

Erik Ll L Sonnhammer

List of Publications by Year in descending order

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151
papers

62,267
citations

26567

56
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7496

151
g-index

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. <i>Journal of Molecular Biology</i> , 2001, 305, 567-580. | 2.0 | 11,404 |
| 2 | The Pfam protein families database. <i>Nucleic Acids Research</i> , 2007, 36, D281-D288. | 6.5 | 6,372 |
| 3 | Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230. | 6.5 | 5,425 |
| 4 | The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D427-D432. | 6.5 | 3,937 |
| 5 | The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012, 40, D290-D301. | 6.5 | 3,306 |
| 6 | The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004, 32, 138D-141. | 6.5 | 3,084 |
| 7 | Pfam: The protein families database in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D412-D419. | 6.5 | 3,068 |
| 8 | The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010, 38, D211-D222. | 6.5 | 2,693 |
| 9 | A Combined Transmembrane Topology and Signal Peptide Prediction Method. <i>Journal of Molecular Biology</i> , 2004, 338, 1027-1036. | 2.0 | 2,145 |
| 10 | The Pfam Protein Families Database. <i>Nucleic Acids Research</i> , 2002, 30, 276-280. | 6.5 | 2,067 |
| 11 | Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006, 34, D247-D251. | 6.5 | 2,030 |
| 12 | Advantages of combined transmembrane topology and signal peptide prediction—the Phobius web server. <i>Nucleic Acids Research</i> , 2007, 35, W429-W432. | 6.5 | 1,461 |
| 13 | The Pfam Protein Families Database. <i>Nucleic Acids Research</i> , 2000, 28, 263-266. | 6.5 | 1,173 |
| 14 | Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. <i>Journal of Molecular Biology</i> , 2001, 314, 1041-1052. | 2.0 | 1,081 |
| 15 | Pfam: A comprehensive database of protein domain families based on seed alignments. , 1997, 28, 405-420. | | 1,036 |
| 16 | A dot-matrix program with dynamic threshold control suited for genomic DNA and protein sequence analysis. <i>Gene</i> , 1995, 167, GC1-GC10. | 1.0 | 677 |
| 17 | Inparanoid: a comprehensive database of eukaryotic orthologs. <i>Nucleic Acids Research</i> , 2004, 33, D476-D480. | 6.5 | 667 |
| 18 | Pfam: multiple sequence alignments and HMM-profiles of protein domains. <i>Nucleic Acids Research</i> , 1998, 26, 320-322. | 6.5 | 644 |

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|----|--|-----|-----------|
| 19 | Kalign—an accurate and fast multiple sequence alignment algorithm. BMC Bioinformatics, 2005, 6, 298. | 1.2 | 615 |
| 20 | InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. Nucleic Acids Research, 2010, 38, D196-D203. | 6.5 | 576 |
| 21 | Pfam 3.1: 1313 multiple alignments and profile HMMs match the majority of proteins. Nucleic Acids Research, 1999, 27, 260-262. | 6.5 | 533 |
| 22 | InParanoid 8: orthology analysis between 273 proteomes, mostly eukaryotic. Nucleic Acids Research, 2015, 43, D234-D239. | 6.5 | 449 |
| 23 | Spatial maps of prostate cancer transcriptomes reveal an unexplored landscape of heterogeneity. Nature Communications, 2018, 9, 2419. | 5.8 | 374 |
| 24 | Orthology, paralogy and proposed classification for paralog subtypes. Trends in Genetics, 2002, 18, 619-620. | 2.9 | 360 |
| 25 | Genomic Gene Clustering Analysis of Pathways in Eukaryotes. Genome Research, 2003, 13, 875-882. | 2.4 | 307 |
| 26 | An HMM posterior decoder for sequence feature prediction that includes homology information. Bioinformatics, 2005, 21, i251-i257. | 1.8 | 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. | 2.0 | 283 |
| 28 | FAT: a novel domain in PIK-related kinases. Trends in Biochemical Sciences, 2000, 25, 225-227. | 3.7 | 265 |
| 29 | Kalign2: high-performance multiple alignment of protein and nucleotide sequences allowing external features. Nucleic Acids Research, 2009, 37, 858-865. | 6.5 | 263 |
| 30 | Automatic clustering of orthologs and inparalogs shared by multiple proteomes. Bioinformatics, 2006, 22, e9-e15. | 1.8 | 227 |
| 31 | Modular arrangement of proteins as inferred from analysis of homology. Protein Science, 1994, 3, 482-492. | 3.1 | 220 |
| 32 | The Imprint of Somatic Hypermutation on the Repertoire of Human Germline V Genes. Journal of Molecular Biology, 1996, 256, 813-817. | 2.0 | 209 |
| 33 | Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430. | 9.0 | 198 |
| 34 | Membrane topology of the <i>Drosophila</i> OR83b odorant receptor. FEBS Letters, 2007, 581, 5601-5604. | 1.3 | 194 |
| 35 | InParanoid 6: eukaryotic ortholog clusters with inparalogs. Nucleic Acids Research, 2007, 36, D263-D266. | 6.5 | 189 |
| 36 | Automated ortholog inference from phylogenetic trees and calculation of orthology reliability. Bioinformatics, 2002, 18, 92-99. | 1.8 | 163 |

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|----|---|-----|-----------|
| 37 | Volume changes in protein evolution. <i>Journal of Molecular Biology</i> , 1994, 236, 1067-1078. | 2.0 | 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. | 3.1 | 158 |
| 39 | Global networks of functional coupling in eukaryotes from comprehensive data integration. <i>Genome Research</i> , 2009, 19, 1107-1116. | 2.4 | 137 |
| 40 | Analysis of Protein Domain Families in <i>Caenorhabditis elegans</i> . <i>Genomics</i> , 1997, 46, 200-216. | 1.3 | 129 |
| 41 | Improved and automated prediction of effective siRNA. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 264-274. | 1.0 | 129 |
| 42 | Automatic assessment of alignment quality. <i>Nucleic Acids Research</i> , 2005, 33, 7120-7128. | 6.5 | 126 |
| 43 | A comprehensive structural, biochemical and biological profiling of the human NUDIX hydrolase family. <i>Nature Communications</i> , 2017, 8, 1541. | 5.8 | 124 |
| 44 | Scoredist: a simple and robust protein sequence distance estimator. <i>BMC Bioinformatics</i> , 2005, 6, 108. | 1.2 | 116 |
| 45 | Quality assessment of multiple alignment programs. <i>FEBS Letters</i> , 2002, 529, 126-130. | 1.3 | 112 |
| 46 | Big data and other challenges in the quest for orthologs. <i>Bioinformatics</i> , 2014, 30, 2993-2998. | 1.8 | 109 |
| 47 | Comprehensive sequence analysis of the 182 predicted open reading frames of yeast chromosome III. <i>Protein Science</i> , 1992, 1, 1677-1690. | 3.1 | 106 |
| 48 | Kalign, Kalignvu and Mumsa: web servers for multiple sequence alignment. <i>Nucleic Acids Research</i> , 2006, 34, W596-W599. | 6.5 | 99 |
| 49 | Domain Tree-Based Analysis of Protein Architecture Evolution. <i>Molecular Biology and Evolution</i> , 2008, 25, 254-264. | 3.5 | 98 |
| 50 | FunCoup 3.0: database of genome-wide functional coupling networks. <i>Nucleic Acids Research</i> , 2014, 42, D380-D388. | 6.5 | 96 |
| 51 | Predicting protein function from domain content. <i>Bioinformatics</i> , 2008, 24, 1681-1687. | 1.8 | 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. | 3.2 | 72 |
| 53 | Reliability of transmembrane predictions in whole-genome data. <i>FEBS Letters</i> , 2002, 532, 415-418. | 1.3 | 70 |
| 54 | A Workbench for large-scale sequence homology analysis. <i>Bioinformatics</i> , 1994, 10, 301-307. | 1.8 | 69 |

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|----|---|------|-----------|
| 55 | What's in a genome?. Nature, 1992, 358, 287-287. | 13.7 | 57 |
| 56 | siRNADB: a database of siRNA sequences. Nucleic Acids Research, 2004, 33, D131-D134. | 6.5 | 57 |
| 57 | OrthoDisease: A database of human disease orthologs. Human Mutation, 2004, 24, 112-119. | 1.1 | 56 |
| 58 | Network-based Identification of Novel Cancer Genes. Molecular and Cellular Proteomics, 2010, 9, 648-655. | 2.5 | 54 |
| 59 | Domain architecture conservation in orthologs. BMC Bioinformatics, 2011, 12, 326. | 1.2 | 54 |
| 60 | Letter to the Editor: SeqXML and OrthoXML: standards for sequence and orthology information. Briefings in Bioinformatics, 2011, 12, 485-488. | 3.2 | 51 |
| 61 | Prognostic Significance in Breast Cancer of a Gene Signature Capturing Stromal PDGF Signaling. American Journal of Pathology, 2013, 182, 2037-2047. | 1.9 | 50 |
| 62 | Comparative interactomics with Funcoup 2.0. Nucleic Acids Research, 2012, 40, D821-D828. | 6.5 | 49 |
| 63 | Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2012, 856, 187-216. | 0.4 | 47 |
| 64 | Dynamic Zebrafish Interactome Reveals Transcriptional Mechanisms of Dioxin Toxicity. PLoS ONE, 2010, 5, e10465. | 1.1 | 47 |
| 65 | A novel transmembrane topology of presenilin based on reconciling experimental and computational evidence. FEBS Journal, 2005, 272, 2727-2733. | 2.2 | 45 |
| 66 | Improved profile HMM performance by assessment of critical algorithmic features in SAM and HMMER. BMC Bioinformatics, 2005, 6, 99. | 1.2 | 45 |
| 67 | A large-scale benchmark of gene prioritization methods. Scientific Reports, 2017, 7, 46598. | 1.6 | 44 |
| 68 | FunCoup 4: new species, data, and visualization. Nucleic Acids Research, 2018, 46, D601-D607. | 6.5 | 44 |
| 69 | Computational antisense oligo prediction with a neural network model. Bioinformatics, 2002, 18, 1567-1575. | 1.8 | 41 |
| 70 | The Quest for Orthologs benchmark service and consensus calls in 2020. Nucleic Acids Research, 2020, 48, W538-W545. | 6.5 | 41 |
| 71 | Comprehensive Analysis of Orthologous Protein Domains Using the HOPS Database. Genome Research, 2003, 13, 2353-2362. | 2.4 | 40 |
| 72 | FunShift: a database of function shift analysis on protein subfamilies. Nucleic Acids Research, 2004, 33, D197-D200. | 6.5 | 39 |

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|----|---|-----|-----------|
| 73 | Functional association networks as priors for gene regulatory network inference. <i>Bioinformatics</i> , 2014, 30, i130-i138. | 1.8 | 39 |
| 74 | Hieranoid: Hierarchical Orthology Inference. <i>Journal of Molecular Biology</i> , 2013, 425, 2072-2081. | 2.0 | 38 |
| 75 | PathwAX: a web server for network crosstalk based pathway annotation. <i>Nucleic Acids Research</i> , 2016, 44, W105-W109. | 6.5 | 36 |
| 76 | Gearing up to handle the mosaic nature of life in the quest for orthologs. <i>Bioinformatics</i> , 2018, 34, 323-329. | 1.8 | 36 |
| 77 | Integrated graphical analysis of protein sequence features predicted from sequence composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 262-273. | 1.5 | 35 |
| 78 | Statistical Assessment of Crosstalk Enrichment between Gene Groups in Biological Networks. <i>PLoS ONE</i> , 2013, 8, e54945. | 1.1 | 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. | 6.5 | 33 |
| 80 | Improving Profile HMM Discrimination by Adapting Transition Probabilities. <i>Journal of Molecular Biology</i> , 2004, 338, 847-854. | 2.0 | 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. | 3.1 | 30 |
| 82 | Evolution of Protein Domain Architectures. <i>Methods in Molecular Biology</i> , 2019, 1910, 469-504. | 0.4 | 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. | 2.4 | 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. | 1.5 | 29 |
| 85 | Orthology confers intron position conservation. <i>BMC Genomics</i> , 2010, 11, 412. | 1.2 | 29 |
| 86 | The Quest for Orthologs orthology benchmark service in 2022. <i>Nucleic Acids Research</i> , 2022, 50, W623-W632. | 6.5 | 29 |
| 87 | MaxLink: network-based prioritization of genes tightly linked to a disease seed set. <i>Bioinformatics</i> , 2014, 30, 2689-2690. | 1.8 | 27 |
| 88 | Comparative analysis and unification of domain-domain interaction networks. <i>Bioinformatics</i> , 2009, 25, 3020-3025. | 1.8 | 26 |
| 89 | MetaTM - a consensus method for transmembrane protein topology prediction. <i>BMC Bioinformatics</i> , 2009, 10, 314. | 1.2 | 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. | 2.0 | 25 |

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|-----|--|-----|-----------|
| 91 | Profiled support vector machines for antisense oligonucleotide efficacy prediction. BMC Bioinformatics, 2004, 5, 135. | 1.2 | 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. | 1.0 | 22 |
| 94 | Improved orthology inference with Hieranoid 2. Bioinformatics, 2017, 33, 1154-1159. | 1.8 | 22 |
| 95 | Genome-wide functional association networks: background, data & state-of-the-art resources. Briefings in Bioinformatics, 2020, 21, 1224-1237. | 3.2 | 20 |
| 96 | Optimal Sparsity Criteria for Network Inference. Journal of Computational Biology, 2013, 20, 398-408. | 0.8 | 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. | 1.8 | 18 |
| 98 | siRNA specificity searching incorporating mismatch tolerance data. Bioinformatics, 2008, 24, 1316-1317. | 1.8 | 17 |
| 99 | HieranoiDB: a database of orthologs inferred by Hieranoid. Nucleic Acids Research, 2017, 45, D687-D690. | 6.5 | 17 |
| 100 | Domainoid: domain-oriented orthology inference. BMC Bioinformatics, 2019, 20, 523. | 1.2 | 17 |
| 101 | Fusion transcript detection using spatial transcriptomics. BMC Medical Genomics, 2020, 13, 110. | 0.7 | 17 |
| 102 | Assessment of Protein Distance Measures and Tree-Building Methods for Phylogenetic Tree Reconstruction. Molecular Biology and Evolution, 2005, 22, 2257-2264. | 3.5 | 16 |
| 103 | jSquid: a Java applet for graphical on-line network exploration. Bioinformatics, 2008, 24, 1467-1468. | 1.8 | 16 |
| 104 | OrthoDisease: tracking disease gene orthologs across 100 species. Briefings in Bioinformatics, 2011, 12, 463-473. | 3.2 | 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. | 1.6 | 16 |
| 108 | Functional characterization in Caenorhabditis elegans of transmembrane worm-human orthologs. BMC Genomics, 2004, 5, 85. | 1.2 | 15 |

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| 109 | PfamAlyzer: domain-centric homology search. <i>Bioinformatics</i> , 2007, 23, 3382-3383. | 1.8 | 15 |
| 110 | The <i>Chironomus tentans</i> genome sequence and the organization of the Balbiani ring genes. <i>BMC Genomics</i> , 2014, 15, 819. | 1.2 | 14 |
| 111 | Benchmarking the next generation of homology inference tools. <i>Bioinformatics</i> , 2016, 32, 2636-2641. | 1.8 | 14 |
| 112 | Discovering viral genomes in human metagenomic data by predicting unknown protein families. <i>Scientific Reports</i> , 2018, 8, 28. | 1.6 | 14 |
| 113 | Dynamic contact maps of protein structures. <i>Journal of Molecular Graphics and Modelling</i> , 1998, 16, 1-5. | 1.3 | 13 |
| 114 | Focusing on RISC assembly in mammalian cells. <i>Biochemical and Biophysical Research Communications</i> , 2008, 368, 703-708. | 1.0 | 13 |
| 115 | OrthoGUI: graphical presentation of Orthostrapper results. <i>Bioinformatics</i> , 2002, 18, 1272-1273. | 1.8 | 12 |
| 116 | Prediction of Function Divergence in Protein Families Using the Substitution Rate Variation Parameter Alpha. <i>Molecular Biology and Evolution</i> , 2006, 23, 1406-1413. | 3.5 | 12 |
| 117 | MGclus: network clustering employing shared neighbors. <i>Molecular BioSystems</i> , 2013, 9, 1670. | 2.9 | 12 |
| 118 | Uncovering cancer gene regulation by accurate regulatory network inference from uninformative data. <i>Npj Systems Biology and Applications</i> , 2020, 6, 37. | 1.4 | 12 |
| 119 | InParanoid-DIAMOND: faster orthology analysis with the InParanoid algorithm. <i>Bioinformatics</i> , 2022, 38, 2918-2919. | 1.8 | 12 |
| 120 | Conspicuous accumulation of transcription elongation repressor hrp130/CA150 on the intron-rich Balbiani ring 3 gene. <i>Chromosoma</i> , 2004, 113, 244-257. | 1.0 | 11 |
| 121 | Benchmarking homology detection procedures with low complexity filters. <i>Bioinformatics</i> , 2009, 25, 2500-2505. | 1.8 | 11 |
| 122 | ChromoWheel: a new spin on eukaryotic chromosome visualization. <i>Bioinformatics</i> , 2004, 20, 576-577. | 1.8 | 10 |
| 123 | A generalized framework for controlling FDR in gene regulatory network inference. <i>Bioinformatics</i> , 2019, 35, 1026-1032. | 1.8 | 10 |
| 124 | Putative regulatory domains in the human and mouse CVADR genes. <i>Gene Function & Disease</i> , 2000, 1, 82-86. | 0.3 | 9 |
| 125 | DASher: a stand-alone protein sequence client for DAS, the Distributed Annotation System. <i>Bioinformatics</i> , 2009, 25, 1333-1334. | 1.8 | 8 |
| 126 | Avoiding pitfalls in gene (co)expression meta-analysis. <i>Genomics</i> , 2014, 103, 21-30. | 1.3 | 8 |

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| 127 | Automatic extraction of reliable regions from multiple sequence alignments. BMC Bioinformatics, 2007, 8, S9. | 1.2 | 7 |
| 128 | PathWAX II: network-based pathway analysis with interactive visualization of network crosstalk. Bioinformatics, 2022, 38, 2659-2660. | 1.8 | 7 |
| 129 | Chromosomal clustering of nuclear genes encoding mitochondrial and chloroplast proteins in Arabidopsis. Trends in Genetics, 2006, 22, 589-593. | 2.9 | 6 |
| 130 | Fast and accurate gene regulatory network inference by normalized least squares regression. Bioinformatics, 2022, 38, 2263-2268. | 1.8 | 6 |
| 131 | Widespread eukaryotic sequences, highly similar to bacterial DNA polymerase I, looking for functions. Current Biology, 1997, 7, R462-R466. | 1.8 | 5 |
| 132 | Transition Priors for Protein Hidden Markov Models: An Empirical Study towards Maximum Discrimination. Journal of Computational Biology, 2004, 11, 181-193. | 0.8 | 5 |
| 133 | NovelFam3000 "Uncharacterized human protein domains conserved across model organisms. BMC Genomics, 2006, 7, 48. | 1.2 | 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, . | 0.9 | 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. | 1.6 | 5 |
| 137 | Sfixem-graphical sequence feature display in Java. Bioinformatics, 2004, 20, 2488-2490. | 1.8 | 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. | 1.8 | 4 |
| 139 | TreeDom: a graphical web tool for analysing domain architecture evolution. Bioinformatics, 2016, 32, 2384-2385. | 1.8 | 4 |
| 140 | Perturbation-based gene regulatory network inference to unravel oncogenic mechanisms. Scientific Reports, 2020, 10, 14149. | 1.6 | 4 |
| 141 | The C. elegans expression pattern database: a beginning. , 1996, 12, 370-370. | | 4 |
| 142 | GRNbenchmark - a web server for benchmarking directed gene regulatory network inference methods. Nucleic Acids Research, 2022, 50, W398-W404. | 6.5 | 4 |
| 143 | Inferring the experimental design for accurate gene regulatory network inference. Bioinformatics, 2021, 37, 3553-3559. | 1.8 | 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. | 0.8 | 2 |
| 146 | Experimental validation of predicted cancer genes using FRET. Methods and Applications in Fluorescence, 2018, 6, 035007. | 1.1 | 2 |
| 147 | MetaCNV - a consensus approach to infer accurate copy numbers from low coverage data. BMC Medical Genomics, 2020, 13, 76. | 0.7 | 2 |
| 148 | Benefits and Challenges of Pre-clustered Network-Based Pathway Analysis. Frontiers in Genetics, 2022, 13, . | 1.1 | 2 |
| 149 | Generation of Realistic Gene Regulatory Networks by Enriching for Feed-Forward Loops. Frontiers in Genetics, 2022, 13, 815692. | 1.1 | 1 |
| 150 | Network Crosstalk as a Basis for Drug Repurposing. Frontiers in Genetics, 2022, 13, 792090. | 1.1 | 0 |
| 151 | Optimal Sparsity Selection Based on an Information Criterion for Accurate Gene Regulatory Network Inference. Frontiers in Genetics, 0, 13, . | 1.1 | 0 |