<div align="center">

Curriculum Vitae

Kimmen Sjölander, Ph.D.

</div>

Current Title: Professor

Contact Information: Department of Bioengineering and Department of Plant and Microbial Biology, QB3 Institute, University of California Berkeley, 308C Stanley Hall, #1762, Berkeley, CA 94720-1762. Email: kimmen@berkeley.edu.

Education and Training: BA, Computer Science, UC Santa Cruz, Highest honors in the major, Phi Beta Kappa, 1993. PhD, Computer Science, UC Santa Cruz, 1997.

Selected Honors

1993   Elected to Phi Beta Kappa
1993   National Science Foundation Three-Year Graduate Research Fellowship
1996   Program in Mathematics and Molecular Biology Fellowship
2003   National Science Foundation CAREER Award
2004   National Science Foundation Presidential Early Career Award in Science and Engineering (PECASE)

Positions and Employment

1997-1999   Chief Scientist, Molecular Applications Group, Palo Alto, California

1999-2001   Principal Scientist, Protein Informatics, Celera Genomics, California

2001-2006   Assistant Professor, Department of Bioengineering, University of California, Berkeley

2006-2012   Associate Professor,   Department of Bioengineering and Department of Plant and Microbial Biology, University of California, Berkeley

2012-present Professor, Department of Bioengineering and Department of Plant and Microbial Biology, University of California, Berkeley

Selected Publications (in chronological order)

1. Krogh, A., Brown, M., Mian, S., **Sjölander, K**. and Haussler, D., "Hidden Markov Models in Computational Biology: Applications to Protein Modeling," Journal of Molecular Biology 1994 Feb 4;235(5):1501-31.
2. Venter, C. et al, "The sequence of the human genome," Science, 2001 Feb 16;291(5507):1304-51. My contributions: the algorithms used for the Panther functional classification of the human genome.
3. Edgar, R., and **Sjölander, K**., "SATCHMO: Sequence Alignment and Tree Construction using Hidden Markov models," Bioinformatics. 2003 Jul 22;19(11):1404-11. Selected by the Faculty of 1000 as a "Must Read" for Technological Advance (rating 6.0).
4. Magnani, E., **Sjölander, K**. and Hake S., "From endonucleases to transcription factors: evolution of the AP2 DNA-binding domain in plants", Plant Cell, 2004 Sep;16(9):2265-77. *Selected by the Faculty of 1000 as a "Must Read".*
5. Kleffmann, T., Russenberger, D., von Zychlinski, A., Christopher, W., **Sjölander, K**., Gruissem, W., and Baginsky, S. "The Arabidopsis thaliana chloroplast proteome reveals pathway abundance and novel protein functions," Current Biology 2004 Mar 9;14(5):354-62.
6. **Sjölander, K**., "Phylogenomic inference of protein molecular function: advances and challenges," Bioinformatics 2004 (20)2:170-179.
7. von Zychlinski A, Kleffmann T, Krishnamurthy N, **Sjölander K**, Baginsky S, Gruissem W., "Proteome analysis of the rice etioplast: metabolic and regulatory networks and novel protein functions", Mol Cell Proteomics. 2005 May 20.
8. Lillian Fritz-Laylin, Nandini Krishamurthy, Mahmut Tor, **Kimmen Sjölander*** and Jonathan Jones. "Phylogenomic analysis of the receptor-like proteins of rice and Arabidopsis", Plant Physiology, June 2005, Vol. 138, pp. 611-623
9. Stephen T. Chisholm, Douglas Dahlbeck, Nandini Krishnamurthy, Brad Day, **Kimmen Sjölander**, and Brian J. Staskawicz, "Molecular characterization of proteolytic cleavage sites of the Pseudomonas syringae effector AvrRpt2", Proceedings of the National Academy of Sciences, February 8, 2005, vol. 102, no. 6, 2087-2092.
10. Rebecca Middleton*, **Kimmen Sjölander***, Nandini Krishnamurthy, Jonathan Foley, and Patricia Zambryski, "Predicted hexameric structure of the Agrobacterium VirB4 C terminus suggests VirB4 acts as a docking site during type IV secretion", Proceedings of the National Academy of Sciences 2005 Feb 1;102(5):1685-90. (*Joint first authors.)

11. Nandini Krishnamurthy, Duncan Brown, Dan Kirshner and **Kimmen Sjölander**, "PhyloFacts: An online structural phylogenomic encyclopedia for protein functional and structural classification," Genome Biology 2006, 7:R83. *Noted as "Highly Accessed" by the journal.*
12. Brown DP, Krishnamurthy N, **Sjölander K**, "Automated Protein Subfamily Identification and Classification," PLoS Computational Biology 2007, 3(8): e160 doi:10.1371/journal.pcbi.0030160. *Selected by the Faculty of 1000 as a technological advance.*
13. Jake Gunn Glanville, Dan Kirshner, Nandini Krishnamurthy and **Kimmen Sjölander**, "Berkeley Phylogenomics Group web servers: resources for structural phylogenomic analysis" Nucleic Acids Research Web Server Issue, 2007; doi:10.1093/nar/gkm325
14. Sriram Sankararaman* and **Kimmen Sjölander**, "INTREPID - INformation-theoretic TREe traversal for Protein functional site IDentification," Bioinformatics 2008; doi: 10.1093/bioinformatics/btn474.
15. Sriram Sankararaman, Bryan Kolaczkowski and **Kimmen Sjölander** "INTREPID: a web server for prediction of functionally important residues by evolutionary analysis," Nucleic Acids Research 2009; doi: 10.1093/nar/gkp339
16. Ruchira S. Datta, Christopher Meacham, Bushra Samad, Christoph Neyer and **Kimmen Sjölander** ,"Berkeley PHOG: PhyloFacts Orthology Group Prediction Web Server," Nucleic Acids Research Web Server Issue 2009; doi: 10.1093/nar/gkp373.
17. Hagopian, R., Davidson, J., Datta, R., Samad, B., Jarvis, G., and **Sjölander,** K. "SATCHMO-JS: a webserver for simultaneous protein multiple sequence alignment and phylogenetic tree construction," Nucleic Acids Research 2010, doi:10.1093/nar/gkq298. *Selected as a Featured Article by NAR.*
18. Sriram Sankararaman, Fei Sha, Jack F. Kirsch, Michael I. Jordan, and **Kimmen Sjölander**, "Active Site Prediction using Evolutionary and Structural Information," Bioinformatics 2010; doi: 10.1093/bioinformatics/btq008.
19. **Sjölander, K**., Datta, R., Shen, Y., Shoffner, G., "Ortholog identification in the presence of domain architecture rearrangement," Briefings in Bioinformatics 2011; doi: 10.1093/bib/bbr036.
20. Shen, Y., Bonnot, F., Imsand, E., Rosefigure, J., **Sjölander,** K*, Klinman*, J., "Distribution and Properties of the Genes Encoding the Biosynthesis of the Bacterial Cofactor, Pyrroloquinoline Quinone," Biochemistry 2012; doi: 10.1021/bi201763d (co-corresponding author)
21. Liberles, D., Teichmann, et al., "The interface of protein structure, protein biophysics, and molecular evolution," Protein Science 2012; doi: 10.1002/pro.2071

Patent held:

Sjölander, K. (2000) U.S. Patent No. 6,128,587: Method and apparatus using Bayesian subfamily identification.

Webservers and databases provided to the scientific community:

PhyloFacts Phylogenomic Encylcopedias, at http://phylogenomics.berkeley.edu/phylofacts/. PhyloFacts release PF3.0.2 contains >7M protein sequences from >99K unique taxa across the Tree of Life grouped into >92K families.