Supporting Information

Crystal Structures of *Trypanosoma cruzi* UDP-Galactopyranose Mutase Implicate Flexibility of the Histidine Loop in Enzyme Activation

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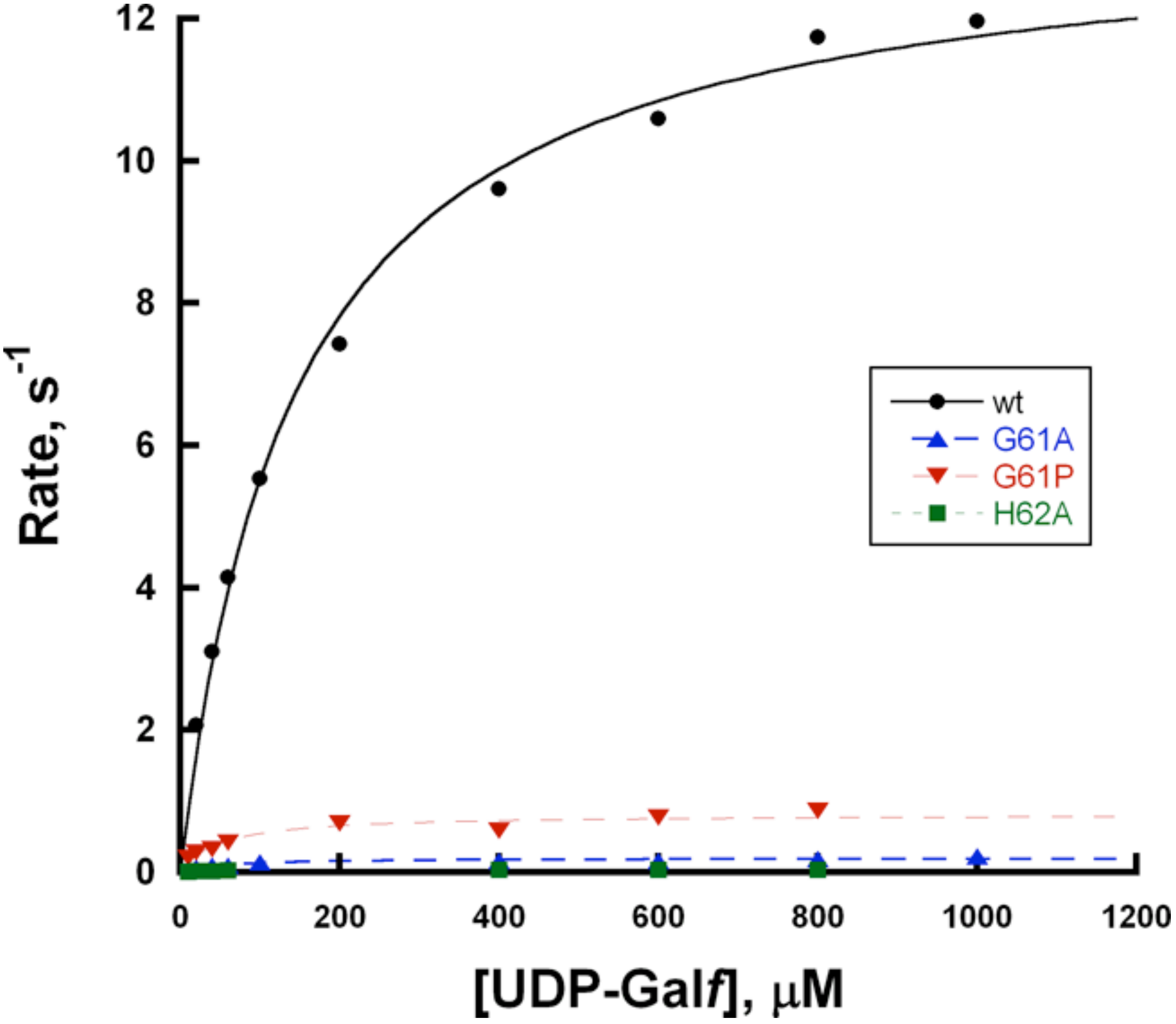

Figure S1. Steady-state kinetic characterization of TcUGM and the TcUGM histidine loop mutants G61A, G61P, and H62A. The activity was determined by monitoring the formation UDP-Gal*p* from UDP-Gal*f*. The data were fit to the Michaelis-Menten equation.

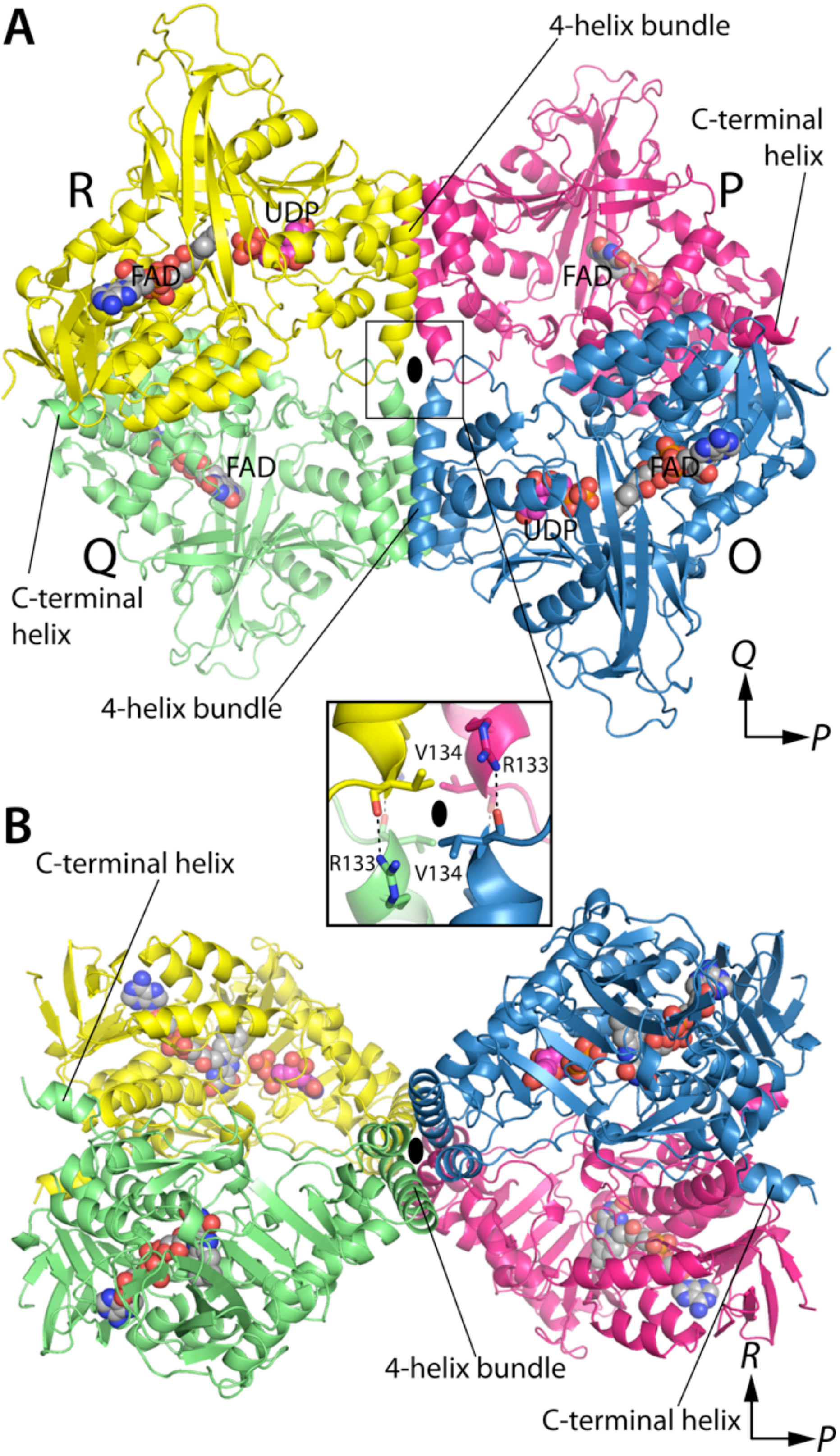

Figure S2. Structure of the AfUGM tetramer. (A) The tetramer is viewed down the *R* molecular 2-fold axis. Each chain has a different color. Inset: Intersubunit hydrogen bonds formed by Arg133 at the intersection of molecular 2-fold axes. (B) The tetramer is viewed down the Q-axis.