of 2.97 Å^3/Da and a solvent content of 59%. The crystal structure has been determined by molecular replacement. The current model was refined at 2.6 Å resolution to an *R*-factor of 23.8% (R_{free} = 31.6%).

In crystals, LsAspR adopts a homodimeric form. The subunit consists of two domains: the N-terminal domain (residues 1-104 and 216-234) and the C-terminal domain (residues 105-215). In each domain, a central four-stranded parallel β-sheet is flanked by six α-helices. The spatial arrangement of the strictly conserved residues Cys84 and Cys196 strongly indicates that the active site of LsAspR must be located in the cleft between the two domains.

Keywords: racemase, aspartate racemase, crystal structure

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Insights into the fumarase reaction mechanism from crystal structures of Rv1098c

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Fumarase (fumarate hydratase: EC 4.2.1.2) catalyzes the reversible conversion of L-malate to fumarate and H_2O during the TCA cycle. In Mycobacteria tuberculosis, this reaction is catalyzed by the essential enzyme Rv1098c encoded by the fum gene [1, 2].

Rv1098c belongs to a superfamily of enzymes that catalyze reactions involving fumarate molecules. This superfamily not only includes fumarases but also L-aspartases, δ-crystalline, 3-carboxy-cis,cis-muconate lactonizing enzymes, arginino-succinatases as members. Despite a low sequence identity (~25%), the crystal structures of several members of this superfamily revealed a conserved overall fold.

We determine the crystal structures of Rv1098c in its apo form as well as its complexes with the competitive inhibitor meso-tartrate and the substrate/product malate. These structures reveal that ligand binding promotes conformational changes at the enzyme C-terminal domain that close the active site. Inspection of the active site clefts allowed us to propose a catalytic mechanism through a detailed description of the interactions between substrate and catalytic residues.

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Cap architecture conservation in monoglyceride lipases from bacteria to humans

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Monoglyceride lipases (MGL) catalyze the hydrolysis of monoglycerides into free fatty acid and glycerol. MGL have been identified in all kingdoms of life and have adopted different substrate specificities with respect to chain lengths, depending on their different roles in the host organisms. In humans, MGL play an integral part in lipid metabolism affecting energy homeostasis and signaling processes. It also hydrolyzes the endocannabinoid 2-arachidonoylglycerol, which regulates a range of physiological processes (e.g. pain sensation). In bacteria, especially short chain monoglycerides are highly toxic. Thus, MGL is crucial for the survival of the bacteria. Despite the biological, pharmacological and biotechnological interest in MGL, the 3D structure of human MGL was the first member of this enzyme family to be solved in 2010. We report the first crystal structures of MGL from a bacterial species (Bacillus sp. H257) in its free form at 1.2Å and covalently complexed to phenylmethanesulfonyl fluoride at 1.8Å resolution, molecular dynamics simulation of bacterial MGL (bMGL, 250 aa) and a comprehensive comparison of the resulting structural insights with the human homolog (303 aa): The core structure is composed of an α/β hydrolase fold. A cap region, which is often observed in α/β hydrolase, is inserted between α4 and β5 elements of the core structure. An ~22Å long tunnel leads from the surface of bMGL to the catalytic triad and thus keeps the active center unexposed to the polar environment. The rim at the entrance to the tunnel has a diameter that is ~12Å wide and is lined with hydrophobic side chains mostly from the cap domain. A hole is located in the cap region of the protein and corresponds to the proposed exit hole for glycerol to leave the active site in human MGL. Molecular dynamics simulation shows open and closed states of the entrance tunnel and the glycerol exit hole.

No electron density was observed for a stretch of 3 aa in the cap region. In human MGL, a corresponding region was also found to be highly flexible and was not visible in one chain of the dimeric structure. Comparison of the cap regions of hMGL and bMGL shows intriguing similarities, despite a sequence identity of only 10%. The 62-amino acid cap of hMGL has been described as U-shaped and comprises of three helices connected by loop regions. The 45-amino acid cap of bMGL harbors a short helical turn and a short two-stranded antiparallel β-sheet connected by linkers. It is very interesting that despite these differences in length and secondary structure composition, the overall shape and arrangement of the cap region of both the proteins superimposes almost precisely in the observed open conformation. It can be speculated that this specific lid architecture is conserved throughout evolution of MGLs.

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A hybrid multifunctional antioxidant system: peroxiredoxin nitroreductase enzyme

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A natural fusion occurring between a peroxiredoxin (Prx) and a nitroreductase (Ntr) motif has been identified in *Thermotoga maritima*. The corresponding protein TmPrxNtr, the mutant TmPrxNtrC40S and its separate modules (TmPrx, TmNtr) have been overexpressed in *Escherichia coli,* then purified and their catalytic activity studied. TmPrxNtr and TmPrxNtrC40S display similar circular dichroism spectra showing that the mutation of cysteine 40 into serine does not