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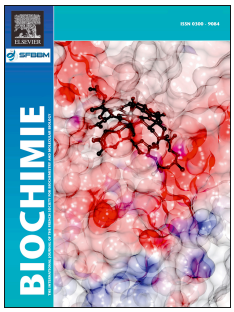

Structure of the monotopic membrane protein (S)-mandelate dehydrogenase at 2.2Å resolution

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The x-ray structure of the monotopic membrane protein (S)-mandelate dehydrogenase (MDH) from *Pseudomonas putida* reveals an inherent flexibility of its membrane binding segment that might be important for its biological activity. The surface of MDH exhibits a concentration of the positive charges on one side and the negative charges on the other side. The putative membrane binding surface of MDH has a concentric circular ridge, formed by positively charged residues, which projects away from the protein surface by ~4Å; this is unique structural feature and not observed in other monotopic membrane proteins to our knowledge. There are three α-helixes in the membrane binding region. Based on the structure of MDH, it is possible to propose that the interaction of MDH with the membrane is stabilized by coplanar electrostatic interactions, between the positively charged concentric circular ridge and the negatively charged head-groups of the phospholipid bilayer, along with three α-helixes that provide additional stability by inserting into the membrane. The structure reveals the possible orientation of these helixes along with possible role for the individual residues which form those helixes. These α-helixes may play a role in the enzyme's mobility. The detergent, N-Dodecyl-β-maltoside, is inserted between the membrane binding region and rest of the molecule and may provide structural stability to intra-protein regions by forming hydrogen bonds and close contacts. From the average B-factor of the MDH structure, it is likely that MDH is highly mobile, which might be essential for its intersection in membrane and non-membrane environments, as its substrate (S)-mandelate, is from the cytoplasm, while its electron acceptor is a component of the membrane electron transport chain.