OsmC (Osmotically inducible protein) from Escherichia coli has a preference for aromatic peroxides according to docking and kinetic experiments

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Detoxification of organic peroxides appears to be important for bacterial survival and proliferation in the host. OsmC (Osmotically inducible protein) belongs to the Ohr/OsmC family of proteins. It was shown that these enzymes share a common structural fold and also metabolizes organic hydroperoxides preferentially over $\mathrm{H}_{2} \mathrm{O}_{2}$ using a highly reactive cysteine thiolate group. In order to further characterize these differences, enzymatic assays and docking experiments were performed. Our docking results showed that OsmC active site does not accommodate very well peroxides derived from long chain fatty acids such as oleic, linoleic acid or tert-butyl-hydroperoxide (t-BHP). In fact, OsmC presented a catalytic efficiency for cumene hydroperoxide (CHP) at least 10 fold higher than $t$-BHP $\left(10^{4} \mathrm{M}^{-1} \mathrm{~s}^{-1}\right.$ and $10^{3} \mathrm{M}^{-1} \mathrm{~s}^{-1}$ respectively). These values are clearly correlated with the affinity for the activity site because OsmC has a Km value lower for CHP than for $t$-BHP. The catalytic efficiency for $\mathrm{H}_{2} \mathrm{O}_{2}$ are too small ( $10^{1}-10^{2} \mathrm{M}^{-1} \mathrm{~s}^{-1}$ ) with a Km value higher than 100 mM indicating that OsmC was not capable to reduce this peroxide in vivo. It was shown that an aromatic residue (phenylalanine) from the uncleaved $\mathrm{His}_{6}$-tag was bound to the entrance of the active-site pocket in an OsmC structure (Shin et al, 2004). These results together indicate that OsmC has a preference for peroxides with an aromatic group.

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