Molecular Dynamic Employment Regarding the Broad Specificity of D-Arginine Dehydrogenase with D-Amino Acids

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Enzymes are ubiquitous in biological systems. They catalyze chemical reactions and are involved in many biochemical processes. The enzyme of interest is D-Arginine dehydrogenase (DADH). This enzyme is a relatively medium sized complex consisting of approximately 180 residues and a proposed catalytic site that has a high binding affinity for D-Arginine. DADH catalyzes the oxidation of D-amino acids into their corresponding imino acids by removing the main chain α-hydride and carboxyl proton using flavin adenine dinucleotide (FAD) as its cofactor. Following the redox reaction with FAD, the imino acid can either be hydrolyzed within the active site or after being released from the enzyme. Many enzymes have distinct specificity for their relative substrates. However, DADH has a broad specificity for D-amino acids, and the reason being is quite ambiguous. The difference in catalytic efficiencies between D-amino acids with DADH proposed an alteration in their corresponding binding energies. Molecular dynamics methods was applied to compare physical traits and properties of all the binding substrates, which included bond energies, partial charges, center of mass, entropy, and distance of residues inside the complex. Coupled with the previous knowledge from enzyme kinetics, more insights regarding extensive DADH/substrate behavior will be provided.