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場所: 臨海副都心センター別館 8 階コラボレーションコーナー
講演者/発表者: Dmitrij Frishman (Technische Universitaet Muenchen, Germany)

タイトル
Exploring the fold space of membrane proteins

概要
Recent progress in structure determination techniques has led to a significant growth in the number of known membrane protein structures. The first structural genomics projects focusing on membrane proteins have been initiated, warranting an investigation of appropriate bioinformatics strategies for optimal structural target selection for these molecules. What determines a membrane protein fold? How many structures need to be solved to provide sufficient structural coverage of the membrane protein sequence space?
In my talk I will describe the CAMPS database (Computational Analysis of the Membrane Protein Space) that automatically classifies alpha-helical membrane proteins into fold classes. I will also present our latest results on predicting interacting helices in membrane proteins and deriving helix connectivity diagrams that represent a convenient level of abstraction for comparing predicted membrane protein structures. Finally, I will review the difficulties in classifying experimentally determined three-dimensional structures of membrane proteins, focusing on the difference between the SCOP and CATH databases.

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3. Neumann S., Fuchs A., Mulkidjanian A, and Frishman D. (2010) Current status of membrane protein structure classification. Proteins, 78, 1760-1773.

4. Fuchs, A., Kirschner, A., Frishman D. (2009) Prediction of helix-helix contacts and interacting helices in polytopic membrane proteins using neural networks. Proteins, 74, 857-71
5. Fuchs, A., Martin-Galiano, A.J., Kalman, M., Fleishman, S., Ben-Tal, S., and Frishman, D. (2007) Co-Evolving Residues in Membrane Proteins. Bioinformatics, 23, 3312-3319.
6. Martin-Galiano, A.J., Frishman, D. (2006) Defining the Fold Space of Membrane Proteins: the CAMPS Database. Proteins, 64, 906-22.