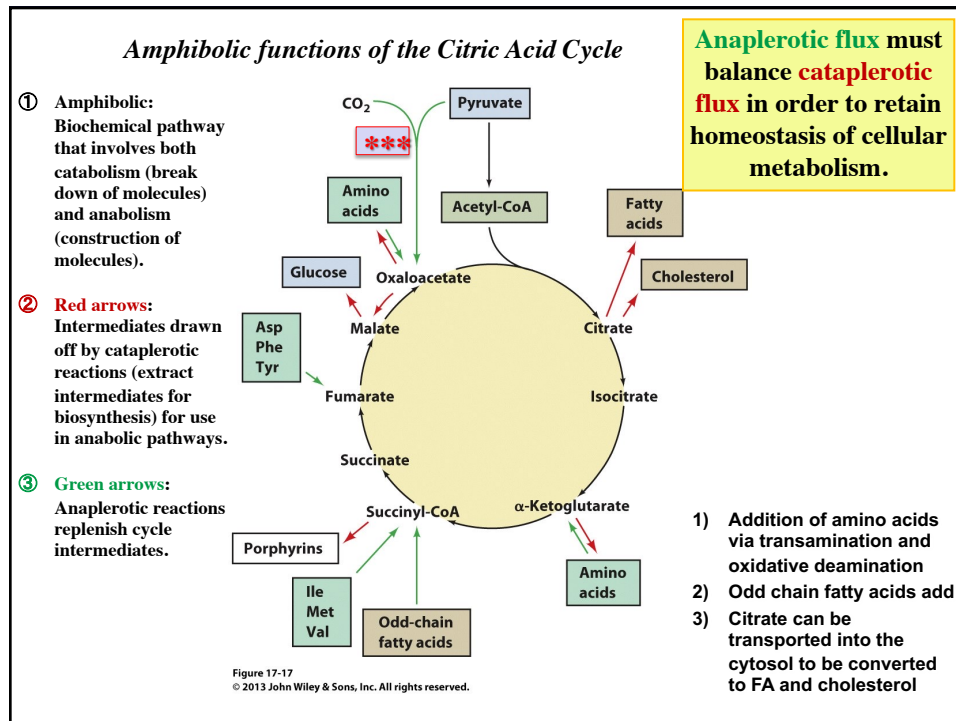
Citrate synthase
inhibited by S-CoA,
citrate, NADH, and ATP

Isocitrate dehydrogenase
inhibited by NADH &
ATP
stimulated by NAD⁺ &
ADP

**α -ketoglutarate
dehydrogenase**
Inhibited by S-CoA,
NADH and high
ATP/AMP ratio



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Getting there - don't forget PC!

Pyruvate Dehydrogenase (PDH) - Entry of glucose metabolites into cycle is through formation of acetyl-CoA by oxidative decarboxylation of pyruvate

- In eukaryotes, all of the TCA enzymes and the PDH are found in the mitochondria. Either in the inner compartment or the matrix of the mitochondrion.
- Pyruvate is made in the cytosol and transported by a H⁺ / pyruvate symporter.

$$\begin{array}{c}
 \text{COO}^- \\
 | \\
 \text{C}=\text{O} \\
 | \\
 \text{CH}_3
 \end{array}
 + \text{NAD}^+ + \text{CoA-SH} \xrightarrow{\text{Pyruvate Dehydrogenase}}
 \begin{array}{c}
 \text{NADH} \\
 \text{CO}_2
 \end{array}
 + \text{CH}_3\text{-CO-S-CoA}$$

Acetyl CoA

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PDH Exists as large multiunit complex

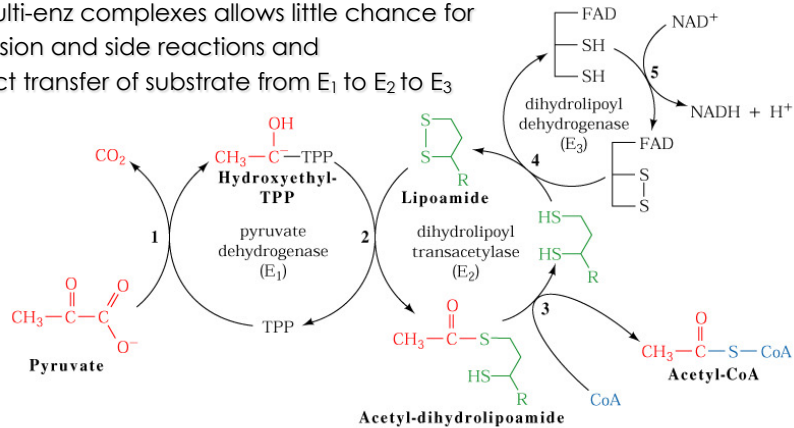
- Coenzymes - Vitamin B1- thiamine pyrophosphate (TPP), pantoic acid (CoA), riboflavin (FAD), Niacin (NAD^+) and lipoamide
- (3 different subunits)

E₁ Pyruvate Dehydrogenase - 24 copies / E₂ Dihydrolipoyl Transacetylase - 24 copies / E₃ Dihydrolipoyl Dehydrogenase - 12 copies

- increases local concentration of substrate for each subunit

- multi-enz complexes allows little chance for diffusion and side reactions and

direct transfer of substrate from E₁ to E₂ to E₃



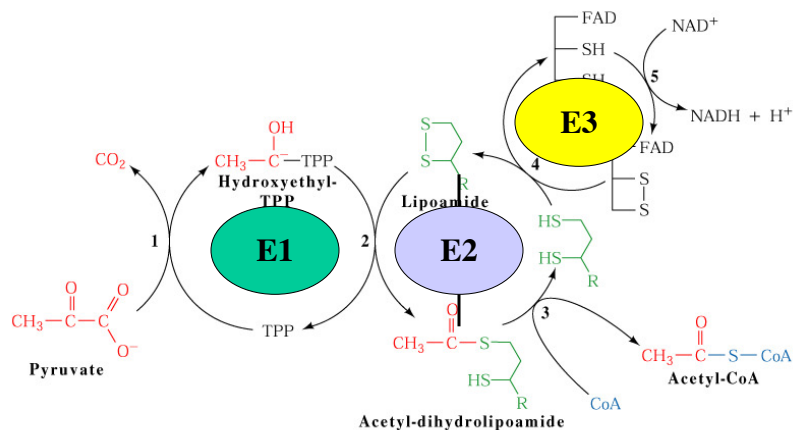
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The three enzymes of the PDH

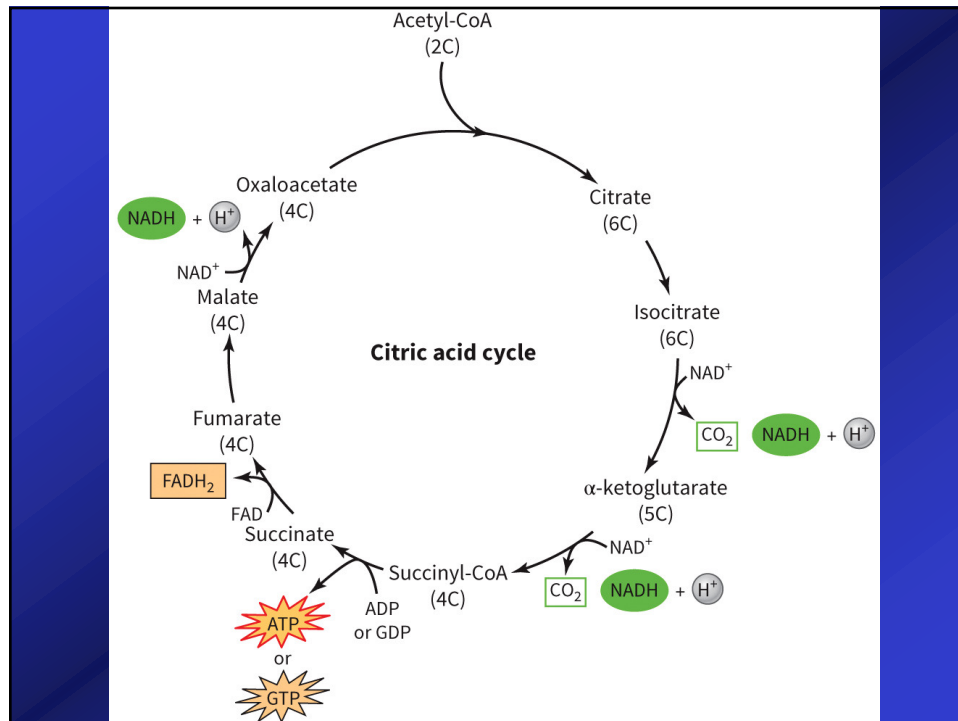
E₁ - Pyruvate dehydrogenase

E₂ Dihydrolipoyl Transacetylase

E₃ - Dihydrolipoyl Dehydrogenase



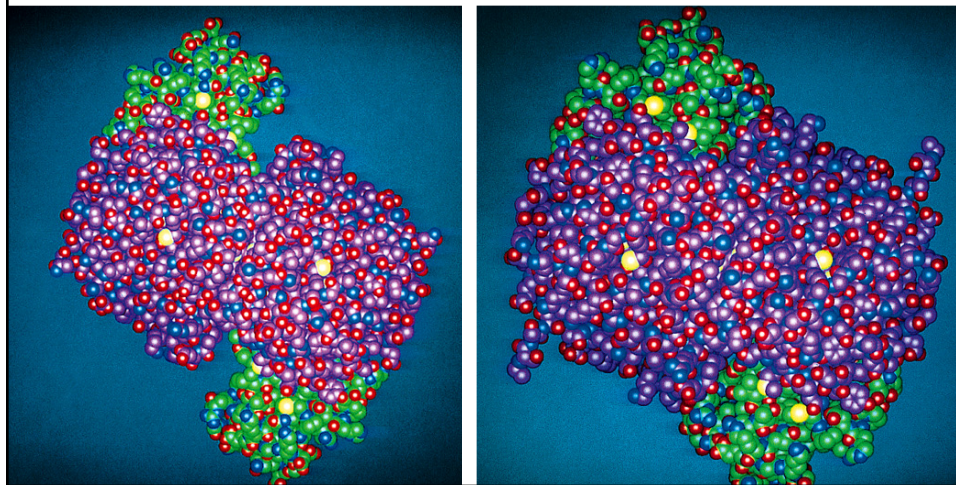
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Reaction of the cycle

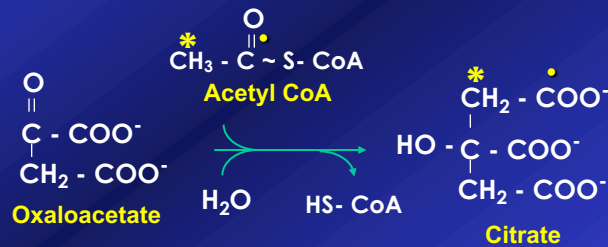
Citrate Synthase (CS) - catalyzes the condensation of acetyl-CoA and OAA in a highly exergonic fashion. There is a substantial conformational change in the enzyme when substrate binds. "hides" water from the active site and then forms A-CoA binding site. - ordered sequential reaction



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Citrate Synthase (CS)

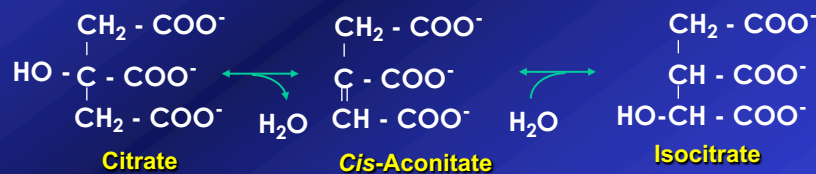
- aldol condensation of Acetyl CoA and oxaloacetate
- involves two His and one Asp
- ordered reaction leading to tertiary changes
- induced fit caused by OAA binding forms reactive site



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Aconitase - catalyzes the isomerization of citrate to isocitrate via stereospecific dehydration and rehydration. (a two step reaction).

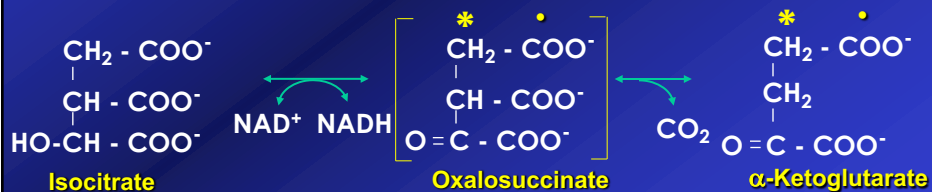
- citrate → isocitrate
- isomerization reaction
- 2 steps removal and addition of water
- Iron required - not heme
- iron-sulfur protein - bound by cys residues



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Isocitrate Dehydrogenase (IDH) - catalyzes the oxidative decarboxylation of isocitrate to produce an α -ketoglutarate and the first loss of CO_2 – remember that to get from citrate to OAA, you need to lose two carbons. This step also produces NADH.

- isocitrate \rightarrow [oxalosuccinate] \rightarrow α ketoglutarate
- first oxidative conversion
- 2 steps - all on same enzyme
 - 1 - oxidation of alcohol to ketone
 $\text{NAD}^+ \rightarrow \text{NADH}$ (reduced) worth 3 ATPs
 - 2 - β decarboxylation

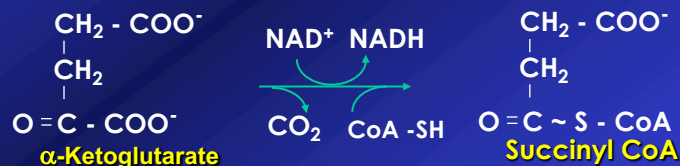


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Alpha Ketoglutarate Dehydrogenase (α KGDH)

- another enzyme multienzyme complex similar to the PDH complex. α KGDH catalyzes the second oxidative decarboxylation. Note that the two carbons released as CO_2 in this round of the cycle are not the carbons that entered the cycle as acetyl-CoA

- generates CO_2 , NADH and succinyl CoA
- analogous to PDH
- includes the same E_3 complex



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Succinate Thiokinase (STK) - AKA Succinyl-CoA synthetase

The GTP is easily converted to ATP by NDPK. In some tissues and specific species this is an ATP specific enzyme

- succinyl CoA + GDP → succinate + GTP + CoASH
- substrate level phosphorylation
- Hydrolysis of thioester bond of succinyl CoA - ΔG°
- GTP used by G proteins or converted to ATP by NDPK
- two forms exist - in birds ATP is produced



Succinate is symmetric and SDH does not differentiate between the COOH groups, all four carbons are labeled after one turn

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Succinate Dehydrogenase (SDH)

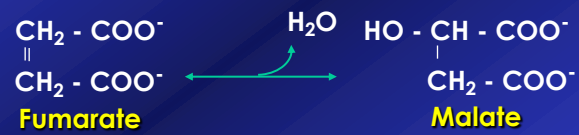
- Succinate + FAD → fumarate + FADH₂
- only non-matrix enzyme
- found bound to inner mitochondrial membrane
- facilitates transfer of FADH₂ electrons to electron transport system
- iron sulfur center
- FAD generally acts to oxidize C-C to C=C
- While NAD⁺ → C-OH to C=O (aldehydes or ketones)
- FAD is covalently bound to protein - consequence?



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Fumarase

- fumarate \rightarrow malate
- specific addition of H_2O



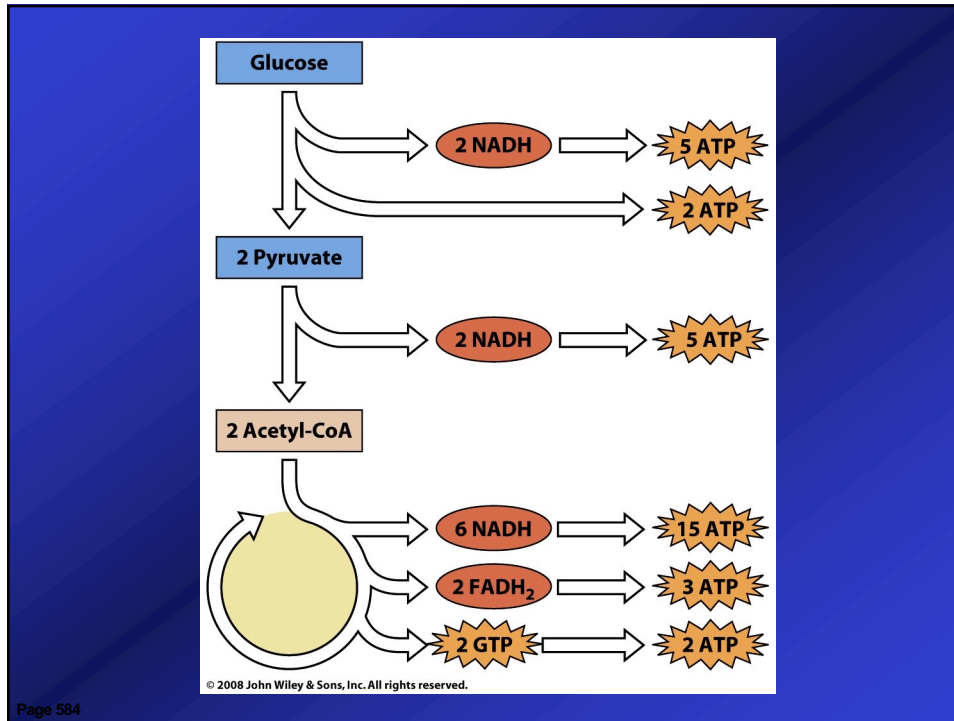
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Malate Dehydrogenase (MDH)

- malate + NAD^+ \rightarrow malate + NADH
- oxidation to reform oxaloacetate



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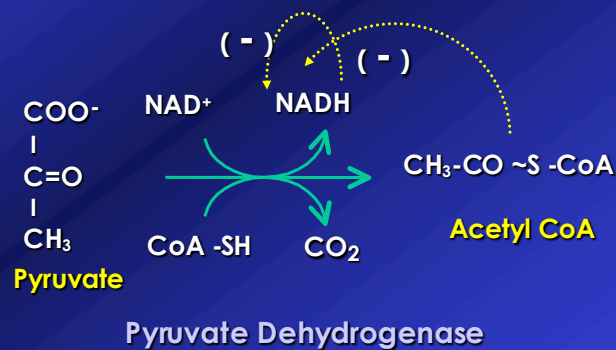
Regulation of PDH and the cycle

Regulated to meet needs of cell - don't waste energy

1 Feed back inhibition at PDH

– ACoA and NADH are allosteric inhibitors

- Act by inhibiting E2 - shifting the equilibrium towards the acylated form. Leads to TPP build up and will decrease decarboxylation



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Mitochondria

- Outer membrane is very porous
- Inner membrane very tight. Transfer into and out of matrix is controlled - important in H^+ and shuttling reducing equivalents.
- membranes are topologically sided - different charge, lipids and proteins



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