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Crystal Structures of two 4-OT Homologues from *Helicobacter pylori* and *Archaeoglobus fulgidus*. Rakhi Dasgupta, Jeffrey Almrud, William Johnson, Chris Whitman, Marvin Hackert, Chemistry & Biochemistry, Univ. of Texas at Austin, 1 University Station A5300, Austin, TX 78712 USA.

The tautomerase superfamily is represented by 4-oxalocrotonate tautomerase (4-OT), 5-(carboxymethyl)-2-hydroxymuconate isomerase and macrophage migration inhibitory factor. 4-OT and most of its homologues are hexameric while the other two are trimeric. The members of this family share two distinguishing features - a β - α - β structural motif and a catalytically important N-terminal Pro residue.

Several new members of the 4-OT family have been identified and categorized into five subfamilies. Crystal structures of a representative member from each group have been solved. Here the structures of two 4-OT homologues from *H. pylori* (*Helicobacter pylori*) and *Arc. fu.* (*Archaeoglobus fulgidus*), belonging to two different subfamilies, will be discussed with reference to other subfamily structures. *H. pylori* and *Arc. fu.* share 34 and 17 % sequence identity with 4-OT from *P. putida* and conserve the β - α - β fold of their monomers and the overall hexameric state of 4-OT. However there are differences in the loop regions connecting the β -sheets and α -helices and striking differences in the architecture and charge characteristics of residues constituting the active sites compared to 4-OT from *P. putida*.