

# Accepted Manuscript

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

N. Sukumar, S. Liu, W. Li, F.S. Mathews, B. Mitra, P. Kandavelu



PII: S0300-9084(18)30212-8

DOI: [10.1016/j.biochi.2018.07.017](https://doi.org/10.1016/j.biochi.2018.07.017)

Reference: BIOCHI 5480

To appear in: *Biochimie*

Received Date: 16 January 2018

Accepted Date: 27 July 2018

Please cite this article as: N. Sukumar, S. Liu, W. Li, F.S. Mathews, B. Mitra, P. Kandavelu, Structure of the monotopic membrane protein (S)-mandelate dehydrogenase at 2.2Å resolution, *Biochimie* (2018), doi: 10.1016/j.biochi.2018.07.017.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

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  $\sim 4\text{\AA}$ ; this is unique structural feature and not observed in other monotopic membrane proteins to our knowledge. There are three  $\alpha$ -helices 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  $\alpha$ -helices that provide additional stability by inserting into the membrane. The structure reveals the possible orientation of these helices along with possible role for the individual residues which form those helices. These  $\alpha$ -helices may play a role in the enzyme's mobility. The detergent, N-Dodecyl- $\beta$ -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.

Download English Version:

<https://daneshyari.com/en/article/8304095>

Download Persian Version:

<https://daneshyari.com/article/8304095>

[Daneshyari.com](https://daneshyari.com)