

## Poster Presentation

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### *Crystallographic analysis of beta-ketoadipyl-coa thiolase from pseudomonas putida*

Sukritee Bhaskar<sup>1</sup>, Santosh Panjikar<sup>2</sup>, Ruchi Anand<sup>3</sup>

<sup>1</sup>Chemistry IITB-Monash Research Academy, Mumbai, India, <sup>2</sup>Department of Biochemistry and Molecular Biology, Monash University, Australian Synchrotron, Clayton, Australia, <sup>3</sup>Department 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

[1] Thompson. S. et.al (1989) *Biochemistry* 14, 5735–42.

[2] Modis. Y. et.al. (1999) *Structure* 7 (10), 1279–90

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