

— Keynote Address —

Membrane Proteins in Vivo and in Silico: Getting the Best of Two Worlds

Gunnar von Heijne

gunnar@dbb.su.se

Stockholm Bioinformatics Center, Department of Biochemistry and Biophysics,
Stockholm University, SE-10691 Stockholm, Sweden

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Abstract

Membrane protein research has gained a lot of momentum in recent years: high-resolution structures are being produced at an increasing rate, membrane proteomics is coming on line, and membrane proteins are recognized as drug targets of major importance. Bioinformatics has always been an integral part of the developments in the field, and today provides the tools necessary to identify the membrane complement of proteomes and to predict topologies and - in lucky cases - full 3D models of membrane proteins.

As in so many other areas, much is to be gained from a tighter integration between bioinformatics and experimental studies of membrane proteins. In our own work, we are reaching towards proteome-wide studies of membrane protein, an area where experimental and theoretical approaches must be combined to push forward.

References

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