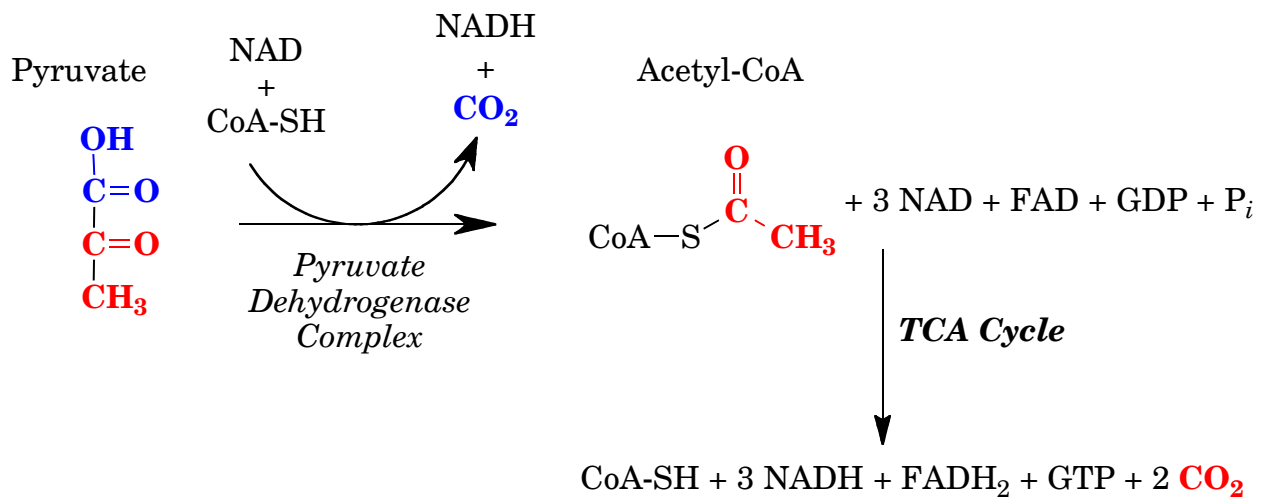
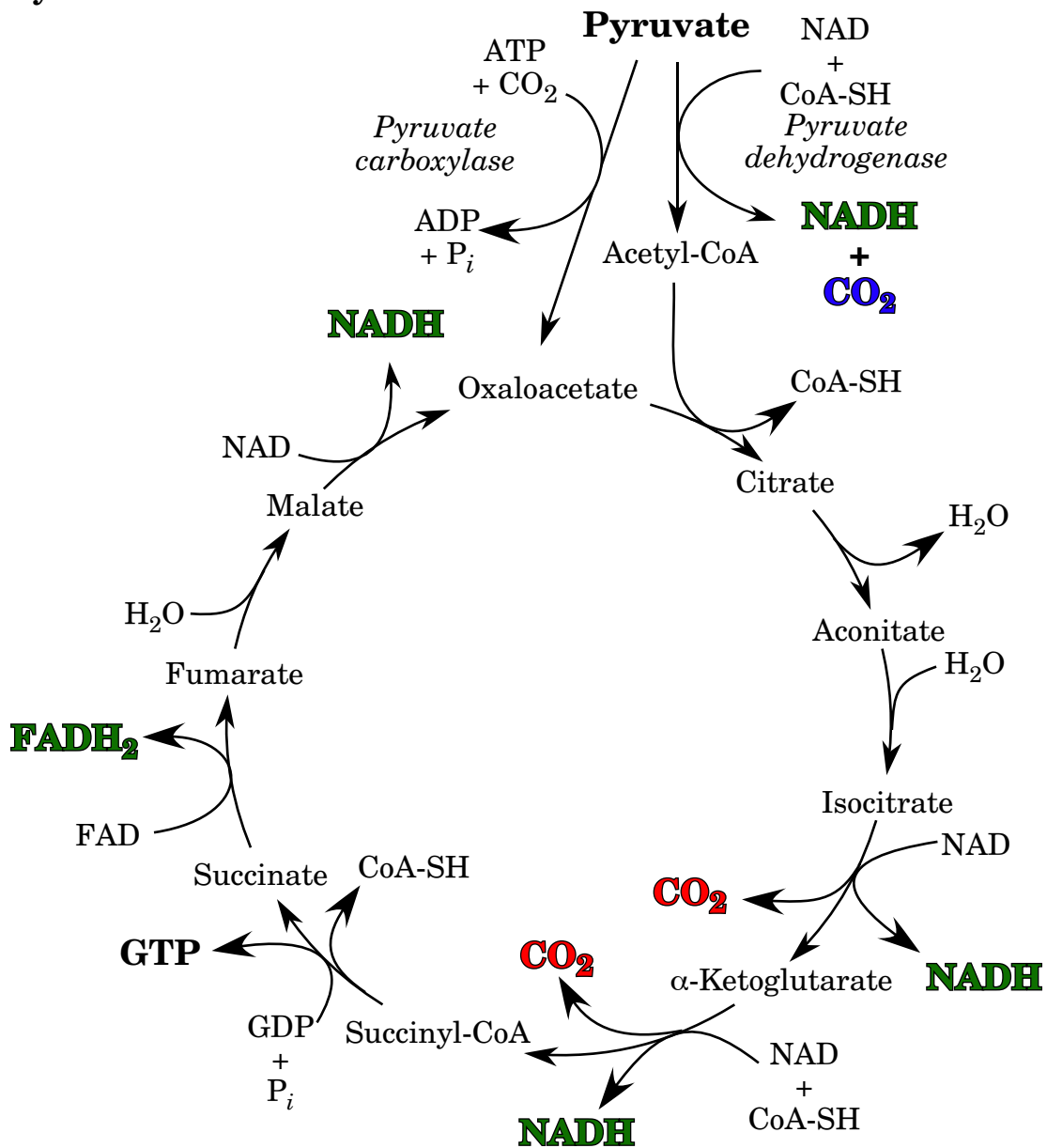


Pyruvate Oxidation



Proteins in the Pyruvate Dehydrogenase Complex

E_1 = Pyruvate dehydrogenase (Pyruvate decarboxylase)

E_2 = Dihydrolipoyl acetyltransferase

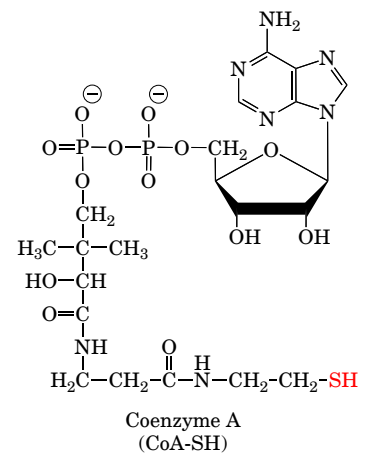
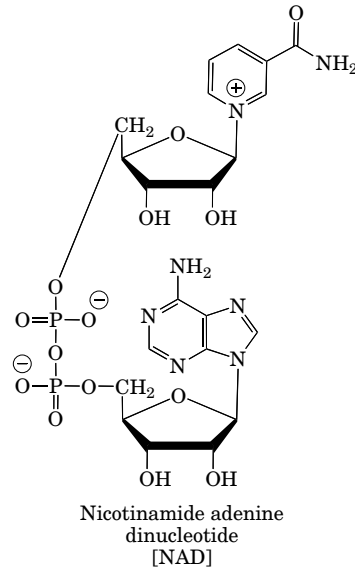
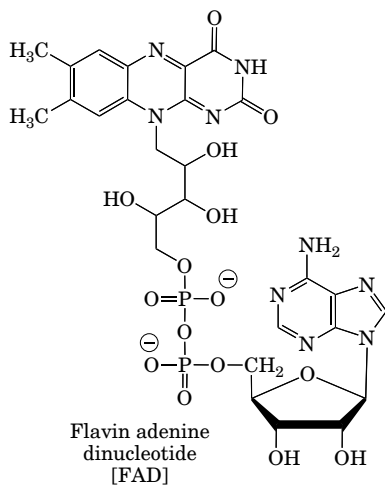
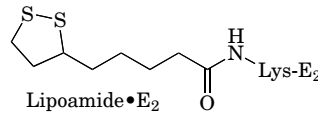
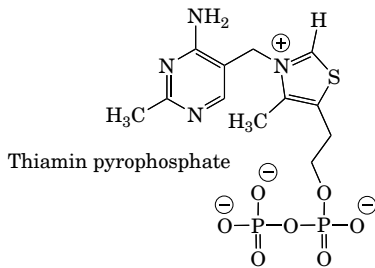
E_3 = Dihydrolipoyl dehydrogenase

Protein X

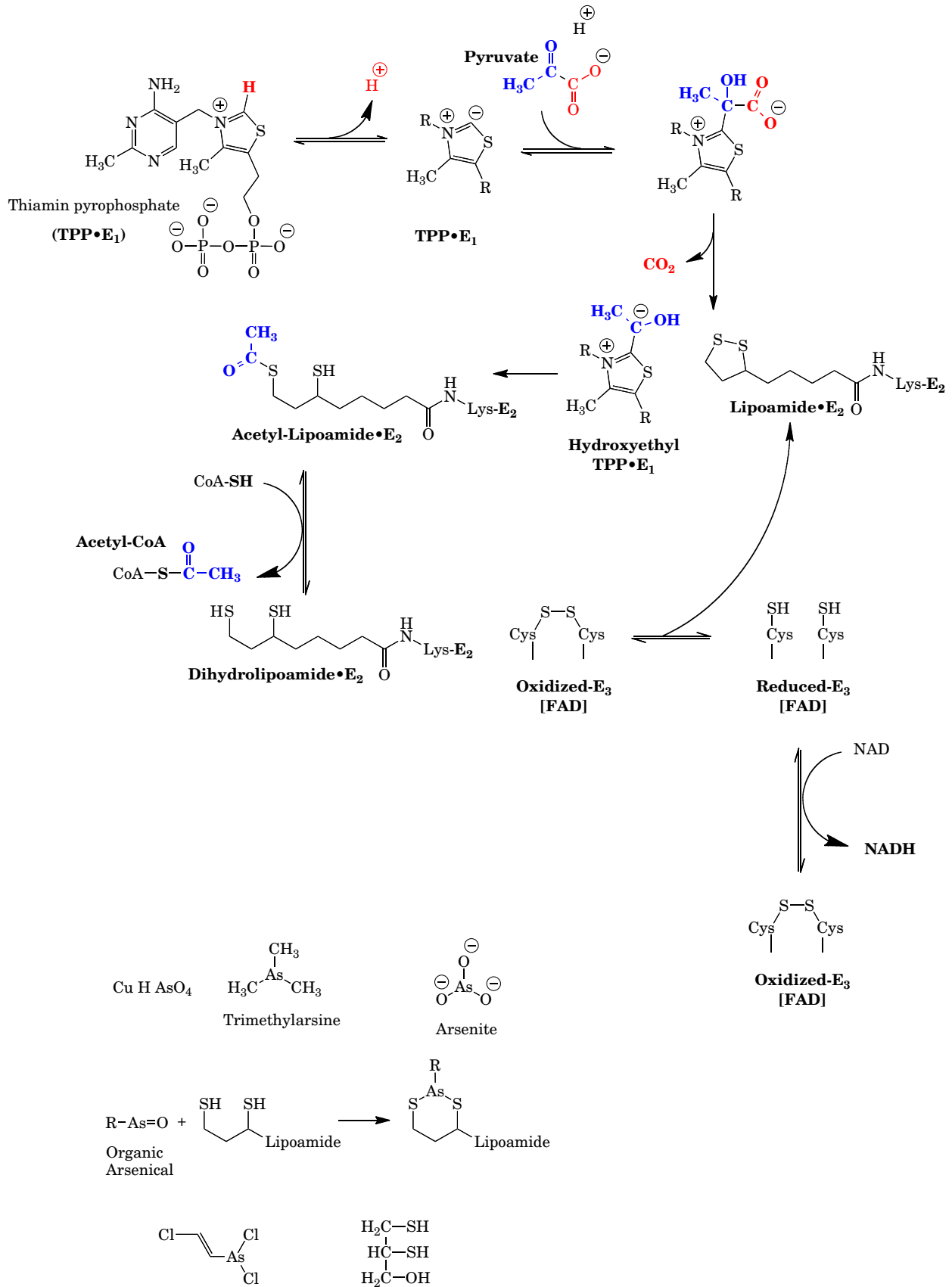
E_1 -kinase

Phospho- E_1 -phosphatase

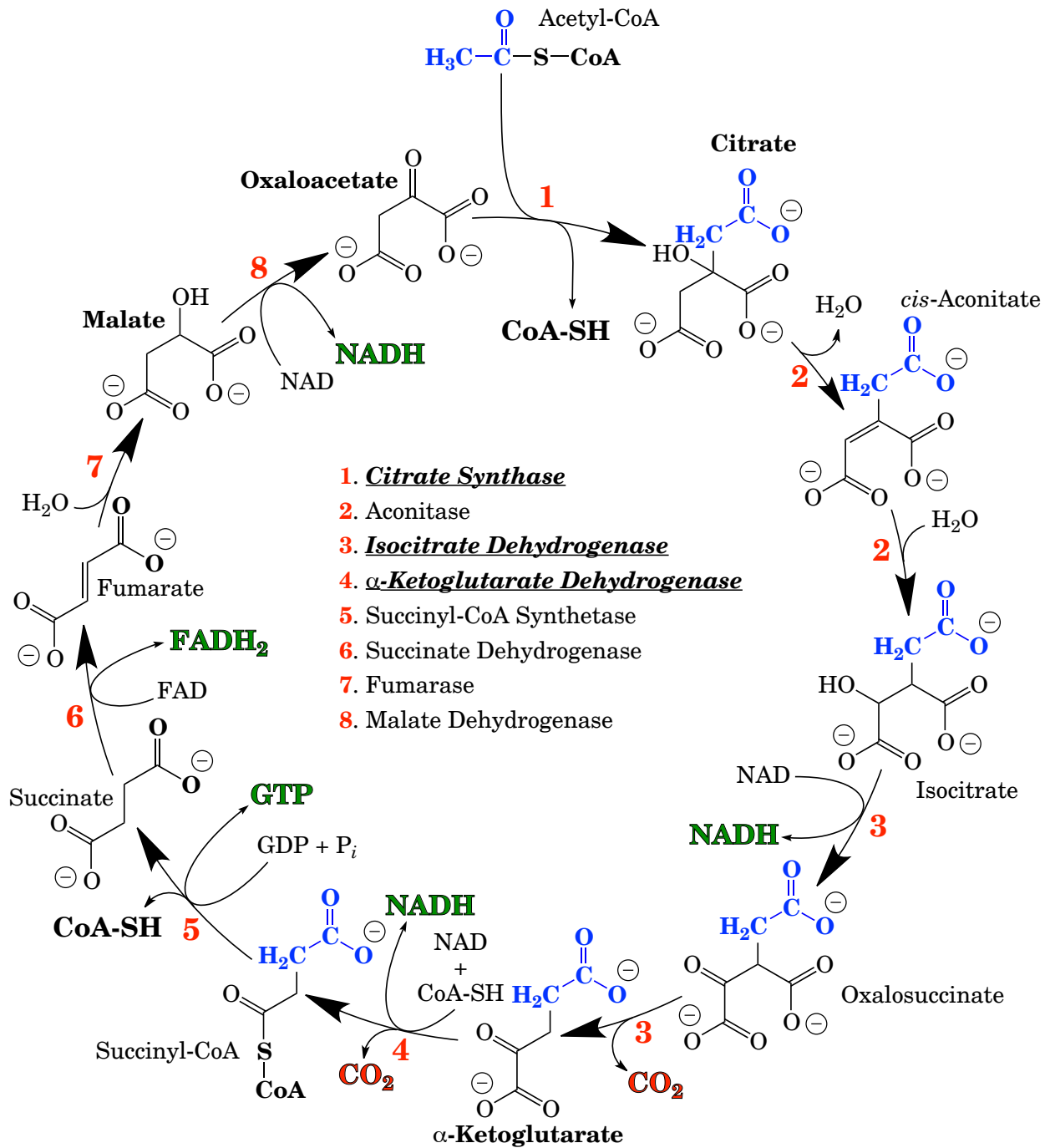
	Size (megaDa)	E_1 peptides	E_2 peptides	E_3 peptides
Eukaryotes gram-positive prokaryotes	10	120 (($\alpha\beta$) ₂ tetramers)	60 (trimers)	24 (dimers)
Gram-negative prokaryotes (<i>E. coli</i>)	4.6	24	24	12
Eukaryotic ribosome	4.2	4 RNA (6880 bases) and ~84 polypeptides		
Prokaryotic ribosome	2.7	3 RNA (4860 bases) and 57 polypeptides		



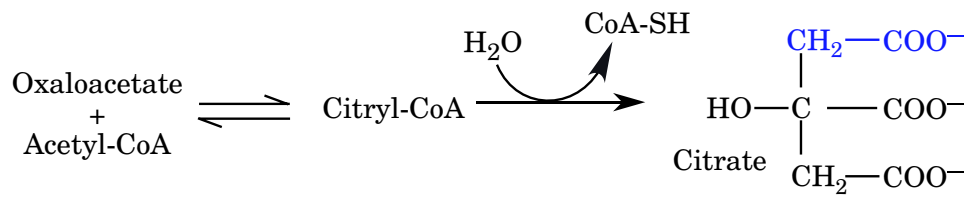
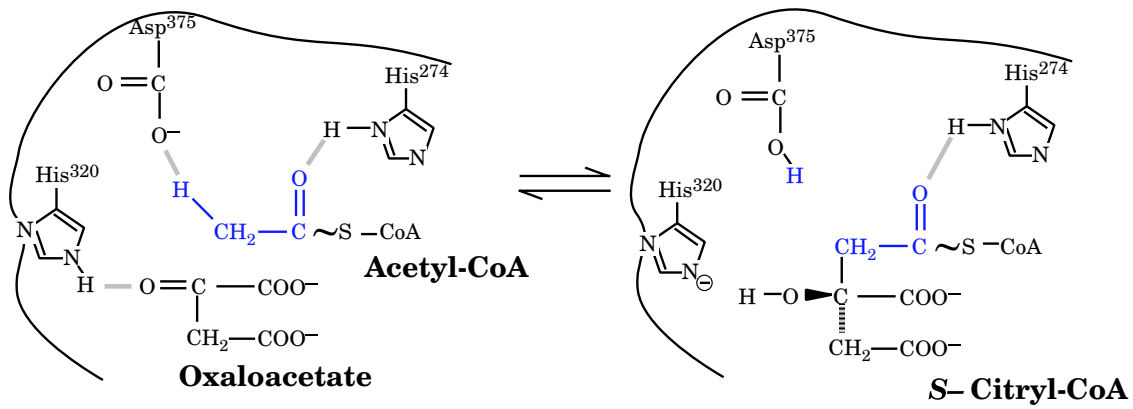
Pyruvate Dehydrogenase Complex



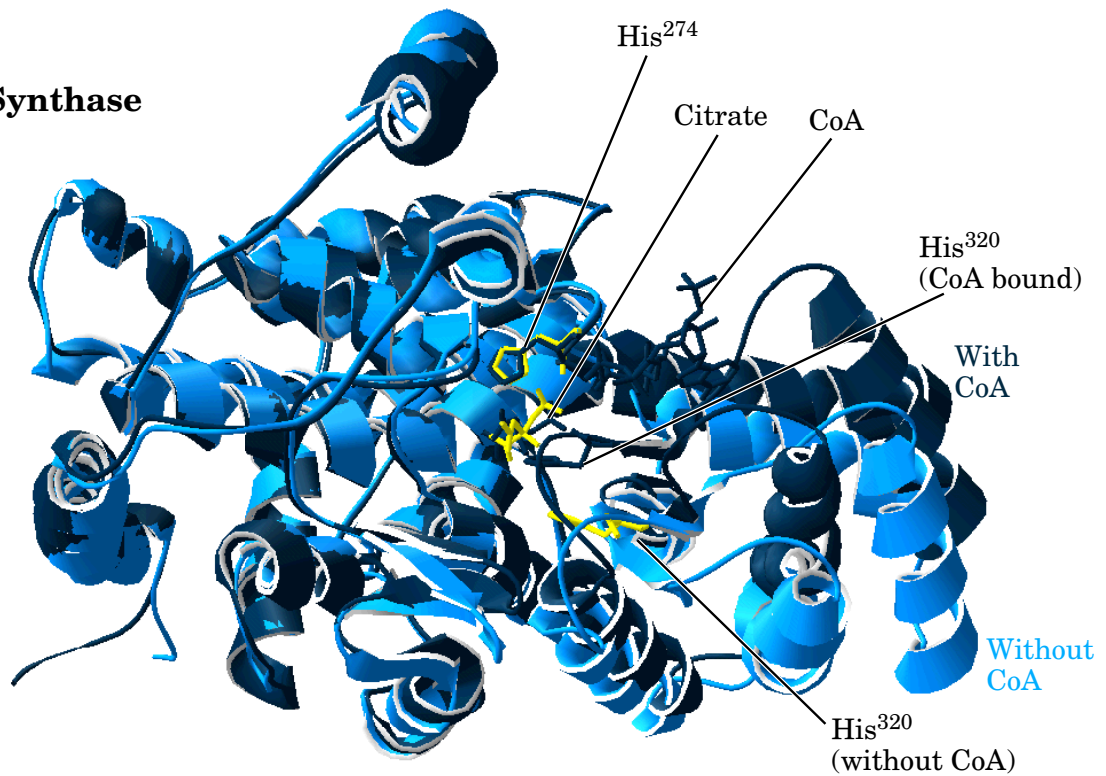
Tricarboxylic Acid (TCA) Cycle



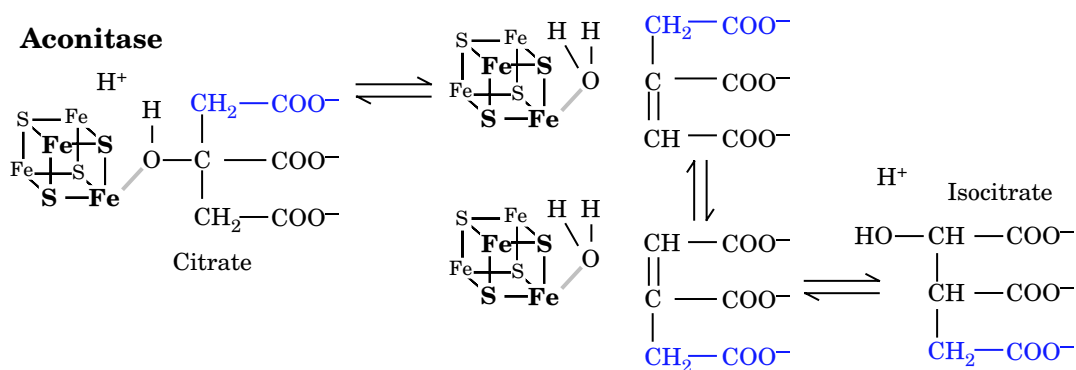
Citrate Synthase



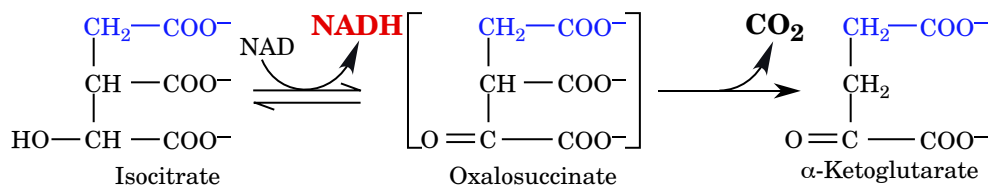
Citrate Synthase



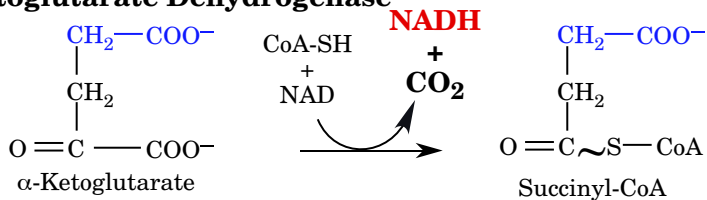
Porcine (*Sus scrofa*) citrate synthase bound to citrate (pdb ID 1CTS) and to both citrate and CoA (pdb ID 2CTS)



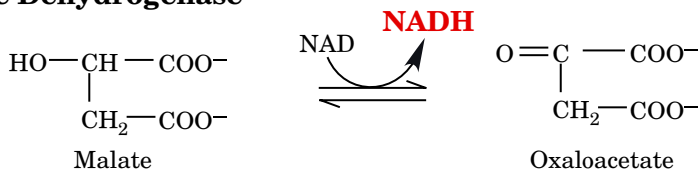
Isocitrate Dehydrogenase



α -Ketoglutarate Dehydrogenase



Malate Dehydrogenase



Reaction	ΔG° (kJ/mol)	Typical ΔG in cells (kJ/mol)
Acetate combustion	-849	
TCA cycle	-40	-115
<i>Citrate synthase</i>	-31.4	-53.9
Aconitase	+6.7	+0.8
<i>Isocitrate Dehydrogenase</i>	-8.4	-17.5
<i>α-ketoglutarate dehydrogenase</i>	-30	-43.9
Succinyl-CoA synthetase	-3.3	~ 0
Succinate dehydrogenase	+0.4	~ 0
Fumarase	-3.8	~ 0
Malate dehydrogenase	+29.7	~ 0

Anaplerotic reactions

