

Curriculum Vitae – Prof. Anders Krogh

Personal Information

Date of Birth: May 2nd, 1959
Private Address: Borgmester Jensens Alle 22, st th, 2100 København Ø, Denmark
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Denmark. +45 3532 1329, krogh@binf.ku.dk
Web: <https://scholar.google.com/citations?user=-vGMjmwAAAAJ>

Education

Sept 1991 Ph.D. (Physics), Niels Bohr Institute, Univ. of Copenhagen, Denmark
June 1987 Cand. Scient. [M. Sc.] (Physics and mathematics), NBI, Univ. of Copenhagen

Professional / Work Experience (since 2000)

2018 – Professor of Bioinformatics, Dept of Computer Science (50%) and Dept of Biology (50%), Univ.
of Copenhagen
2002 – 2018 Professor of Bioinformatics, Dept of Biology, Univ. of Copenhagen
2009 – 2018 Head of Section for Computational and RNA Biology, Dept. of Biology, Univ. of Copenhagen
2000–2002 Associate Prof., Technical Univ. of Denmark (DTU), Copenhagen

Prices and Awards

2017 – Fellow of the International Society for Computational Biology <https://www.iscb.org/iscb-fellows-program>
2008 – Fellow, Royal Danish Academy of Sciences and Letters

Public Activities & Appointments (since 2009)

2014 – Board member, Elixir, European Infrastructure for Life Science.
2014 – Steering committee member, Danish Elixir Node.
2012 – 2016 Board member, Bioinformatics Infrastructure for Life Sciences (BILS), Swedish Research Council
2011 – 2016 Director, Centre for Computational and Applied Transcriptomics (COAT)
2009 – Associate editor, *BMC Bioinformatics*

Publications

- Google Scholar: <https://scholar.google.com/citations?user=-vGMjmwAAAAJ>
- ORCID: 0000-0002-5147-6282. ResearcherID: M-1541-2014
- Co-author of 130 peer-reviewed papers and 2 monographs
- 63,000 citations and h-index of 74 (Google Scholar, June 2019)
- H-index of 54 in Web of science (June 2019)
- Publications in high-impact journals: Nature (5), Science (1), Cell (1), Nature Genetics (2), Nature Biotechnology (2), Nature Communications (4), Cell (1, to appear), Genome Res. (6), EMBO Journal (1), PNAS (2)

Supervision

- 20 postdocs + 2 ongoing
- 23 phd students + 2 ongoing
- Around 70 Master thesis projects

Anders Krogh Publications – 10 selected

Bold names indicate that a (shared) first author was a student or a postdoc in my group while the work was done.
Citations are from Google Scholar, June 2019

Sibbesen, J, Maretty, L, The Danish Pan-Genome Consortium, Krogh A. Accurate genotyping across variant classes and lengths using variant graphs. Nature Genetics 50 1054–1059, 2018. Citations: 7

S. Liu, S. Huang, F. Chen, L. Zhao, Y. Yuan, S. S. Francis, L. Fang, Z. Li, L. Lin, R. Liu, Y. Zhang, H. Xu, S. Li, Y. Zhou, R. W. Davies, Q. Liu, R. G. Walters, K. Lin, J. Ju, T. Korneliussen, M. A. Yang, Q. Fu, J. Wang, L. Zhou, A. Krogh, H. Zhang, W. Wang, Z. Chen, Z. Cai, Y. Yin1, H. Yang, M. Mao, J. Shendure, J. Wang, A. Albrechtsen, X. Jin, R. Nielsen, and X. Xu. Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. Cell 175, 347-359.e14, 2018. Citations: 15

L. Maretty, J. M. Jensen, B. Petersen, J. A. Sibbesen, S. Liu, P. Villesen, L. Skov, K. Belling, C. Theil Have, J. M. G. Izarzugaza, M. Grosjean, J. Bork-Jensen, J. Grove, T. D. Als, S. Huang, Y. Chang, R. Xu, W. Ye, J. Rao, X. Guo, J. Sun, H. Cao, C. Ye, J. van Beusekom, T. Espeseth, E. Flindt, R. M. Friberg, A. E. Halager, S. Le Hellard, C. M. Hultman, F. Lescai, S. Li, O. Lund, P. Løngren, T. Mailund, M. L. Matey-Hernandez, O. Mors, C. N. S. Pedersen, T. Sicheritz-Ponten, P. Sullivan, A. Syed, D. Westergaard, R. Yadav, N. Li, X. Xu, T. Hansen, A. Krogh, L. Bolund, T. I. A. Sørensen, O. Pedersen, R. Gupta, S. Rasmussen, S. Besenbacher, A. D. Brøglum, J. Wang, H. Eiberg, K. Kristiansen, S. Brunak, and M. H. Schierup.. Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature 548, 87–91, 2017. Citations: 37

Menzel P, Ng KL, Krogh A. Fast and sensitive taxonomic classification for metagenomics with Kaiju. Nature Communications 7, 11257, 2016. Citations: 209

Maretty L, Sibbesen J, Krogh A. Bayesian transcriptome assembly. Genome Biology 15(10): 501, 2014. Citations: 39

Kerpedjiev PK, Frellsen J, Lindgreen S, Krogh A. Adaptable probabilistic mapping of short reads using position specific scoring matrices. BMC Bioinformatics 15:100, 2014. Citations: 42

M. Rasmussen, Y. Li, **S. Lindgreen**, J. S. Pedersen, A. Albrechtsen, I. Moltke, M. Metspalu, E. Metspalu, T. Kivisild, R. Gupta, M. Bertalan, K. Nielsen, M. T. Gilbert, Y. Wang, M. Raghavan, P. F. Campos, H. M. Kamp, A. S. Wilson, A. Gledhill, S. Tridico, M. Bunce, E. D. Lorenzen, J. Binladen, X. Guo, J. Zhao, X. Zhang, H. Zhang, Z. Li, M. Chen, L. Orlando, K. Kristiansen, M. Bak, N. Tommerup, C. Bendixen, T. L. Pierre, B. Grønow, M. Meldgaard, C. Andreasen, S. A. Fedorova, L. P. Osipova, T. F. Higham, C. B. Ramsey, T. V. Hansen, F. C. Nielsen, M. H. Crawford, S. Brunak, T. Sicheritz-Ponten, R. Villemans, R. Nielsen, **A. Krogh**, J. Wang, and E. Willerslev. Ancient human genome sequence of an extinct Palaeo-Eskimo. Nature, 463:757-762, 2010.

Citations: 653

Krogh A. What are artificial neural networks? Nature Biotech., 26(2):195-197, 2008. Citations: 201

Krogh A, Larsson B, von Heijne G, Sonnhammer, E. Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes, J.Mol. Biol. 305: 567, 2001. Citations: 8892

Krogh, A, Brown, N, Mian, IS, Sjolander, K, Haussler, D. Hidden Markov-Models in computational biology – applications to protein modeling, J. Mol. Biol. 235: 1501-1531, 1994. Citations: 2368