

Role of conserved Arginine in GH70 family: A Computational study on the Structural Features and its Implications on the Catalytic Mechanism of GTF-SI from *Streptococcus mutans*

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Supporting Information

1. Root Means Square Displacements (RMSD) from MD simulations.....p.1
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3. QM/MM scan along the reaction coordinate defined as $RC = d(C1 - O_G) - d(C1 - OD1) - d(HE2 - O_G)$p.2
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Figure S1. Root Means Square Displacements (RMSD) of the MD simulations carried out.

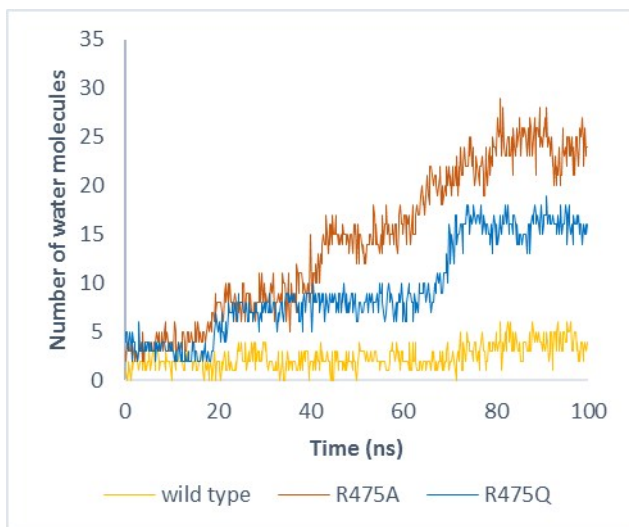


Figure S2. Average of water molecules in the active site along of MD simulations

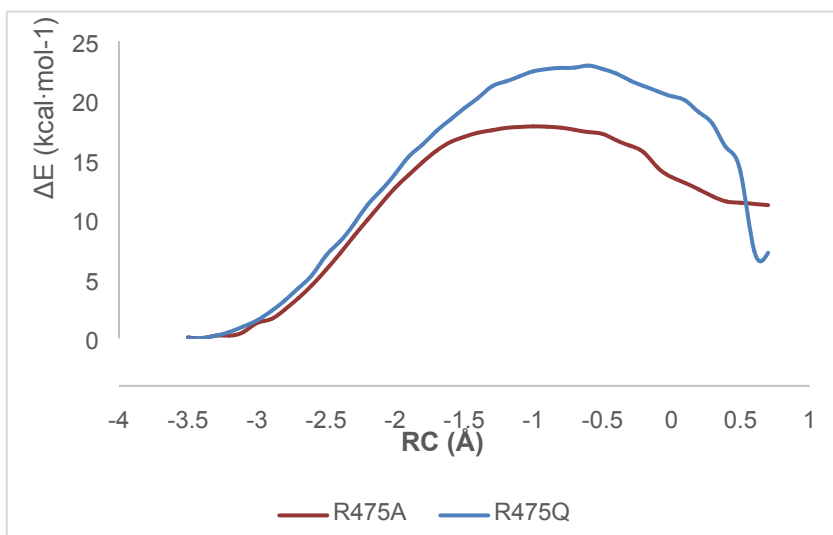


Figure S3. QM/MM scan along the reaction coordinate defined as $RC = d(C1 - O_G) - d(C1 - OD1) - d(HE2 - O_G)$.

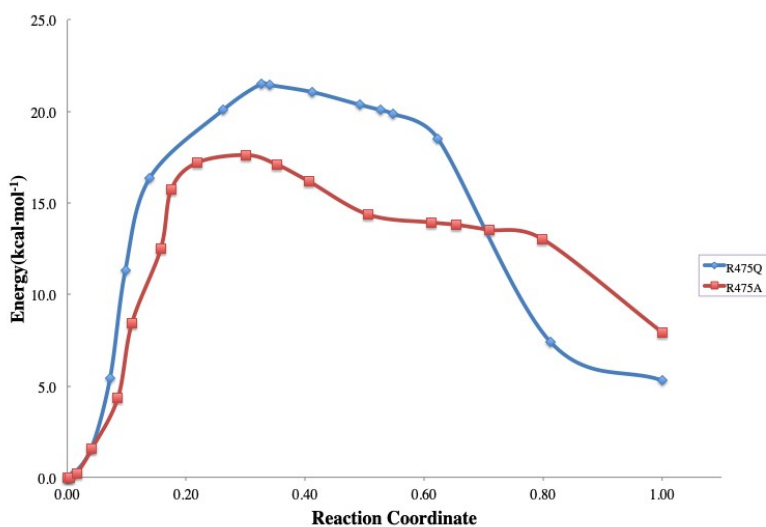


Figure S4. Minimum energy path (MEP) for the formation of CGE. The energy values are relative to the energy of the reactant and were obtained at BP86/6-31G(d) level of theory. The reaction coordinate is based on the structural difference between points along the CPR trajectory and the reactant structure. It was normalized between 0 for the reactant and 1 for the product.