Kevin Bryson

List of Publications by Year
in descending order

30 papers	5,067 citations	394286 19 h-index	477173 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. Bioinformatics, 2022, 38, 730-737.	1.8	23
2	A Continuously Benchmarked and Crowdsourced Challenge for Rapid Development and Evaluation of Models to Predict COVID-19 Diagnosis and Hospitalization. JAMA Network Open, 2021, 4, e2124946.	2.8	8
3	The breast cancer oncogene IKKÎµ coordinates mitochondrial function and serine metabolism. EMBO Reports, 2020, 21, e48260.	2.0	6
4	Host-Microbe-Drug-Nutrient Screen Identifies Bacterial Effectors of Metformin Therapy. Cell, 2019, 178, 1299-1312.e29.	13.5	186
5	Host-Microbe Co-metabolism Dictates Cancer Drug Efficacy in C.Âelegans. Cell, 2017, 169, 442-456.e18.	13.5	198
6	Highly polygenic architecture of antidepressant treatment response: Comparative analysis of SSRI and NRI treatment in an animal model of depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 235-250.	1.1	10
7	MCbiclust: a novel algorithm to discover large-scale functionally related gene sets from massive transcriptomics data collections. Nucleic Acids Research, 2017, 45, 8712-8730.	6.5	13
8	Epigenetic Differences In Monozygotic Twins Discordant For Major Depressive Disorder. European Neuropsychopharmacology, 2017, 27, S382-S383.	0.3	0
9	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
10	Epigenetic differences in monozygotic twins discordant for major depressive disorder. Translational Psychiatry, 2016, 6, e839-e839.	2.4	38
11	Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models. PLoS Computational Biology, 2015, 11, e1004096.	1.5	35
12	Protein function prediction by massive integration of evolutionary analyses and multiple data sources. BMC Bioinformatics, 2013, 14, S1.	1.2	72
13	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
14	Scalable web services for the PSIPRED Protein Analysis Workbench. Nucleic Acids Research, 2013, 41, W349-W357.	6.5	1,206
15	SwiftLink: parallel MCMC linkage analysis using multicore CPU and GPU. Bioinformatics, 2013, 29, 413-419.	1.8	8
16	Sequetyping: Serotyping Streptococcus pneumoniae by a Single PCR Sequencing Strategy. Journal of Clinical Microbiology, 2012, 50, 2419-2427.	1.8	63
17	Detecting Gene Duplications in the Human Lineage. Annals of Human Genetics, 2010, 74, 555-565.	0.3	6
18	A Meta-Analysis of Microarray Gene Expression in Mouse Stem Cells: Redefining Stemness. PLoS ONE, 2008, 3, e2712.	1.1	11

#	Article	IF	Citations
19	Computer-Assisted Protein Domain Boundary Prediction Using the Dom-Pred Server. Current Protein and Peptide Science, 2007, 8, 181-188.	0.7	52
20	High throughput profile-profile based fold recognition for the entire human proteome. BMC Bioinformatics, 2006, 7, 288.	1.2	19
21	AGMIAL: implementing an annotation strategy for prokaryote genomes as a distributed system. Nucleic Acids Research, 2006, 34, 3533-3545.	6.5	84
22	The complete genome sequence of Lactobacillus bulgaricus reveals extensive and ongoing reductive evolution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9274-9279.	3.3	382
23	Protein structure prediction servers at University College London. Nucleic Acids Research, 2005, 33, W36-W38.	6.5	646
24	The Genomic Threading Database: a comprehensive resource for structural annotations of the genomes from key organisms. Nucleic Acids Research, 2004, 32, 196D-199.	6.5	40
25	The DISOPRED server for the prediction of protein disorder. Bioinformatics, 2004, 20, 2138-2139.	1.8	659
26	Predicting Metal-binding Site Residues in Low-resolution Structural Models. Journal of Molecular Biology, 2004, 342, 307-320.	2.0	126
27	Agent interaction for bioinformatics data management. Applied Artificial Intelligence, 2001, 15, 917-947.	2.0	16
28	Binding Sites of the Polyamines Putrescine, Cadaverine, Spermidine and Spermine on A- and B-DNA Located by Simulated Annealing. Journal of Biomolecular Structure and Dynamics, 2000, 18, 393-412.	2.0	32
29	Successful recognition of protein folds using threading methods biased by sequence similarity and predicted secondary structure. Proteins: Structure, Function and Bioinformatics, 1999, 37, 104-111.	1.5	29
30	Molecular dynamics of putrescine. Journal of the Chemical Society, Faraday Transactions, 1996, 92, 913.	1.7	2