Structural Analysis, Discrimination and Prediction of Membrane Spanning β-strands in Outer Membrane Proteins

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Prediction of membrane spanning β-strands in outer membrane proteins (OMPs) is one of the important problems in computational biology. In this work, we have systematically analyzed the characteristic features of amino acid residues in OMPs, and developed algorithms for discriminating OMPs and predicting their membrane spanning β-strands.

Structural analysis of outer membrane proteins

A conformational parameter set for the 20 amino acid residues in globular and OMPs has been developed from the ratio between the frequency of occurrence (%) of amino acid residues in the β-strand part of globular/OMPs and that of the whole protein. We found that all aromatic residues have the preference to be in β-strands of globular and OMPs. Isoleucine has the highest preference to be in the β-strand of globular proteins and an opposite trend is observed in OMPs[(1)].

We have delineated the inter-residue contacts in globular and OMPs based on the sequence and structural information. Residues that are close to each other in space and are distant in sequence are termed as long-range contacts[(2)]. We found that the positively charged residues are making significant contacts with other residues in the membrane.

Discrimination of outer membrane proteins

We have devised a simple, statistical method based on amino acid composition for discriminating OMPs from other folding types of globular and membrane proteins. Our method could correctly identify the OMPs and exclude globular/transmembrane helical proteins at an accuracy of 89% and 80%, respectively[(3)].

Prediction of membrane spanning β-strand segments

We have developed an algorithm based on neural networks for predicting the transmembrane β-strands in OMPs. We introduced the concept of "residue probability" for assigning residues in transmembrane β-strand segments. The performance of our method is evaluated with single residue accuracy, correlation, specificity and sensitivity. We observed a good agreement between predicted β-strand segments and experimental observations[(4)]. We have developed a web interface in which users can input the amino acid sequence and obtain the probable membrane spanning segments (Fig 1). It is available at http://psfs.cbrc.jp/tmbeta-net/ [(5)].

References

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(4) Gromiha, M.M., Ahmad, S., Suwa, M.: "Neural network based prediction of membrane spanning β-strands in outer membrane proteins", *J. Comp. Chem.*, **25**, pp.762-767 (2004).
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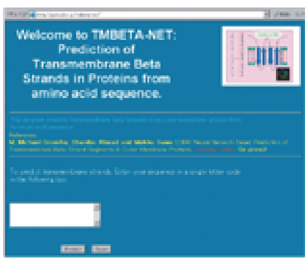

Fig.1

Top page image of **TMBETA-NET** web site (http://psfs.cbrc.jp/tmbeta-net/)

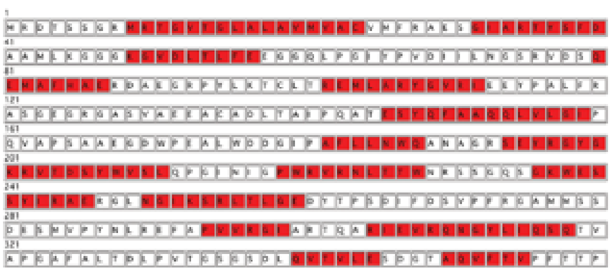

Fig.2

Online prediction of membrane spanning β-strand segments in outer membrane proteins. The predicted membrane spanning segments in the outer membrane protein is highlighted in red.