Comparative analysis of membrane protein structure databases

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Comparative analysis of membrane protein structure databases

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Abstract

Background

Membrane proteins play important roles in cell survival and cell communication, as they function as transporters, receptors, anchors and enzymes. They are also potential targets for drugs that block receptors or inhibit enzymes related to diseases. Although the number of known structures of membrane proteins is still small relative to the size of the proteome as a whole, many new membrane protein structures have been determined recently.

Scope of the article

We compared and analyzed the widely used membrane protein databases, mpstruc, Orientations of Proteins in Membranes(OPM), and PDBTM, as well as the extended dataset of mpstruc based on sequence similarity, the PDB structures whose classification field indicates that they are "membrane proteins" and the proteins with Structural Classification of Proteins (SCOP) class-f domains. We evaluated the relationships between these databases or datasets based on the overlap in their contents and the degree of consistency in the structural, topological, and functional classifications and in the trans-

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