
Curriculum Vitae

Name: **Lukas Käll**
Academic Title: Docent i Statistisk Bioteknik
Employment form: Biträdande Lektor (Associate Professor)
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Higher Level Education

Docent I was accepted as a Docent in Statistical Biotechnology, June 2012 at KTH, Stockholm.

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

Royal Institute of Technology (2013-) My present position is Associate Professor ("Lektor") at School of Biotechnology at the Royal Institute of Technology (KTH).

Royal Institute of Technology (2011-2013) I worked as an Assistant Professor ("Bitädande Lektor") at School of Biotechnology at the Royal Institute of Technology (KTH).

Stockholm University (2008-2011) I was employed as an Assistant Professor ("Forskarassistent") at Center for Biomembrane Research, in the Department of Biochemistry and Biophysics at Stockholm university.

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.

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.

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.

Supervision

I have supervised the following persons (PhD students or higher):

Name	Postion	Years
Luminita Moruz	PhD Student	2009 - (Nov 2013)
Viktor Granholm	PhD Student	2010 - (Apr 2014)
Jesper Lind	Postdoc	2010
Haipeng Wang	Postdoc	2012 - 2013
Magnus Rosenlund	Researcher	2012 -

PhD defense committe tasks

I have acted as an opponent at the following PhD defenses:

- Xiaobei Zhao, “On Gene Regulation in Eukaryotes Computational approaches to decipher transcriptional regulation at genetic and epigenetic level”, 9th of March 2012, at Faculty of Science, University of Copenhagen, Denmark.
- Niklaas Colaert, “Digging deeper in the data, novel approaches and analysis methods in quantitative peptide-centric proteomics”, 17th May 2011, at Faculty of Medicine and Health Sciences of University of Gent, Belgium.
- Harald Bransnes, “Development of tools for analyzing and sharing proteomics data”, at Matematisk-naturvitenskapelige fakultet of Universitetet i Bergen, Norway, the 22nd of March 2010.

I have worked as a comittee member in the defences of Møarten Neijman (30 May, 2013), MEB, Karolinska Institutet; Sverker Lundin (7 Dec, 2012), School of Biotechnology, KTH; and Johanna Hasmats (22 Nov, 2012), School of Biotechnology, KTH

Other scientific experience

- I was a friendly pre-reviewer of Génome Québec’s applications for Genome Canada competition in Bioinformatics and Computational Biology 2012.
- I was chairing the session “Data Analysis of Proteomics Assays” at the SocBin Bioinformatics 2012 conference, Karolinska Institutet, Sweden, June 11-14. socbin.org/bioinfo2012/
- I was chairing the session “Informatics: Identification” at 60th ASMS Conference on Mass Spectrometry and Allied Topics Vancouver, BC, Canada May 20 - 24, 2012 asms.org.
- I am since May 2012 an ASMS bioinformatics interest group coordinator
- I was a member of the program committe of RECOMB Satellite Conference on Computational Proteomics 2012 proteomics.ucsd.edu/recombcp2012/, San Diego, USA.
- I have acted as an project officer evaluating Project Grant proposals for the Mathematics panel of the Portuguese Foundation for Science and Technology, summer 2009.

Teaching experience

Bioinformatics and Biostatistics, BB2440 I was course responsible for this 7.0hp course at KTH Biotechnology, Fall 2013.

Analysis of data from high-throughput molecular biology experiments, BB2490 2013 I was course responsible for this 7.5hp course, taught together with Lars Arvestad and Olof Emanuelsson.

Bioinformatics and Biostatistics, BB2440 I gave two 2h lectures in this course at KTH Biotechnology, Fall 2012.

Functional regulation in development and disease, FRDD2012 I gave a 1.5 hour lecture on “Mass spectrometry-based proteomics” at the Karolinska Institutet - RIKEN Joint International Doctoral Course, 28th February, 2012

<http://www.osc.riken.jp/english/event/FRDD2012/>

Analysis of data from high-throughput molecular biology experiments, BB2490 2012 I developed, organized and taught this 7.5hp course together with Olof Emanuelsson.

ISMB2011 Summer 2011, “An insight into computational and statistical mass spectrometry-based proteomics”, A 4h Tutorial held at ISMB/ECCB, together with Olga Vitek, Purdue University

<http://www.iscb.org/ismbeccb2011-program/tutorials#am2>

Analysis of data from high-throughput molecular biology experiments, KB8018 2011 I developed, organized and taught this 7.5hp course. The course was co-localized with the KTH course BB2490, that was organized by Olof Emanuelsson.

Proteins - from gene to function, KB5001 2010 I organized the bioinformatics part of this course. (6h teaching)

Advanced biochemical methods, KB8002 2010 I organized the bioinformatics and biostatistics part of this course. (4h teaching)

Proteomics Data Analysis (PDA10) Fall 2010 I held the lectures and practicals for this one week course at the Instituto Gulbenkian, Portugal organized by me and Lennart Martens, University of Gent (2,5 days teaching and practicals)

ISMB2010 Summer 2010, “An insight into computational and statistical mass spectrometry-based proteomics”, A 4h Tutorial held at ISMB, together with Olga Vitek, Purdue University

Advanced biochemical methods, KB8002 2009 I organized the bioinformatics and biostatistics part of this course. (4h teaching)

Introduction to Bioinformatics (KB7004) I organized the machine learning and biostatistics part of this course. (4h teaching)

HMMs in Bioinformatics - Fall 2005 I organized a PhD course on the usage of hidden Markov models in bioinformatics at the Stockholm Bioinformatics Center. The participants read and present a pre-selected set of papers.

http://www.pdc.kth.se/~hakanv/HMM_course/index.html

Guest lecture - October 2004 I taught one of the session in Arne Leijons class on Pattern Recognition (2F1510) at the Royal Institute of Technology, Stockholm. I taught the students about how to employ hidden Markov models in bioinformatics.

<http://www.ee.kth.se/sip/courses/EN2200/>

Teacher assistant (“amanuens”) - Fall 2004 I assisted the biomedicine masters students through the computer labs of the course *Bioinformatics* organized by Bengt Persson at Karolinska Institutet, Stockholm.

<http://www.ifm.liu.se/bioinfo/biomedicin/schemaht04.html>

Refereed Publications

I have a h-index of 17 and a total of 2291 citations according to Google Scholar (Sep 2013).

1. **Lukas Käll** and Erik L.L.Sonnhammer,
Reliability of transmembrane predictions in whole-genome data.
FEBS Letters, 532:415-418, Dec 2002.
2. **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 588 times according to Google Scholar, Sep 2012

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3. 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.
 4. **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.
 5. 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.
 6. **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.
 7. **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.
 8. 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
 9. **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
 10. **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
 11. 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
 12. **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
 13. 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
 14. 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
 15. Nir Yosef and **Lukas Käll**,
From sequence to structure to networks,
Genome Biology, **9**(11):3022, November 2008
 16. **Lukas Käll**, John D. Storey, William Stafford Noble
qquality: Nonparametric estimation of q values and posterior error probabilities
Bioinformatics, **25**(7):964-966, February 2009

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17. 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
 18. Luminita Moruz, Daniela Tomazela and **Lukas Käll**
Training, Selection, and Robust Calibration of Retention Time Models for Targeted Proteomics. *J Proteome Res*, **9**(10):5209-5216, 2010
 19. **Lukas Käll**
Prediction of transmembrane topology and signal peptide given a protein's amino acid sequence. *Methods Mol Biol* **673**: 53-62, 2010.
 20. Viktor Granholm and **Lukas Käll**
Quality assessments of peptide-spectrum matches in shotgun proteomics. *Proteomics*, **11**(6):1086-1093, 2011.
 21. Viktor Granholm, William Stafford Noble and **Lukas Käll**
On using samples of known protein content to assess the statistical calibration of scores assigned to peptide-spectrum matches in shotgun proteomics. *Journal of Proteome Research*, **10**(5):2671-2678, 2011.
 22. **Lukas Käll** and Olga Vitek. Computational mass spectrometry-based proteomics. *PLoS Comp Biol* **7**(12):e1002277, 2011.
 23. Serang, O., Moruz, L., Hoopmann, M.R. and **Käll, L.** "Recognizing Uncertainty Increases Robustness and Reproducibility of Mass Spectrometry-based Protein Inferences." *J Proteome Res* **2012**, **11**(12):5586-5591
 24. Granholm, V., Noble, W.S. and **Käll, L.** "A cross-validation scheme for machine learning algorithms in shotgun proteomics." *BMC Bioinformatics* **2012**, **13** Suppl 16():S3
 25. Granholm, V., Navarro, J.F., Noble, W.S. and **Käll, L.** "Determining the calibration of confidence estimation procedures for unique peptides in shotgun proteomics." *J Proteomics* **2012**, **80C**():123-131
Number of citations: 0, Impact Factor: 3.851
 26. James C. Wright, Mark O. Collins, Lu Yu, **Lukas Käll**, Markus Broch and Jyoti S. Choudhary
Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator. *Molecular & Cellular Proteomics*, **11**(8):478-491, 2012
 27. Luminita Moruz, An Staes, Joe Foster, Maria Hatzou, Evy Timmerman, Lennart Martens, **Lukas Käll**
Chromatographic Retention Time Prediction for Post-translationally Modified Peptides. *Proteomics*, **12**(8):1151-1159, 2012
 28. Kostas D. Tsirigos, Aron Hennerdal, **Lukas Käll** and Arne Elofsson
A guideline to proteome-wide alpha-helical membrane protein topology predictions. *Proteomics* **12**(14):2282-2294, 2012
 29. Bendz, M., Skwark, M., Nilsson, D., Granholm, V., Cristobal, S., **Käll, L.** and Elofsson, A. "Membrane protein shaving with thermolysin can be used to evaluate topology predictors." *Proteomics* **2013**, **13**(9):1467-1480
 30. Moruz, L., Pichler, P., Stranzl, T., Mechtler, K. and **Käll, L.** "Optimized nonlinear gradients for reversed-phase liquid chromatography in shotgun proteomics." *Anal Chem* **2013**, **85**(16):7777-7785
 31. Serang, O., Cansizoglu, A. E., **Käll, L.**, Steen, H. and Steen, J. A. "Nonparametric Bayesian evaluation of differential protein quantification" *J Proteome Res*, **12**(10):4556-4565, 2013
 32. Moruz, L., Hoopmann, M., Rosenlund, M., Granholm, V., Moritz, R. and **Käll, L.** "Mass fingerprinting of complex mixtures: protein inference from high-resolution peptide masses and predicted retention times." *J Proteome Res*, **12**(12):4741-4741, 2013

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33. Granholm, V., Kim, S., Navarro, J.C.F., Sjölund, E., Smith, R.D. and Käll, L. "Fast and accurate database searches with MS-GF+Percolator", *J Proteome Res*, **13**(2):890-897, 2014.
34. Branca, R.M., Orre, L.M., Johansson, H.J., Granholm, V., Huss, M., Perez-Bercoff, A., Forshed, J., Käll, L. and Lehtio, J. "HiRIEF LC-MS enables deep proteome coverage and unbiased proteogenomics." *Nat Methods* **11** (1) : 59-62.

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>

Invited talks

- I was an invited speaker at the mass spectrometry special interest group (MS-SIG) at ISMB/ECCB 2013 in Berlin, in July 2013, the talk had the title "Protein inferences from unfragmented peptides' masses and predicted retention times"
- I was an invited speaker at the First Austrian Proteomics Association Computational Proteomics Workshop: Novel and Future Developments in Computational Proteomics, Salzburg, 3-5 July 2013, "Two applications of predictions of peptides' chromatographic retention time".
- I gave an introductory talk for the session "Informatics: Validation" at 60th ASMS Conference on Mass Spectrometry and Allied Topics Vancouver, BC, Canada May 20 - 24, 2012 asms.org, "Inference from mass spectrometry-based proteomics data".
- I was invited speaker at the "1st Annual Proteome Discoverer User Meeting" at Atlantic Hotel in Bremen, Germany, 5-6th of December, 2011, "Assessing confidence in identifications using Percolator".
- I was invited speaker at the "Late Summer Practical Proteomics Seminar" at the Institute of Molecular Biotechnology in Vienna, Austria, 29-30 August, 2011, "Machine learning techniques to increase yield and assess confidence for shotgun proteomics".
- I was invited speaker at the mini-symposium: Specific Yet Sensitive Proteomics Bioinformatics, Institute Rommelaere, VIB, Gent, Belgium, 13th May 2011, "Assessing and improving confidence in peptide-spectrum matches".
- I was an invited speaker at the ESF sponsored workshop "Biochemistry of Proteomics" in Zakopane, Poland, 11-15 April 2011, "How to assess confidence in peptide-spectrum matches for shotgun proteomics".
- I was a keynote speaker at the Netherlands Proteomics Centre progress meeting, Utrecht, 13-14th of January 2011, "Machine Learning techniques to assess confidence and increase yield for shotgun proteomics".
- I was a keynote speaker at the 5th Conference of the Hellenic Society for Computational Biology and Bioinformatics, Alexandroupolis Greece, 17-19 October 2010, "Semi-supervised machine learning for the peptide identification problem in shotgun proteomics".
- I was invited to speak at the European Science Foundation (ESF) workshop on "Quality Control in Proteomics" in Cambridge, UK 25-27 November 2009, "Assigning confidence to Peptide-Spectrum Matches".

- 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 12 was one of the 18% accepted papers at the largest European Bioinformatics conference, ECCB 2008, Cagliari, Italy.
- I was a keynote 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 7 was one of 56 out of 189 submitted papers that were presented at the highlights track of ISMB 2008, Toronto, Canada.
- Paper 4 was one of 56 out of 426 submitted papers that were accepted to the largest annual bioinformatics conference, ISMB 2005, Detroit, USA.

Software

Phobius Combined prediction of transmembrane topology and signal peptides

More than 12,000 pageviews by more than 1600 unique users and every month. 25 standalone licenses have been distributed.

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

HomologHMM An HMM decoder able to handle homologs.

<http://phobius.sbc.su.se/data.html>

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

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

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

<http://per-colator.com>

quality A statistical tool for determining posterior error probabilities and q values for high-throughput experiments.

<http://per-colator.com>

Elude A peptide's retention time predictor for reversed phase chromatography.

<http://per-colator.com>

Active Grants

I have listed our funding first as a table, and subsequently describe the grants in detail.

PI	Years	Total Amount	Body
Lukas Käll, KTH	2011-2015	1 600 kkr	KTH
Lukas Käll, KTH	2011-13	1 000 kkr	SciLifeLab
Lukas Käll, KTH	2013-14	600 kkr	SeRC
Juleen Zierath, KI	2013-18	28 Msek	AstraZenica

Biträdande Lektorat, KTH

I receive a 400 000 SEK per year coverage for my position at the Royal Institute of Technology. The end date is set to 2015-04-31.

Recruitment grant, SciLifeLab

I receive a recruitment grant of 1 000 000 SEK from the Science for Life Laboratory over two years. The grant period is 2011-2013, with the possibility to extend the grant for two more years.

Project grant, SeRC

I receive a grant of 300 000 SEK/year from the Swedish e-Science Research Center, for the project "Software for post-measurement re-calibration of data from mass spectrometers". The grant period is 2013-2014, with a possible extension.

AstraZenica-SciLifeLab - Joint Research Collaboration

I take part of Juleen Zierath's AstraZenica-SciLifeLab grant of at least 28 MSEK (actual sum is still under negotiation) during 5 years project time. My share is still under negotiation.