

Supporting Information

Mapping the Intramolecular Communications Among Different Glutamate Dehydrogenase States using Molecular Dynamics

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Supplementary Figure 1

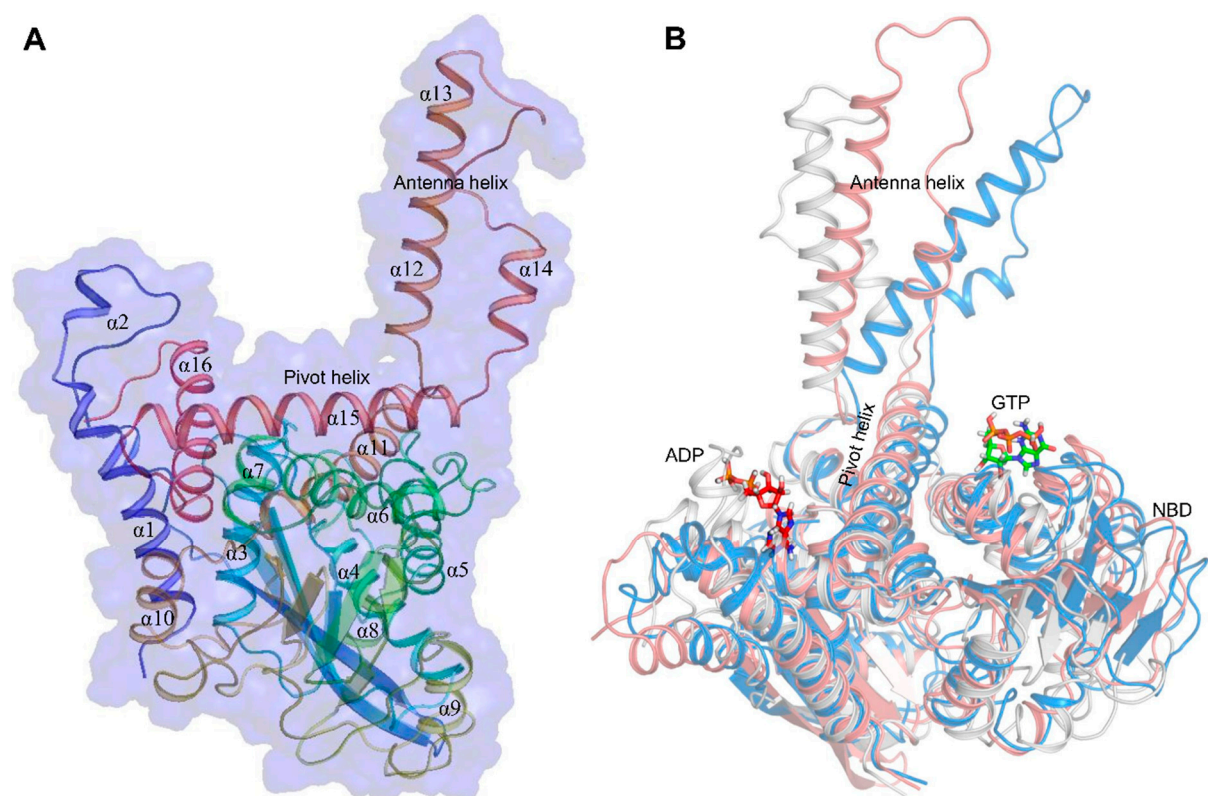


Figure S1. Structural architecture and superposition of GDH monomer structure. (A) Sixteen α -helices including intermediate, elongated, antenna, and pivot helices, and conserved nucleotide-binding domain (NBD) is shown. (B) The minimum energy structures of GDH in the apo, agonist- and antagonist-bound forms are superimposed to show that the most significant differences among the three forms is in the ligand binding regions, NBD, intermediate helix ($\alpha 6$), elongated helix ($\alpha 11$), antenna helices, and pivot helix.