MS07-P11 | Differences In Crystallization Of Several Selected Haloalkane Dehalogenases And Their Mutation Variants

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Knowledge of the structure of proteins is a key in identifying and describing the detailed mechanism of biological processes, the development of therapeutics, the degradation of pollutants from the environment, etc. One of the methods used to determine the structure of proteins on atomic resolution is X-ray crystallography. For many years, our laboratory has been researching structures of different types and mutant variants of haloalkane dehalogenases (HLDs) that are responsible for one of the key reactions in the bacterial degradation of various halogenated pollutants - environmentally unfriend compounds. HLDs can be potentially applying in bioremediation, biosensing of pollution, biosynthesis, cellular imaging and protein immobilization. These enzymes catalyze the cleavage of a carbon-halogen bond in haloalkanes with water as the sole co-substrate, resulting in formation of a halide ion, a corresponding alcohol, and a proton. To date, several tertiary structures of different HLDs enzymes have been solving by X-ray diffraction analysis, providing a good theoretical framework for their modification by protein engineering. Crystallization conditions for haloalkane dehalogenases such as DhaA from *Rhodococcus rhodochrous* NCIMB 13064, LinB from *Sphingobium japonicum* UT26, and DbeA from *Bradyrhizobium elkanii* USDA94 and their mutant variants were comparing and analyzing. Based on carefully designed experiments and by combination of the information obtained from complementary techniques it was possible to get inside into conformational changes of selected enzymes upon their interactions with substrates as well as location of hydrogen atoms inside the enzyme active site and the access tunnels.

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