Theoretical study of acceptance features of adenosine and its aza-, carba- and deoxyanalogues in active site of adenosine deaminase

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Abstract

Conformational models of enzyme-ligand complexes of adenosine deaminase with adenosine and it aza-, carba- and deoxyanalogues appling methods of docking and molecular mechanical optimization are constructed. Optimization conformational energy of enzyme-ligand complexes was made using molecular mechanics of MM3 force field. Features of adenosine deaminase acception of molecules of adenosine and its analogues in N- and S-areas of pseudorotation of furanose cycle are considered. Interrelations between structure of enzyme-ligand complexes and biochemical properties of ligands in the relation adenosine deaminase are established.