

A novel dehalogenase structure determined by a new approach to Synchrotron data collection.

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Halo acid dehalogenases are enzymes that degrade short-chained organic acids with bound halide substituents, through cleavage of the carbon-halogen bond. They are common in microbial species and have been classified into two distinct evolutionary lineages. Group II dehalogenases have been well studied both biochemically and structurally, with four structures published, including one by this author. The group has a rossmanoid core domain, have specificity for the L-enantiomers of substrate molecules, and belong to the mechanistically diverse HAD superfamily of enzymes. Less attention has been paid to group I dehalogenases, and no structural information of this functionally interesting group of enzymes is yet available. What is interesting from a mechanistic point of view though is this groups' specificity for D-enantiomers, unlike the group II enzymes. We report the first structure of a group I dehalogenase, determined from MAD data collected on the Stanford Synchrotron in the USA via remote access system (Blue Ice), Stanford Synchrotron Radiation Laboratory (SSRL).