

Erik Ll L Sonnhammer

List of Publications by Year in Descending Order

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Version: 2024-04-17

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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.

141
papers

44,279
citations

53
h-index

159
g-index

159
ext. papers

53,058
ext. citations

9.3
avg, IF

7.39
L-index

#	Paper	IF	Citations
141	Generation of Realistic Gene Regulatory Networks by Enriching for Feed-Forward Loops.. <i>Frontiers in Genetics</i> , 2022 , 13, 815692	4.5	
140	Network Crosstalk as a Basis for Drug Repurposing.. <i>Frontiers in Genetics</i> , 2022 , 13, 792090	4.5	
139	Drug repurposing improves disease targeting 11-fold and can be augmented by network module targeting, applied to COVID-19. <i>Scientific Reports</i> , 2021 , 11, 20687	4.9	1
138	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	6.5	4
137	Pfam: The protein families database in 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D412-D419	20.1	620
136	DNA Methylation Levels in Mononuclear Leukocytes from the Mother and Her Child Are Associated with IgE Sensitization to Allergens in Early Life. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	5
135	Uncovering cancer gene regulation by accurate regulatory network inference from uninformative data. <i>Npj Systems Biology and Applications</i> , 2020 , 6, 37	5	1
134	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, W538-W545	20.1	17
133	Fusion transcript detection using spatial transcriptomics. <i>BMC Medical Genomics</i> , 2020 , 13, 110	3.7	7
132	MetaCNV - a consensus approach to infer accurate copy numbers from low coverage data. <i>BMC Medical Genomics</i> , 2020 , 13, 76	3.7	1
131	Pathway-specific model estimation for improved pathway annotation by network crosstalk. <i>Scientific Reports</i> , 2020 , 10, 13585	4.9	4
130	Perturbation-based gene regulatory network inference to unravel oncogenic mechanisms. <i>Scientific Reports</i> , 2020 , 10, 14149	4.9	0
129	Genome-wide functional association networks: background, data & state-of-the-art resources. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1224-1237	13.4	5
128	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	12.9	37
127	Evolution of Protein Domain Architectures. <i>Methods in Molecular Biology</i> , 2019 , 1910, 469-504	1.4	11
126	Domainoid: domain-oriented orthology inference. <i>BMC Bioinformatics</i> , 2019 , 20, 523	3.6	3
125	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D427-D432	20.1	2298

124	A generalized framework for controlling FDR in gene regulatory network inference. <i>Bioinformatics</i> , 2019 , 35, 1026-1032	7.2	5
123	Experimental validation of predicted cancer genes using FRET. <i>Methods and Applications in Fluorescence</i> , 2018 , 6, 035007	3.1	1
122	Discovering viral genomes in human metagenomic data by predicting unknown protein families. <i>Scientific Reports</i> , 2018 , 8, 28	4.9	11
121	Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity. <i>Nature Communications</i> , 2018 , 9, 2419	17.4	195
120	Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018 , 34, 323-329	7.2	25
119	FunCoup 4: new species, data, and visualization. <i>Nucleic Acids Research</i> , 2018 , 46, D601-D607	20.1	29
118	GeneSPIDER - gene regulatory network inference benchmarking with controlled network and data properties. <i>Molecular BioSystems</i> , 2017 , 13, 1304-1312		9
117	A large-scale benchmark of gene prioritization methods. <i>Scientific Reports</i> , 2017 , 7, 46598	4.9	30
116	A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family. <i>Nature Communications</i> , 2017 , 8, 1541	17.4	62
115	HieranoiDB: a database of orthologs inferred by Hieranoid. <i>Nucleic Acids Research</i> , 2017 , 45, D687-D690	20.1	9
114	A novel method for crosstalk analysis of biological networks: improving accuracy of pathway annotation. <i>Nucleic Acids Research</i> , 2017 , 45, e8	20.1	20
113	Improved orthology inference with Hieranoid 2. <i>Bioinformatics</i> , 2017 , 33, 1154-1159	7.2	11
112	PathwAX: a web server for network crosstalk based pathway annotation. <i>Nucleic Acids Research</i> , 2016 , 44, W105-9	20.1	22
111	TreeDom: a graphical web tool for analysing domain architecture evolution. <i>Bioinformatics</i> , 2016 , 32, 2384-5	7.2	2
110	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016 , 13, 425-30	21.6	133
109	Benchmarking the next generation of homology inference tools. <i>Bioinformatics</i> , 2016 , 32, 2636-41	7.2	10
108	InParanoid 8: orthology analysis between 273 proteomes, mostly eukaryotic. <i>Nucleic Acids Research</i> , 2015 , 43, D234-9	20.1	337
107	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	22.3	17

106	Avoiding pitfalls in L1-regularised inference of gene networks. <i>Molecular BioSystems</i> , 2015 , 11, 287-96		8
105	Avoiding pitfalls in gene (co)expression meta-analysis. <i>Genomics</i> , 2014 , 103, 21-30	4.3	6
104	MaxLink: network-based prioritization of genes tightly linked to a disease seed set. <i>Bioinformatics</i> , 2014 , 30, 2689-90	7.2	22
103	The <i>Chironomus tentans</i> genome sequence and the organization of the Balbiani ring genes. <i>BMC Genomics</i> , 2014 , 15, 819	4.5	12
102	Functional association networks as priors for gene regulatory network inference. <i>Bioinformatics</i> , 2014 , 30, i130-8	7.2	30
101	FunCoup 3.0: database of genome-wide functional coupling networks. <i>Nucleic Acids Research</i> , 2014 , 42, D380-8	20.1	89
100	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014 , 42, D222-30	20.1	3975
99	Prognostic significance in breast cancer of a gene signature capturing stromal PDGF signaling. <i>American Journal of Pathology</i> , 2013 , 182, 2037-47	5.8	42
98	Hieranoid: hierarchical orthology inference. <i>Journal of Molecular Biology</i> , 2013 , 425, 2072-2081	6.5	31
97	MGclus: network clustering employing shared neighbors. <i>Molecular BioSystems</i> , 2013 , 9, 1670-5		8
96	Optimal sparsity criteria for network inference. <i>Journal of Computational Biology</i> , 2013 , 20, 398-408	1.7	11
95	Statistical assessment of crosstalk enrichment between gene groups in biological networks. <i>PLoS ONE</i> , 2013 , 8, e54945	3.7	28
94	Quality criteria for finding genes with high mRNA-protein expression correlation and coexpression correlation. <i>Gene</i> , 2012 , 497, 228-36	3.8	18
93	Network analysis of functional genomics data: application to avian sex-biased gene expression. <i>Scientific World Journal, The</i> , 2012 , 2012, 130491	2.2	2
92	Evolution of protein domain architectures. <i>Methods in Molecular Biology</i> , 2012 , 856, 187-216	1.4	35
91	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012 , 40, D290-301	20.1	2844
90	Comparative interactomics with Funcoup 2.0. <i>Nucleic Acids Research</i> , 2012 , 40, D821-8	20.1	41
89	Domain architecture conservation in orthologs. <i>BMC Bioinformatics</i> , 2011 , 12, 326	3.6	32

88	Letter to the editor: SeqXML and OrthoXML: standards for sequence and orthology information. <i>Briefings in Bioinformatics</i> , 2011 , 12, 485-8	13.4	44
87	OrthoDisease: tracking disease gene orthologs across 100 species. <i>Briefings in Bioinformatics</i> , 2011 , 12, 463-73	13.4	12
86	InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. <i>Nucleic Acids Research</i> , 2010 , 38, D196-203	20.1	500
85	Network-based Identification of novel cancer genes. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 648-55	7.6	46
84	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010 , 38, D211-22	20.1	2467
83	Orthology confers intron position conservation. <i>BMC Genomics</i> , 2010 , 11, 412	4.5	25
82	Dynamic zebrafish interactome reveals transcriptional mechanisms of dioxin toxicity. <i>PLoS ONE</i> , 2010 , 5, e10465	3.7	41
81	Benchmarking homology detection procedures with low complexity filters. <i>Bioinformatics</i> , 2009 , 25, 2500-5	7.2	11
80	Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009 , 19, 1107-16	9.7	123
79	DASher: a stand-alone protein sequence client for DAS, the Distributed Annotation System. <i>Bioinformatics</i> , 2009 , 25, 1333-4	7.2	8
78	Kalign2: high-performance multiple alignment of protein and nucleotide sequences allowing external features. <i>Nucleic Acids Research</i> , 2009 , 37, 858-65	20.1	214
77	Comparative analysis and unification of domain-domain interaction networks. <i>Bioinformatics</i> , 2009 , 25, 3020-5	7.2	22
76	MetaTM - a consensus method for transmembrane protein topology prediction. <i>BMC Bioinformatics</i> , 2009 , 10, 314	3.6	22
75	Employing conservation of co-expression to improve functional inference. <i>BMC Systems Biology</i> , 2008 , 2, 81	3.5	5
74	Focusing on RISC assembly in mammalian cells. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 368, 703-8	3.4	12
73	siRNA specificity searching incorporating mismatch tolerance data. <i>Bioinformatics</i> , 2008 , 24, 1316-7	7.2	15
72	Domain tree-based analysis of protein architecture evolution. <i>Molecular Biology and Evolution</i> , 2008 , 25, 254-64	8.3	70
71	Predicting protein function from domain content. <i>Bioinformatics</i> , 2008 , 24, 1681-7	7.2	60

70	jSquid: a Java applet for graphical on-line network exploration. <i>Bioinformatics</i> , 2008 , 24, 1467-8	7.2	16
69	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2008 , 36, D281-8	20.1	1806
68	InParanoid 6: eukaryotic ortholog clusters with inparalogs. <i>Nucleic Acids Research</i> , 2008 , 36, D263-6	20.1	176
67	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
66	Automatic extraction of reliable regions from multiple sequence alignments. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 5, S9	3.6	4
65	PfamAlyzer: domain-centric homology search. <i>Bioinformatics</i> , 2007 , 23, 3382-3	7.2	14
64	Membrane topology of the Drosophila OR83b odorant receptor. <i>FEBS Letters</i> , 2007 , 581, 5601-4	3.8	165
63	Chromosomal clustering of nuclear genes encoding mitochondrial and chloroplast proteins in Arabidopsis. <i>Trends in Genetics</i> , 2006 , 22, 589-93	8.5	6
62	NovelFam3000--uncharacterized human protein domains conserved across model organisms. <i>BMC Genomics</i> , 2006 , 7, 48	4.5	2
61	Automatic clustering of orthologs and inparalogs shared by multiple proteomes. <i>Bioinformatics</i> , 2006 , 22, e9-15	7.2	200
60	Kalign, Kalignvu and Mumsa: web servers for multiple sequence alignment. <i>Nucleic Acids Research</i> , 2006 , 34, W596-9	20.1	79
59	Prediction of function divergence in protein families using the substitution rate variation parameter alpha. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1406-13	8.3	10
58	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
57	Overview and comparison of ortholog databases. <i>Drug Discovery Today: Technologies</i> , 2006 , 3, 137-43	7.1	17
56	A general model of G protein-coupled receptor sequences and its application to detect remote homologs. <i>Protein Science</i> , 2006 , 15, 509-21	6.3	139
55	Automatic assessment of alignment quality. <i>Nucleic Acids Research</i> , 2005 , 33, 7120-8	20.1	102
54	FunShift: a database of function shift analysis on protein subfamilies. <i>Nucleic Acids Research</i> , 2005 , 33, D197-200	20.1	37
53	Inparanoid: a comprehensive database of eukaryotic orthologs. <i>Nucleic Acids Research</i> , 2005 , 33, D476-80	20.1	541

52	siRNAdb: a database of siRNA sequences. <i>Nucleic Acids Research</i> , 2005 , 33, D131-4	20.1	51
51	A novel transmembrane topology of presenilin based on reconciling experimental and computational evidence. <i>FEBS Journal</i> , 2005 , 272, 2727-33	5.7	43
50	Scoredist: a simple and robust protein sequence distance estimator. <i>BMC Bioinformatics</i> , 2005 , 6, 108	3.6	89
49	Kalign--an accurate and fast multiple sequence alignment algorithm. <i>BMC Bioinformatics</i> , 2005 , 6, 298	3.6	476
48	Improved profile HMM performance by assessment of critical algorithmic features in SAM and HMMER. <i>BMC Bioinformatics</i> , 2005 , 6, 99	3.6	40
47	Large-scale prediction of function shift in protein families with a focus on enzymatic function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 758-68	4.2	26
46	Assessment of protein distance measures and tree-building methods for phylogenetic tree reconstruction. <i>Molecular Biology and Evolution</i> , 2005 , 22, 2257-64	8.3	13
45	An HMM posterior decoder for sequence feature prediction that includes homology information. <i>Bioinformatics</i> , 2005 , 21 Suppl 1, i251-7	7.2	246
44	transition priors for protein hidden Markov models: an empirical study towards maximum discrimination. <i>Journal of Computational Biology</i> , 2004 , 11, 181-93	1.7	3
43	Sfixem--graphical sequence feature display in Java. <i>Bioinformatics</i> , 2004 , 20, 2488-90	7.2	4
42	ChromoWheel: a new spin on eukaryotic chromosome visualization. <i>Bioinformatics</i> , 2004 , 20, 576-7	7.2	7
41	Profiled support vector machines for antisense oligonucleotide efficacy prediction. <i>BMC Bioinformatics</i> , 2004 , 5, 135	3.6	21
40	Functional characterization in <i>Caenorhabditis elegans</i> of transmembrane worm-human orthologs. <i>BMC Genomics</i> , 2004 , 5, 85	4.5	14
39	Conspicuous accumulation of transcription elongation repressor hrp130/CA150 on the intron-rich Balbiani ring 3 gene. <i>Chromosoma</i> , 2004 , 113, 244-57	2.8	10
38	OrthoDisease: a database of human disease orthologs. <i>Human Mutation</i> , 2004 , 24, 112-9	4.7	48
37	Exploring the foundation of genomics: a northern blot reference set for the comparative analysis of transcript profiling technologies. <i>Comparative and Functional Genomics</i> , 2004 , 5, 584-95		2
36	Improved and automated prediction of effective siRNA. <i>Biochemical and Biophysical Research Communications</i> , 2004 , 319, 264-74	3.4	115
35	A combined transmembrane topology and signal peptide prediction method. <i>Journal of Molecular Biology</i> , 2004 , 338, 1027-36	6.5	1669

34	Improving profile HMM discrimination by adapting transition probabilities. <i>Journal of Molecular Biology</i> , 2004 , 338, 847-54	6.5	24
33	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
32	Comprehensive analysis of orthologous protein domains using the HOPS database. <i>Genome Research</i> , 2003 , 13, 2353-62	9.7	34
31	Genomic gene clustering analysis of pathways in eukaryotes. <i>Genome Research</i> , 2003 , 13, 875-82	9.7	243
30	Orthology, paralogy and proposed classification for paralog subtypes. <i>Trends in Genetics</i> , 2002 , 18, 619-20	20.5	299
29	Automated ortholog inference from phylogenetic trees and calculation of orthology reliability. <i>Bioinformatics</i> , 2002 , 18, 92-9	7.2	148
28	Computational antisense oligo prediction with a neural network model. <i>Bioinformatics</i> , 2002 , 18, 1567-75	7.2	37
27	OrthoGUI: graphical presentation of Orthostrapper results. <i>Bioinformatics</i> , 2002 , 18, 1272-3	7.2	12
26	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2002 , 30, 276-80	20.1	1839
25	Quality assessment of multiple alignment programs. <i>FEBS Letters</i> , 2002 , 529, 126-30	3.8	95
24	Reliability of transmembrane predictions in whole-genome data. <i>FEBS Letters</i> , 2002 , 532, 415-8	3.8	58
23	Integrated graphical analysis of protein sequence features predicted from sequence composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 262-73	4.2	34
22	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
21	Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. <i>Journal of Molecular Biology</i> , 2001 , 314, 1041-52	6.5	959
20	Putative regulatory domains in the human and mouse CVADR genes. <i>Gene Function & Disease</i> , 2000 , 1, 82-86		5
19	FAT: a novel domain in PIK-related kinases. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 225-7	10.3	243
18	Classification of transmembrane protein families in the <i>Caenorhabditis elegans</i> genome and identification of human orthologs. <i>Genome Research</i> , 2000 , 10, 1679-89	9.7	26
17	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2000 , 28, 263-6	20.1	1074

16	Pfam 3.1: 1313 multiple alignments and profile HMMs match the majority of proteins. <i>Nucleic Acids Research</i> , 1999 , 27, 260-2	20.1	488
15	Dynamic contact maps of protein structures. <i>Journal of Molecular Graphics and Modelling</i> , 1998 , 16, 1-5, 33	2.8	10
14	Pfam: multiple sequence alignments and HMM-profiles of protein domains. <i>Nucleic Acids Research</i> , 1998 , 26, 320-2	20.1	527
13	Analysis of protein domain families in <i>Caenorhabditis elegans</i> . <i>Genomics</i> , 1997 , 46, 200-16	4.3	106
12	Sequence of the human immunoglobulin diversity (D) segment locus: a systematic analysis provides no evidence for the use of DIR segments, inverted D segments, "minor" D segments or D-D recombination. <i>Journal of Molecular Biology</i> , 1997 , 270, 587-97	6.5	265
11	Widespread eukaryotic sequences, highly similar to bacterial DNA polymerase I, looking for functions. <i>Current Biology</i> , 1997 , 7, R463-5	6.3	5
10	Pfam: a comprehensive database of protein domain families based on seed alignments. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 28, 405-20	4.2	841
9	The imprint of somatic hypermutation on the repertoire of human germline V genes. <i>Journal of Molecular Biology</i> , 1996 , 256, 813-17	6.5	178
8	The <i>C. elegans</i> expression pattern database: a beginning 1996 , 12, 370-370		3
7	Comparison of the human germline and rearranged VH repertoire reveals complementarity between germline variability and somatic mutation. <i>Annals of the New York Academy of Sciences</i> , 1995 , 764, 180-2	6.5	4
6	A dot-matrix program with dynamic threshold control suited for genomic DNA and protein sequence analysis. <i>Gene</i> , 1995 , 167, GC1-10	3.8	563
5	A workbench for large-scale sequence homology analysis. <i>Bioinformatics</i> , 1994 , 10, 301-7	7.2	44
4	Modular arrangement of proteins as inferred from analysis of homology. <i>Protein Science</i> , 1994 , 3, 482-926.3		174
3	Volume changes in protein evolution. <i>Journal of Molecular Biology</i> , 1994 , 236, 1067-78	6.5	139
2	Comprehensive sequence analysis of the 182 predicted open reading frames of yeast chromosome III. <i>Protein Science</i> , 1992 , 1, 1677-90	6.3	98
1	What's in a genome?. <i>Nature</i> , 1992 , 358, 287	50.4	44