COMPUTATIONAL MODELING OF ACTIVITIES OF PROTEASES AND THEIR SYNTHETIC ANALOGUES

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The selective hydrolysis of the extremely stable peptide or amide bond of peptides and proteins by proteases is required in a wide range of biological, biotechnological and industrial applications. We have applied innovative theoretical techniques including molecular dynamic (MD) simulations, quantum mechanics (QM/MM) and quantum mechanics/molecular mechanics (QM/MM) to elucidate the mechanisms of enzymes and their synthetic analogues. In the first step, we have investigated the roles of active sites, second coordination shell residues and protein environment in the catalytic functioning of natural enzymes. In the next step, the knowledge of the mechanisms of existing synthetic analogues of proteases will be combined with the information acquired in the first step to design more efficient synthetic analogues in collaboration with experimentalists. The information provided by our theoretical studies cannot be readily obtained through existing experimental techniques.