

CURRICULUM VITAE

Arne Elofsson

13 mars 2012

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Date of Birth: 10 Dec. 1966
Citizenship: Swedish.
Place of Birth: Stockholm, Sweden

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Affiliations

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Stockholm Bioinformatics Center, Stockholm University
Center for Biomembrane Research, Stockholm University
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 forskar-inriktning) 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

For up to date information on publications, citations and links to PDF versions of most papers see <http://bioinfo.se/papers/>

- Total number of scientific publications: 101
- Number of peer reviewed original publications in journals: 87
- Number of peer reviewed original publications in conference proceedings: 2
- Number of review articles: 5
- Number of book chapters: 5
- Number of citations: 6414
- H-index: 44
- G-index: 73

Grants

- | | |
|--|-------------|
| • Since 1995 received individual research grants for | 45 MSEK |
| • Research councils | 13 400 KSEK |
| • European Union | 1 303 KEuro |
| • Strategic foundation | 9 835 KSEK |
| • Other foundations | 8 392 KSEK |

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/>

- Total number of scientific publications: 101
- Number of peer reviewed original publications in journals: 88
- Number of peer reviewed original publications in conference proceedings: 2
- Number of review articles: 6
- Number of book chapters: 5
- Number of citations: 6470
- H-index: 44
- G-index: 73

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: 807, 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: 581, Impact Factor: 5.039
3. 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: 242, Impact Factor: 5.039
4. 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: 229, Impact Factor: 3.135
5. Bujnicki, J.M., Elofsson, A., Fischer, D. and Rychlewski, L. "Structure prediction meta server." *Bioinformatics* **2001**, 17(8):750-751
Number of citations: 215, Impact Factor: 5.039

Top cited papers

1. Elofsson, A. and von Heijne, G. "Membrane protein structure: prediction versus reality." *Annu Rev Biochem* **2007**, 76():125-140
Number of citations: 122, Impact Factor: 31.19
2. Contreras, F.X., Ernst, A.M., Haberkant, P., Bjorkholm, P., Lindahl, E., Gonen, B., Tischler, C., Elofsson, A., von Heijne, G., Thiele, C., Pepperkok, R., Wieland, F. and Brugger, B. "Molecular recognition of a single sphingolipid species by a protein's transmembrane domain." *Nature* **2012**, 481(7382):525-529
Number of citations: 0, Impact Factor: 28.751
3. 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: 66, Impact Factor: 23.308
4. 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: 62, Impact Factor: 14.994
5. Basmärke-Wehelie, R., Sjolinder, H., Jurkowski, W., Elofsson, A., Arnqvist, A., Engstrand, L., Hagner, M., Wallin, E., Guan, N., Kuranasekera, H., Aro, H. and Jonsson, A.B. "The Complement Regulator CD46 Is Bactericidal to *Helicobacter pylori* and Blocks Urease Activity." *Gastroenterology* **2011**, 141(3):918-928
Number of citations: 0, Impact Factor: 12.182

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: 4, 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: 17, Impact Factor: 3.368

• 1992

3. Sander, C., Vriend, G., Bazan, F., Horovitz, A., Nakamura, H., Ribas, L., Finkelstein, A.V., Lockhart, A., Merkl, R., Perry, L.J. and others "Protein design on computers. Five new proteins: Shpilka, Grendel, Fingerclasp, Leather, and Aida." *Proteins* **1992**, 12(2):105-110
Number of citations: 31, Impact Factor: 3.354

• 1993

4. 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: 8, Impact Factor: 3.354
5. 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: 40, Impact Factor: 5.501
6. 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: 9, Impact Factor: -1

• 1995

7. 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: 67, Impact Factor: 3.354

• 1996

8. 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: 136, Impact Factor: 0
9. 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: 58, Impact Factor: -1
10. 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**

11. 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: 123, Impact Factor: 3.135
12. 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: 36, Impact Factor: 5.501
13. 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: 807, Impact Factor: 2.662

• **1998**

14. 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: 43, Impact Factor: 3.135

• **1999**

15. 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: 71, Impact Factor: 5.501
16. 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: 57, Impact Factor: 5.039
17. Garemyr, R. and Elofsson, A. “Study of the electrostatics treatment in molecular dynamics simulations.” *Proteins* **1999**, 37(3):417-428
Number of citations: 24, Impact Factor: 3.354

18. 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: 74, Impact Factor: 3.354
19. 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: 176, Impact Factor: 3.354
20. 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: 20, Impact Factor: 5.501

• **2000**

21. 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: 242, Impact Factor: 5.039
22. 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: 153, Impact Factor: 5.501
23. 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**

24. 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: 98, Impact Factor: 3.493
25. 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: 107, Impact Factor: 3.354
26. 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: 78, Impact Factor: 3.354
27. Bujnicki, J.M., Elofsson, A., Fischer, D. and Rychlewski, L. "Structure prediction meta server." *Bioinformatics* **2001**, 17(8):750-751
Number of citations: 215, Impact Factor: 5.039
28. 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: 229, Impact Factor: 3.135

29. Eriksson, O., Xhou, Y. and Elofsson, A. "Side chain-positioning as an integer programming problem." *WABI* **2001**, 1():1-1
Number of citations: 42, Impact Factor: -1
30. 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: 122, Impact Factor: 3.135

• **2002**

31. 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: 25, Impact Factor: 3.135
32. Donnes, P. and Elofsson, A. "Prediction of MHC class I binding peptides, using SVMHC." *BMC Bioinformatics* **2002**, 3():25
Number of citations: 194, Impact Factor: 3.493
33. Elofsson, A. "A study on protein sequence alignment quality." *Proteins* **2002**, 46(3):330-339
Number of citations: 66, Impact Factor: 3.354
34. 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: 30, Impact Factor: 0.573

• **2003**

35. 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: 581, Impact Factor: 5.039
36. 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: 72, Impact Factor: 3.354
37. 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: 65, Impact Factor: 3.354
38. Wallner, B. and Elofsson, A. "Can correct protein models be identified?" *Protein Sci* **2003**, 12(5):1073-1086
Number of citations: 213, Impact Factor: 3.135
39. 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: 126, Impact Factor: 3.354
40. 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: 73, Impact Factor: 5.501

- **2004**

41. 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: 135, Impact Factor: 3.135
42. 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: 34, Impact Factor: 3.354
43. 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: 71, Impact Factor: 3.354

- **2005**

44. 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: 28, Impact Factor: 3.234
45. 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: 23, Impact Factor: 3.493
46. 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: 80, Impact Factor: 5.501
47. 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: 112, Impact Factor: 3.135
48. Light, S., Kraulis, P. and Elofsson, A. "Preferential attachment in the evolution of metabolic networks." *BMC Genomics* **2005**, 6():159
Number of citations: 44, Impact Factor: 4.18
49. 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: 75, Impact Factor: 5.501
50. 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: 96, Impact Factor: 5.501
51. Wallner, B. and Elofsson, A. "Pcons5: combining consensus, structural evaluation and fold recognition scores." *Bioinformatics* **2005**, 21(23):4248-4254
Number of citations: 49, Impact Factor: 5.039

- **2006**

52. 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: 140, Impact Factor: 6.589
 53. Bjorklund, A.K., Ekman, D. and Elofsson, A. "Expansion of Protein Domain Repeats." *PLoS Comput Biol* **2006**, 2(8):e114
Number of citations: 78, Impact Factor: 6.236
 54. 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: 28, Impact Factor: 5.039
 55. 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: 49, Impact Factor: 5.501
 56. 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: 90, Impact Factor: 3.135
 57. 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: 30, Impact Factor: 6.954
 58. 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: 1, Impact Factor: 0.573
 59. 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**
60. 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: 33, Impact Factor: 6.954
 61. 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: 28, Impact Factor: 5.501
 62. 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: 51, Impact Factor: 3.354

63. 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: 11, Impact Factor: 6.589

• **2008**

64. 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: 10, Impact Factor: 3.135
65. 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: 5, Impact Factor: 3.354
66. 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: 24, Impact Factor: 3.135
67. 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: 85, Impact Factor: 9.598
68. 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: 10, Impact Factor: 5.501
69. 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: 52, Impact Factor: 5.039
70. 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: 10, Impact Factor: 5.479
71. 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: 22, Impact Factor: 5.039

• **2009**

72. 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: 66, Impact Factor: 23.308
73. 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: 14, Impact Factor: 3.354

74. 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: 54, Impact Factor: 6.954
75. 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: 19, Impact Factor: 3.354

• **2010**

76. Ekman, D. and Elofsson, A. "Identifying and Quantifying Orphan Protein Sequences in Fungi." *J Mol Biol* **2010**, 396(2):396-405
Number of citations: 3, Impact Factor: 5.501
77. 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: 18, Impact Factor: 5.501
78. 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: 15, Impact Factor: 5.501
79. 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: 4, Impact Factor: 3.493
80. 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: 2, Impact Factor: 5.501
81. 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: 2, Impact Factor: 2.175
82. 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: 5, Impact Factor: 3.232
83. 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: 1, Impact Factor: 3.135

• **2011**

84. 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: 2, Impact Factor: 3.354

85. 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: 2, Impact Factor: 5.039
86. Basmarke-Wehelie, R., Sjolinder, H., Jurkowski, W., Elofsson, A., Arnqvist, A., Engstrand, L., Hagner, M., Wallin, E., Guan, N., Kuranasekera, H., Aro, H. and Jonsson, A.B. "The Complement Regulator CD46 Is Bactericidal to *Helicobacter pylori* and Blocks Urease Activity." *Gastroenterology* **2011**, 141(3):918-928
Number of citations: 0, Impact Factor: 12.182
87. Hennerdal, A. and Elofsson, A. "Rapid membrane protein topology prediction." *Bioinformatics* **2011**, 27(9):1322-1323
Number of citations: 2, Impact Factor: 5.039
88. Shu, N. and Elofsson, A. "KalignP: Improved multiple sequence alignments using position specific gap penalties in Kalign2." *Bioinformatics* **2011**, 27(12):1702-1703
Number of citations: 0, Impact Factor: 5.039

- **2012**

89. Contreras, F.X., Ernst, A.M., Haberkant, P., Bjorkholm, P., Lindahl, E., Gonen, B., Tischer, C., Elofsson, A., von Heijne, G., Thiele, C., Pepperkok, R., Wieland, F. and Brugger, B. "Molecular recognition of a single sphingolipid species by a protein's transmembrane domain." *Nature* **2012**, 481(7382):525-529
Number of citations: 0, Impact Factor: 28.751
90. Hayat, S. and Elofsson, A. "BOCTOPUS: improved topology prediction of transmembrane beta barrel proteins." *Bioinformatics* **2012**, 28(4):516-522
Number of citations: 0, Impact Factor: 5.039

Review articles

- **1997**

91. 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: -1

- **2002**

92. 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: 4, Impact Factor: 6.589

- **2007**

93. Elofsson, A. and von Heijne, G. "Membrane protein structure: prediction versus reality." *Annu Rev Biochem* **2007**, 76():125-140
Number of citations: 122, Impact Factor: 31.19

- **2008**

94. 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: 62, Impact Factor: 14.994

• **2011**

95. Hedin, L.E., Illergard, K. and Elofsson, A. "An Introduction to Membrane Proteins (dagger)." *J Proteome Res* **2011**, 10(8):3324-3331
Number of citations: 0, Impact Factor: 5.675

• **2012**

96. Norholm, M.H., Light, S., Virkki, M.T., Elofsson, A., von Heijne, G. and Daley, D.O. "Manipulating the genetic code for membrane protein production: What have we learnt so far?" *Biochim Biophys Acta (Epub ahead of print)* **2012**, 1818(4):1091-1096
Number of citations: 0, Impact Factor: 2.59

Book chapters

• **1991**

97. 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**, (0):1-1
Number of citations: 4, Impact Factor: 0

• **1994**

98. 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: 0, Impact Factor: 2.269

• **1998**

99. Zhang, X.-P., Elofsson, A. and Glaser, E. "Interaction of mt-HSP70 with mitochondrial presequences" *Plant Mitochondria: From gene to Function (Moller, I.M., Gardeström, P., Glimelius, K. and Glaser, E., eds)* **1998**, 1():1-1
Number of citations: 0, Impact Factor: 2.269

• **2001**

100. Fang, H., Wallner, B. Lundström, J., von Wowern, C. and Elofsson, A. "Improved fold recognition by using the Pcons consensus approach" *Chapter in Protein structure prediction: Bioinformatic approach I IUL biotechnology Series, La Jolla*, **2001**, 1():397-41
Number of citations: 2, Impact Factor: 2.269

• **2008**

101. 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

In press

102. Kenichiro Imai, Sikander Hayat, Noriyuki Sakiyama, Naoya Fujita, Kentaro Tomii, Arne Elofsson and Paul Horton "Localization prediction and structure-based *in silico* analysis of bacterial proteins – with emphasis on outer membrane proteins", *Methods in Mol. Biol.* in press
103. Light, S, Sagit, R, Ithychanda, SS, Qin J and Elofssonm A "The evolution of filamin - a protein domain repeat perspective", *J. Struct Biol* in press
Number of citations: 0, Impact Factor: 2.986

Submitted

104. K.D. Tsirigos, A. Hennerdal, L. Kall and A. Elofsson "A guideline to proteome-wide α -helical membrane protein topology predictions", submitted to *Proteomics*.
105. S. Hayat and A. Elofsson "TMBMODEL: Toward 3D modeling of transmembrane β barrel proteins based on z-coordinate and topology prediction", submitted to ISCB-2012
106. D. Liberles... A.Elofsson... "The Interface of Protein Structure, Protein Biophysics, and Molecular Evolution", minor revision in *Protein Science*.

Manuscripts

107. M. Bendz, M. Skwark, D. Nilsson, V. Granholm, S. Cristobal, L. Kall and A. Elofsson "Membrane shaving - the search for the optimal method", manuscript
108. D. Nilsson, M. Virkii, L. Hedin, C. Peters, B. Wallner, S. Cristobal and A. Elofsson "A study of interactions affecting the insertion of marginally hydrophobic TM-helices", manuscript in preparation.

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 homology 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)

Research Group

Graduate Students:

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

Postdocs

- | | |
|------------------------------------|---------------------------------|
| 1. Sara Light <i>July-2009-</i> | Protein interactions |
| 2. Sikander Hayat <i>Apr-2010-</i> | Membrane proteins |
| 3. Nanjiang Shu <i>Jul-2010-</i> | Membrane protein bioinformatics |

Alumni

Guest professors

- Costas Papaloukas, *Jul 2006 - Jan 2007* 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" (Co-supervised)
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"
13. Aron Hennerdal, Oct 14, 2011 "Membrane protein predictions"

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
10. Dr. Maria Bendz, *June-2008-Dec 2011* MS on membrane proteins