

Ronald Taylor

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

6,005
citations

361045

20
h-index

344852

36
g-index

42
all docs

42
docs citations

42
times ranked

10249
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimum information about a microarray experiment (MIAME)â€”toward standards for microarray data. <i>Nature Genetics</i> , 2001, 29, 365-371.	9.4	3,750
2	Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. <i>Current Biology</i> , 2015, 25, 690-701.	1.8	522
3	Predicting Species-Resolved Macronutrient Acquisition during Succession in a Model Phototrophic Biofilm Using an Integrated â€”Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 1020.	1.5	287
4	Standards for Microarray Data. <i>Science</i> , 2002, 298, 539b-539.	6.0	147
5	The <i>Toxoplasma gondii</i> Cyst Wall Protein CST1 Is Critical for Cyst Wall Integrity and Promotes Bradyzoite Persistence. <i>PLoS Pathogens</i> , 2013, 9, e1003823.	2.1	134
6	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). <i>Nature Biotechnology</i> , 2008, 26, 305-312.	9.4	111
7	Microbial Community Metabolic Modeling: A Community Dataâ€”Driven Network Reconstruction. <i>Journal of Cellular Physiology</i> , 2016, 231, 2339-2345.	2.0	107
8	Submission of Microarray Data to Public Repositories. <i>PLoS Biology</i> , 2004, 2, e317.	2.6	102
9	Evidence supporting dissimilatory and assimilatory lignin degradation in <i>Enterobacter lignolyticus</i> SCF1. <i>Frontiers in Microbiology</i> , 2013, 4, 280.	1.5	92
10	Network Inference Algorithms Elucidate Nrf2 Regulation of Mouse Lung Oxidative Stress. <i>PLoS Computational Biology</i> , 2008, 4, e1000166.	1.5	78
11	The frameshift signal of HIV-1 involves a potential intramolecular triplex RNA structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5331-5336.	3.3	76
12	Bottlenecks and Hubs in Inferred Networks Are Important for Virulence in <i>Salmonella typhimurium</i> . <i>Journal of Computational Biology</i> , 2009, 16, 169-180.	0.8	73
13	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. <i>Methods in Molecular Biology</i> , 2011, 719, 31-69.	0.4	73
14	Reverse engineering adverse outcome pathways. <i>Environmental Toxicology and Chemistry</i> , 2011, 30, 22-38.	2.2	72
15	The Highly Conserved MraZ Protein Is a Transcriptional Regulator in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2014, 196, 2053-2066.	1.0	69
16	An open letter to the scientific journals. <i>Bioinformatics</i> , 2002, 18, 1409-1409.	1.8	40
17	Distinct Strains of <i>Toxoplasma gondii</i> Feature Divergent Transcriptomes Regardless of Developmental Stage. <i>PLoS ONE</i> , 2014, 9, e111297.	1.1	37
18	CO2 exposure at pressure impacts metabolism and stress responses in the model sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> strain Hildenborough. <i>Frontiers in Microbiology</i> , 2014, 5, 507.	1.5	31

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19	Coregulation of Terpenoid Pathway Genes and Prediction of Isoprene Production in <i>Bacillus subtilis</i> Using Transcriptomics. <i>PLoS ONE</i> , 2013, 8, e66104.	1.1	30
20	Microarray Data Standards: An Open Letter. <i>Environmental Health Perspectives</i> , 2004, 112, A666-7.	2.8	23
21	Proteome of <i>Salmonella Enterica</i> Serotype Typhimurium Grown in a Low Mg ²⁺ /pH Medium. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 388-397.	0.4	21
22	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 205-208.	1.0	19
23	Transcriptomic and proteomic dynamics in the metabolism of a diazotrophic cyanobacterium, <i>Cyanothece</i> sp. PCC 7822 during a diurnal light-dark cycle. <i>BMC Genomics</i> , 2014, 15, 1185.	1.2	18
24	PACAP interactions in the mouse brain: Implications for behavioral and other disorders. <i>Gene</i> , 2012, 491, 224-231.	1.0	15
25	Using the gene ontology to enrich biological pathways. <i>International Journal of Computational Biology and Drug Design</i> , 2009, 2, 221.	0.3	12
26	A guide to microarray experiments-an open letter to the scientific journals. <i>Lancet</i> , The, 2002, 360, 1019.	6.3	11
27	Biological Network Inference and Analysis Using SEBINI and CABIN. <i>Methods in Molecular Biology</i> , 2009, 541, 551-576.	0.4	10
28	Nucleic acid sequences coding for internal antisense peptides: are there implications for protein folding and evolution?. <i>Nucleic Acids Research</i> , 1994, 22, 3373-3380.	6.5	7
29	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 1819.	1.5	7
30	Modeling Dynamic Regulatory Processes in Stroke. <i>PLoS Computational Biology</i> , 2012, 8, e1002722.	1.5	6
31	Wrestling with SUMO and bio-ontologies. <i>Nature Biotechnology</i> , 2006, 24, 21-22.	9.4	5
32	A Network Inference Workflow Applied to Virulence-Related Processes in <i>Salmonella typhimurium</i> . <i>Annals of the New York Academy of Sciences</i> , 2009, 1158, 143-158.	1.8	5
33	NEW CHALLENGES FACING INTEGRATIVE BIOLOGICAL SCIENCE IN THE POST-GENOMIC ERA. <i>Journal of Biological Systems</i> , 2006, 14, 275-293.	0.5	4
34	Enriching regulatory networks by bootstrap learning using optimised GO-based gene similarity and gene links mined from PubMed abstracts. <i>International Journal of Computational Biology and Drug Design</i> , 2011, 4, 56.	0.3	4
35	Searching for genomic organizational motifs: Explorations of the <i>Escherichia coli</i> chromosome. <i>Computers & Chemistry</i> , 1993, 17, 209-217.	1.2	3
36	An analysis pipeline for the inference of protein-protein interaction networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 409.	0.1	3

#	ARTICLE	IF	CITATIONS
37	An integrated approach to predictive genomic analytics. , 2010, , .		1
38	COMPARATIVE ANALYSIS OF GENOMIC DATA: A GLOBAL LOOK AT STRUCTURAL AND REGULATORY FEATURES. , 1993, , .		0
39	The Microarray Explorer analysis package. Briefings in Bioinformatics, 2001, 2, 392-394.	3.2	0
40	Learning biological networks via bootstrapping with optimized go-based gene similarity. , 2010, , .		0
41	Modular Semantic Tagging of Medline Abstracts and Its Use in Inferring Regulatory Networks. , 2011, , .		0