

Anders Krogh

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

140 papers	35,400 citations	61 h-index	150 g-index
150 ext. papers	41,413 ext. citations	11.7 avg, IF	6.92 L-index

#	Paper	IF	Citations
140	Context dependency of nucleotide probabilities and variants in human DNA.. <i>BMC Genomics</i> , 2022 , 23, 87	4.5	1
139	High-throughput proteomics of breast cancer interstitial fluid: identification of tumor subtype-specific serologically relevant biomarkers. <i>Molecular Oncology</i> , 2021 , 15, 429-461	7.9	4
138	CAnker bioMarker Prediction Pipeline (CAMPP)-A standardized framework for the analysis of quantitative biological data. <i>PLoS Computational Biology</i> , 2020 , 16, e1007665	5	2
137	Secreted breast tumor interstitial fluid microRNAs and their target genes are associated with triple-negative breast cancer, tumor grade, and immune infiltration. <i>Breast Cancer Research</i> , 2020 , 22, 73	8.3	8
136	Taxonomic classification method for metagenomics based on core protein families with Core-Kaiju. <i>Nucleic Acids Research</i> , 2020 , 48, e93	20.1	5
135	CAnker bioMarker Prediction Pipeline (CAMPP)A standardized framework for the analysis of quantitative biological data 2020 , 16, e1007665		
134	CAnker bioMarker Prediction Pipeline (CAMPP)A standardized framework for the analysis of quantitative biological data 2020 , 16, e1007665		
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132	CAnker bioMarker Prediction Pipeline (CAMPP)A standardized framework for the analysis of quantitative biological data 2020 , 16, e1007665		
131	CAnker bioMarker Prediction Pipeline (CAMPP)A standardized framework for the analysis of quantitative biological data 2020 , 16, e1007665		
130	Sensitive detection of circular DNAs at single-nucleotide resolution using guided realignment of partially aligned reads. <i>BMC Bioinformatics</i> , 2019 , 20, 663	3.6	21
129	Accurate genotyping across variant classes and lengths using variant graphs. <i>Nature Genetics</i> , 2018 , 50, 1054-1059	36.3	35
128	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. <i>Cell</i> , 2018 , 175, 347-359.e14	56.2	123
127	Highly accessible AU-rich regions in 3'Untranslated regions are hotspots for binding of regulatory factors. <i>PLoS Computational Biology</i> , 2017 , 13, e1005460	5	33
126	Sugar Metabolism of the First Thermophilic Planctomycete : Comparative Genomic and Transcriptomic Approaches. <i>Frontiers in Microbiology</i> , 2017 , 8, 2140	5.7	12
125	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017 , 548, 87-91	50.4	87
124	Fast and sensitive taxonomic classification for metagenomics with Kaiju. <i>Nature Communications</i> , 2016 , 7, 11257	17.4	677

123	RNA Sequencing of Trigeminal Ganglia in Rattus Norvegicus after Glyceryl Trinitrate Infusion with Relevance to Migraine. <i>PLoS ONE</i> , 2016 , 11, e0155039	3.7	7
122	Novel viral genomes identified from six metagenomes reveal wide distribution of archaeal viruses and high viral diversity in terrestrial hot springs. <i>Environmental Microbiology</i> , 2016 , 18, 863-74	5.2	40
121	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015 , 6, 5969	17.4	119
120	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. <i>Microbial Ecology</i> , 2015 , 70, 411-24	4.4	79
119	Transcriptome dynamics of the microRNA inhibition response. <i>Nucleic Acids Research</i> , 2015 , 43, 6207-21	20.1	3
118	Drosophila Imp iCLIP identifies an RNA assemblage coordinating F-actin formation. <i>Genome Biology</i> , 2015 , 16, 123	18.3	23
117	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015 , 33, 617-22	44.5	57
116	Cancers of unknown primary origin (CUP) are characterized by chromosomal instability (CIN) compared to metastasis of know origin. <i>BMC Cancer</i> , 2015 , 15, 151	4.8	34
115	SHAPE Selection (SHAPES) enrich for RNA structure signal in SHAPE sequencing-based probing data. <i>Rna</i> , 2015 , 21, 1042-52	5.8	35
114	Discovery, genotyping and characterization of structural variation and novel sequence at single nucleotide resolution from de novo genome assemblies on a population scale. <i>GigaScience</i> , 2015 , 4, 64	7.6	16
113	Comparing cancer vs normal gene expression profiles identifies new disease entities and common transcriptional programs in AML patients. <i>Blood</i> , 2014 , 123, 894-904	2.2	82
112	Adaptable probabilistic mapping of short reads using position specific scoring matrices. <i>BMC Bioinformatics</i> , 2014 , 15, 100	3.6	36
111	Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax. <i>Nature Communications</i> , 2014 , 5, 3966	17.4	101
110	Rapid detection of structural variation in a human genome using nanochannel-based genome mapping technology. <i>GigaScience</i> , 2014 , 3, 34	7.6	113
109	SNPest: a probabilistic graphical model for estimating genotypes. <i>BMC Research Notes</i> , 2014 , 7, 698	2.3	6
108	Alternative polyadenylation of tumor suppressor genes in small intestinal neuroendocrine tumors. <i>Frontiers in Endocrinology</i> , 2014 , 5, 46	5.7	10
107	Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. <i>Genome Research</i> , 2014 , 24, 454-66	9.7	113
106	Whole-genome sequencing of cultivated and wild peppers provides insights into Capsicum domestication and specialization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5135-40	11.5	466

105	Adaptations to a subterranean environment and longevity revealed by the analysis of mole rat genomes. <i>Cell Reports</i> , 2014 , 8, 1354-64	10.6	124
104	Bayesian transcriptome assembly. <i>Genome Biology</i> , 2014 , 15, 501	18.3	43
103	cWords - systematic microRNA regulatory motif discovery from mRNA expression data. <i>Silence: A Journal of RNA Regulation</i> , 2013 , 4, 2		19
102	Genome analysis reveals insights into physiology and longevity of the Brandt's bat <i>Myotis brandtii</i> . <i>Nature Communications</i> , 2013 , 4, 2212	17.4	160
101	A short-read multiplex sequencing method for reliable, cost-effective and high-throughput genotyping in large-scale studies. <i>Human Mutation</i> , 2013 , 34, 1715-20	4.7	37
100	Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013 , 499, 74-8	50.4	563
99	Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. <i>Nature Communications</i> , 2013 , 4, 2172	17.4	79
98	Alterations in polyadenylation and its implications for endocrine disease. <i>Frontiers in Endocrinology</i> , 2013 , 4, 53	5.7	26
97	Loss of miR-10a activates lpo and collaborates with activated Wnt signaling in inducing intestinal neoplasia in female mice. <i>PLoS Genetics</i> , 2013 , 9, e1003913	6	34
96	On the accuracy of short read mapping. <i>Methods in Molecular Biology</i> , 2013 , 1038, 39-59	1.4	6
95	Improving The Analysis Of Gene Expression Profiles By Comparing AML Blasts With Their Nearest Normal Counterparts. <i>Blood</i> , 2013 , 122, 2568-2568	2.2	
94	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. <i>Genome Biology</i> , 2012 , 13, R35	18.3	90
93	Improving ancient DNA read mapping against modern reference genomes. <i>BMC Genomics</i> , 2012 , 13, 178	4.5	178
92	MicroRNA-143 down-regulates Hexokinase 2 in colon cancer cells. <i>BMC Cancer</i> , 2012 , 12, 232	4.8	109
91	microRNA-146a inhibits G protein-coupled receptor-mediated activation of NF- κ B by targeting CARD10 and COPS8 in gastric cancer. <i>Molecular Cancer</i> , 2012 , 11, 71	42.1	75
90	microRNA-101 is a potent inhibitor of autophagy. <i>EMBO Journal</i> , 2011 , 30, 4628-41	13	275
89	An Aboriginal Australian genome reveals separate human dispersals into Asia. <i>Science</i> , 2011 , 334, 94-8	33.3	528
88	miR-449 inhibits cell proliferation and is down-regulated in gastric cancer. <i>Molecular Cancer</i> , 2011 , 10, 29	42.1	181

87	The genome of the leaf-cutting ant <i>Acromyrmex echinatior</i> suggests key adaptations to advanced social life and fungus farming. <i>Genome Research</i> , 2011 , 21, 1339-48	9.7	183
86	MicroRNA transfection and AGO-bound CLIP-seq data sets reveal distinct determinants of miRNA action. <i>Rna</i> , 2011 , 17, 820-34	5.8	56
85	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010 , 463, 757-62	50.4	567
84	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. <i>Genome Research</i> , 2010 , 20, 1010-9	9.7	86
83	miR Maid: a unified programming interface for microRNA data resources. <i>BMC Bioinformatics</i> , 2010 , 11, 29	3.6	12
82	Long- and short-term selective forces on malaria parasite genomes. <i>PLoS Genetics</i> , 2010 , 6, e1001099	6	20
81	MicroRNA-145 targets YES and STAT1 in colon cancer cells. <i>PLoS ONE</i> , 2010 , 5, e8836	3.7	138
80	Discovery of regulatory elements is improved by a discriminatory approach. <i>PLoS Computational Biology</i> , 2009 , 5, e1000562	5	23
79	CCHMM_PROF: a HMM-based coiled-coil predictor with evolutionary information. <i>Bioinformatics</i> , 2009 , 25, 2757-63	7.2	38
78	Identification and analysis of miRNAs in human breast cancer and teratoma samples using deep sequencing. <i>BMC Medical Genomics</i> , 2009 , 2, 35	3.7	38
77	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
76	Genome-wide detection and analysis of hippocampus core promoters using DeepCAGE. <i>Genome Research</i> , 2009 , 19, 255-65	9.7	116
75	What are artificial neural networks?. <i>Nature Biotechnology</i> , 2008 , 26, 195-7	44.5	207
74	BayesMD: flexible biological modeling for motif discovery. <i>Journal of Computational Biology</i> , 2008 , 15, 1347-63	1.7	6
73	A generative, probabilistic model of local protein structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8932-7	11.5	84
72	Programmed cell death 4 (PDCD4) is an important functional target of the microRNA miR-21 in breast cancer cells. <i>Journal of Biological Chemistry</i> , 2008 , 283, 1026-33	5.4	871
71	Modeling promoter grammars with evolving hidden Markov models. <i>Bioinformatics</i> , 2008 , 24, 1669-75	7.2	11
70	Hidden Markov Models for prediction of protein features. <i>Methods in Molecular Biology</i> , 2008 , 413, 173-94	9.4	10

69	A code for transcription initiation in mammalian genomes. <i>Genome Research</i> , 2008 , 18, 1-12	9.7	179
68	JASPAR, the open access database of transcription factor-binding profiles: new content and tools in the 2008 update. <i>Nucleic Acids Research</i> , 2008 , 36, D102-6	20.1	541
67	Asap: a framework for over-representation statistics for transcription factor binding sites. <i>PLoS ONE</i> , 2008 , 3, e1623	3.7	35
66	Advantages of combined transmembrane topology and signal peptide prediction--the Phobius web server. <i>Nucleic Acids Research</i> , 2007 , 35, W429-32	20.1	1033
65	An evolutionary method for learning HMM structure: prediction of protein secondary structure. <i>BMC Bioinformatics</i> , 2007 , 8, 357	3.6	35
64	Multiple alignment and structure prediction of non-coding RNA sequences. <i>BMC Bioinformatics</i> , 2007 , 8,	3.6	1
63	Molecular composition of IMP1 ribonucleoprotein granules. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 798-811	7.6	160
62	MASTR: multiple alignment and structure prediction of non-coding RNAs using simulated annealing. <i>Bioinformatics</i> , 2007 , 23, 3304-11	7.2	57
61	Intragenomic matching reveals a huge potential for miRNA-mediated regulation in plants. <i>PLoS Computational Biology</i> , 2007 , 3, e238	5	52
60	Prediction of Structurally-Determined Coiled-Coil Domains with Hidden Markov Models 2007 , 292-302		12
59	A hidden Markov model approach for determining expression from genomic tiling micro arrays. <i>BMC Bioinformatics</i> , 2006 , 7, 239	3.6	22
58	Automatic generation of gene finders for eukaryotic species. <i>BMC Bioinformatics</i> , 2006 , 7, 263	3.6	20
57	PONGO: a web server for multiple predictions of all-alpha transmembrane proteins. <i>Nucleic Acids Research</i> , 2006 , 34, W169-72	20.1	36
56	Sampling realistic protein conformations using local structural bias. <i>PLoS Computational Biology</i> , 2006 , 2, e131	5	66
55	Measuring covariation in RNA alignments: physical realism improves information measures. <i>Bioinformatics</i> , 2006 , 22, 2988-95	7.2	37
54	Evolving the structure of hidden Markov models. <i>IEEE Transactions on Evolutionary Computation</i> , 2006 , 10, 39-49	15.6	9
53	Novel overlapping coding sequences in Chlamydia trachomatis. <i>FEMS Microbiology Letters</i> , 2006 , 265, 106-17	2.9	15
52	Large-scale prokaryotic gene prediction and comparison to genome annotation. <i>Bioinformatics</i> , 2005 , 21, 4322-9	7.2	113

51	Computational evidence for hundreds of non-conserved plant microRNAs. <i>BMC Genomics</i> , 2005 , 6, 119	4.5	59
50	An HMM posterior decoder for sequence feature prediction that includes homology information. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i251-7	7.2	246
49	Training HMM structure with genetic algorithm for biological sequence analysis. <i>Bioinformatics</i> , 2004 , 20, 3613-9	7.2	33
48	Teaching computers to fold proteins. <i>Physical Review E</i> , 2004 , 70, 030903	2.4	10
47	A combined transmembrane topology and signal peptide prediction method. <i>Journal of Molecular Biology</i> , 2004 , 338, 1027-36	6.5	1669
46	The Block Hidden Markov Model for Biological Sequence Analysis. <i>Lecture Notes in Computer Science</i> , 2004 , 64-70	0.9	1
45	EasyGene--a prokaryotic gene finder that ranks ORFs by statistical significance. <i>BMC Bioinformatics</i> , 2003 , 4, 21	3.6	120
44	Prediction of lipoprotein signal peptides in Gram-negative bacteria. <i>Protein Science</i> , 2003 , 12, 1652-62	6.3	880
43	RpoD promoters in <i>Campylobacter jejuni</i> exhibit a strong periodic signal instead of a -35 box. <i>Journal of Molecular Biology</i> , 2003 , 326, 1361-72	6.5	70
42	Reliability measures for membrane protein topology prediction algorithms. <i>Journal of Molecular Biology</i> , 2003 , 327, 735-44	6.5	181
41	Bias of purine stretches in sequenced chromosomes. <i>Computers & Chemistry</i> , 2002 , 26, 531-41		31
40	A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins. <i>Bioinformatics</i> , 2002 , 18 Suppl 1, S46-53	7.2	158
39	Prediction of human protein function from post-translational modifications and localization features. <i>Journal of Molecular Biology</i> , 2002 , 319, 1257-65	6.5	274
38	Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18. <i>Nature</i> , 2001 , 413, 848-52	50.4	1010
37	On the total number of genes and their length distribution in complete microbial genomes. <i>Trends in Genetics</i> , 2001 , 17, 425-8	8.5	170
36	Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes. <i>Journal of Molecular Biology</i> , 2001 , 305, 567-80	6.5	8822
35	Genome organisation and chromatin structure in <i>Escherichia coli</i> . <i>Biochimie</i> , 2001 , 83, 201-12	4.6	71
34	Sigma A recognition sites in the <i>Bacillus subtilis</i> genome. <i>Microbiology (United Kingdom)</i> , 2001 , 147, 2417-2424	24.24	56

33	Using database matches with for HMMGene for automated gene detection in Drosophila. <i>Genome Research</i> , 2000 , 10, 523-8	9.7	50
32	A General Method for Combining Predictors Tested on Protein Secondary Structure Prediction. <i>Perspectives in Neural Computing</i> , 2000 , 259-264		2
31	No evidence that mRNAs have lower folding free energies than random sequences with the same dinucleotide distribution. <i>Nucleic Acids Research</i> , 1999 , 27, 4816-22	20.1	149
30	Hidden neural networks. <i>Neural Computation</i> , 1999 , 11, 541-63	2.9	33
29	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. <i>Nature</i> , 1998 , 393, 537-44	50.4	6341
28	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. <i>Nature</i> , 1998 , 396, 190-190	50.4	70
27	An introduction to hidden Markov models for biological sequences. <i>New Comprehensive Biochemistry</i> , 1998 , 32, 45-63		63
26	Markov chains and hidden Markov models 1998 , 47-80		1
25	Gene Finding: Putting the Parts Together 1998 , 261-274		14
24	Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids 1998 ,		2271
23	Statistical mechanics of ensemble learning. <i>Physical Review E</i> , 1997 , 55, 811-825	2.4	81
22	Nonlinear backpropagation: doing backpropagation without derivatives of the activation function. <i>IEEE Transactions on Neural Networks</i> , 1997 , 8, 1321-7		13
21	Hidden Markov Models for Human Genes 1997 , 15-32		
20	Naturally occurring nucleosome positioning signals in human exons and introns. <i>Journal of Molecular Biology</i> , 1996 , 263, 503-10	6.5	62
19	Improving prediction of protein secondary structure using structured neural networks and multiple sequence alignments. <i>Journal of Computational Biology</i> , 1996 , 3, 163-83	1.7	117
18	Hidden Markov models for sequence analysis: extension and analysis of the basic method. <i>Bioinformatics</i> , 1996 , 12, 95-107	7.2	160
17	Dirichlet mixtures: a method for improved detection of weak but significant protein sequence homology. <i>Bioinformatics</i> , 1996 , 12, 327-45	7.2	139
16	A hidden Markov model that finds genes in E. coli DNA. <i>Nucleic Acids Research</i> , 1994 , 22, 4768-78	20.1	219

15	. <i>IEEE Transactions on Information Theory</i> , 1994 , 40, 1215-1218	2.8	3
14	Hidden Markov models in computational biology. Applications to protein modeling. <i>Journal of Molecular Biology</i> , 1994 , 235, 1501-31	6.5	1331
13	A quantitative study of pruning by optimal brain damage. <i>International Journal of Neural Systems</i> , 1993 , 4, 159-69	6.2	18
12	Generalization in a linear perceptron in the presence of noise. <i>Journal of Physics A</i> , 1992 , 25, 1135-1147		60
11	Learning with noise in a linear perceptron. <i>Journal of Physics A</i> , 1992 , 25, 1119-1133		21
10	Phase transitions in simple learning. <i>Journal of Physics A</i> , 1989 , 22, 2133-2150		43
9	Dynamics of Learning in Simple Perceptrons. <i>Physica Scripta</i> , 1989 , T25, 149-151	2.6	6
8	Mean-field analysis of hierarchical associative networks with magnetisation <i>Journal of Physics A</i> , 1988 , 21, 2211-2224		17
7	Hierarchical associative networks. <i>Journal of Physics A</i> , 1987 , 20, 4449-4455		23
6	Introduction to the Theory of Neural Computation		68
5	Low Pass Genomes of 141,431 Chinese Reveal Patterns of Viral Infection, Novel Phenotypic Associations, and the Genetic History of China. <i>SSRN Electronic Journal</i> ,	1	1
4	Early Pleistocene enamel proteome sequences from Dmanisi resolve <i>Stephanorhinus</i> phylogeny		5
3	Sensitive detection of circular DNAs at single-nucleotide resolution using guided realignment of partially aligned reads		2
2	Prediction of DNA from context using neural networks		2
1	Context dependency of nucleotide probabilities and variants in human DNA		1