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## *Curriculum Vitae* – Lukas Käll

### **Address**

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### **Higher Level Education**

**Postdoc** University of Washington, Department of Genome Sciences 2006-08.  
I worked under the supervision of William Stafford Noble with a set of computational and statistical proteomics projects.

**PhD Bioinformatics** Karolinska Institutet, 2002-06.  
I worked in Erik Sonnhammer's lab at the Center of Genomics and Bioinformatics. I defended my thesis "Predicting transmembrane topology and signal peptides with hidden Markov models" the 7th of April 2006.

**M.Sc. Engineering Physics** Uppsala University, 1989-94

**Licence de Physique** Ecole Normal Supérieur de Lyon, 1991-92

### **Professional experience**

**Stockholm University (2008-)** I currently work as an Assistant Professor at Center for Biomembrane Research at Stockholm university. I primarily work with large scale mapping of membrane proteins with mass spectrometry.

**University of Washington (2006-08)** I worked as a postdoctoral research fellow in William Stafford Noble's lab at Department of Genome Sciences between July 2006 and August 2008. I primarily worked with peptide identification by mass spectrometry, and how to improve peptide identification software using machine learning algorithms. I also investigated how to enforce transmembrane topology prediction using mass spectrometry data.

**Stockholm Bioinformatics Center (2006)** I worked as a postdoctoral research fellow in Erik Sonnhammer's lab at the Stockholm Bioinformatics Center between April and June 2006. I mainly worked with transmembrane topology prediction.

**Karolinska Institutet (2002-06)** I worked as a PhD Student in Erik Sonnhammer's lab at Karolinska Institutet between April 2002 and April 2006. See above.

**Spacemetric (2001-02)** At the small start-up company Spacemetric I took part in the development of a satellite image processing application.

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**Swedish Space Corporation (1997-2001)** My time at SSC was completely devoted to the SMART-1 lunar probe. SSC was the prime contractor for this European Space Agency driven project. I held various positions within the project including Software Coordinator, where I was responsible for the procurement of the on-board software (~1M Euro, ~20 thousand lines of code). I was also Project Leader for the Spacecraft Simulator. In this role, I was economically and technically responsible for a team of 6 people (~1M Euro, ~50 thousand lines of code)

**Pharmacia Biotech AB (1994-97)** At Pharmacia Biotech, (now called General Electric Healthcare,) I primarily worked with the DNA sequencer ALF Express. Among other things, I was involved in the algorithmic design of lane tracking and base calling algorithms.

## Refereed Publications

- I **Lukas Käll** and Erik L.L.Sonnhammer,  
Reliability of transmembrane predictions in whole-genome data.  
*FEBS Letters*, **532**:415-418, Dec 2002.
- II **Lukas Käll**, Anders Krogh and Erik L. L. Sonnhammer,  
A Combined Transmembrane Topology and Signal Peptide Prediction Method.  
*JMB*, **338**(5):1027-1036, May 2004.  
*Cited 155 times according to Google Scholar, Mar 2008*
- III Anna Henricson, **Lukas Käll** and Erik Sonnhammer,  
Transmembrane topology of presenilin by reconciling experimental and computational approaches,  
*FEBS Journal*, **272**(11):2727-2733, June 2005.
- IV **Lukas Käll**, Anders Krogh and Erik Sonnhammer,  
An HMM posterior decoder for sequence feature prediction that includes homology information,  
*Bioinformatics*, **21**(Suppl 1):i251-i257, June 2005.
- V Markus Wistrand\*, **Lukas Käll**\* and Erik Sonnhammer,  
A general model of G protein-coupled receptor sequences and its application to detect remote homologs,  
*Protein Science*, **15**(3):509-21, Mars 2006.  
\* These authors contributed equally to this work.
- VI **Lukas Käll**, Anders Krogh and Erik Sonnhammer,  
Advantages of combined transmembrane topology and signal peptide prediction – the Phobius web server,  
*Nucleic Acids Research*, **35**(Suppl 2):W429-W432Web, May 2007.
- VII **Lukas Käll**, Jesse Canterbury, Jason Weston, William Stafford Noble and Michael J. MacCoss,  
Semi-supervised learning for peptide identification from shotgun proteomics datasets  
*Nature Methods*, **4**:923-25, November 2007.

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- VIII Carolina Lundin, **Lukas Käll**, Scott Kreher, Erik Sonnhammer, John Carlson, Gunnar von Heijne and IngMarie Nilsson,  
Membrane topology of the *Drosophila* OR83b odorant receptor  
*FEBS Letters*, **581**:5601-4, December 2007
- IX **Lukas Käll**, John D. Storey, Michael J. MacCoss and William Stafford Noble,  
Assigning confidence measures to peptides identified by tandem mass spectrometry  
*Journal of Proteome Research*, **7**(1):29-34, January 2008
- X **Lukas Käll**, John D. Storey, Michael J. MacCoss and William Stafford Noble,  
Posterior error probabilities and false discovery rates: two sides of the same coin  
*Journal of Proteome Research*, **7**(1):40-44, January 2008
- XI Christopher Park, Aaron Klammer, **Lukas Käll**, Michael J. MacCoss and William Stafford Noble,  
Rapid and accurate peptide identification from tandem mass spectra,  
*Journal of Proteome Research*, **7**(7):3022-7, July 2008
- XII **Lukas Käll**, John D. Storey, William Stafford Noble,  
Nonparametric estimation of posterior error probabilities associated with peptides identified by tandem mass spectrometry,  
*Bioinformatics*, **24**(16):i42-i48, August 2008
- XIII Gennifer E. Merrihew, Colleen Davis, Brent Ewing, Anthony Rogers, **Lukas Käll**, Phil Green, James H. Thomas and Michael J. MacCoss,  
Use of Shotgun Proteomics for the Identification, Confirmation, and Correction of *C. elegans* Gene Annotations,  
*Genome Research*, **18**(10):1660-1669, October 2008
- XIV Sheila M. Reynolds, **Lukas Käll**, Michael E. Riffle, Jeff A. Bilmes and William Stafford Noble  
Transmembrane Protein Topology Prediction using Dynamic Bayesian Networks  
*PLOS Computational Biology*, **4**(11):e1000213, November 2008
- XV Nir Yosef and **Lukas Käll**,  
From sequence to structure to networks,  
*Genome Biology*, **9**(11):3022, November 2008
- XVI **Lukas Käll**, John D. Storey, William Stafford Noble  
quality: Nonparametric estimation of q values and posterior error probabilities  
*Bioinformatics*, **25**(7):964-966, February 2009
- XVII Marina Spivak, Jason Weston, Léon Bottou, **Lukas Käll**, William Stafford Noble  
Improvements to the Percolator algorithm for peptide identification from shotgun proteomics data sets  
*Journal of Proteome Research*, **8**(7):3737-3745, July 2009

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## Other Publications

- I **Lukas Käll** and Erik L.L.Sonnhammer,  
Predicting membrane proteins,  
Chapter in Dunn, M., ed., *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, John Wiley & Sons, 2005.
- II **Lukas Käll**,  
Predicting transmembrane topology and signal peptides with hidden Markov models,  
*PhD Thesis*.  
<http://diss.kib.ki.se/2006/91-7140-719-7/thesis.pdf>
- III **Lukas Käll**,  
Prediction of transmembrane topology and signal peptide given a proteins amino acid sequence,  
Chapter in Fenyo, D., ed., *Topics in Computational Biology*, Humana Press, 2009.

## Invited talks

- I was invited to speak at the European Science Foundation (ESF) workshop on "Quality Control in Proteomics" in Cambridge, UK 25-27 November 2009
- I was invited to speak at the "Characterization of Membrane Proteins" section of the largest annual mass spectrometry conference, the 57th American Society for Mass Spectrometry Conference, May-June 2009, Philadelphia, USA
- Paper XII was one of the 18% accepted papers at the largest European Bioinformatics conference, ECCB 2008, Cagliari, Italy.
- I was invited speaker at the Second International Workshop on Machine Learning in Systems Biology in the Palace of the Royal Academy of Belgium, Brussels September 13-14 2008
- Paper VII was one of 56 out of 189 submitted papers that were presented at the highlights track of ISMB 2008, Toronto, Canada.
- Paper IV was one of 56 out of 426 submitted papers that were accepted to the largest annual bioinformatics conference, ISMB 2005, Detroit, USA.

## Software

**HomologHMM** An HMM decoder able to handle homologs.

<http://phobius.cgb.ki.se/data.html>

**GPCRHMM** Prediction of G protein-coupled receptors and their transmembrane topology.

<http://noble.gs.washington.edu/~lukall/gpcrhmh>.

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**Percolator** A shotgun proteomics post-processor using semi-supervised machine learning.

<http://noble.gs.washington.edu/proj/percolator>

### **Prediction servers**

**Phobius** Combined prediction of transmembrane topology and signal peptides

More than 900 unique users and every month. 25 standalone licenses have been distributed.

<http://phobius.cbr.su.se/> or <http://phobius.binf.ku.dk/>.