Poster Presentation

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Structural studies on dehydroshikimate dehydratase

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The soil bacterium, Pseudomonas putida, is capable of using the alicyclic compound quinate as a sole carbon source. During this process, quinate is converted to 3-dehydroshikimate, which subsequently undergoes a dehydration to form protocatechuate. The latter transformation is performed by the enzyme dehydroshikimate dehydratase (DSD). We have recombinantly produced DSD from P. putida and are currently performing x-ray crystallographic studies on the enzyme to gain structural insight into its catalytic mechanism and mode of substrate recognition. Initial crystals of DSD diffracted to 2.7 Ä resolution, but exhibited strong twinning. A redesigned construct has recently yielded crystals that diffract to similar resolution, but with a significantly reduced tendency toward twinning. Interestingly, sequence analysis of P. putida DSD reveals that the protein is in fact a fusion of two distinct domains: an N-terminal sugar phosphate isomerase-like domain associated with DSD activity, and a C-terminal hydroxyphenylpyruvate dioxygenase (HPPD)-like domain with unknown functional significance. Structural characterization of the protein may provide novel insight into the functional relevance of the unusual HPPD-like domain.

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