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Title:

From Photosynthesis via the Membrane Proteome Interactome to Structure Prediction and Design

המפגש יתקיים
ביום א', 1 מרץ 2015, בשעה 9:00
מועדון סגל
(3/1/2015, 9:00, Faculty Club)

Abstract:

The photosynthetic reaction center is the first structurally elucidated membrane protein. Today, a hundred membrane protein structures provide a representative dataset[1] suggesting thumb-rules governing the main target of medicine. Still, the photosynthetic apparatus is unique not only as it is responsible for harvesting light into biomass but also as it has spectroscopic pigments that report structure-function-dynamics relationships. Using structural bioinformatics and computational biophysics[2] along with biophysical and biochemical characterization I will describe the mechanism and (thermo-)stability governing the photosynthetic reaction center Q_A-Q_B rate determining step[3, 4]. Identified motifs such as kinks[5] and novel flexibility profiles explain the mechanism of other membrane proteins, e.g. the influenza M2 proton channel[6]. In the membrane proteome level such parameterization enables the prediction of membrane protein pseudo-energy topological landscapes[7] as well as characterization of the soluble- and membrane-proteome interactome[8]. Interestingly, while soluble- and membrane-proteins share similar helix-helix geometries, while the former interactome is governed by hydrophobic residues, the latter are governed by backbone-mediated H-bonds facilitated by small residues. The data presents new understanding of membrane protein biology and disease as well as new opportunities for protein structure prediction and design[9, 10].

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