

Erik Ll L Sonnhhammer

List of Publications by Year in descending order

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151
papers

62,267
citations

26630

56
h-index

7160

153
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159
all docs

159
docs citations

159
times ranked

64450
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting transmembrane protein topology with a hidden markov model: application to complete genomes ¹¹ Edited by F. Cohen. Journal of Molecular Biology, 2001, 305, 567-580.	4.2	11,404
2	The Pfam protein families database. Nucleic Acids Research, 2007, 36, D281-D288.	14.5	6,372
3	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	14.5	5,425
4	The Pfam protein families database in 2019. Nucleic Acids Research, 2019, 47, D427-D432.	14.5	3,937
5	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	14.5	3,306
6	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	14.5	3,084
7	Pfam: The protein families database in 2021. Nucleic Acids Research, 2021, 49, D412-D419.	14.5	3,068
8	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	14.5	2,693
9	A Combined Transmembrane Topology and Signal Peptide Prediction Method. Journal of Molecular Biology, 2004, 338, 1027-1036.	4.2	2,145
10	The Pfam Protein Families Database. Nucleic Acids Research, 2002, 30, 276-280.	14.5	2,067
11	Pfam: clans, web tools and services. Nucleic Acids Research, 2006, 34, D247-D251.	14.5	2,030
12	Advantages of combined transmembrane topology and signal peptide prediction—the Phobius web server. Nucleic Acids Research, 2007, 35, W429-W432.	14.5	1,461
13	The Pfam Protein Families Database. Nucleic Acids Research, 2000, 28, 263-266.	14.5	1,173
14	Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. Journal of Molecular Biology, 2001, 314, 1041-1052.	4.2	1,081
15	Pfam: A comprehensive database of protein domain families based on seed alignments. Proteins: Structure, Function and Bioinformatics, 1997, 28, 405-420.	2.6	1,036
16	A dot-matrix program with dynamic threshold control suited for genomic DNA and protein sequence analysis. Gene, 1995, 167, GC1-GC10.	2.2	677
17	Inparanoid: a comprehensive database of eukaryotic orthologs. Nucleic Acids Research, 2004, 33, D476-D480.	14.5	667
18	Pfam: multiple sequence alignments and HMM-profiles of protein domains. Nucleic Acids Research, 1998, 26, 320-322.	14.5	644

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19	Kalign—an accurate and fast multiple sequence alignment algorithm. BMC Bioinformatics, 2005, 6, 298.	2.6	615
20	InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. Nucleic Acids Research, 2010, 38, D196-D203.	14.5	576
21	Pfam 3.1: 1313 multiple alignments and profile HMMs match the majority of proteins. Nucleic Acids Research, 1999, 27, 260-262.	14.5	533
22	InParanoid 8: orthology analysis between 273 proteomes, mostly eukaryotic. Nucleic Acids Research, 2015, 43, D234-D239.	14.5	449
23	Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity. Nature Communications, 2018, 9, 2419.	12.8	374
24	Orthology, paralogy and proposed classification for paralog subtypes. Trends in Genetics, 2002, 18, 619-620.	6.7	360
25	Genomic Gene Clustering Analysis of Pathways in Eukaryotes. Genome Research, 2003, 13, 875-882.	5.5	307
26	An HMM posterior decoder for sequence feature prediction that includes homology information. Bioinformatics, 2005, 21, i251-i257.	4.1	292
27	Sequence of the human immunoglobulin diversity (D) segment locus: a systematic analysis provides no evidence for the use of DIR segments, inverted D segments, æœminorâ€•D segments or D-D recombination 1 1 Edited By J. Karn. Journal of Molecular Biology, 1997, 270, 587-597.	4.2	283
28	FAT: a novel domain in PIK-related kinases. Trends in Biochemical Sciences, 2000, 25, 225-227.	7.5	265
29	Kalign2: high-performance multiple alignment of protein and nucleotide sequences allowing external features. Nucleic Acids Research, 2009, 37, 858-865.	14.5	263
30	Automatic clustering of orthologs and inparalogs shared by multiple proteomes. Bioinformatics, 2006, 22, e9-e15.	4.1	227
31	Modular arrangement of proteins as inferred from analysis of homology. Protein Science, 1994, 3, 482-492.	7.6	220
32	The Imprint of Somatic Hypermutation on the Repertoire of Human Germline V Genes. Journal of Molecular Biology, 1996, 256, 813-817.	4.2	209
33	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	19.0	198
34	Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. FEBS Letters, 2007, 581, 5601-5604.	2.8	194
35	InParanoid 6: eukaryotic ortholog clusters with inparalogs. Nucleic Acids Research, 2007, 36, D263-D266.	14.5	189
36	Automated ortholog inference from phylogenetic trees and calculation of orthology reliability. Bioinformatics, 2002, 18, 92-99.	4.1	163

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37	Volume changes in protein evolution. <i>Journal of Molecular Biology</i> , 1994, 236, 1067-1078.	4.2	160
38	A general model of G protein-coupled receptor sequences and its application to detect remote homologs. <i>Protein Science</i> , 2006, 15, 509-521.	7.6	158
39	Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009, 19, 1107-1116.	5.5	137
40	Analysis of Protein Domain Families in <i>Caenorhabditis elegans</i> . <i>Genomics</i> , 1997, 46, 200-216.	2.9	129
41	Improved and automated prediction of effective siRNA. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 264-274.	2.1	129
42	Automatic assessment of alignment quality. <i>Nucleic Acids Research</i> , 2005, 33, 7120-7128.	14.5	126
43	A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family. <i>Nature Communications</i> , 2017, 8, 1541.	12.8	124
44	Scoredist: a simple and robust protein sequence distance estimator. <i>BMC Bioinformatics</i> , 2005, 6, 108.	2.6	116
45	Quality assessment of multiple alignment programs. <i>FEBS Letters</i> , 2002, 529, 126-130.	2.8	112
46	Big data and other challenges in the quest for orthologs. <i>Bioinformatics</i> , 2014, 30, 2993-2998.	4.1	109
47	Comprehensive sequence analysis of the 182 predicted open reading frames of yeast chromosome III. <i>Protein Science</i> , 1992, 1, 1677-1690.	7.6	106
48	Kalign, Kalignvu and Mumsa: web servers for multiple sequence alignment. <i>Nucleic Acids Research</i> , 2006, 34, W596-W599.	14.5	99
49	Domain Tree-Based Analysis of Protein Architecture Evolution. <i>Molecular Biology and Evolution</i> , 2008, 25, 254-264.	8.9	98
50	FunCoup 3.0: database of genome-wide functional coupling networks. <i>Nucleic Acids Research</i> , 2014, 42, D380-D388.	14.5	96
51	Predicting protein function from domain content. <i>Bioinformatics</i> , 2008, 24, 1681-1687.	4.1	83
52	A Novel ACKR2-Dependent Role of Fibroblast-Derived CXCL14 in Epithelial-to-Mesenchymal Transition and Metastasis of Breast Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 3702-3717.	7.0	72
53	Reliability of transmembrane predictions in whole-genome data. <i>FEBS Letters</i> , 2002, 532, 415-418.	2.8	70
54	A Workbench for large-scale sequence homology analysis. <i>Bioinformatics</i> , 1994, 10, 301-307.	4.1	69

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55	What's in a genome?. Nature, 1992, 358, 287-287.	27.8	57
56	siRNAdb: a database of siRNA sequences. Nucleic Acids Research, 2004, 33, D131-D134.	14.5	57
57	OrthoDisease: A database of human disease orthologs. Human Mutation, 2004, 24, 112-119.	2.5	56
58	Network-based Identification of Novel Cancer Genes. Molecular and Cellular Proteomics, 2010, 9, 648-655.	3.8	54
59	Domain architecture conservation in orthologs. BMC Bioinformatics, 2011, 12, 326.	2.6	54
60	Letter to the Editor: SeqXML and OrthoXML: standards for sequence and orthology information. Briefings in Bioinformatics, 2011, 12, 485-488.	6.5	51
61	Prognostic Significance in Breast Cancer of a Gene Signature Capturing Stromal PDGF Signaling. American Journal of Pathology, 2013, 182, 2037-2047.	3.8	50
62	Comparative interactomics with Funcoup 2.0. Nucleic Acids Research, 2012, 40, D821-D828.	14.5	49
63	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2012, 856, 187-216.	0.9	47
64	Dynamic Zebrafish Interactome Reveals Transcriptional Mechanisms of Dioxin Toxicity. PLoS ONE, 2010, 5, e10465.	2.5	47
65	A novel transmembrane topology of presenilin based on reconciling experimental and computational evidence. FEBS Journal, 2005, 272, 2727-2733.	4.7	45
66	Improved profile HMM performance by assessment of critical algorithmic features in SAM and HMMER. BMC Bioinformatics, 2005, 6, 99.	2.6	45
67	A large-scale benchmark of gene prioritization methods. Scientific Reports, 2017, 7, 46598.	3.3	44
68	FunCoup 4: new species, data, and visualization. Nucleic Acids Research, 2018, 46, D601-D607.	14.5	44
69	Computational antisense oligo prediction with a neural network model. Bioinformatics, 2002, 18, 1567-1575.	4.1	41
70	The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545.	14.5	41
71	Comprehensive Analysis of Orthologous Protein Domains Using the HOPS Database. Genome Research, 2003, 13, 2353-2362.	5.5	40
72	FunShift: a database of function shift analysis on protein subfamilies. Nucleic Acids Research, 2004, 33, D197-D200.	14.5	39

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73	Functional association networks as priors for gene regulatory network inference. <i>Bioinformatics</i> , 2014, 30, i130-i138.	4.1	39
74	Hieranoid: Hierarchical Orthology Inference. <i>Journal of Molecular Biology</i> , 2013, 425, 2072-2081.	4.2	38
75	PathwAX: a web server for network crosstalk based pathway annotation. <i>Nucleic Acids Research</i> , 2016, 44, W105-W109.	14.5	36
76	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329.	4.1	36
77	Integrated graphical analysis of protein sequence features predicted from sequence composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 262-273.	2.6	35
78	Statistical Assessment of Crosstalk Enrichment between Gene Groups in Biological Networks. <i>PLoS ONE</i> , 2013, 8, e54945.	2.5	34
79	A novel method for crosstalk analysis of biological networks: improving accuracy of pathway annotation. <i>Nucleic Acids Research</i> , 2017, 45, e8-e8.	14.5	33
80	Improving Profile HMM Discrimination by Adapting Transition Probabilities. <i>Journal of Molecular Biology</i> , 2004, 338, 847-854.	4.2	30
81	A genome-wide IR-induced RAD51 foci RNAi screen identifies CDC73 involved in chromatin remodeling for DNA repair. <i>Cell Discovery</i> , 2015, 1, 15034.	6.7	30
82	Evolution of Protein Domain Architectures. <i>Methods in Molecular Biology</i> , 2019, 1910, 469-504.	0.9	30
83	Classification of Transmembrane Protein Families in the <i>Caenorhabditis elegans</i> Genome and Identification of Human Orthologs. <i>Genome Research</i> , 2000, 10, 1679-1689.	5.5	29
84	Large-scale prediction of function shift in protein families with a focus on enzymatic function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 758-768.	2.6	29
85	Orthology confers intron position conservation. <i>BMC Genomics</i> , 2010, 11, 412.	2.8	29
86	The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632.	14.5	29
87	MaxLink: network-based prioritization of genes tightly linked to a disease seed set. <i>Bioinformatics</i> , 2014, 30, 2689-2690.	4.1	27
88	Comparative analysis and unification of domain-domain interaction networks. <i>Bioinformatics</i> , 2009, 25, 3020-3025.	4.1	26
89	MetaTM - a consensus method for transmembrane protein topology prediction. <i>BMC Bioinformatics</i> , 2009, 10, 314.	2.6	25
90	FunCoup 5: Functional Association Networks in All Domains of Life, Supporting Directed Links and Tissue-Specificity. <i>Journal of Molecular Biology</i> , 2021, 433, 166835.	4.2	25

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91	Profiled support vector machines for antisense oligonucleotide efficacy prediction. BMC Bioinformatics, 2004, 5, 135.	2.6	24
92	Overview and comparison of ortholog databases. Drug Discovery Today: Technologies, 2006, 3, 137-143.	4.0	24
93	Quality criteria for finding genes with high mRNAâ€“protein expression correlation and coexpression correlation. Gene, 2012, 497, 228-236.	2.2	22
94	Improved orthology inference with Hieranoid 2. Bioinformatics, 2017, 33, 1154-1159.	4.1	22
95	Genome-wide functional association networks: background, data & state-of-the-art resources. Briefings in Bioinformatics, 2020, 21, 1224-1237.	6.5	20
96	Optimal Sparsity Criteria for Network Inference. Journal of Computational Biology, 2013, 20, 398-408.	1.6	18
97	DNA Methylation Levels in Mononuclear Leukocytes from the Mother and Her Child Are Associated with IgE Sensitization to Allergens in Early Life. International Journal of Molecular Sciences, 2021, 22, 801.	4.1	18
98	siRNA specificity searching incorporating mismatch tolerance data. Bioinformatics, 2008, 24, 1316-1317.	4.1	17
99	HieranoiDB: a database of orthologs inferred by Hieranoid. Nucleic Acids Research, 2017, 45, D687-D690.	14.5	17
100	Domainoid: domain-oriented orthology inference. BMC Bioinformatics, 2019, 20, 523.	2.6	17
101	Fusion transcript detection using spatial transcriptomics. BMC Medical Genomics, 2020, 13, 110.	1.5	17
102	Assessment of Protein Distance Measures and Tree-Building Methods for Phylogenetic Tree Reconstruction. Molecular Biology and Evolution, 2005, 22, 2257-2264.	8.9	16
103	jSquid: a Java applet for graphical on-line network exploration. Bioinformatics, 2008, 24, 1467-1468.	4.1	16
104	OrthoDisease: tracking disease gene orthologs across 100 species. Briefings in Bioinformatics, 2011, 12, 463-473.	6.5	16
105	Avoiding pitfalls in L_1 -regularised inference of gene networks. Molecular BioSystems, 2015, 11, 287-296.	2.9	16
106	GeneSPIDER â€“ gene regulatory network inference benchmarking with controlled network and data properties. Molecular BioSystems, 2017, 13, 1304-1312.	2.9	16
107	Pathway-specific model estimation for improved pathway annotation by network crosstalk. Scientific Reports, 2020, 10, 13585.	3.3	16
108	Functional characterization in Caenorhabditis elegans of transmembrane worm-human orthologs. BMC Genomics, 2004, 5, 85.	2.8	15

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109	PfamAlyzer: domain-centric homology search. Bioinformatics, 2007, 23, 3382-3383.	4.1	15
110	The Chironomus tentans genome sequence and the organization of the Balbiani ring genes. BMC Genomics, 2014, 15, 819.	2.8	14
111	Benchmarking the next generation of homology inference tools. Bioinformatics, 2016, 32, 2636-2641.	4.1	14
112	Discovering viral genomes in human metagenomic data by predicting unknown protein families. Scientific Reports, 2018, 8, 28.	3.3	14
113	Dynamic contact maps of protein structures. Journal of Molecular Graphics and Modelling, 1998, 16, 1-5.	2.4	13
114	Focusing on RISC assembly in mammalian cells. Biochemical and Biophysical Research Communications, 2008, 368, 703-708.	2.1	13
115	OrthoGUL: graphical presentation of Orthostrapper results. Bioinformatics, 2002, 18, 1272-1273.	4.1	12
116	Prediction of Function Divergence in Protein Families Using the Substitution Rate Variation Parameter Alpha. Molecular Biology and Evolution, 2006, 23, 1406-1413.	8.9	12
117	MGclus: network clustering employing shared neighbors. Molecular BioSystems, 2013, 9, 1670.	2.9	12
118	Uncovering cancer gene regulation by accurate regulatory network inference from uninformative data. Npj Systems Biology and Applications, 2020, 6, 37.	3.0	12
119	InParanoid-DIAMOND: faster orthology analysis with the InParanoid algorithm. Bioinformatics, 2022, 38, 2918-2919.	4.1	12
120	Conspicuous accumulation of transcription elongation repressor hrp130/CA150 on the intron-rich Balbiani ring 3 gene. Chromosoma, 2004, 113, 244-257.	2.2	11
121	Benchmarking homology detection procedures with low complexity filters. Bioinformatics, 2009, 25, 2500-2505.	4.1	11
122	ChromoWheel: a new spin on eukaryotic chromosome visualization. Bioinformatics, 2004, 20, 576-577.	4.1	10
123	A generalized framework for controlling FDR in gene regulatory network inference. Bioinformatics, 2019, 35, 1026-1032.	4.1	10
124	Putative regulatory domains in the human and mouse CVADR genes. Gene Function & Disease, 2000, 1, 82-86.	0.3	9
125	DASher: a stand-alone protein sequence client for DAS, the Distributed Annotation System. Bioinformatics, 2009, 25, 1333-1334.	4.1	8
126	Avoiding pitfalls in gene (co)expression meta-analysis. Genomics, 2014, 103, 21-30.	2.9	8

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127	Automatic extraction of reliable regions from multiple sequence alignments. BMC Bioinformatics, 2007, 8, S9.	2.6	7
128	PathwAX II: network-based pathway analysis with interactive visualization of network crosstalk. Bioinformatics, 2022, 38, 2659-2660.	4.1	7
129	Chromosomal clustering of nuclear genes encoding mitochondrial and chloroplast proteins in Arabidopsis. Trends in Genetics, 2006, 22, 589-593.	6.7	6
130	Fast and accurate gene regulatory network inference by normalized least squares regression. Bioinformatics, 2022, 38, 2263-2268.	4.1	6
131	Widespread eukaryotic sequences, highly similar to bacterial DNA polymerase I, looking for functions. Current Biology, 1997, 7, R462-R466.	3.9	5
132	Transition Priors for Protein Hidden Markov Models: An Empirical Study towards Maximum Discrimination. Journal of Computational Biology, 2004, 11, 181-193.	1.6	5
133	NovelFam3000 “Uncharacterized human protein domains conserved across model organisms. BMC Genomics, 2006, 7, 48.	2.8	5
134	Employing conservation of co-expression to improve functional inference. BMC Systems Biology, 2008, 2, 81.	3.0	5
135	PathBIX “a web server for network-based pathway annotation with adaptive null models. Bioinformatics Advances, 2021, 1, .	2.4	5
136	Drug repurposing improves disease targeting 11-fold and can be augmented by network module targeting, applied to COVID-19. Scientific Reports, 2021, 11, 20687.	3.3	5
137	Sfixem-graphical sequence feature display in Java. Bioinformatics, 2004, 20, 2488-2490.	4.1	4
138	Comparison of the Human Germline and Rearranged V _H Repertoire Reveals Complementarity between Germline Variability and Somatic Mutation. Annals of the New York Academy of Sciences, 1995, 764, 180-182.	3.8	4
139	TreeDom: a graphical web tool for analysing domain architecture evolution. Bioinformatics, 2016, 32, 2384-2385.	4.1	4
140	Perturbation-based gene regulatory network inference to unravel oncogenic mechanisms. Scientific Reports, 2020, 10, 14149.	3.3	4
141	The C. elegans expression pattern database: a beginning. Trends in Genetics, 1996, 12, 370-371.	6.7	4
142	GRNbenchmark - a web server for benchmarking directed gene regulatory network inference methods. Nucleic Acids Research, 2022, 50, W398-W404.	14.5	4
143	Inferring the experimental design for accurate gene regulatory network inference. Bioinformatics, 2021, 37, 3553-3559.	4.1	3
144	Exploring the Foundation of Genomics: A Northern Blot Reference set for the Comparative Analysis of Transcript Profiling Technologies. Comparative and Functional Genomics, 2004, 5, 584-595.	2.0	2

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145	Network Analysis of Functional Genomics Data: Application to Avian Sex-Biased Gene Expression. Scientific World Journal, The, 2012, 2012, 1-10.	2.1	2
146	Experimental validation of predicted cancer genes using FRET. Methods and Applications in Fluorescence, 2018, 6, 035007.	2.3	2
147	MetaCNV - a consensus approach to infer accurate copy numbers from low coverage data. BMC Medical Genomics, 2020, 13, 76.	1.5	2
148	Benefits and Challenges of Pre-clustered Network-Based Pathway Analysis. Frontiers in Genetics, 2022, 13, .	2.3	2
149	Generation of Realistic Gene Regulatory Networks by Enriching for Feed-Forward Loops. Frontiers in Genetics, 2022, 13, 815692.	2.3	1
150	Network Crosstalk as a Basis for Drug Repurposing. Frontiers in Genetics, 2022, 13, 792090.	2.3	0
151	Optimal Sparsity Selection Based on an Information Criterion for Accurate Gene Regulatory Network Inference. Frontiers in Genetics, 0, 13, .	2.3	0