

CURRICULUM VITAE

Arne Elofsson

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Affiliations

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Swedish E-science Research Center, Stockholm University
Science for Life Laboratory, Stockholm University

Degrees, positions and examinas

Scientific positions

- Jul 1989 - Aug 1993 PhD-position in Medical Biophysics at Dep. of Medical Biophysics, Karolinska Institutet.
- Sep 1993 - Aug 1995 Postdoctoral fellowship from Swedish Research Council for engineering Sciences, with David Eisenberg at Molecular Biology Institute, UCLA.
- Sep 1995 - Nov 1999 Assistant Professor at Dep. of Biochemistry, University of Stockholm
- Dec 1999 -Jan 2006 Associate Professor at Dep. of Biochemistry and Stockholm Bioinformatics Center (SBC)
- Dec 1999 -June 2005 Vice director at Stockholm Bioinformatics Center
- Feb 2006 - Professor in Bioinformatics at Dep. of Biochemistry and Biophysics, Stockholm University

Schools:

- Aug 1973 - Jun 1985 Studies at Smedslättens skola, Ålstens skola, Äppelvikens skola and Bromma Gymnasium Stockholm, Sweden
- Aug 1985 - Jun 1986 Studies in engineering physics (Teknisk fysik) at Uppsala University, Uppsala, Sweden.

- Aug 1986 - Jun 1988 Studies in the MD/PhD program (läkarlinjen med forskarinriktning) at Karolinska Institutet, Stockholm, Sweden.
- Aug 1988 - Jun 1989 Studies in engineering physics at Uppsala University and Royal Institute of Technology, Stockholm, Sweden.
- Jul 1989 - Aug 1993 PhD. Studies in Molecular Biophysics at Dept. of Medical Biophysics, Karolinska Institutet.

Exams and Degrees:

- Med Kand degree at Karolinska Institutet: June 13 1988
- PhD (dr Med. Vetenskap) at Karolinska Institutet: May 7 1993.
- Docentur at Department of Biochemistry and Biophysics, Stockholm University April 28 1999
- Professor at Department of Biochemistry and Biophysics, Stockholm University Febr 1, 2006

Publication record

Please note that this list is generated automatic and might therefore contain errors. All citation reports are obtained from Google Scholar, except for a few papers not found by Google Scholar where records are taken from Thomson. Impact factors for the journals are taken from the year 2007 and not from the year the articles are published. For up to date information on publications, citations and links to PDF versions of most papers see <http://bioinfo.se/papers/>

- Number of scientific publications: 96
- Number of citations: 5738
- H-index: 41

Top cited papers

1. Cserzo, M., Wallin, E., Simon, I., von Heijne, G. and Elofsson, A. "Prediction of transmembrane alpha-helices in prokaryotic membrane proteins: the dense alignment surface method." *Protein Eng* **1997**, 10(6):673-676
Number of citations: 710, Impact Factor: 2.662
2. Ginalski, K., Elofsson, A., Fischer, D. and Rychlewski, L. "3D-Jury: a simple approach to improve protein structure predictions." *Bioinformatics* **2003**, 19(8):1015-1018
Number of citations: 514, Impact Factor: 5.039
3. Lundstrom, J., Rychlewski, L., Bujnicki, J. and Elofsson, A. "Pcons: a neural-network-based consensus predictor that improves fold recognition." *Protein Sci* **2001**, 10(11):2354-2362
Number of citations: 226, Impact Factor: 3.135
4. Siew, N., Elofsson, A., Rychlewski, L. and Fischer, D. "MaxSub: an automated measure for the assessment of protein structure prediction quality." *Bioinformatics* **2000**, 16(9):776-785
Number of citations: 204, Impact Factor: 5.039
5. Bujnicki, J.M., Elofsson, A., Fischer, D. and Rychlewski, L. "Structure prediction meta server." *Bioinformatics* **2001**, 17(8):750-751
Number of citations: 203, Impact Factor: 5.039

Peer reviewed articles**• 1990**

1. Elofsson, A., Nilsson, L. and Rigler, R. "Studies on somatostatin with time-resolved spectroscopy and molecular dynamics simulations." *Int J Pept Protein Res* **1990**, 36(3):297-301
Number of citations: 3, Impact Factor: 2.269

• 1991

2. Elofsson, A., Rigler, R., Nilsson, L., Roslund, J., Krause, G. and Holmgren, A. "Motion of aromatic side chains, picosecond fluorescence, and internal energy transfer in Escherichia coli thioredoxin studied by site-directed mutagenesis, time-resolved fluorescence spectroscopy, and" *Biochemistry* **1991**, 30(40):9648-9656
Number of citations: 16, Impact Factor: 3.368
3. Rigler, R., Wennerberg, A. B. A., Cooke, R. M., Elofsson, A., Nilsson, L., Vogel, H., Holley, L. H., Carlquist, M., Langel, U., Bartfai, T., and Campbell, I. "On the solution structure of Galanin" *Galanin* **1991**, :1-1
Number of citations: 4, Impact Factor: 0

• 1992

4. Sander, C., Vriend, G., Bazan, F., Horovitz, A., Nakamura, H., Ribas, L., Finkelstein, A.V., Lockhart, A., Merkl, R., Perry, L.J., Elofsson A and others "Protein design on computers. Five new proteins: Shpilka, Grendel, Fingerclasp, Leather, and Aida." *Proteins* **1992**, 12(2):105-110
Number of citations: 19, Impact Factor: 3.354

• 1993

5. Elofsson, A., Kulinski, T., Rigler, R. and Nilsson, L. "Site specific point mutation changes specificity: a molecular modeling study by free energy simulations and enzyme kinetics of the thermodynamics in ribonuclease T1 substrate interactions." *Proteins* **1993**, 17(2):161-175
Number of citations: 6, Impact Factor: 3.354
6. Elofsson, A. and Nilsson, L. "How consistent are molecular dynamics simulations? Comparing structure and dynamics in reduced and oxidized Escherichia coli thioredoxin." *J Mol Biol* **1993**, 233(4):766-780
Number of citations: 31, Impact Factor: 4.472
7. Elofsson, A and Nilsson, L "Free Energy Perturbations in Ribonuclease T1 Substrate Binding. Study of the Influence of Simulation Length, Internal Freedom and structure in Free Energy Perturbations" *Molecular Simulations* **1993**, 10(2-6):255-276
Number of citations: 8, Impact Factor: 2.269

• 1994

8. LeGrand, S.M., Elofsson A. and Eisenberg, D. "The Effect of a Distance Cutoff on the Performance of the Distance Matrix Error when Used as a Potential Function to Drive Conformational Search" *In: Distance-based Approaches to Protein Structure Determination I* **1994**, 2:1-1
Number of citations: 1, Impact Factor: 2.269

- **1995**

9. Elofsson, A., Le Grand, S.M. and Eisenberg, D. "Local moves: an efficient algorithm for simulation of protein folding" *Proteins* **1995**, 23(1):73-82
Number of citations: 57, Impact Factor: 3.354

- **1996**

10. Fischer, D, Elofsson, A and Rice, DW, LeGrand, S, Eisenberg, D "Assessing the Performance of Fold Recognition Methods By Means of a Comprehensive Benchmark" *Proc. Pacific Symposium on Biocomputing, Hawaii*, **1996**, 100:300-318
Number of citations: 130, Impact Factor: 0
11. Elofsson, A., Fischer, D., Rice, D.W., Le Grand, S.M. and Eisenberg, D. "A study of combined structure/sequence profiles." *Fold Des* **1996**, 1(6):451-461
Number of citations: 61, Impact Factor: 5.025
12. Elofsson, A and Nilsson, L "A 1.2 ns Molecular Dynamic Simulation of Ribonuclease T1-3-Guanosine monophosphate complex" *J Phys Chem* **1996**, 100:2480-2488
Number of citations: 4, Impact Factor: 3.265

- **1997**

13. Wallin, E., Tsukihara, T., Yoshikawa, S., von Heijne, G. and Elofsson, A. "Architecture of helix bundle membrane proteins: an analysis of cytochrome c oxidase from bovine mitochondria." *Protein Sci* **1997**, 6(4):808-815
Number of citations: 115, Impact Factor: 3.135
14. Mingarro, I., Elofsson, A. and von Heijne, G. "Helix-helix packing in a membrane-like environment." *J Mol Biol* **1997**, 272(4):633-641
Number of citations: 33, Impact Factor: 4.472
15. Cserzo, M., Wallin, E., Simon, I., von Heijne, G. and Elofsson, A. "Prediction of transmembrane alpha-helices in prokaryotic membrane proteins: the dense alignment surface method." *Protein Eng* **1997**, 10(6):673-676
Number of citations: 710, Impact Factor: 2.662
16. Elofsson, A "Recent advances in how to test knowledge based energy functions for protein folding studies" *Recent Research Developments in Physical Chemistry* **1997**, 1:1-1
Number of citations: 0, Impact Factor: 2.269

- **1998**

17. Seshadri, K., Garemyr, R., Wallin, E., von Heijne, G. and Elofsson, A. "Architecture of beta-barrel membrane proteins: analysis of trimeric porins." *Protein Sci* **1998**, 7(9):2026-2032
Number of citations: 37, Impact Factor: 3.135
18. Zhang, X.-P., Elofsson, A. and Glaser, E. "Interaction of mt-HSP70 with mitochondrial presequences" *Plant Mitochondria: From gene to Function (Moller, I.M., Gardestrom, P., Glimelius, K. and Glaser, E., eds)* **1998**, 1:1-1
Number of citations: 0, Impact Factor: 2.269

- **1999**

19. Monne, M., Nilsson, I., Elofsson, A. and von Heijne, G. "Turns in transmembrane helices: determination of the minimal length of a "helical hairpin" derivation of a fine-grained turn propensity scale." *J Mol Biol* **1999**, 293(4):807-814
Number of citations: 57, Impact Factor: 4.472
20. Elofsson, A. and Sonnhammer, E.L. "A comparison of sequence and structure protein domain families as a basis for structural genomics." *Bioinformatics* **1999**, 15(6):480-500
Number of citations: 55, Impact Factor: 5.039
21. Garemyr, R. and Elofsson, A. "Study of the electrostatics treatment in molecular dynamics simulations." *Proteins* **1999**, 37(3):417-428
Number of citations: 20, Impact Factor: 3.354
22. Hargbo, J. and Elofsson, A. "Hidden Markov models that use predicted secondary structures for fold recognition." *Proteins* **1999**, 36(1):68-76
Number of citations: 69, Impact Factor: 3.354
23. Fischer, D., Barret, C., Bryson, K., Elofsson, A., Godzik, A., Jones, D., Karplus, K.J., Kelley, L.A., MacCallum, R.M., Pawowski, K., Rost, B., Rychlewski, L. and Sternberg, M. "CAFASP-1: critical assessment of fully automated structure prediction methods." *Proteins* **1999**, Suppl 3:209-217
Number of citations: 161, Impact Factor: 3.354
24. Zhang, X.P., Elofsson, A., Andreu, D. and Glaser, E. "Interaction of mitochondrial presequences with DnaK and mitochondrial hsp70." *J Mol Biol* **1999**, 288(1):177-190
Number of citations: 19, Impact Factor: 4.472

- **2000**

25. Siew, N., Elofsson, A., Rychlewski, L. and Fischer, D. "MaxSub: an automated measure for the assessment of protein structure prediction quality." *Bioinformatics* **2000**, 16(9):776-785
Number of citations: 204, Impact Factor: 5.039
26. Lindahl, E. and Elofsson, A. "Identification of related proteins on family, superfamily and fold level." *J Mol Biol* **2000**, 295(3):613-625
Number of citations: 146, Impact Factor: 4.472
27. Fischer, D., Elofsson, A. and Rychlewski, L. "The 2000 Olympic Games of protein structure prediction; fully automated programs are being evaluated vis-a-vis human teams in the protein structure prediction experiment CAFASP2." *Protein Eng* **2000**, 13(10):667-670
Number of citations: 19, Impact Factor: 2.662

- **2001**

28. Cristobal, S., Zemla, A., Fischer, D., Rychlewski, L. and Elofsson, A. "A study of quality measures for protein threading models." *BMC Bioinformatics* **2001**, 2:5
Number of citations: 86, Impact Factor: 3.493
29. Fischer, D., Elofsson, A., Rychlewski, L., Pazos, F., Valencia, A., Rost, B., Ortiz, A.R. and Dunbrack, Jr., R.L. "CAFASP2: the second critical assessment of fully automated structure prediction methods." *Proteins* **2001**,

Suppl 5:171-183

Number of citations: 103, Impact Factor: 3.354

30. Bujnicki, J.M., Elofsson, A., Fischer, D. and Rychlewski, L. "LiveBench-2: large-scale automated evaluation of protein structure prediction servers." *Proteins* **2001**, Suppl 5:184-191

Number of citations: 76, Impact Factor: 3.354

31. Bujnicki, J.M., Elofsson, A., Fischer, D. and Rychlewski, L. "Structure prediction meta server." *Bioinformatics* **2001**, 17(8):750-751

Number of citations: 203, Impact Factor: 5.039

32. Lundstrom, J., Rychlewski, L., Bujnicki, J. and Elofsson, A. "Pcons: a neural-network-based consensus predictor that improves fold recognition." *Protein Sci* **2001**, 10(11):2354-2362

Number of citations: 226, Impact Factor: 3.135

33. Eriksson, O., Xhou, Y. and Elofsson, A. "Side chain-positioning as an integer programming problem." *WABI* **2001**, 1:1-1

Number of citations: 41, Impact Factor: 2.269

34. Fang, H., Wallner, B. Lundstrom, J., von Wowern, C. and Elofsson, A. "Improved fold recognition by using the Pcons consensus approach" *Chapter in "Protein structure prediction: Bioinformatic approach" IUL biotechnology Series, La Jolla, 2001*, 1:397-41

Number of citations: 2, Impact Factor: 2.269

35. Bujnicki, J.M., Elofsson, A., Fischer, D. and Rychlewski, L. "LiveBench-1: continuous benchmarking of protein structure prediction servers." *Protein Sci* **2001**, 10(2):352-361

Number of citations: 118, Impact Factor: 3.135

• **2002**

36. Milchert, L.E., Liberles, D.A. and Elofsson, A. "The salmon genome (and other issues in bioinformatics)." *Genome Biol* **2002**, 3(7):REPORTS4022

Number of citations: 3, Impact Factor: 6.589

37. Hedman, M., Deloof, H., Von Heijne, G. and Elofsson, A. "Improved detection of homologous membrane proteins by inclusion of information from topology predictions." *Protein Sci* **2002**, 11(3):652-658

Number of citations: 22, Impact Factor: 3.135

38. Donnes, P. and Elofsson, A. "Prediction of MHC class I binding peptides, using SVMHC." *BMC Bioinformatics* **2002**, 3:25

Number of citations: 188, Impact Factor: 3.493

39. Elofsson, A. "A study on protein sequence alignment quality." *Proteins* **2002**, 46(3):330-339

Number of citations: 64, Impact Factor: 3.354

40. David A. Liberles, Anna Thoren, Gunnar von Heijne and Arne Elofsson "The use of Phylogenetic profiles for Gene Predictions" *Current Genomics* **2002**, 3:131-138

Number of citations: 28, Impact Factor: 0.573

• **2003**

41. Ginalski, K., Elofsson, A., Fischer, D. and Rychlewski, L. "3D-Jury: a simple approach to improve protein structure predictions." *Bioinformatics*

2003, 19(8):1015-1018

Number of citations: 514, Impact Factor: 5.039

42. Wallner, B., Fang, H. and Elofsson, A. "Automatic consensus-based fold recognition using Pcons, ProQ, and Pmodeller." *Proteins* **2003**, 53 Suppl 6:534-541

Number of citations: 65, Impact Factor: 3.354

43. Rychlewski, L., Fischer, D. and Elofsson, A. "LiveBench-6: large-scale automated evaluation of protein structure prediction servers." *Proteins* **2003**, 53 Suppl 6:542-547

Number of citations: 61, Impact Factor: 3.354

44. Wallner, B. and Elofsson, A. "Can correct protein models be identified?" *Protein Sci* **2003**, 12(5):1073-1086

Number of citations: 179, Impact Factor: 3.135

45. Fischer, D., Rychlewski, L., Dunbrack, Jr., R.L., Ortiz, A.R. and Elofsson, A. "CAFASP3: the third critical assessment of fully automated structure prediction methods." *Proteins* **2003**, 53 Suppl 6:503-516

Number of citations: 120, Impact Factor: 3.354

46. Emanuelsson, O., Elofsson, A., von Heijne, G. and Cristobal, S. "In silico prediction of the peroxisomal proteome in fungi, plants and animals." *J Mol Biol* **2003**, 330(2):443-456

Number of citations: 65, Impact Factor: 4.472

● **2004**

47. Viklund, H. and Elofsson, A. "Best alpha-helical transmembrane protein topology predictions are achieved using hidden Markov models and evolutionary information." *Protein Sci* **2004**, 13(7):1908-1917

Number of citations: 128, Impact Factor: 3.135

48. Wallner, B., Fang, H., Ohlson, T., Frey-Skott, J. and Elofsson, A. "Using evolutionary information for the query and target improves fold recognition." *Proteins* **2004**, 54(2):342-350

Number of citations: 35, Impact Factor: 3.354

49. Ohlson, T., Wallner, B. and Elofsson, A. "Profile-profile methods provide improved fold-recognition: a study of different profile-profile alignment methods." *Proteins* **2004**, 57(1):188-197

Number of citations: 66, Impact Factor: 3.354

● **2005**

50. Berglund, A.C., Wallner, B., Elofsson, A. and Liberles, D.A. "Tertiary windowing to detect positive diversifying selection." *J Mol Evol* **2005**, 60(4):499-504

Number of citations: 25, Impact Factor: 3.234

51. Ohlson, T. and Elofsson, A. "ProfNet, a method to derive profile-profile alignment scoring functions that improves the alignments of distantly related proteins." *BMC Bioinformatics* **2005**, 6:253

Number of citations: 21, Impact Factor: 3.493

52. Bjorklund, A.K., Ekman, D., Light, S., Frey-Skott, J. and Elofsson, A. "Domain rearrangements in protein evolution." *J Mol Biol* **2005**, 353(4):911-923

Number of citations: 64, Impact Factor: 4.472

53. Wallner, B. and Elofsson, A. "All are not equal: a benchmark of different homology modeling programs." *Protein Sci* **2005**, 14(5):1315-1327
Number of citations: 108, Impact Factor: 3.135
54. Light, S., Kraulis, P. and Elofsson, A. "Preferential attachment in the evolution of metabolic networks." *BMC Genomics* **2005**, 6:159
Number of citations: 41, Impact Factor: 4.18
55. Ekman, D., Bjorklund, A.K., Frey-Skott, J. and Elofsson, A. "Multi-domain proteins in the three kingdoms of life: orphan domains and other unassigned regions." *J Mol Biol* **2005**, 348(1):231-243
Number of citations: 69, Impact Factor: 4.472
56. Granseth, E., von Heijne, G. and Elofsson, A. "A study of the membrane-water interface region of membrane proteins." *J Mol Biol* **2005**, 346(1):377-385
Number of citations: 83, Impact Factor: 4.472
57. Wallner, B. and Elofsson, A. "Pcons5: combining consensus, structural evaluation and fold recognition scores." *Bioinformatics* **2005**, 21(23):4248-4254
Number of citations: 43, Impact Factor: 5.039

• **2006**

58. Ekman, D., Light, S., Bjorklund, A.K. and Elofsson, A. "What properties characterize the hub proteins of the protein-protein interaction network of *Saccharomyces cerevisiae*?" *Genome Biol* **2006**, 7(6):R45
Number of citations: 108, Impact Factor: 6.589
59. Bjorklund, A.K., Ekman, D. and Elofsson, A. "Expansion of Protein Domain Repeats." *PLoS Comput Biol* **2006**, 2(8):e114
Number of citations: 62, Impact Factor: 6.236
60. Granseth, E., Viklund, H. and Elofsson, A. "ZPRED: predicting the distance to the membrane center for residues in alpha-helical membrane proteins." *Bioinformatics* **2006**, 22(14):e191-6
Number of citations: 27, Impact Factor: 5.039
61. Viklund, H., Granseth, E. and Elofsson, A. "Structural classification and prediction of reentrant regions in alpha-helical transmembrane proteins: application to complete genomes." *J Mol Biol* **2006**, 361(3):591-603
Number of citations: 43, Impact Factor: 4.472
62. Wallner, B. and Elofsson, A. "Identification of correct regions in protein models using structural, alignment, and consensus information." *Protein Sci* **2006**, 15(4):900-913
Number of citations: 79, Impact Factor: 3.135
63. Amico, M., Finelli, M., Rossi, I., Zauli, A., Elofsson, A., Viklund, H., von Heijne, G., Jones, D., Krogh, A., Fariselli, P., Luigi Martelli, P. and Casadio, R. "PONGO: a web server for multiple predictions of all-alpha transmembrane proteins." *Nucleic Acids Res* **2006**, 34(Web Server issue):W169-72
Number of citations: 29, Impact Factor: 6.954
64. Asa Bjorklund, Anna Thoren, Gunnar von Heijne and Arne Elofsson "The use of Phylogenetic profiles for Gene Predictions Revisited" *Current Genomics* **2006**, 7(2):79-86
Number of citations: 28, Impact Factor: 0.573

65. Ohlson, T., Aggarwal, V., Elofsson, A. and MacCallum, R.M. "Improved alignment quality by combining evolutionary information, predicted secondary structure and self-organizing maps." *BMC Bioinformatics* **2006**, 7:357
Number of citations: 8, Impact Factor: 3.493

• **2007**

66. Elofsson, A. and von Heijne, G. "Membrane protein structure: prediction versus reality." *Annu Rev Biochem* **2007**, 76:125-140
Number of citations: 105, Impact Factor: 31.19
67. Wallner, B., Larsson, P. and Elofsson, A. "Pcons.net: protein structure prediction meta server." *Nucleic Acids Res* **2007**, 35(suppl 2):W369-W374
Number of citations: 28, Impact Factor: 6.954
68. Ekman, D., Bjorklund, A.K. and Elofsson, A. "Quantification of the elevated rate of domain rearrangements in metazoa." *J Mol Biol* **2007**, 372(5):1337-1348
Number of citations: 21, Impact Factor: 4.472
69. Wallner, B. and Elofsson, A. "Prediction of global and local model quality in CASP7 using Pcons and ProQ." *Proteins* **2007**, 69(S8):184-193
Number of citations: 46, Impact Factor: 3.354
70. Hughes, T., Ekman, D., Ardawatia, H., Elofsson, A. and Liberles, D.A. "Evaluating dosage compensation as a cause of duplicate gene retention in *Paramecium tetraurelia*." *Genome Biol* **2007**, 8(5):213
Number of citations: 7, Impact Factor: 6.589

• **2008**

71. Papaloukas, C., Granseth, E., Viklund, H. and Elofsson, A. "Estimating the length of transmembrane helices using Z-coordinate predictions." *Protein Sci* **2008**, 17(2):271-278
Number of citations: 11, Impact Factor: 3.135
72. Bernsel, A., Viklund, H. and Elofsson, A. "Remote homology detection of integral membrane proteins using conserved sequence features." *Proteins* **2008**, 71(3):1387-1399
Number of citations: 6, Impact Factor: 3.354
73. Larsson, P., Wallner, B., Lindahl, E. and Elofsson, A. "Using multiple templates to improve quality of homology models in automated homology modeling." *Protein Sci* **2008**, 17(6):990-1002
Number of citations: 17, Impact Factor: 3.135
74. Bernsel, A., Viklund, H., Falk, J., Lindahl, E., von Heijne, G. and Elofsson, A. "Prediction of membrane-protein topology from first principles." *Proc Natl Acad Sci U S A* **2008**, 105(20):7177-7181
Number of citations: 70, Impact Factor: 9.598
75. Kauko, A., Illergard, K. and Elofsson, A. "Coils in the membrane core are conserved and functionally important." *J Mol Biol* **2008**, 380(1):170-180
Number of citations: 11, Impact Factor: 4.472
76. Viklund, H. and Elofsson, A. "OCTOPUS: improving topology prediction by two-track ANN-based preference scores and an extended topological grammar." *Bioinformatics* **2008**, 24(15):1662-1668
Number of citations: 40, Impact Factor: 5.039

77. Wallner, B., and Elofsson, A. "Prediction of global and local model qualities using MQAPs" *Eds Bujnicki* **2008**, 1:1-1
Number of citations: 0, Impact Factor: 2.269
78. Moore, A.D., Bjorklund, A.K., Ekman, D., Bornberg-Bauer, E. and Elofsson, A. "Arrangements in the modular evolution of proteins." *Trends Biochem Sci* **2008**, 33(9):444-451
Number of citations: 44, Impact Factor: 14.994
79. Bjorklund, A.K., Light, S., Hedin, L. and Elofsson, A. "Quantitative assessment of the structural bias in protein-protein interaction assays." *Proteomics* **2008**, 8(22):4657-4667
Number of citations: 8, Impact Factor: 5.479
80. Viklund, H., Bernsel, A., Skwark, M. and Elofsson, A. "SPOCTOPUS: a combined predictor of signal peptides and membrane protein topology." *Bioinformatics* **2008**, 24(24):2928-2929
Number of citations: 16, Impact Factor: 5.039

• **2009**

81. Michino, M., Abola, E., Brooks, 3rd, C.L., Dixon, J.S., Moulton, J. and Stevens, R.C. "Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008." *Nat Rev Drug Discov* **2009**, 8(6):455-463
Number of citations: 29, Impact Factor: 23.308
82. Illergard, K., Ardell, D.H. and Elofsson, A. "Structure is three to ten times more conserved than sequence-A study of structural response in protein cores." *Proteins* **2009**, 77(3):499-508
Number of citations: 7, Impact Factor: 3.354
83. Bernsel, A., Viklund, H., Hennerdal, A. and Elofsson, A. "TOPCONS: consensus prediction of membrane protein topology." *Nucleic Acids Res* **2009**, 37(Web Server issue):W465-8
Number of citations: 26, Impact Factor: 6.954
84. Larsson, P., Skwark, M.J., Wallner, B. and Elofsson, A. "Assessment of global and local model quality in CASP8 using Pcons and ProQ." *Proteins* **2009**, 77(S9):167-172
Number of citations: 6, Impact Factor: 3.354

• **2010**

85. Ekman, D. and Elofsson, A. "Identifying and Quantifying Orphan Protein Sequences in Fungi." *J Mol Biol* **2010**, 396(2):396-405
Number of citations: 0, Impact Factor: 4.472
86. Hedin, L.E., Ojemalm, K., Bernsel, A., Hennerdal, A., Illergard, K., Enquist, K., Kauko, A., Cristobal, S., von Heijne, G., Lerch-Bader, M., Nilsson, I. and Elofsson, A. "Membrane Insertion of Marginally Hydrophobic Transmembrane Helices Depends on Sequence Context." *J Mol Biol* **2010**, 396(1):221-229
Number of citations: 7, Impact Factor: 4.472
87. Kauko, A., Hedin, L.E., Thebaud, E., Cristobal, S., Elofsson, A. and von Heijne, G. "Repositioning of Transmembrane alpha-Helices during Membrane Protein Folding." *J Mol Biol* **2010**, 397(1):190-201
Number of citations: 7, Impact Factor: 4.472

88. Illergard, K., Callegari, S. and Elofsson, A. "MPRAP: An accessibility predictor for alpha-helical transmembrane proteins that performs well inside and outside the membrane." *BMC Bioinformatics* **2010**, 11(1):333
Number of citations: 3, Impact Factor: 3.493
89. Bjorklund, A.K., Light, S., Sagit, R. and Elofsson, A. "Nebulin: A Study of Protein Repeat Evolution." *J Mol Biol* **2010**, 402(1):38-51
Number of citations: 1, Impact Factor: 4.472
90. Runesson, J., Sollenberg, U.E., Jurkowski, W., Yazdi, S., Eriksson, E.E., Elofsson, A. and Langel, U. "Determining receptor-ligand interaction of human galanin receptor type 3." *Neurochem Int* **2010**, 57(7):804-811
Number of citations: 0, Impact Factor: 2.175
91. Lima, M.F., Eloy, N.B., Pegoraro, C., Sagit, R., Rojas, C., Bretz, T., Vargas, L., Elofsson, A., Oliveira, A.C., Hemerly, A.S. and Ferreira, P.C. "Genomic evolution and complexity of the Anaphase-promoting Complex (APC) in land plants." *BMC Plant Biol* **2010**, 10(1):254
Number of citations: 0, Impact Factor: 3.232
92. Hennerdal, A., Falk, J., Lindahl, E. and Elofsson, A. "Internal duplications in alpha-helical membrane protein topologies are common but the nonduplicated forms are rare." *Protein Sci* **2010**, 19(12):2305-2318
Number of citations: 0, Impact Factor: 3.135

• **2011**

93. Illergard, K., Kauko, A. and Elofsson, A. "Why are polar residues within the membrane core evolutionary conserved?" *Proteins* **2011**, 79(1):79-91
Number of citations: 0, Impact Factor: 3.354
94. Larsson, P., Skwark, M.J., Wallner, B. and Elofsson, A. "Improved predictions by Pcons.net using multiple templates." *Bioinformatics* **2011**, 27(3):426-427
Number of citations: 0, Impact Factor: 5.039
95. Hennerdal, A. and Elofsson, A. "Rapid membrane protein topology prediction." *Bioinformatics* **2011**, 27(9):1322-1323
Number of citations: 0, Impact Factor: 5.039
96. Shu, N. and Elofsson, A. "KalignP: Improved multiple sequence alignments using position specific gap penalties in Kalign2." *Bioinformatics (Epub ahead of print)* **2011**
Number of citations: 0, Impact Factor: 5.039

Submitted

97. none

Freely available GPL licensed computer programs

All programs are available from <http://bioinfo.se/> and are licensed under the GPL license.

1. Palign - a flexible and powerful sequence alignment and search program. <http://bioinfo.se/palign/>
2. modHMM - A modular HMM program that can use profile-profile comparisons. <http://www.modhmm.org/>

3. ProQ - A set of programs to predict the quality of a protein model. <http://bioinfo.se/ProQ/>
4. LGscore - A program to measure the quality of a protein model. <http://bioinfo.se/lgscore/>
5. Pfrag - a fast and free homology modelling program

Freely available web-applications

These services are freely available

- For globular protein structure predictions. All tools are now available through <http://pcons.net/> - a meta-server using pcons and Pfrag to predict structures.
 - Pcons - A consensus fold recognition server receiving than ten thousand requests per year.
 - Pmodeller - A consensus homology modelling server.
 - Pfrag - A fast an accurate homolgy modelling method.
 - ProQ - A quality predictor for protein models.
 - Pmembr - A fold recognition server for membrane proteins.
- For membrane proteins. All servers are now available through <http://topcons.net/>
 - TOPCONS - Consensus based topology predictor
 - Spoctopus - Combined predictor of Signal peptides, topology and reentrant regions
 - Octopus - Combined predictor of topology and reentrant regions
 - SCAMPI - A scale based membrane protein predictor
 - pro/prodiv-TMHMM - a predictor of transmembrane regions.
 - DAS - A predictor of transmembrane regions.
 - Zpred - a predictor of the distance to the membrane center.

Research grants

Current grants

- Research councils:
 - 2010-2012 VR (NT) “Structure, folding and evolution of membrane proteins” 2 700 KSEK
 - 2011-2013 VR (M) “ Evolution, variation, structure and interactions of repeat domain containing proteins.” 2 400 KSEK
- European union
 - 2008-2012 IRP: “EDICT European Drug Initiative on Channels and Transporters”, FP7-HEALTH-F4-2007-201924 517 KEuro
 - 2008-2011 ITN: “Transys - A systems approach to defining membrane protein networks and applications”, FP7-PEOPLE-2007-1-1-ITN 200 KEuro
- Other
 - 2011- SeRC “Development of E-science tools to study membrane proteins”. 600 KSEK/year
 - 2011-2013 SciLifeLab: “Accurate assignment of indels in repeat domain containing proteins” 1 000 KSEK
 - 2009-2012 Vinnova/SSF-JSP “Elucidating the import, membrane integration, architecture and interactions of mitochondrial β -barrel outer membrane proteins” 2 100 KSEK

Historical overview of received grants

- Since 1995 received individual research grants for 45 MSEK (4.7 MEuro)
 - Research councils 13 400 KSEK
 - European Union 1 303 KEuro
 - Strategic foundation 9 835 KSEK
 - Other foundations 9 992 KSEK
- Equipment (computing clusters) 11 300 KSEK
- Co-applicant in center grants 110 000 KSEK (10 MEuro)

Other merits

Awards

- Sven och Ebba-Christina Högbergs pris 1999

Invited talks and lectures since 2006

- Invited talk to “Public CASP meeting”, New York (May 2006)
- Selected talk at ISMB’06 (Aug, 2006) Delivered by Erik Granseth
- Invited talk to “III International Symposium on Biochemistry and Molecular Biology”, Havana October, 2006
- Invited talk at CASP7 (Dec, 2006) Delivered by Björn Wallner
- Invited talk to “Biosapiens workshop”, Israel (Jan 2007)
- Selected talk at highlight track at ISMB’07 (Aug, 2007) Delivered by Åsa K. Björklund
- Invited talk at “EMBN workshop”, Groningen Jan 2008
- Invited talk at “EBI membrane workshop”, Hinxton, Feb 2008
- Invited talk at “Bioinformatics winter school”, Bologna Feb 2008
- Invited talk to “CASP 7.5 meeting”, Madrid pril 2008
- Selected talk at “CASP8”, Italy, Dec 2008
- Keynote talk to “3D-sig, ISMB”, Stockholm June 2009
- Invited talk to “Protein Structure Prediction workshop”, Budapest Aug 2009
- Invited talk to “Systems biology on microorganisms”, Mar 2010, Paris
- Selected talk at “3d-sig, ISMB”, Boston, July 2010
- Invited talk at Tokyo University, Nagoya University and CBRC, Japan Oct 2010
- Invited talks at Saarbrucken University, Germany, Nov 2010
- Invited lecturer at Workshop on membrane protein structure, Bilbao, Sep 2011

International assignments

- 1998-2000 Secretary in the Swedish Biophysical society.
- 2004-2012 President of the Society for Bioinformatics in the Nordic countries (SocBiN)
- 2010- Member of “Working Group on Theoretical Structural Models Validation”

Editorial boards

- 2008-14 Associate editor for Protein science
- 2009- Associate editor for PLOS computational biology
- 2010- Editorial Board Member of BMC Bioinformatics
- 2010- Editorial Board Member of IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)
- 2011- Academic Editor for Plos ONE

Conferences

- Organized workshop “Biophysical aspects of protein folding” (60 participants) 1997
- Organized the SocBiN conference Bioinformatics’99 (250 participants)
- Member of organization committee for protein society meeting in Stockholm 2007 (800 participants)
- Local organizer of ISMB/ECCB-09 (1500 participants)

Program committees and refereeing

- Member of editorial board for highlight track for ISMB’07 and ISMB’08
- Reviewing >20 articles annually from J. Mol. Biol., Proteins, Bioinformatics, Nucleic Acids Research, BMC Bioinformatics, Nat Biotech. Plos. Comp Biol.
- Member of program committee at the Annual Conference on Intelligent Systems for Molecular Biology (ISMB) since 2001
- 1999-2012 Member of program committee for Bioinformatics’XX (chair 1999, 2004 and 2012)
- 2006 Member of program committee for The European Symposium of the Protein Society, 2007
- 2006 Member of the CASP7 consultancy group
- 2006 Member of program committee for GCB’06
- 2006 One of the top 100 active reviewers/writers for open access journals in the BMC series.
- 2009 Local organizer of ISMB/ECCB’09 in Stockholm

Review committees

- Member of the National Research Council review group for biochemistry and biotechnology, 2006, 2007, 2008, 2010, 2011
- External reviewer for grants from:
 - Danish Supercomputing Center, 2007,2008
 - Welcome Trust, 2006
 - Norwegian Research Council, 2005
 - Cancer UK, 2005
 - Science Foundation Ireland, 2003
 - Israel Science Foundation , 2002-2010
 - Netherlands Genomics Initiative, 2001
 - Singapore Science program , 2001
- External reviewers for academic positions
 - 2006 Skövde - external reviewer for lectureship.
 - 2009 UmeåUniversity - external reviewer for forskarassistent.
 - 2009 Danish Technical University - external reviewer for professorship.

PhD-reviews and assignments as opponent

- 2000 Helsinki University (examiner) Jarmo Alander
- 2006 Karolinska Institutet (Chair of Committee) Markus Wistrand
- 2007 University of Sydney (external examiner)
- 2008 Turku University (opponent) Virpi Ahola
- 2008 Copenhagen University (opponent) Martin Paluszewski
- Member of more than 10 PhD committees.

Research Group

Graduate Students:

- | | |
|---|-------------------------|
| 1. Aron Hennerdal, <i>Sep-2006-</i> | Membrane proteins |
| 2. Rauan Sagit, <i>June-2008-</i> | Domain evolution |
| 3. Marcin Skwark, <i>Aug-2008-</i> | Structure prediction |
| 4. Minttu Virkki, <i>Nov-2009-</i> | Membrane Proteins (exp) |
| 5. Daniel Nilsson, <i>Nov-2009-</i> | Membrane Proteins (exp) |
| 6. Patrik Björkholm (Co-supervised), <i>Nov-2009-</i> | Membrane Proteins |
| 7. Christoph Peters <i>Dec-2010-</i> | Protein Bioinformatics |
| 8. Walter Basile <i>Mar-2011-</i> | Orphan Proteins |

Postdocs

- | | |
|------------------------------------|---------------------------------|
| 1. Maria Bendz, <i>June-2008-</i> | MS on membrane proteins |
| 2. Sara Light <i>July-2009-</i> | Protein interactions |
| 3. Sikander Hayat <i>Apr-2010-</i> | Membrane proteins |
| 4. Nanjiang Shu <i>Jul-2010-</i> | Membrane protein bioinformatics |
| 5. Linnea Hedin <i>Dec-2010-</i> | Membrane proteins |
| 6. Erik Granseth <i>Jan-2011-</i> | Membrane proteins |

External Collaborators

- | | |
|--------------------------------------|----------------------------------|
| • Prof Erik Lindahl, KTH | Protein and membrane simulations |
| • Björn Wallner, KTH, | Protein structure predictions |
| • Doc. Susana Cristobal, LiU | Biochemistry |
| • Prof. Gunnar von Heijne, SU | Membrane proteins |
| • Felix Goni, EHU, Spain, | Membranes |
| • Bernd Wollscheid, ETH, Switzerland | Mass-spectrometry |
| • Peter James, Lund | Mass-spectrometry |
| • Paul Horton, CBRC, Japan | β -barrel proteins |
| • Toshiya Endo, Nagoya, Japan | β -barrel proteins |

Alumni

Guest professors

- | | |
|---|--------|
| • Costas Papaloukas, <i>Jul 2006 - Jan 2007</i> | Zpred2 |
|---|--------|

Associated professors

- Erik Lindahl, *2004 - 2009* Gromacs
- Lukas Käll, *2008-2011* Mass-spectrometry

Supervised PhD students

1. Björn Wallner Sept 30, 2005 “Protein structure prediction: Model Building and Quality Assessment”
2. Tomas Ohlson Feb 24, 2006 “The use of evolutionary information in protein alignments and homology identification”
3. Sara Light May 19, 2006 “Investigations into the evolution of biological networks”
4. Erik Granseth, Sep 24, 2007 “Structure, prediction, evolution and genome wide studies of membrane proteins”
5. Håkan Viklund, Nov 23, 2007 “The structural grammar of transmembrane proteins”
6. Andreas Bernsel, Sep 19, 2008 “Sequence-based predictions of membrane-protein topology, homology and insertion” (Co-supervised)
7. Diana Ekman, Nov 28, 2008 “Domain rearrangement and creation in protein evolution”
8. Olivia Eriksson, Dec 12, 2008 “Simplicity within Complexity- Understanding dynamics of cellular networks by model reduction”
9. Kristoffer Illergård, Feb 19, 2010 “On the effects of structure and function on protein evolution”
10. Per Larsson, May 12, 2010 “Prediction, modeling and refinement of protein structures”
11. Åsa Björklund, Apr 23, 2010 “Creation of new proteins - domain rearrangements and tandem duplications.”
12. Linnea Hedin, Oct 15, 2010 “Intra and intermolecular interactions in proteins”

Post-docs

1. Dr. Miklos Cserző, *Jan 1996 - Jun 1996* Membrane proteins
2. Dr. K. Seshadri, *Jun 1997 - Feb 1998* Analysis of Membrane proteins
3. Dr. Mats Eriksson, *Sep 1998 -Apr 2000* Drug design
4. Dr. Huisheng Fang, *Dec 2000-Dec 2002* Fold Recognition
5. Dr. Meftun Ahmed, *Jan 2002-Aug 2002* Peroxisomes
6. Dr. Nick Braun, *Nov 2002-Apr 2003* Evolution of protein thermodynamics
7. Dr. Erik Sandelin, *Mar 2003-Sep 2006* Protein structure predictions
8. Dr. Wiktor Jurkowski *June-2008-2010* Membrane protein docking
9. Dr. Karin Julenius *June-2009-2010* Posttranslational modifications