

Supplementary Information for

Kinetic Evidence for Inter-Domain Communication in the Allosteric Regulation of α -
Isopropylmalate Synthase from *M. tuberculosis*.

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Table S1. Ultracentrifugation Results for Wild-Type and Mutant IPMS

Protein	$S_{20,w}$
Dimer (HydroPro)	7.9 S^a
Monomer (HydroPro)	4.3 S^a
Wild type	8.5 S
Wild type + Leucine	8.2 S
E218A IPMS	7.5 S
E218A + Leucine	7.7 S
H379A IPMS	8.6 S
H379A + Leucine	8.1 S
Y410F IPMS	8.7 S
Y410F + Leucine	9.2 S

^avalues were calculated in Hydropro (Garcia De La Torre, J., Huertas, M. L., and Carrasco, B. (2000) Calculation of hydrodynamic properties of globular proteins from their atomic-level structure, *Biophys J* 78, 719-730.) using the coordinates of PDB file 1SR9

Supplemental Figure Legends

Figure S1. ClustalW was used to align the amino acid sequence of α -IPMS enzymes from eubacteria (*E. coli*, *S. aureus*, *S. enteric* serovar *typhimurium*, *M. tuberculosis*, *C. glutamicum*, *H. influenza*, and *R. eutropha*), archaea (*S. solfataricus* and *A. fulgidus*), plants (*A. thaliana*), and fungi (*S. cerevisiae* and *N. crassa*). Residues colored red are strictly conserved and residues colored blue are strongly similar in at least 90% of the sequences (*i.e.* only one outlier)

Figure S2. Eadie-Hofstee plot of wild-type, E218A, and H379A IPMS. The Eadie-Hofstee plot ($v/[\alpha\text{-KIV}]$ vs. v) is superior to the Lineweaver-Burk plot for ensuring that curvature in initial velocity replots is real (and not due to a one or two bad points) because the data are evenly weighted relative to the Lineweaver-Burk plot.

Figure S3. $^1\text{H-NMR}$ analysis of the reaction of Y410F IPMS. The initial spectrum (upper) was taken prior to addition of enzyme. A second spectrum was taken after the reaction had reached completion (lower spectrum).

Figure S2.

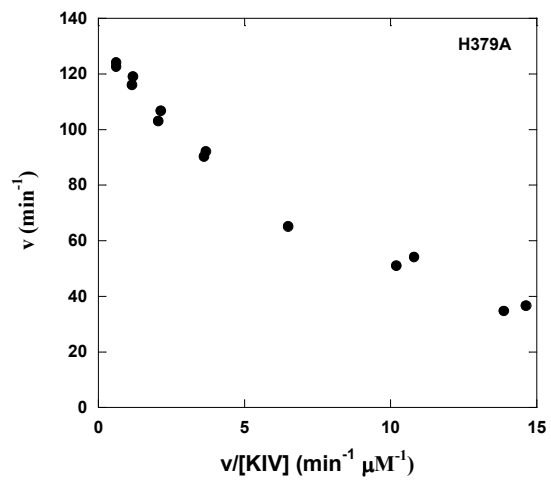
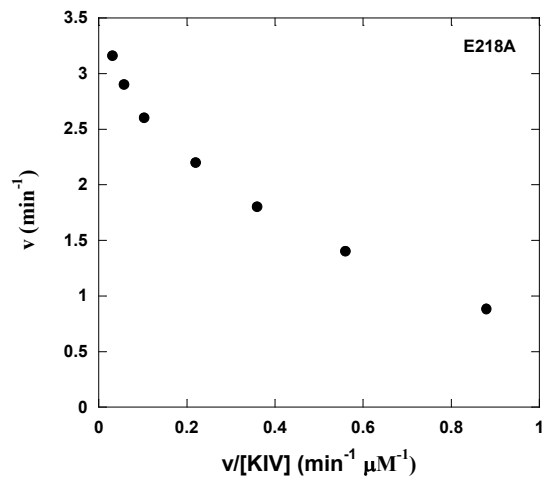
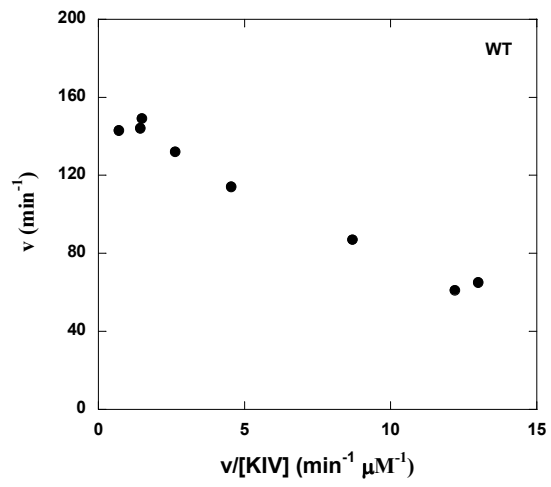


Figure S3.

