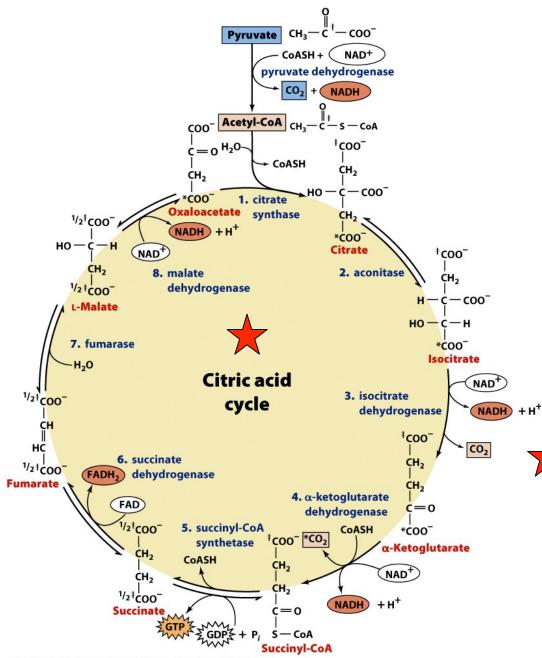
Chapter 17 Citric Acid Cycle (II) (4/26/11) Summary and Conclusion

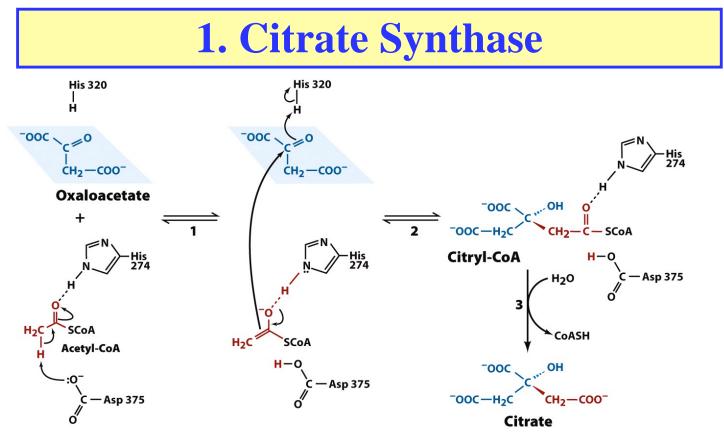


You MUST know this entire figure, including molecules, enzymes, and cofactors.

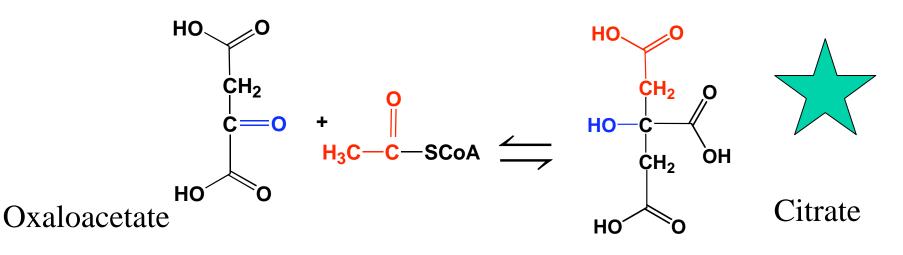
•In eukaryotes, all of the enzymes in the TCA are located in the mitochondria, so all substrates including NAD+ and GDP must be generated or transported there

•The carbon atoms of the 2CO₂ molecules generated in one turn of the cycle do not come from the acetyl group of acetyl-CoA but from oxaloacetate

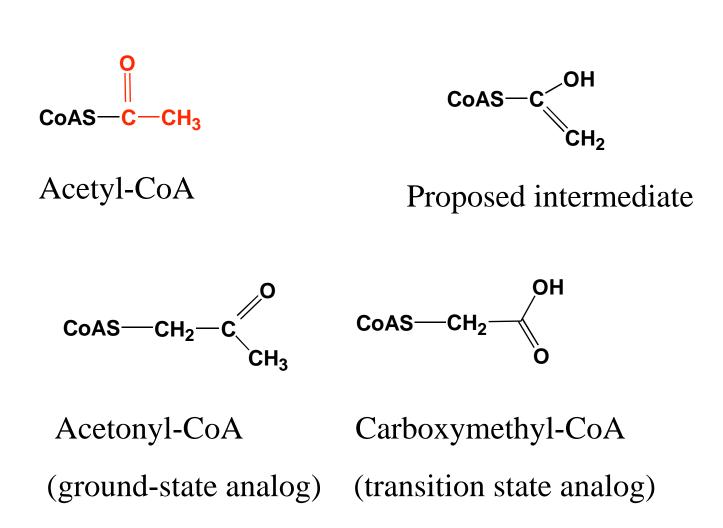
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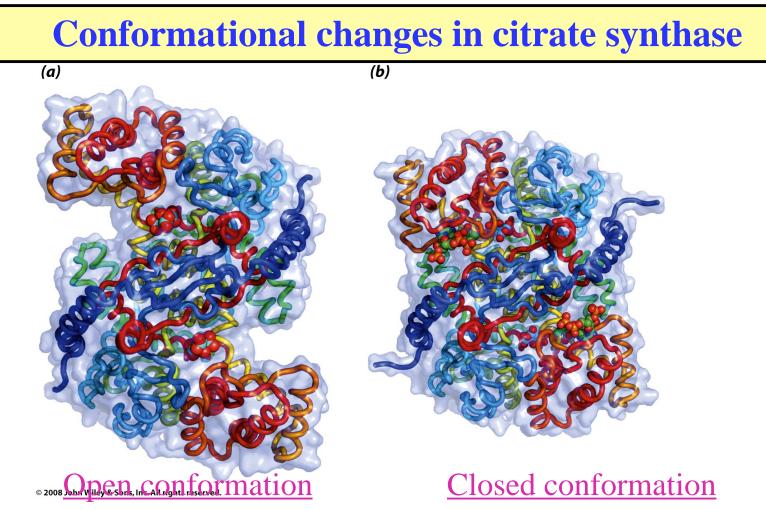


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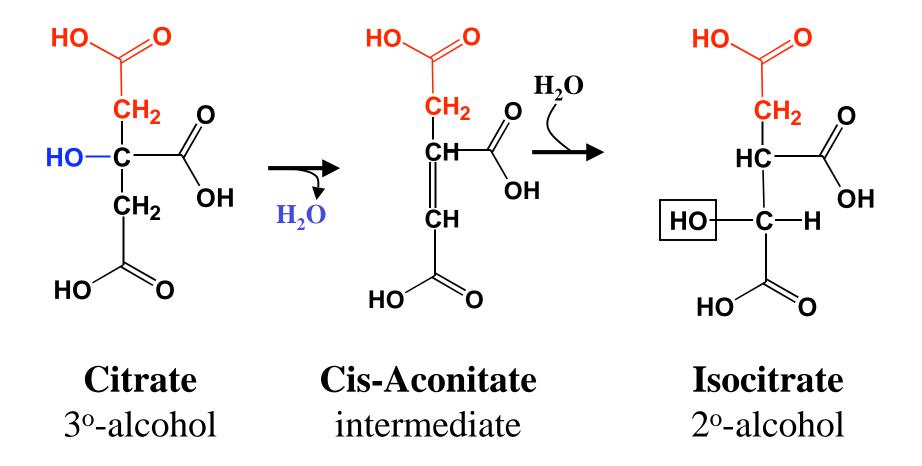
Induced fit needs binding of oxaloacetate before Acetyl-CoA can bind.





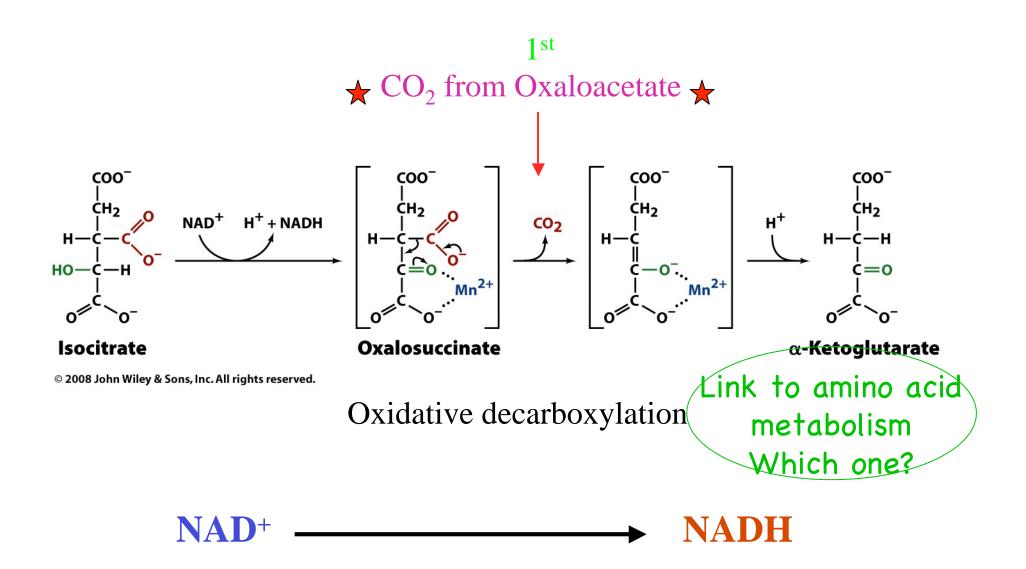
- Oxaloacetate binding causes a conformational change that creates the acetyl-CoA binding site and seals the oxaloacetate binding site so that solvent cannot reach the bound substrate
- Asp375 (base), His274 (acid), and His320 (acid) are the catalytic residues

2. Aconitase

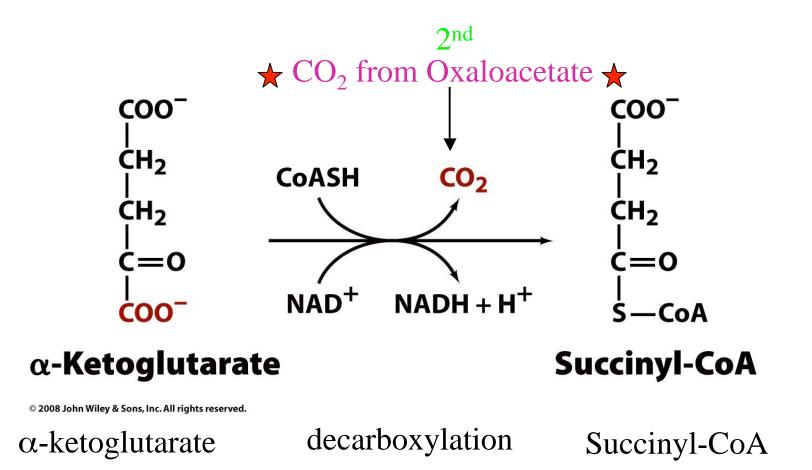


Aconitase has an iron-sulfur cluster (Fe_4S_4) at the active site. These are normally involved in e⁻-transfer but not in this case.

3. NAD⁺/Mn²⁺-Dependent Isocitrate dehydrogenase

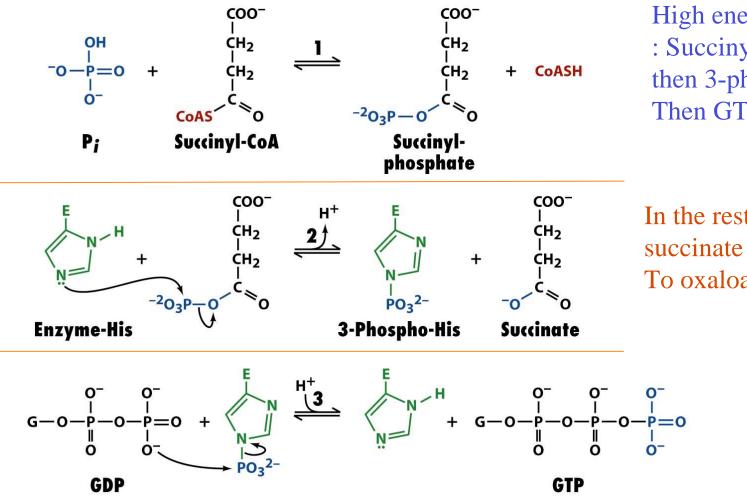


4. α-Ketoglutarate dehydrogenase



This enzyme is just like pyruvate dehydrogenase - a multienzyme complex that is specific for longer CoA derivatives

5. Succinyl-CoA Synthetase or Succinate Thiokinase

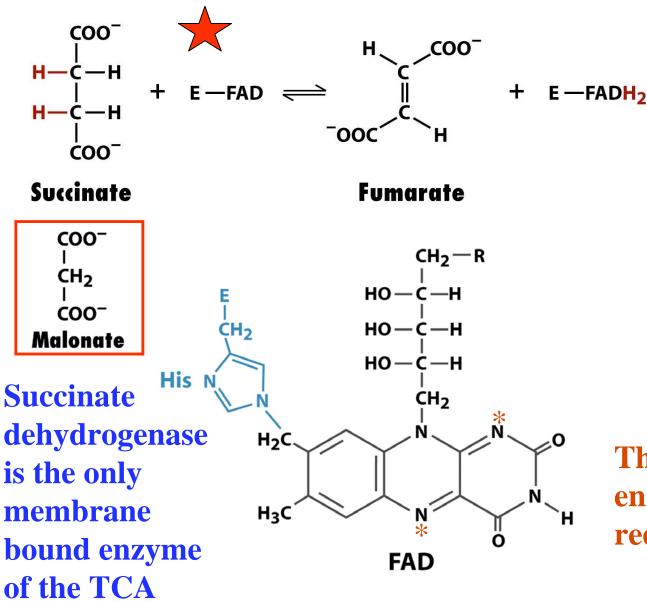


High energy compound : Succinyl-CoA, then 3-phospho-His, Then GTP

In the rest of the cycle, succinate will be converted To oxaloacetate

High-energy compound

6. Succinate dehydrogenase

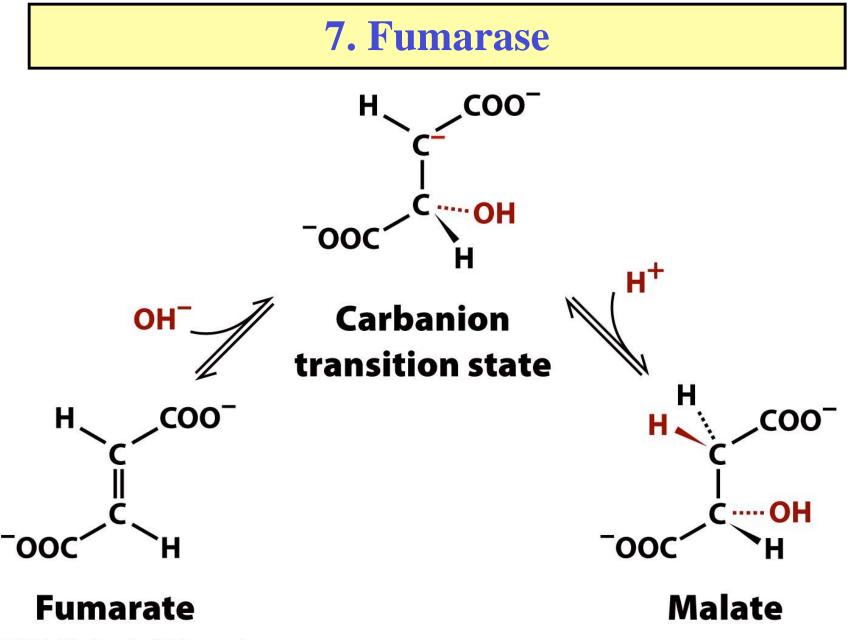


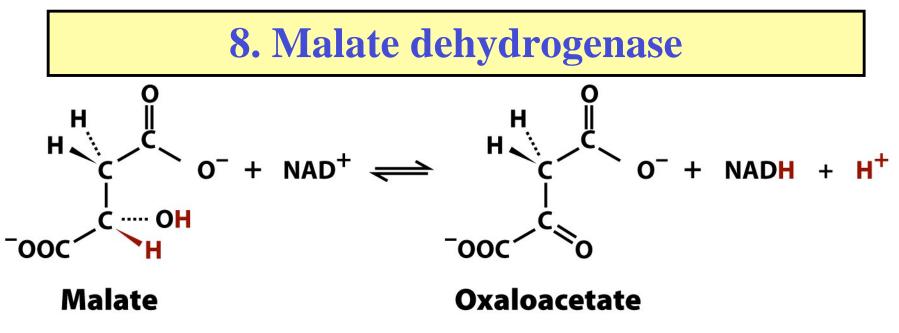
2e⁻ + 2H⁺

The FADH₂ is attached to the enzyme and must be re-oxidized before next rxn. This liberates 2eand 2H+

The FAD on the enzyme itself is reduced to FADH₂(*) Succinate dehydrogenase is the only membrane bound enzyme in the citrate cycle

- **FAD** functions to oxidize <u>alkanes to alkenes</u> (as in step 6)
- NAD+ functions to oxidize <u>alcohols to aldehydes</u> or ketones (as in step 8)
- Reoxidation of $FADH_2$ to FAD occurs in the mitochondrial electron transport chain
- This occurs via Succinate DH because it is membrane bound as is the electron transport chain

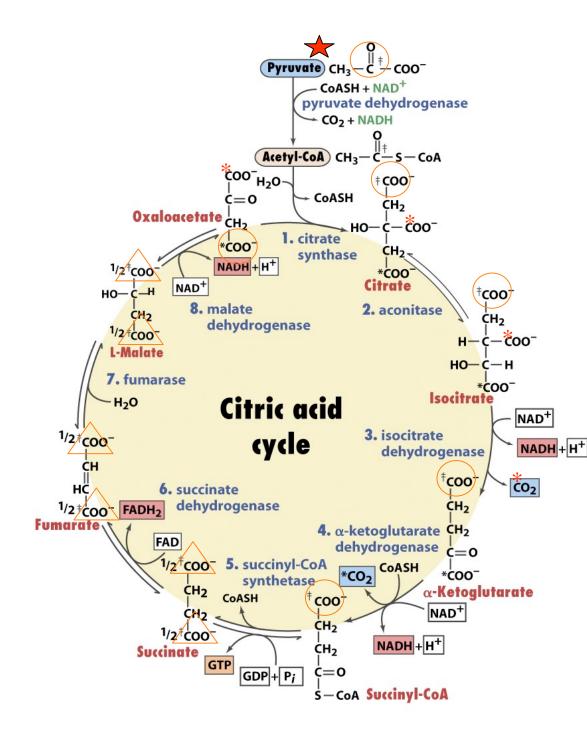




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Oxaloacetate is regenerated for the next turn of the TCA cycle. This reaction is very unfavorable (+29.7 kJ/mol) so very little oxaloacetate is made.

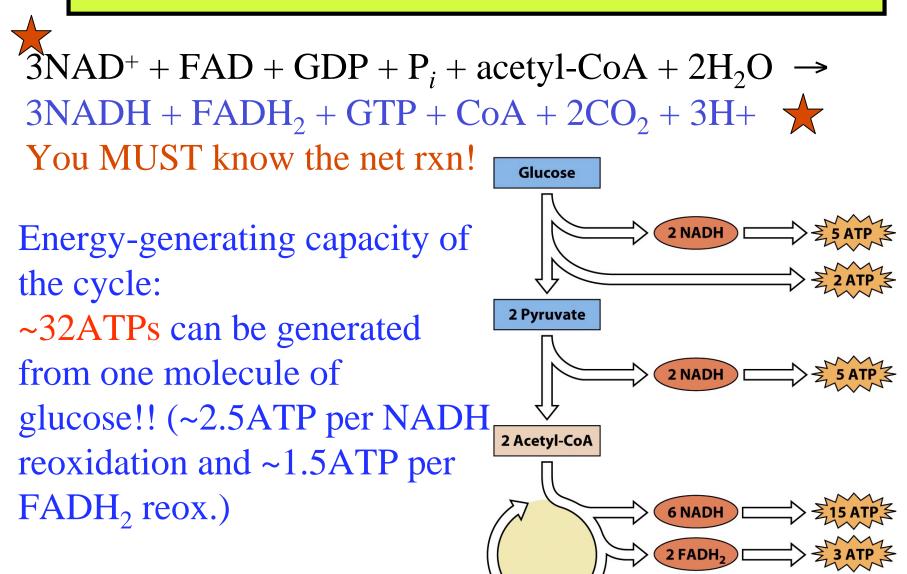
However, remember that the first rxn. of the cycle is *highly* exergonic (-31.5 kJ/mol). Citrate synthase requires oxaloacetate and so drives the creation of oxaloacetate by malate dehydrogenase.



You MUST know this entire figure, including molecules, enzymes, and cofactors.

- •In eukaryotes, all of the enzymes in the TCA are located in the mitochondria, so all substrates including NAD+ and GDP must be generated or transported there
- •The carbon atoms of the 2CO₂ molecules generated in one turn of the cycle do not come from the acetyl group of acetyl-CoA but from oxaloacetate

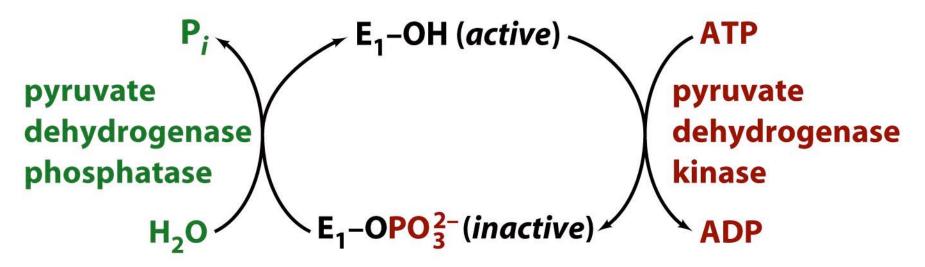
Overall net TCA reaction



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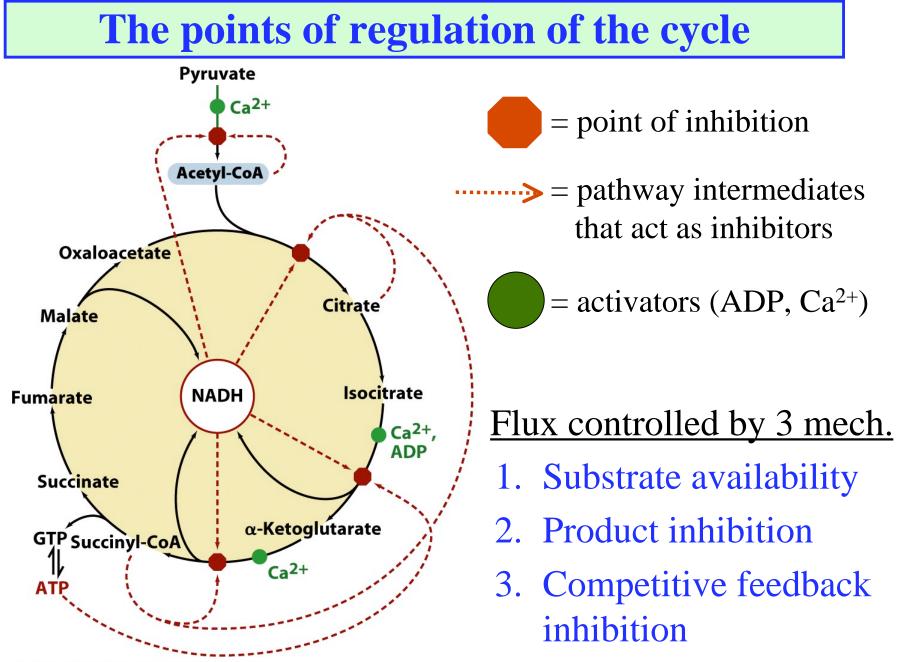
Regulation of Pyruvate Dehydrogenase

- 1. Product inhibition by NADH and acetyl-CoA
 - NADH and acetyl-CoA compete for binding with NAD+ and CoA
 - They also drive the reversible transacetylase (E_2) and dihydrolipoyl dehydrogenase (E_3) reactions in the backward directions.
- 2. Covalent modification by phosphorylation/dephosporylation of E_1
 - The products NADH and acetyl-CoA can activate the pyruvate dehydrogenase kinase associated with the enzyme complex which deactivates PDH
 - Insulin (which is a signal of fuel abundance) turns on the pyruvate dehydrogenase phosphatase which reactivates PDH



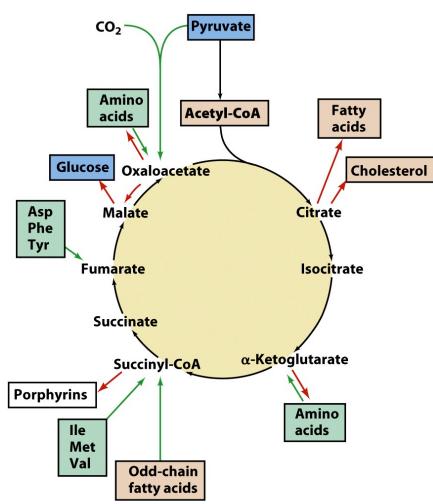
Regulation of the citric acid cycle

| Table 17-2 | Standard Free Energy Changes (ΔG°) and Physiological Free Energy Changes (ΔG) of Citric Acid Cycle Reactions | | |
|------------|--|--|---------------------------------|
| Reaction | Enzyme | ∆ <i>G</i> °′ (kJ · mol ^{−1}) | ∆G (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 |



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Citric acid cycle intermediates are always in flux



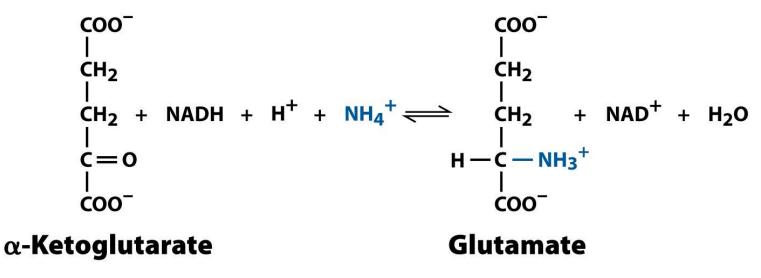
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Pathways using intemediates

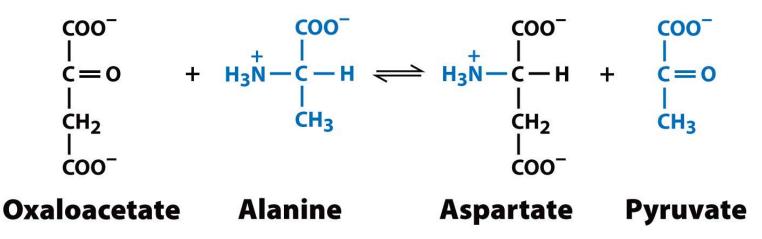
- 1. Gluconeogenesis
- 2. Fatty acid biosynthesis
- 3. Amino acid biosynthesis
- 4. Porphyrin biosynthesis

<u>Reactions replenishing</u> <u>intermediates</u>

- 1. Oxidation of odd-chain fatty acids
- 2. Breakdown of Ile, Met, Val, Asp, Phe, Tyr
- 3. Transamination/deamination of amino acids

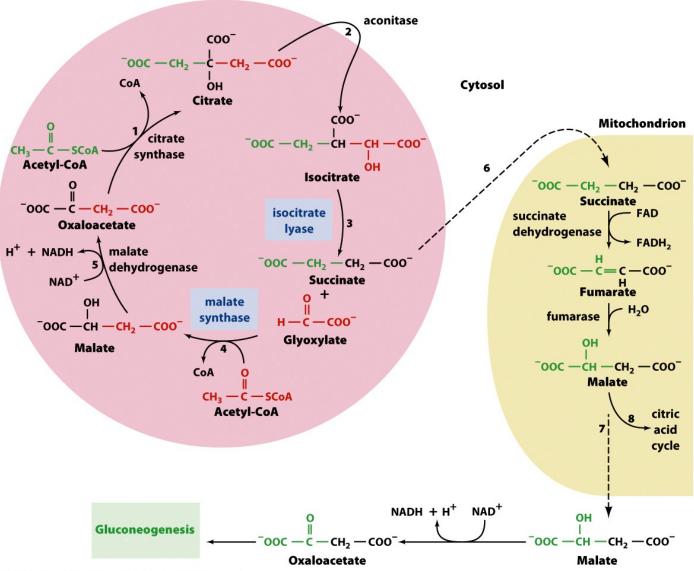


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Glyoxalate cycle vs. Citric acid cycle

Glyoxysome



Questions:

1 (Companion#7). Which of the following labeled glucose molecule would yield ¹⁴CO₂ following glycolysis and the pyruvate dehydrogenase reaction?

(a) $1-[^{14}C]$ -glucose (b) $3-[^{14}C]$ -glucose (c) $4-[^{14}C]$ -glucose (d) $6-[^{14}C]$ -glucose

- 2 (Book#5). The CO_2 produced in one round of the citric acid cycle does not originate in the acetyl carbons that entered that round.
- (a) If acetyl-CoA is labeled with ¹⁴C at its carbonyl carbon, how many rounds of the cycle are required before ¹⁴CO₂ is released?
- (b) How many rounds are required if acetyl-CoA is labeled at its methyl group?