

CURRICULUM VITAE

Arne Elofsson

March 30, 2008

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. Scientific positions

- Jul 1989 - Aug 1993 PhD-position in Medical Biophysics at Dept. of Medical Biophysics, Karolinska Institutet. 7 May 1993 Thesis, "Biophysical Aspects of Proteins", Supervised by Rudolf Rigler and Lennart Nilsson.
- 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 Forskarassistent at Dept. of Biochemistry, University of Stockholm
- Dec 1999 -Jan 2006 Lektor at Dept of Biochemistry and Stockholm Bioinformatics Center (SBC)
- Dec 1999 -June 2005 Vice director at SBC
- Feb 2006 - Professor in Bioinformatics at Department of Biochemistry and Biophysics, Stockholm University

. Parental leave

- April - July 2005

. Schools:

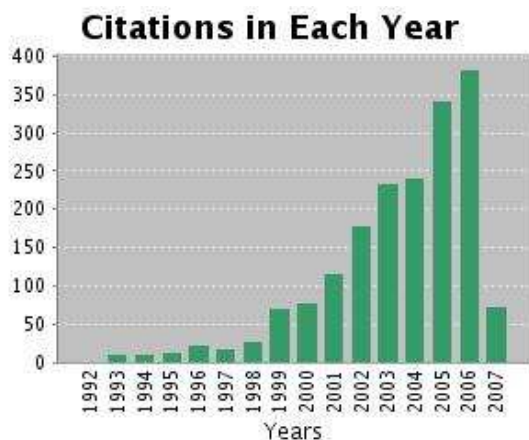
- Aug 1973 - Jun 1985 Studies at Smedslättens skola, Ålstens skola, Äppelvikens skola and Bromma Gymnasium Stockholm, Sweden
- Aug 1985 - Jun 1986 Studies in engineering physics (Teknisk fysik) at Uppsala University, Uppsala, Sweden.
- Aug 1986 - Jun 1988 Studies in the MD/PhD program (läkarlinjen med 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
- Full Professorship at Department of Biochemistry and Biophysics, Stockholm University Febr 1, 2006

Summary

- 75 scientific publications including
 - 61 publication in peer reviewed journals
 - 5 review articles
 - 6 publication in books/proceedings
 - 3 submitted articles
- Cited more than 2100 times (From Citation Index)
- More than 200 (300) citations per year since 2003 (2005)
- Average citation per paper: 34
- H-index 25 (since 1990, i.e. 1.5/year)



Articles in peer reviewed journals

- **1990**
 1. Arne Elofsson, Lennart Nilsson and Rudolf Rigler “Studies on somatostatin with time-resolved spectroscopy and molecular dynamics simulations”, *Int. J. Pept. Prot. Res.* **1990**:36, 297–301.
- **1991**
 2. Arne Elofsson, Rudolf Rigler, Lennart Nilsson, Johnny Roslund, Günter Krause and Arne Holmgren, “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 molecular dynamic simulations.” *Biochemistry*, **1991**:30 9648–9656.
- **1992**

3. Chris Sander, Gerrit Vriend, Fernando Bazan, Amnon Horovitz, Haruki Nakamura, Luis Ribas, Alexei V. Finkelstein, Andrew Lockhart, Rainer Merkl, L. Jeanne Perry, Stephen C. Emery, Christine Gaboriaud, Cara Marks, John Moulton, Christophe Verlinde, Marc Eberhard, Arne Elofsson, Tim J. P. Hubbard, Lynne Regan, Jay Banks, Roberto Jappelli, Arthur M. Lesk and Anna Tramontano, "Protein Design on Computers. Five New Proteins: Shpilka, Grendel, Fingerclasp, Leather and Aida" *Proteins, Structure Function and Genetics*; **1992**:12, 105–110
- **1993**
 4. Arne Elofsson and Lennart Nilsson, "How consistent are Molecular Dynamics simulations ? A comparison between the structure and Dynamics of Reduced and Oxidised Escherichia Coli Thioredoxin." *J. Mol. Biol.* **1993**:233, 766–780.
 5. Arne Elofsson and Lennart Nilsson, "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.
 6. Arne Elofsson, Tadeusz Kolinski, Rudolf Rigler and Lennart Nilsson "Site Specific Point Mutations Changes Specificity. A Molecular Modelling Study by Free Energy Simulations of the Thermodynamics in Ribonuclease T1 Substrate Interactions" *Proteins, Structure Function and Genetics* **1993** 17:161–175
 - **1995**
 7. Arne Elofsson, Scott LeGrand and David Eisenberg "Local moves, an efficient method for protein folding simulations" *Proteins, Structure Function and Genetics* **1995** 23:73–82
 - **1996**
 8. Arne Elofsson and Lennart Nilsson, "A 1.2 ns Molecular Dynamic Simulation of Ribonuclease T1-3'-Guanosine monophosphate complex" *J. Phys. Chem*, **1996** 100:2480–2488
 9. Arne Elofsson, Daniel Fischer, Danny W. Rice, Scott M. LeGrand and David Eisenberg "A study of combined structure-sequence profiles" **1996** *Folding & Design* 1:451–461
 - **1997**
 10. Miklos Cserzö, Erik Wallin, Istvan Simon, Gunnar von Heijne and Arne Elofsson, "Prediction of transmembrane α -helices: Application of the Dense Alignment Surface method" *Protein Engineering*, **1997**, 10(6):673–676
 11. Erik Wallin, Tomotake Tsukihara, Shinya Yoshikawa, Gunnar von Heijne and Arne Elofsson "Architecture of helix bundle membrane proteins. An analysis of cytochrome c oxidase from bovine mitochondria.", *Protein Science* **1997** 6:808–815
 12. Ismael Mingarro, Arne Elofsson, Gunnar von Heijne "Helix-helix packing in a membrane-like environment." , *J. Mol. Biol.* **1997** 272(4):633–541

- **1998**

13. K. Seshadri, Robert Garemyr, Erik Wallin, Gunnar von Heijne and Arne Elofsson “Architecture of β -barrel membrane proteins: Analysis of trimeric porins” *Protein Science* **1998** 7(9):2026–2032

- **1999**

14. Jeanette Hargbo and Arne Elofsson “Hidden Markov models that use predicted secondary structure for fold recognition” , *Proteins: Struct. Funct. Genet.* **1999** 36(1):68–76.
15. Xiao-Ping Zhang, Arne Elofsson, David Andreu and Elzbieta Glaser “Interaction of Mitochondrial presequences with DnaK and Mitochondrial hsp70” , *J. Mol. Biol.* **1999** 23;288(1):177–190.
16. Arne Elofsson and Erik L.L. Sonnhammer “A comparison of sequence and structure protein domain families as a basis for structural genomics.” *Bioinformatics* **1999** 15(6):480–500
17. Lawrence A. Kelley, Robert M. MacCallum, Michael Sternberg, Kevin Karplus, Daniel Fischer, Arne Elofsson, Adam Godzik, Leszek Rychlewski, Krysztof Pawlowski, David Jones and Kevin Bryson “CAFASP-1: Critical assessment of fully automated structure prediction.” *Proteins Struct. Funct. Genet.* **1999**; Suppl 3:209–217.
18. Robert Garemyr and Arne Elofsson “A study of the electrostatic treatment in molecular dynamics simulations” *Proteins, Struct. Funct. Genet.* **1999** 37(3):417–428
19. Magnus Monné, IngMarie Nilsson, Arne Elofsson and Gunnar von Heijne “Turns in transmembrane helices. Derivation of the minimal length of a “helical hairpin” and derivation of a fine-grained turn propensity scale. , *J. Mol. Biol.* **1999** 293(4):807–814.

- **2000**

20. Erik Lindahl and Arne Elofsson “Identification of related proteins, on family, superfamily and fold level.” *J. Mol. Biol.* **2000** 295:613–625
21. Naomi Siew, Arne Elofsson, Leszek Rychlewski and Daniel Fischer “Max-Sub: An automated measure to assess the quality of protein structure predictions.” *Bioinformatics* **2000** 16(9):776–785
22. Daniel Fischer, Arne Elofsson and Leszek Rychlewski “The 2000 Olympic Games of Protein Structure Prediction” *Protein Engineering* **2000** 13(10):667–670

- **2001**

23. Janusz M. Bujnicki, Arne Elofsson, Daniel Fischer and Leszek Rychlewski “LiveBench-1: Continuous Benchmarking of Protein Structure Prediction Servers” *Protein Science* **2001** 10(2):352–361.
24. Janusz M Bujnicki, Arne Elofsson, Daniel Fischer and Leszek Rychlewski “Structure Prediction Meta Server”, *Bioinformatics* **2001** 17: 750–751

25. Olivia Eriksson, Yishao Zhou and Arne Elofsson “Side chain-positioning as an integer programming problem.” “*WABI 2001 1st Workshop on Algorithms in BioInformatics*” **2001**
26. Susana Cristobal, Adam Zemla, Daniel Fischer, Leszek Rychlewski and Arne Elofsson “A study of quality measures for protein threading models.”, *BMC Bioinformatics* **2001** 2:5.
27. Jesper Lundström, Leszek Rychlewski, Janusz Bujnicki and Arne Elofsson “Pcons: A neural network based consensus predictor that improves fold recognition.” *Protein Science* **2001** 10(11):2354–2362
28. Daniel Fischer, Arne Elofsson, Leszek Rychlewski, Florencio Pazos, Alfonso Valencia, Burkhard Rost, Angel R. Ortiz, Roland L. Dunbrack “CAFASP2: The second critical assessment of fully automated structure prediction methods”, *Proteins Struct. Funct. Genet.* **2001**45(Suppl 5):171–183
29. Janusz M Bujnicki, Arne Elofsson, Daniel Fischer, Leszek Rychlewski “LiveBench-2: large-scale automated evaluation of protein structure prediction servers.” **2001** *Proteins Struct. Funct. Genet.* 45(Suppl 5):184–191
- **2002**
 30. Arne Elofsson “A study on protein sequence alignment quality.” *Proteins Struct. Funct. Genet.* **2002** 46(3):330–339
 31. David A. Liberles, Anna Thoren, Gunnar von Heijne and Arne Elofsson. “The use of Phylogenetic profiles for Gene Predictions”, *Current Genomics* **2002** 3:131–137
 32. Maria Hedman, Hans De Loof, Gunnar von Heijne and Arne Elofsson “Improved detection of homologous membrane proteins by inclusion of information from topology predictions,” *Protein Science* **2002** 11(3):652–658
 33. Pierre Dönnes and Arne Elofsson Prediction of MHC Class I Binding Peptides, using SVMHC, *BMC: bioinformatics* **2002** 3(1):25
This paper was rated “highly accessed” by BMC bioinformatics.
- **2003**
 34. Krzysztof Ginalski, Arne Elofsson, Daniel Fischer and Leszek Rychlewski, “3D-Jury: a simple approach to improve protein structure predictions” *Bioinformatics* **2003** 19(8):1015–1018.
 35. * Björn Wallner and Arne Elofsson “Can correct protein models be identified ?” , *Protein Science* **2003** 12(5):1073–1086
 36. Olof Emanuelsson, Arne Elofsson, Gunnar von Heijne and Susana Cristobal “In silico prediction of the peroxisomal proteome in fungi, plants and animals.” , *J. Mol. Biol* **2003** 330:443–456
 37. Björn Wallner, Huishang Fang and Arne Elofsson, “Automatic consensus based fold recognition using Pcons, ProQ and Pmodeller.” *Proteins Struct. Funct. Genet.* **2003** 53(S6):534–541
 38. Leszek Rychlewski, Daniel Fischer and Arne Elofsson “LiveBench-6: large-scale automated evaluation of protein structure prediction servers.” *Proteins Struct. Funct. Genet.* **2003** 53(S6):542–547

39. Daniel Fischer, Leszek Rychlewski, Roland L. Dunbrack, Angel R. Ortiz and Arne Elofsson, "CAFASP3: The third critical assessment of Fully Automated protein structure prediction methods." *Proteins Struct. Funct. Genet.* **2003** 53(S6):503–516

• **2004**

40. Björn Wallner, Huisheng Fang, Tomas Ohlson, Johannes Frey-Skött and Arne Elofsson "Using evolutionary information for the query and target improves fold recognition." , **2004** *Proteins Struct. Funct. Genet.* 54(2):342–350
41. * Håkan Viklund and Arne Elofsson "Best α -helical transmembrane protein topology prediction are achieved using hidden Markov models and evolutionary information.", *Protein Science* **2004** 13(7):1908–1917.
42. Tomas Ohlson, Björn Wallner and Arne Elofsson "Profile–profile methods provide improved fold–recognition. A study of different profile–profile alignment methods.", *Proteins Struct. Funct. Genet.* **2004** 57(1):188–197.

• **2005**

43. * Ann-Charlotte Berglund, Björn Wallner, Arne Elofsson, and David A. Liberles. "Tertiary Windowing to Detect Positive Selection" *J. Mol. Evol.* **2005** 60(4), 499-504
44. * Erik Granseth, Gunnar von Heijne, Arne Elofsson "A Study of the Membrane-Water Interface Region of Membrane Proteins" *J. Mol. Biol* **2005** 346(1):377-385.
This paper was the 9'th hottest paper from JMB published between Jan and Mar of 2005.
45. * Diana Ekman, Åsa K. Björklund, Sara Light, Johannes Frey-Skött and Arne Elofsson "Multi-domain proteins in the three kingdoms of life - Orphan domains and other unassigned regions." *J. Mol. Biol* **2005** 348(1):231-243
46. Björn Wallner and Arne Elofsson "All are not equal. A benchmark of different homology modeling programs." *Protein Science* **2005** 14(5), 1315-1327
47. * Åsa K. Björklund, Diana Ekman, Sara Light, Johannes Frey-Skött and Arne Elofsson "Domain rearrangements in protein evolution" *J. Mol. Biol* **2005** 353(4):911-923
This paper was the 7'th hottest paper from J. Mol. Biol. published between Oct and Dec of 2005.
48. Björn Wallner and Arne Elofsson "Pcons5: combining consensus, structural evaluation and fold recognition scores," **2005** *Bioinformatics* 21(23):4248–4254.
49. Tomas Ohlson and Arne Elofsson "Profnet, a method to derive profile–profile alignment scoring functions that improves the alignments of distantly related proteins.", *BMC Bioinformatics* **2005** 6:253
50. Sara Light, Per Kraulis and Arne Elofsson "Preferential attachment in the evolution of metabolic networks", *BMC Genomics*, **2005** 6:159
This paper was rated "highly accessed" by BMC genomics.

- **2006**

51. Björn Wallner and [Arne Elofsson](#) “Identification of correct regions in protein models using structural, alignment and consensus information”, *Protein Science* **2006** 15(4):900-913.
52. * Diana Ekman, Sara Light, Åsa K. Björklund and [Arne Elofsson](#) “What properties characterize the hub proteins of the protein-protein interaction network of *Saccharomyces cerevisiae*?”, *Genome Biology* 7(6):R45 **2006**. This paper was featured on the cover picture and ranked as 10:th most downloaded article in July 2006 and ranked as “highly accessed” by Genome Biology
53. * Erik Granseth, Håkan Viklund and [Arne Elofsson](#) “ZPRED: Predicting the distance to the membrane center for residues in alpha-helical membrane proteins”, *Bioinformatics* **2006** 22(14):e191-196
54. Mauro Amico, Michele Finelli, Ivan Rossi Andrea Zauli, [Arne Elofsson](#), Håkan Viklund, Gunnar von Heijne, David Jones, Anders Krogh, Piero Fariselli, Pier Luigi Martelli, Rita Casadio “PONGO: a web server for multiple predictions of all-alpha transmembrane proteins” *Nucleic Acids Research* **2006** 1;34(Web Server issue):W169-72.
55. * Håkan Viklund, Erik Granseth and [Arne Elofsson](#) “Reentrant regions in α -helical transmembrane proteins are divided in 3 structural classes and abundant in small residues”, *J. Mol. Biol.* **2006** 361(3):591-603
56. * Åsa K. Björklund, Diana Ekman and [Arne Elofsson](#) “Expansion of protein domain repeats” *PLOS Comp. Biol.* **2006** 2(8): e114
57. Tomas Ohlson, Varun Aggerwal, [Arne Elofsson](#) and Robert M MacCallum “Improved alignment quality by combining information, predicted secondary structure and self-organising maps.” *BMC Bioinformatics* **2006** 7(1):357

- **2007**

58. Björn Wallner, Per Larsson and [Arne Elofsson](#) “Pcons.net: Protein Structure Prediction Meta Server” *Nucleic Acids Research* **2007** 35:W369-74
59. Diana Ekman, Åsa K. Björklund and [Arne Elofsson](#) “Quantification of the elevated rate of domain rearrangements in metazoan.” *J. Mol. Biol.* **2007** 372(5):1337-48.
60. Björn Wallner and [Arne Elofsson](#) “Assessment of global and local model quality in CASP7 using Pcons and ProQ” *Proteins* **2007**Sep 25;69(S8):184-193
61. Andreas Bernsel, Håkan Viklund and [Arne Elofsson](#) “Remote homology detection of integral membrane proteins using conserved sequence features” *Proteins* **2007** Dec 12

- **2008**

62. Costas Papaloukas, Erik Granseth, Håkan Viklund and [Arne Elofsson](#) “Estimating the Length of Transmembrane Helices Using Z-coordinate Predictions”, *Protein Science* **2008** 17: 271-278;

63. Andreas Bernsel, Håkan Viklund, Jenny Falk, Erik Lindahl, Gunnar von Heijne, Arne Elofsson “Prediction of membrane-protein topology from first principles *Proc. Natl. Acad. Sci* **2008**, in press

Review articles

64. Lena EF Milchert, David A Liberles and Arne Elofsson “The salmon genome (and other issues in bioinformatics)” *Genome Biology* **2002** 3(7):reports4022.1-4022.4
65. David A. Liberles, Anna Thoren, Gunnar von Heijne and Arne Elofsson. “The use of Phylogenetic profiles for Gene Predictions”, *Current Genomics* **2002** 3:131–137
66. Åsa Björklund, Anna Thoren, Gunnar von Heijne and “The use of Phylogenetic profiles for Gene Predictions Revisited”, *Current Genomics* **2006** 7(2):79–86
67. Arne Elofsson and Gunnar von Heijne “Membrane Protein Structure: Prediction vs Reality”, *Annu Rev. Biochem* **2007** Jan 17
68. Timothy Hughes, Diana Ekman, Himanshu Ardawatia, Arne Elofsson, and David A. Liberles “Gene duplication, whole genome duplication, and Paramecium tetraurelia” *Genome Biology* **2007** 8(5):213

Chapters in books

69. Rigler, R., Wennerberg, A. B. A., Cooke, R. M., Arne Elofsson, Nilsson, L., Vogel, H., Holley, L. H., Carlquist, M., Langel, U., Bartfai, T., and Campbell, I. “On the solution structure of Galanin.”. In *Galanin* ed. T. Hökfelt and T. Bartfai, McMillan, (1991)
70. Arne Elofsson, “Recent advances in how to test knowledge based energy functions for protein folding studies.” in “*Recent Research Developments in Physical Chemistry*” **1997**
71. Xiao-Ping Zhang, Arne Elofsson and Elzbieta Glaser “Interaction of mt-HSP70 with mitochondrial presequences” *Plant Mitochondria: From gene to Function* (Moller, I.M., Gardeström, P., Glimelius, K. and Glaser, E., eds), *Bacjays Publ*, pp. 101-105 **1998**
72. Huisheng Fang, Björn Wallner, Jesper Lundström, Christer von Wower and Arne Elofsson “Improved fold recognition by using the Pcons consensus approach” Chapter in “*Protein structure prediction:Bioinformatic approach*” *IUL biotechnology Series, La Jolla, pp. 397-416* **2001**
73. Björn Wallner and Arne Elofsson “Prediction of global and local model qualities using MQAPs” Chapter in *In press* **2007**

Articles in conference proceedings

74. Scott LeGrand, Arne Elofsson and David Eisenberg, “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 II*. Edited by Henrik Bohr **1994**

75. Daniel Fischer, [Arne Elofsson](#), Danny W Rice, Scott LeGrand. and David Eisenberg “Assessing the Performance of Fold Recognition Methods By Means of a Comprehensive Benchmark.” in *Proc. Pacific Symposium on Biocomputing, Hawaii*, 300-318 January **1996**.

Submitted articles

76. Håkan Viklund and [Arne Elofsson](#) “OCTOPUS: A topology predictor for transmembrane proteins that includes reentrant regions in the topological grammar.”, submitted
77. Per Larsson, Björn Wallner, Erik Lindahl and [Arne Elofsson](#) “On the use of multiple templates to improve quality of homology model”, submitted

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 and 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/>
 - octopus - Combined predictor of topology and reentrant regions
 - SCAMPI - A scale based membrane protein predictor
 - pro/prodiv-TMHMM - The state of the art predictor of transmembrane regions.
 - DAS - A predictor of transmembrane regions.
 - Zpred - a predictor of the distance to the membrane center.

The 10 most important articles (that also are the most important for this project) are marked with a *

Grants

- Since 1995 received individual research grants for 32 286 KSEK (3.5 MEuro)
 - Research councils 8 265 kSEK
 - European Union 1 195 kEuro
 - Strategic foundation 8 835 kSEK
 - Other foundations 4 192 KSEK
- Equipment (computing clusters) 10 200 KSEK
- Co-applicant in center grants 98 000 KSEK (10.5 MEuro)

Grants received per year in kSEK

Year	VR	SSF	EU	other	Equipment	Centers
2007	1575	1855	8740	-	2700	
2006	1500	430	-	-		
2005						58 000
2004	1200	1800	1850	1044		
2003			4300	163		
2002	970					
2001				2375		
2000		4750		400	7500	40 000

Research councils

- 1995 TFR “Computing resources” 300 kSEK
- 1995-1997 TFR “Protein bioinformatics in the post genomic era. Interactions, multi domain, membrane proteins and other challenges.” 1 300 kSEK
- 1997-1999 NFR “Protein structure prediction” 300 kSEK
- 1999-2000 TFR “Protein structure prediction” 620 kSEK
- 2000-2002 NFR “Protein structure prediction” 500 kSEK
- 2003 VR (NT) “Development of improved methods to predict the function and structure of proteins” 160 kSEK
- 2003-2005 VR (NT) “Development of improved methods to predict the function and structure of proteins.” 810 kSEK
- 2005-2006 VR (M) “Classification, identification and prediction of GPCRs and other membrane protein families” 1 200 kSEK
- 2007-2009 VR (NT) “Structure based classification, identification and prediction of GPCRs and other membrane protein families” 1 500 kSEK
- 2007 Cluster for computational chemistry (Co-app) 2 700 kSEK
- 2008-2010 VR (M) “The evolution of protein domain repeats and their implication for signalling and disease” 1 575 kSEK

Strategic Foundation

- 2000-2004 Stockholm Bioinformatics Center (Co Applicant) 40 000 kSEK
 - My grant 1 500 kSEK
 - My salary 3 250 kSEK
- 2005-2008 Bio-X: Studies of membrane protein interactions 5 000 kSEK
 - My part 1 800 kSEK
- Center for Biomembrane Research (Co-applicant) 58 000 kSEK
 - 2006 CBR grant to me 430 kSEK 2007 CBR grant to me 1 855 kSEK

European Union

- FP6
 - 2004-2006 STREP: “GeneFun - Gene Function Predictions” LSHG-CT-2004-503567 240 kEuro
 - 2004-2009 NoE: “Biosapiens A European Virtual Institute for Genome Annotation” (Co-applicant) 200 kEuro
 - 2005-2010 NoE: “EMBRACE A European Model for Bioinformatics Research and Community Education” LSHG-CT-2004-512092 205 kEuro
- FP7
 - 2008-2012 IRP: “POCEMON Personal health systems for monitoring and point of care” 233 kEuro
 - 2008-2012 IRP: “EDICT European Drug Initiative on Channels and Transporters” 517 kEuro
 - 2008-2010 ITN: “Transys - A systems approach to defining membrane protein networks and applications”, 200 kEuro

Others grants

- 1996 Magnus Bergvall 60 kSEK
- 1999 Sven och Ebba-Christina Högbergs prize 150 kSEK
- 2000-2004 K.A.Wallenberg Computer cluster (Co-applicant) 7.500 kSEK
- 2000-2005 K.A.Wallenberg SweLL Teaching grant (Co-applicant) (my part) 400 kSEK
- 2001-2005 PhD position “Research shool in genomics and bioinformaics” 2.075 kSEK
- 2001-2004 Lawski PhD scholarship to Olivia Eriksson 300 kSEK
- 2002-2003 Carl Trygger 163 kSEK
- 2004-2005 Research position from Walleberg Consortium North 1.044 kSEK

Invited talks and lectures

- Invited to talk at International society for molecular modelings conference on Structural Genomics in Cambridge, UK 2000
- Invited to workshop Algorithmique et Biologie at Pasteur, Paris 2000
- Invited talk at Bioinformatics'2001 (2001)
- Invited talk at CASP5 (Dec, 2002)
- Invited talk at TERAPROT workshop in Paris (Jan, 2003)
- Invited talk at University of Saarbrucken (Jun, 2003)
- Invited talk at University of Bergen (Nov, 2003)
- Invited talk at UCLA (Mar, 2004)
- Invited talk at the Biotech Forum in Copenhagen (Oct 2004)
- Invited talk at the Computational Biology Workshop in Stockholm in Stockholm (Oct 2004)
- Invited talk at the COST meeting in Toulouse (Oct 2004)
- vited talk to "Sequence-structure-function: Theoretical and experimental approaches" in Warsaw (Apr 2005)
- Invited short talk at CASP6 (Dec, 2007) Delivered by Björ Wallner
- 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"m Havanna 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 (April 2008)

Organizing international conferences

- Organized workshop "Biophysical aspects of protein folding" (60 participants) 1997
- Organized the conference Bioinformatics'99 (app. 250 participants/conference)
- Member of organization committee for Bioinformatics'2000, '2001, '2002 and '2007
- Co-founder of the ABC-meeting in computational chemistry. A bi-annual meeting of computational chemistry scientists in the Stockholm-Uppsala area.
- Co-founder of the meetings in bioinformatics. An annual meeting of bioinformaticians in the Stockholm-Uppsala area.

Awards

- Sven och Ebba-Christina Högbergs pris 1999

Memberships

- 1998-2000 Secretary in the Swedish Biophysical society.
- 2004-2010 President of the Society for Bioinformatics in the Nordic countries

Editorial boards

- 1997 Editor of “Internet journal of science”
- 2007 Member of editorial board for highlight track for ISMB’07
- 2008 Member of editorial board for highlight track for ISMB’08
- 2008-11 Associate editor for Protein science

Program committees

- 2001-2008 member of program committee at the Annual Conference on Intelligent Systems for Molecular Biology (ISMB)
- 1999-2008 Member of program committee for Bioinformatics’XX (chair 1999 and 2004)
- 2004 Member of program committee Data Mining in Functional Genomics and Proteomics:Current Trends and Future Directions, ECAI-2004 workshop
- 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
- 2008 Member of program committee for ECCB’08

Reviewing

- Member of the National Research Council review group for biotechnology, 2006, 2007
- Reviewing >20 articles annually from J. Mol. Biol., Proteins, Bioinformatics, Nucleic Acids Research, BMC Bioinformatics, Nat Biotech. Plos. Comp Biol. and other journals.
- external reviewer for ESF grant, 2008
- external reviewer for grant submitted to Wellcome Trust, 2006
- external reviewer for grant submitted to Norwegian Research Council, 2005
- external reviewer for grant submitted to Cancer UK, 2005
- external reviewer for grant submitted to Science Foundation Ireland, 2003
- external reviewer for grant submitted to Israel Science Foundation , 2002
- external reviewer for grant submitted to Netherlands Genomics Initiative, 2001
- external reviewer for grant submitted to Singapore Science program , 2001

PhD-reviews/committees

- 2000 Helsinki University Jarmo Alander
- 2002 Karolinska Institutet Pekka Mark
- 2003 Karolinska Institutet Nina Stålberg
- 2004 Karolinska Institutet Christian Storm
- 2006 Karolinska Institutet (Chair) Markus Wistrand
- 2006 Karolinska Institutet ???
- 2006 Stockholm University ??
- 2007 University of Sydney (opponent) ??

. Research Group

. Graduate Students:

- PhD students

- | | |
|--|-----------------------------|
| 1. Olivia Eriksson, <i>Jun-2001-current</i> | Mathematical Bioinformatics |
| 2. Åsa Björklund, <i>May-2004-current</i> | Protein domain networks |
| 3. Diana Ekman, <i>May-2004-current</i> | Protein domain networks |
| 4. Andreas Bernsel <i>Sep-2004-current</i> | Membrane proteins |
| 5. Kristoffer Illergård, <i>Mar-2005-current</i> | Domain evolution |
| 6. Per Larsson, <i>Mar-2005-current</i> | Homology Modelling |
| 7. Linnea Hedin, <i>Sep-2005-current</i> | Bio-X, proteomics |
| 8. Aron Hennerdahl, <i>Sep-2006-current</i> | Membrane proteins |
| 9. Jenny Falk, <i>Sep-2006-current</i> | Membrane proteins |

. Postdoctoral visitors:

- | | |
|---|---------------------------------------|
| 1. Anni Kauko <i>Feb 2007 - Current</i> | “Membrane protein structure analysis” |
| 2. Håkan Viklund, <i>Nov-2007-current</i> | Hidden Markov Models |

. Most important Collaborators

- Dr. Erik Lindahl, Protein and membrane simulations
- Doc. Susana Cristobal, Stockholm University Biochemistry
- Prof. Gunnar von Heijne, Stockholm University Membrane proteins

. Alumni

- Guest professors at sabbatical in my group

- | | |
|--|--------|
| 1. Dr. Costas Papaloukas, <i>Jul 2006 - Jan 2007</i> | Zpred2 |
|--|--------|

- Post-docs

- | | |
|--|-------------------------------------|
| 1. Dr. Miklos Cserzö, <i>Jan 1996 - Jun 1996</i> | DAS |
| 2. Dr. K. Seshadri, <i>Jun 1997 - Feb 1998</i> | Analysis of Membrane proteins |
| 3. Dr. Mats Eriksson, <i>Sep 1998 -Apr 2000</i> | Drug design |
| 4. Dr. Huisheng Fang, <i>Dec 2000-Dec 2002</i> | Fold Recognition |
| 5. Dr. Meftun Ahmed, <i>Jan 2002-Aug 2002</i> | Peroxisomes |
| 6. Dr. Nick Braun, <i>Nov 2002-Apr 2003</i> | Evolution of protein thermodynamics |
| 7. Erik Sandelin, <i>Mar 2003-Sep 2006</i> | Protein structure predictions |

- Supervised doctoral thesis

1. Håkan Viklund, Nov 23, 2007 “Membrane proteins”
2. Erik Granseth, Sep 24, 2007 “Membrane protein structures”
3. Sara Light May 19, 2006 “Investigations into the evolution of biological networks”

4. Tomas Ohlson Feb 24, 2006 “The use of evolutionary information in protein alignments and homology identification”
 5. Björn Wallner Sept 30, 2005 “Protein structure prediction: Model Building and Quality Assessment”
- Supervised licentiate thesis
 1. Robert Garemyr “A study of the electrostatic treatment in molecular dynamics simulations.”, Sept 1999
 2. Jakob Halaska “BioScript3D - A Biomolecular Visualization & Animation Tool”
 - Supervised more than 30 “Master” thesis (Examensarbeten)