

Effects of a Buried Cysteine-To-Serine Mutation on Yeast Triosephosphate Isomerase Structure and Stability

Supplementary Information

Figure S1. Structural superposition of triosephosphate isomerases from *Plasmodium falciparum*. (A) Wild-type enzyme without ligand (1YDV, light blue), wild type enzyme with ligand (2VFI, dark blue), C126S mutant with ligand (3PVF, gold) and C126S mutant without ligand (3PY2, green); (B) Close-up view of the monomer A that shows the main differences between them.

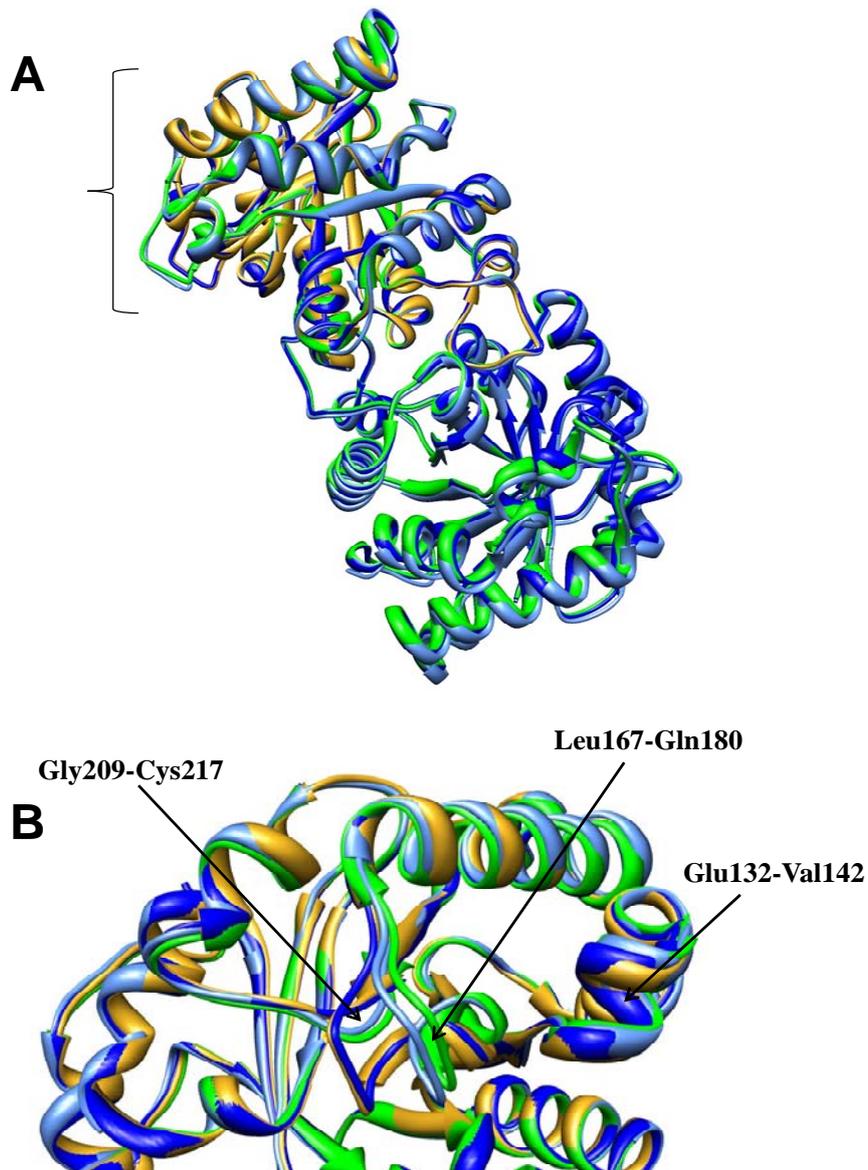
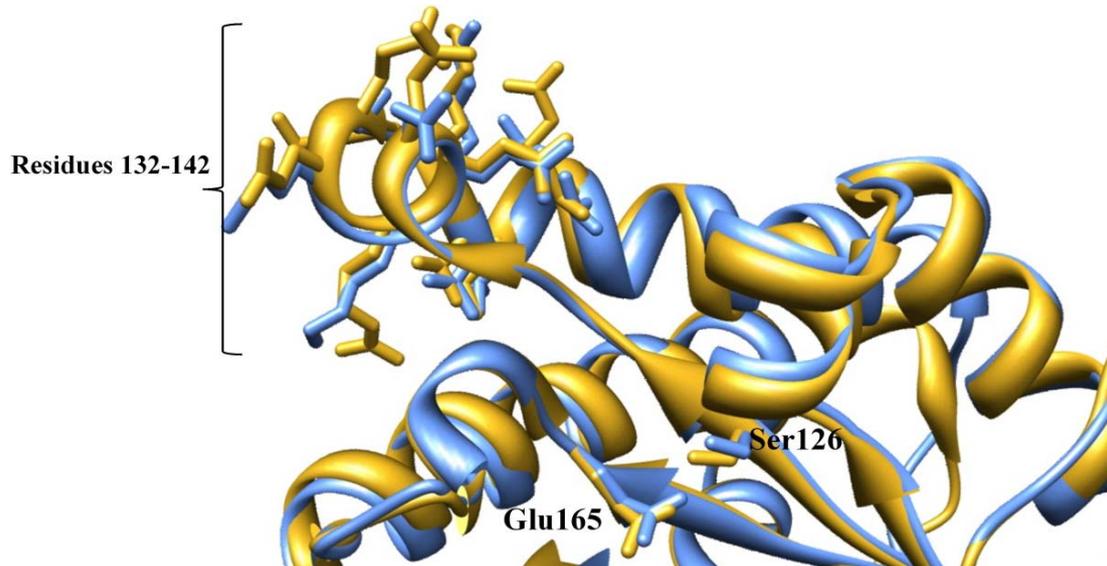


Figure S2. Superposition of the region containing the mutation C126S in the triosephosphate isomerases from *Saccharomyces cerevisiae* (light blue) and *Plasmodium falciparum* (gold). The orientation of Ser126 is the same in both structures. Side chains for residues in the 132–142 region are shown in both structures.



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