You are cordially invited to a talk in the Edmond J. Safra Center for Bioinformatics Distinguished Speaker Series, held jointly with The Department of Biochemistry and Molecular Biology, The George S. Wise Faculty of Life Sciences.

The speaker is Prof. Arne Elofsson, Dept of Biochemistry and Biophysics and Science for Life Laboratory, Stockholm University.

Title: "What is missing from a complete structural map of the cell"

Time: Sunday, 17 May 2015, at 11:15 sharp (refreshments from 11:00)

Place: Sherman building, room 632, Tel Aviv University

Host: Prof. Nir Ben-Tal, bental@tauex.tau.ac.il , The Department of Biochemistry and Molecular Biology, Life Sciences Faculty, Tel Aviv University

Abstract: The ultimate goal of structural bioinformatics research is to provide a complete structural map of all macromolecules and their interactions within a cell. Knowledge about the structure of proteins and other macromolecules is essential for our understanding of biological processes. Proteins do most of the work in a cell and therefore the studies of proteins structure has been an essential part of life science research during the last decades. The performance of structure prediction methods has been blindly tested in CASP since 1994. It is clear that progress in both experimental and theoretical methods have been of uttermost importance for the progress. The rapid growth of determined protein structures has made it possible to build homology models for many proteins. However, surprisingly the exponential reduction in sequencing costs has also been fundamental for the progress since it (a) allows more distant homologies to be detected and (b) it can nowadays be used to predict contacts in proteins reliably.

However, most proteins do not act alone but through interactions with other proteins (and other molecules). Therefore, it is essential to understand not only the structure of a protein but also its interactions. Here, systems biology approaches are often used to understand what interactions are made but these studies mostly ignore the atomistic details about the interactions, i.e. how, the interactions are made.

Here, I will present recent progress in the structural bioinformatics field with a focus on what is still missing to provide a complete picture of all interacting macromolecules in a cell. In particular there are three problems that need to be solved: (i) improved detection of the parts that make up a cell (ii) accurate predictions of interactions of intra- and inter-residue contacts for all type of proteins; (iii) improved accuracy of both experimental and theoretical methods to identify protein-protein interactions.