Crystallographic analysis of beta-ketoadipyl-coa thiolase from psedomonas putida

Sukritee Bhaskar1, Santosh Panjikar2, Ruchi Anand3

1Chemistry IITB-Monash Research Academy, Mumbai, India, 2Department of Biochemistry and Molecular Biology, Monash University, Australian Synchrotron, Clayton, Australia, 3Department of Chemistry, Indian Institute of Technology Bombay, Mumbai, India

E-mail: bhaskarsukritee@gmail.com

Beta-ketoadipyl-CoA thiolase (EC 2.3.1.9) from Pseudomonas Putida is a common enzyme for both protocatechuate and catechol branches of the beta-keto adipate pathway. The enzyme catalyzes thiolytic cleavage of beta-ketoadipyl-CoA to succinyl-CoA and acetyl-CoA. The degradative thiolase (Thiolase-I) process the long acyl chain ranging from 4 to 22 carbons while the biosynthetic thiolase (Thiolase-II) prefer short acyl chain up to 4 carbon atoms. Both classes of thiolase possess similar architecture of active site residues and mode of mechanism. A number of inactive mutants of the degradative thiolase has been co-crystallised with various substrates such as acetoacetyl CoA, Butryl CoA, higher fatty acid chain ketoacyl CoA and the ligand–complex structures have been determined. We will be presenting the analyzed data along with the thiolase assays to show the determinant of degradative and biosynthetic thiolase


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