

Postdoc Protein Bioinformatics

Arne Elofsson, Stockholm University.

<http://bioinfo.se/>

Theme: We are developing state of the art method to predict protein features, including membrane protein topology, protein structure and protein model quality. In addition we have a general interest in protein evolution.

Location: We are located at Science for Life Laboratory, Stockholm Sweden.

Group: Friendly environment with significant freedom.

Positions: Tax Free postdoc scholarships for two years, medical insurance etc.

Contact: arne@bioinfo.se

Position 1: Deep learning in protein bioinformatics.

We apply modern machine learning methods for various protein structure prediction problems.

Position 2: Ab-Initio Structure Prediction using PconsC3.

We have recently developed an ab-initio method to predict the structure of more than 2000 Pfam families. Here we will both improve this method and use it to gain biological insights in these proteins.

Position 3: Evolution of transporters and channels.

We are studying the evolution of protein transporters and channels both to understand their function and predict their structures. Here, we are closely collaborating with experimental colleagues.

Selected Publications

- Uziela, K., Menendez Hurtado, D., Shu, N., Wallner, B. and Elofsson, A. (Epub 2017) ProQ3D: improved model quality assessments using deep learning. *Bioinformatics*
- Hayat, S., Peters, C., Shu, N., Tsirigos, K.D. and Elofsson, A. (2016) Inclusion of dyad-repeat pattern improves topology prediction of transmembrane beta-barrel proteins. *Bioinformatics* **32** (10) : 1571-1573.
- Shiota, T., Imai, K., Qiu, J., Hewitt, V.L., Tan, K., Shen, H.H., Sakiyama, N., Fukasawa, Y., Hayat, S., Kamiya, M., Elofsson, A., Tomii, K., Horton, P., Wiedemann, N., Pfanner, N., Lithgow, T. and Endo, T. (2015) Molecular architecture of the active mitochondrial protein gate. *Science* **349** (6255) : 1544-1548.
- Tsirigos, K.D., Peters, C., Shu, N., Kall, L. and Elofsson, A. (2015) The TOPCONS web server for consensus prediction of membrane protein topology and signal peptides. *Nucleic Acids Res* **43** (W1) : W401-W407.
- Hayat, S., Sander, C., Marks, D.S. and Elofsson, A. (2015) All-atom 3D structure prediction of transmembrane beta-barrel proteins from sequences. *Proc Natl Acad Sci U S A* **112** (17) : 5413-5418.