

Citrate Synthase

Enzyme

2.3.3.1

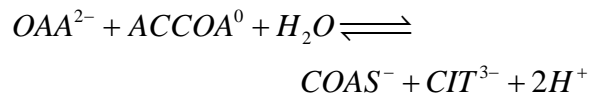
Author(s): Daniel A. Beard, Kalyan Vinnakota, Fan Wu
Biotechnology and Bioengineering Center, Department of Physiology
Medical College of Wisconsin

Contact: dbeard@mcw.edu

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Reactants and Reaction

Citrate synthase is the first step in the oxidation of acetyl-CoA in the citric acid cycle. The reference chemical reaction, is



where the abbreviations for the biochemical species are listed below. The biochemical reaction, involving biochemical reactants that are sums of species is

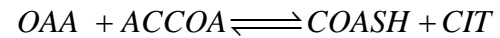


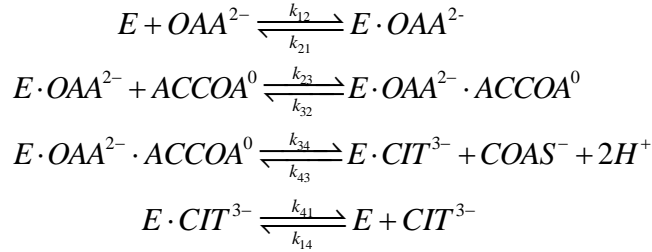
Table 1: Thermodynamic Parameter Values for Citrate Synthase. $\Delta_r G^\circ$ correspond to $T = 298.15$ K, 1 M reactants, $I = 0.0$ M, $P = 1$ atm; pK values correspond to $T = 298.15$ K, 1 M reactants, $I = 0.10$ M, $P = 1$ atm.

| Reactant | Abbreviation | Reference species | $\Delta_r G^\circ$ (kJ/mol) | Ion-bound species | pK |
|-------------------------|------------------|--------------------|-----------------------------|---------------------|-------|
| water | H ₂ O | H ₂ O | -237.19 | - | - |
| coenzyme A | COASH | COAS ⁻ | 0 | COASH ⁰ | 8.09 |
| acetyl-co-enzyme A | ACCOA | ACCOA ⁰ | -188.52 | - | - |
| oxaloacetate | OAA | OAA ²⁻ | -791.77 | MgOAA ⁰ | 1.02 |
| | | | | HOAA ⁻ | 3.9 |
| citrate | CIT | CIT ³⁻ | -1157.36 | HCIT ²⁻ | 5.67 |
| | | | | MgCIT ⁻ | 3.517 |
| | | | | KCIT ²⁻ | 0.60 |
| adenosine triphosphate | ATP | ATP ⁴⁻ | | HATP ³⁻ | 6.71 |
| | | | | MgATP ²⁻ | 4.28 |
| | | | | KATP ³⁻ | 1.00 |
| adenosine diphosphate | ADP | ADP ³⁻ | | HADP ²⁻ | 6.496 |
| | | | | MgADP ⁻ | 3.30 |
| | | | | KADP ²⁻ | 1.17 |
| adenosine monophosphate | AMP | AMP ²⁻ | | HAMP ⁻ | 6.16 |
| | | | | MgAMP ⁰ | 1.74 |
| | | | | KAMP ⁻ | 1.00 |
| succinyl-coenzyme A | SCOA | SCOA ⁻ | -509.59 | HSCOA ⁰ | 3.99 |

All values from [1].

Mechanism

The enzyme catalyzed reaction is assumed to proceed via the compulsory-ordered ternary mechanism, with dead-end binding of succinyl-CoA, ATP, ADP, and AMP. The mechanism involves four enzyme state transitions:



where each state transition is assumed to proceed by mass action.

Equations

Thermodynamics

The standard Gibbs free energy is computed [2]:

$$\begin{aligned}
 \Delta_r G_{cits}^0 &= \Delta_f G_{COASH}^0 + \Delta_f G_{CIT}^0 - \Delta_f G_{OAA}^0 \\
 &\quad - \Delta_f G_{ACCOA}^0 - \Delta_f G_{H_2O}^0 = 60.12 \text{ kJ/mol},
 \end{aligned}$$

where the basic thermodynamic data are listed in Table 1. The equilibrium constant for the reference biochemical reaction is computed from the standard Gibbs free energy

$$K_{eq,cits}^0 = \frac{1}{h^2} \exp\left(-\frac{\Delta_r G_{cits}^0}{RT}\right),$$

where we have introduced the definition $h = 10^{-pH}$ and this equilibrium constant explicitly accounts for pH. Therefore $K_{eq,cits}^0$ represents the equilibrium ratio

$$[COAS^-][CIT^{3-}] / [OAA^{2-}][ACCOA^0]$$

at $T = 298.15 \text{ K}$ and $I = 0.0 \text{ M}$.

The species concentrations are computed:

$$\begin{aligned}
 [OAA^{2-}] &= [OAA] / P_{OAA} \\
 [ACCOA^0] &= [ACCOA] / P_{ACCOA} \\
 [CIT^{3-}] &= [CIT] / P_{CIT} \\
 [COAS^-] &= [COASH] / P_{COASH} \\
 [ATP^{4-}] &= [ATP] / P_{ATP} \\
 [ADP^{3-}] &= [ADP] / P_{ADP} \\
 [AMP^{2-}] &= [AMP] / P_{AMP} \\
 [SCOA^-] &= [SCOA] / P_{SCOA}
 \end{aligned}$$

where the binding polynomials are expressed:

$$\begin{aligned}
 P_{OAA} &= 1 + \frac{[Mg^{2+}]}{K_{Mg,OAA}} \\
 P_{ACCOA} &= 1 \\
 P_{CIT} &= 1 + \frac{h}{K_{H,CIT}} + \frac{[Mg^{2+}]}{K_{Mg,CIT}} + \frac{[K^+]}{K_{K,CIT}} \\
 P_{COASH} &= 1 + \frac{h}{K_{H,COASH}} \\
 P_{ATP} &= 1 + \frac{h}{K_{H,ATP}} + \frac{[Mg^{2+}]}{K_{Mg,ATP}} + \frac{[K^+]}{K_{K,ATP}} \\
 P_{ADP} &= 1 + \frac{h}{K_{H,ADP}} + \frac{[Mg^{2+}]}{K_{Mg,ADP}} + \frac{[K^+]}{K_{K,ADP}} \\
 P_{AMP} &= 1 + \frac{h}{K_{H,AMP}} + \frac{[Mg^{2+}]}{K_{Mg,AMP}} + \frac{[K^+]}{K_{K,AMP}} \\
 P_{SCOA} &= 1 + \frac{h}{K_{H,COASH}}
 \end{aligned}$$

Flux Expression

We use the variables a , b , p , and q to denote species concentrations: $a = [OAA^{2-}]$, $b = [ACCOA^0]$, $p = [COAS^-]$, $q = [CIT^{3-}]$.

The flux expression has the form:

$$J = \frac{n}{d}$$

where



$$n = \frac{V_m}{K_{eA}K_{mB}} \left(\frac{ab - \frac{pq}{K_{eq}}}{1 + \frac{h}{K_{iH}}} \right)$$

and

$$d = \left(1 + \frac{K_{mA}b}{K_{eA}K_{mB}} + \frac{K_{mQ}p}{K_{eQ}K_{mP}} \right) I_1 + \left(\frac{a}{K_{eA}} + \frac{K_{mQ}ap}{K_{eA}K_{mP}K_{eQ}} + \frac{K_{mA}pq}{K_{eA}K_{mB}K_{eQ}} \right) I_2 + \left(\left[\frac{1}{K_{eA}K_{mB}} - \frac{K_{mQ}K'_{eQ}}{K_{eQ}^2K_{mP}} \right] ab + \left[\frac{1}{K_{mP}K_{eQ}} - \frac{K_{mA}}{K_{eA}^2K_{mB}K_{eQ}} \right] pq + \frac{K_{mQ}abp}{K_{eA}K_{eB}K_{mP}K_{eQ}} + \frac{K_{mA}bpq}{K_{eA}K_{mB}K_{eB}K_{eQ}} \right) I_3 + \left(\frac{q}{K_{eQ}} + \frac{K_{mQ}K'_{eQ}ab}{K_{eQ}^2K_{mP}} + \frac{K_{mA}bq}{K_{eA}K_{mB}K_{eQ}} \right) I_4$$

and

$$K_{eP} = \frac{K_{eq,cits}^0 K_{eA} K_{eB}}{K_{eQ}}$$

The rate constant k_{43} is assumed to depend on pH according to the formula $k_{43} = (h/10^{-7})^2 k'_{43}$ where k'_{43} is independent of pH. Therefore the kinetic constant K_{mP} is defined to depend on pH as

$$K_{mP} = \left(\frac{10^{-7}}{h} \right)^2 K'_{mP}$$

The inhibition factors I_1 , I_2 , I_3 , and I_4 , are computed:

$$I_1 = I_3 = I_4 = 1$$

$$I_2 = 1 + \frac{[ATP^4]}{K_{iATP}} + \frac{[ADP^3]}{K_{iADP}} + \frac{[AMP^2]}{K_{iAMP}} + \frac{[SCOA^-]}{K_{iSCOA}}$$

simulating dead-end binding of adenine nucleotides and SCOA at state 2 of the catalytic cycle.

Parameter Values

Table 2: Kinetic Parameter Values for Citrate Synthase (some estimates not available)*

| Parameter | Rat kidney 28°C (based on data from [2]) | Rat liver 25°C (based on data from [3]) | Bovine heart 21°C (based on data from [4]) |
|--|--|---|--|
| V_{max} ($\mu\text{mol} \cdot \text{min}^{-1} \cdot \mu\text{g}^{-1}$) | 0.290 | --- | --- |
| K_{mA} (μM) | 5.79 | 1.33 | 1.00 |
| K_{mB} (μM) | 4.55 | 13.6 | 5.42 |
| K'_{mP} (μM) | 0.180 | --- | --- |
| K_{mQ} (mM) | 2.25 | --- | --- |
| K_{eA} (μM) | 3.09 | 1.96 | 1.50 |
| K_{eB} (mM) | 283 | --- | -- |
| K_{eQ} (mM) | 0.443 | --- | --- |
| K_{iATP} (mM) | --- | 0.215 | 0.357 |
| K_{iADP} (mM) | --- | 0.475 | --- |
| K_{iAMP} (mM) | --- | 1.97 | --- |
| K_{iSCOA} (μM) | --- | --- | 53.8 |
| K_{iH} (μM) | --- | 0.055 | --- |

* These parameter estimates have been adjusted from the values in the original publication to be consistent with the thermodynamic property data estimated in Li et al. [1]. All model fits shown in Figures 1-5 of this document reflect these updated values for the thermodynamic data and the kinetic parameters.

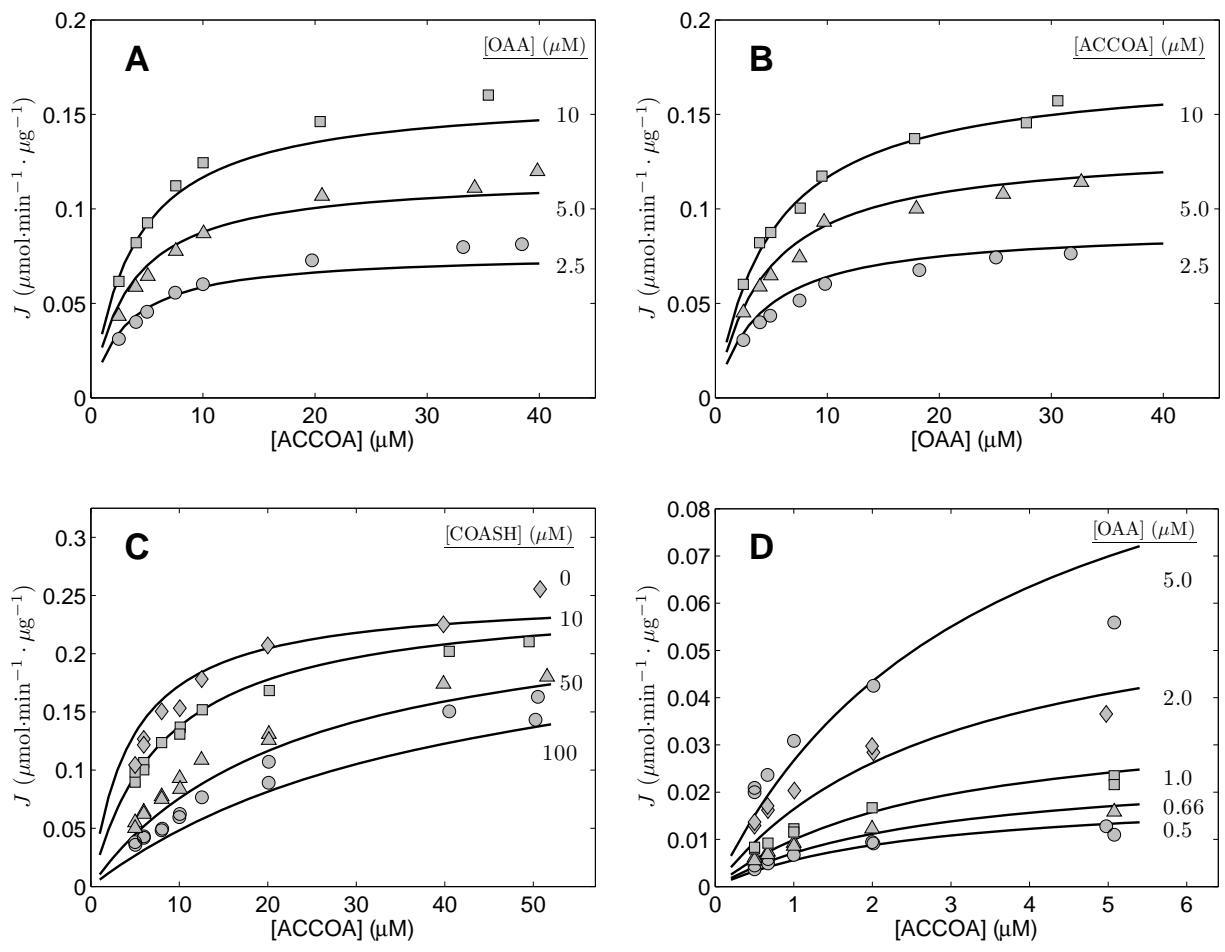


Figure 1: Fits to kinetic data from [3] on the forward operation of kidney enzyme. Measured flux as a function of substrate concentrations was obtained from Figures 2, 3, 6, 7, and 9 of [3]. Initial fluxes (μmol of COASH (or CIT) synthesized per minute per μg of enzyme) measured at the substrate concentrations indicated in the figures. For **A**, **B**, and **D**, the initial product (CIT and COASH) concentrations are zero. **C**. Flux measured with COASH added in various concentrations to investigate the kinetics of product inhibition. All data were obtained at $\text{pH} = 8.1$ at 28°C . Model fits are plotted as solid lines.

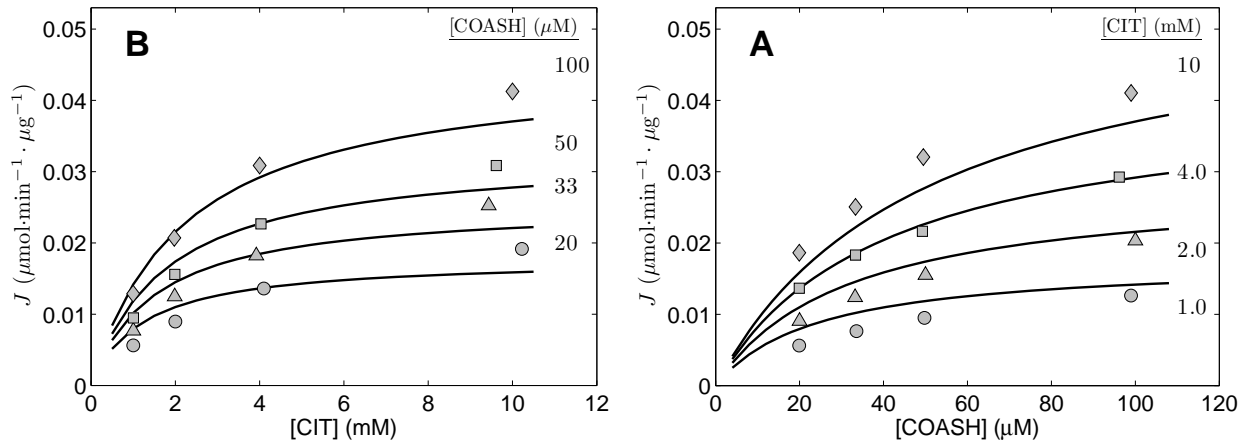


Figure 2: Fits to kinetic data from [3] on the reverse operation of kidney enzyme. Measured reverse flux as a function of concentrations of CIT and COASH was obtained from Figures 4 and 5 of [3]. Initial fluxes (μmol of COASH (or CIT) synthesized per minute per μg of enzyme) measured at the substrate concentrations indicated in the figures. All data were obtained at $\text{pH} = 8.1$ at 28°C . Model fits are plotted as solid lines.

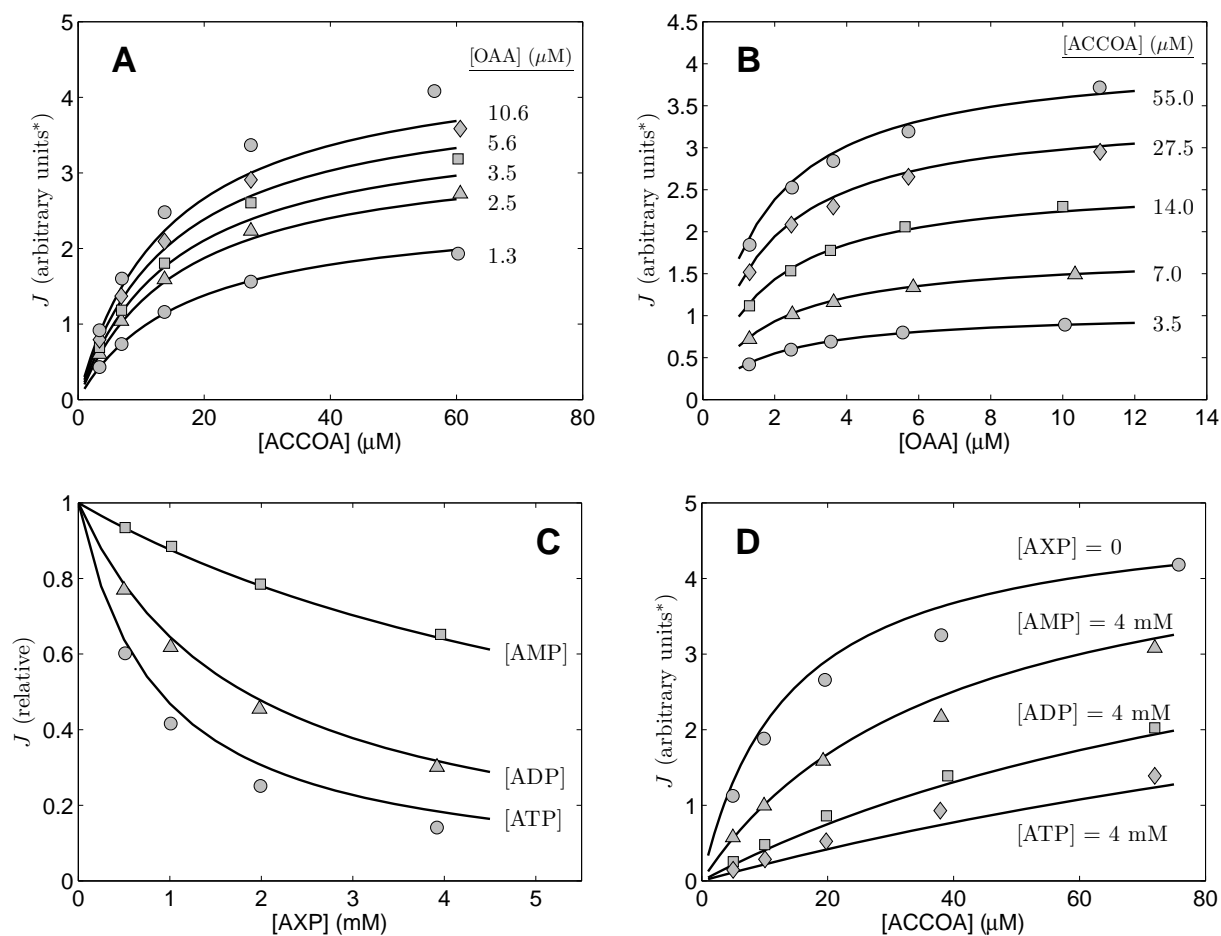


Figure 3: Fits to kinetic data from [4] on the forward operation of liver enzyme. Measured flux in arbitrary units was obtained from Figures 1,2,5, and 6 of [4]. For all cases the product (CIT and COASH) concentrations are zero and total substrate and inhibitor concentrations are indicated in the figure. **A** and **B** report data obtained with no inhibitors present. **C.** The relative activity (normalized to its maximum) of the enzyme is plotted as functions of [ATP], [ADP], and [AMP] measured at [ACCOA] = 11 μM and [OAA] = 1.9 μM . **D.** The measured flux is plotted as a function of [ACCOA] at [OAA] = 34 μM with ATP, ADP, and AMP present as indicated in the figure. All data were obtained at pH = 7.4 at 25° C. Model fits are plotted as solid lines.

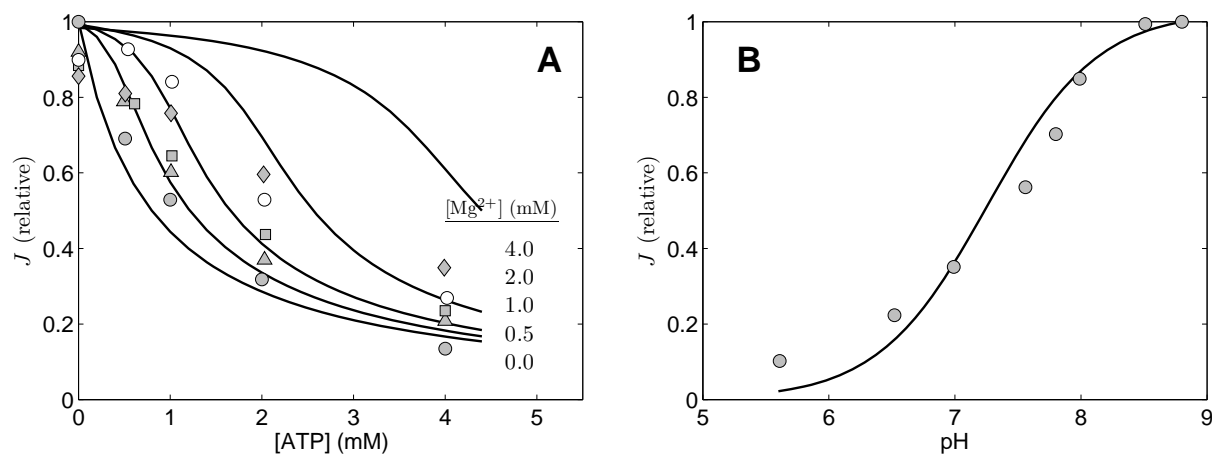


Figure 4: Impact of $[Mg^{2+}]$ and pH on liver enzyme. Measured flux in arbitrary units was obtained from Figures 13 and 14 of [4]. **A.** The relative activity (normalized to its maximum) of the enzyme is plotted as functions of [ATP] at $[Mg^{2+}] = 0$ mM (shaded circles), 0.5 mM (shaded triangles), 1.0 mM (shaded squares), 2.0 mM (open circles), and 4.0 mM (diamonds). **B.** Relative activity is plotted as a function of pH. Substrate concentrations are $[ACCOA] = 21 \mu\text{M}$ and $[OAA] = 8.6 \mu\text{M}$. All data were obtained at 25°C . pH is fixed at 7.4 for **A**. Model fits are plotted as solid lines.

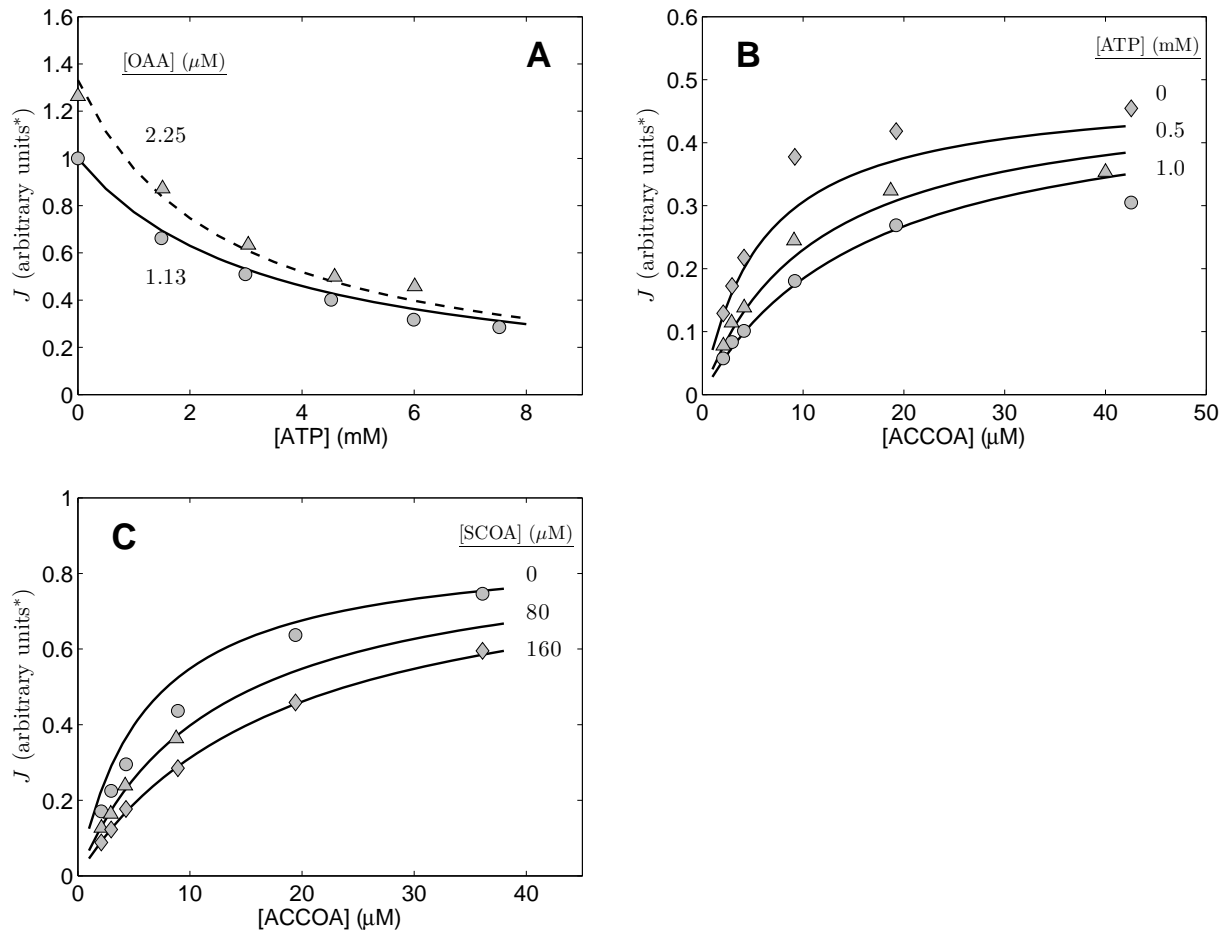


Figure 5: Inhibition of cardiac enzyme. Measured flux in arbitrary units was obtained from Figures 1 and 2 of [5]. **A.** Flux is plotted as a function inhibitor ATP concentration for $[\text{ACCOA}] = 16 \mu\text{M}$ and $[\text{OAA}] = 1.13$ and $2.25 \mu\text{M}$. **B.** Flux is plotted as a function of $[\text{ACCOA}]$ at $[\text{OAA}] = 5 \mu\text{M}$ at three different concentrations of ATP indicated in figure. **C.** Flux is plotted as a function of $[\text{ACCOA}]$ at $[\text{OAA}] = 3.1 \mu\text{M}$ at three different concentrations of SCOA indicated in figure. All data were obtained at $\text{pH} = 7.4$ at 21°C . Model fits are plotted as solid lines.

References

1. Li, X., et al., *A database of thermodynamic quantities for the reactions of glycolysis and the tricarboxylic acid cycle*. J. Phys. Chem. B, 2010(in press).
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