

Kevin Bryson

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

5,067
citations

394421

19
h-index

477307

29
g-index

31
all docs

31
docs citations

31
times ranked

9608
citing authors

#	ARTICLE	IF	CITATIONS
1	Adversarial generation of gene expression data. <i>Bioinformatics</i> , 2022, 38, 730-737.	4.1	23
2	A Continuously Benchmarked and Crowdsourced Challenge for Rapid Development and Evaluation of Models to Predict COVID-19 Diagnosis and Hospitalization. <i>JAMA Network Open</i> , 2021, 4, e2124946.	5.9	8
3	The breast cancer oncogene <i>IKK$\hat{\mu}$</i> coordinates mitochondrial function and serine metabolism. <i>EMBO Reports</i> , 2020, 21, e48260.	4.5	6
4	Host-Microbe-Drug-Nutrient Screen Identifies Bacterial Effectors of Metformin Therapy. <i>Cell</i> , 2019, 178, 1299-1312.e29.	28.9	186
5	Host-Microbe Co-metabolism Dictates Cancer Drug Efficacy in <i>C.Âelegans</i> . <i>Cell</i> , 2017, 169, 442-456.e18.	28.9	198
6	Highly polygenic architecture of antidepressant treatment response: Comparative analysis of SSRI and NRI treatment in an animal model of depression. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 235-250.	1.7	10
7	MCbiclust: a novel algorithm to discover large-scale functionally related gene sets from massive transcriptomics data collections. <i>Nucleic Acids Research</i> , 2017, 45, 8712-8730.	14.5	13
8	Epigenetic Differences In Monozygotic Twins Discordant For Major Depressive Disorder. <i>European Neuropsychopharmacology</i> , 2017, 27, S382-S383.	0.7	0
9	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
10	Epigenetic differences in monozygotic twins discordant for major depressive disorder. <i>Translational Psychiatry</i> , 2016, 6, e839-e839.	4.8	38
11	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. <i>PLoS Computational Biology</i> , 2015, 11, e1004096.	3.2	35
12	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. <i>BMC Bioinformatics</i> , 2013, 14, S1.	2.6	72
13	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
14	Scalable web services for the PSIPRED Protein Analysis Workbench. <i>Nucleic Acids Research</i> , 2013, 41, W349-W357.	14.5	1,206
15	SwiftLink: parallel MCMC linkage analysis using multicore CPU and GPU. <i>Bioinformatics</i> , 2013, 29, 413-419.	4.1	8
16	Sequotyping: Serotyping <i>Streptococcus pneumoniae</i> by a Single PCR Sequencing Strategy. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2419-2427.	3.9	63
17	Detecting Gene Duplications in the Human Lineage. <i>Annals of Human Genetics</i> , 2010, 74, 555-565.	0.8	6
18	A Meta-Analysis of Microarray Gene Expression in Mouse Stem Cells: Redefining Stemness. <i>PLoS ONE</i> , 2008, 3, e2712.	2.5	11

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19	Computer-Assisted Protein Domain Boundary Prediction Using the Dom-Pred Server. <i>Current Protein and Peptide Science</i> , 2007, 8, 181-188.	1.4	52
20	High throughput profile-profile based fold recognition for the entire human proteome. <i>BMC Bioinformatics</i> , 2006, 7, 288.	2.6	19
21	AGMIAL: implementing an annotation strategy for prokaryote genomes as a distributed system. <i>Nucleic Acids Research</i> , 2006, 34, 3533-3545.	14.5	84
22	The complete genome sequence of <i>Lactobacillus bulgaricus</i> reveals extensive and ongoing reductive evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9274-9279.	7.1	382
23	Protein structure prediction servers at University College London. <i>Nucleic Acids Research</i> , 2005, 33, W36-W38.	14.5	646
24	The Genomic Threading Database: a comprehensive resource for structural annotations of the genomes from key organisms. <i>Nucleic Acids Research</i> , 2004, 32, 196D-199.	14.5	40
25	The DISOPRED server for the prediction of protein disorder. <i>Bioinformatics</i> , 2004, 20, 2138-2139.	4.1	659
26	Predicting Metal-binding Site Residues in Low-resolution Structural Models. <i>Journal of Molecular Biology</i> , 2004, 342, 307-320.	4.2	126
27	Agent interaction for bioinformatics data management. <i>Applied Artificial Intelligence</i> , 2001, 15, 917-947.	3.2	16
28	Binding Sites of the Polyamines Putrescine, Cadaverine, Spermidine and Spermine on A- and B-DNA Located by Simulated Annealing. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000, 18, 393-412.	3.5	32
29	Successful recognition of protein folds using threading methods biased by sequence similarity and predicted secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 104-111.	2.6	29
30	Molecular dynamics of putrescine. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1996, 92, 913.	1.7	2