

Biological Statistics and
Computational Biology

Weill Institute for Cell
and Molecular Biology

Candidate for Cellular Systems Biology Position

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University of Washington

Thursday, March 12, 2009
10:00 – 11:00 am
226 Weill Hall, above Synapsis Cafe

Structure prediction and design of membrane proteins

Membrane proteins constitute roughly 30 % of all proteins and perform crucial functions that range from cell-cell communication, to energy transduction, to the transport of key small molecules. Despite recent progress, the experimental determination of membrane protein structures remains difficult, making structure prediction an important alternative approach. However, single membrane protein polypeptide chains are typically longer than 200 amino acids, representing a formidable challenge for structure prediction. To address this problem, I have developed the method RosettaMembrane for the high-resolution structure prediction and design of membrane proteins. Using limited constraints predicted from sequence/structure correlations, RosettaMembrane can predict *de novo* the structure of large and complex membrane proteins. Accurate structure prediction of G protein-coupled receptors is now being achieved using comparative modeling approaches. Experimental constraints can also be combined with RosettaMembrane to model the structure of receptors with associating transmembrane domains on the cell surface.

Short Bio:

Patrick Barth received a B.A. in Physics and Chemistry in 1995 from the Pierre and Marie Curie University of Paris and a M.S. in Bioinorganic Chemistry in 1996 from the Paris-Sud University / Ecole Normale Supérieure. He received his Ph.D. in Biophysics in 2000 from Paris-Sud University / C.E.A. Saclay studying the interactions between photosystem I and ferredoxin by Nuclear Magnetic Resonance and time-resolved spectroscopies. He then joined the groups of Professor Tom Alber at UC Berkeley and Professor Pehr Harbury at Stanford University to develop computational methods for modeling protein electrostatics and designing specific peptide inhibitors to proteins involved in cell division. Recently, he accepted a Senior Fellow and Instructor positions in the group of Professor David Baker at the University of Washington where he develops the method RosettaMembrane for the high-resolution structure prediction and design of membrane proteins.

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