

Micheal J Wise

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

2,958
citations

304602

22
h-index

168321

53
g-index

73
all docs

73
docs citations

73
times ranked

3634
citing authors

#	ARTICLE	IF	CITATIONS
1	The continuing conundrum of the LEA proteins. <i>Die Naturwissenschaften</i> , 2007, 94, 791-812.	0.6	629
2	POPP the question: what do LEA proteins do?. <i>Trends in Plant Science</i> , 2004, 9, 13-17.	4.3	396
3	LEAPing to conclusions: a computational reanalysis of late embryogenesis abundant proteins and their possible roles. <i>BMC Bioinformatics</i> , 2003, 4, 52.	1.2	211
4	Amyloidogenic nature of spider silk. <i>FEBS Journal</i> , 2002, 269, 4159-4163.	0.2	184
5	Consideration of RNA Secondary Structure Significantly Improves Likelihood-Based Estimates of Phylogeny: Examples from the Bilateria. <i>Molecular Biology and Evolution</i> , 2005, 22, 1129-1136.	3.5	168
6	Intrinsically disordered proteins as molecular shields. <i>Molecular BioSystems</i> , 2012, 8, 210-219.	2.9	158
7	Mind the Gaps: Evidence of Bias in Estimates of Multiple Sequence Alignments. <i>Molecular Biology and Evolution</i> , 2007, 24, 2433-2442.	3.5	108
8	Role of Pro-oncogenic Protein Disulfide Isomerase (PDI) Family Member Anterior Gradient 2 (AGR2) in the Control of Endoplasmic Reticulum Homeostasis. <i>Journal of Biological Chemistry</i> , 2011, 286, 44855-44868.	1.6	95
9	Glycogen with short average chain length enhances bacterial durability. <i>Die Naturwissenschaften</i> , 2011, 98, 719-729.	0.6	85
10	Regionalized GC content of template DNA as a predictor of PCR success. <i>Nucleic Acids Research</i> , 2003, 31, 99e-99.	6.5	68
11	YAP3. <i>SIGCSE Bulletin</i> , 1996, 28, 130-134.	0.1	57
12	Bioinformatics and protein expression analyses implicate LEA proteins in the drought response of <i>Collembola</i> . <i>Journal of Insect Physiology</i> , 2009, 55, 210-217.	0.9	44
13	Heuristic RNA pseudoknot prediction including intramolecular kissing hairpins. <i>Rna</i> , 2011, 17, 27-38.	1.6	41
14	Expression profiling and cross-species RNA interference (RNAi) of desiccation-induced transcripts in the anhydrobiotic nematode <i>Aphelenchus avenae</i> . <i>BMC Molecular Biology</i> , 2010, 11, 6.	3.0	35
15	Distribution Patterns of Polyphosphate Metabolism Pathway and Its Relationships With Bacterial Durability and Virulence. <i>Frontiers in Microbiology</i> , 2018, 9, 782.	1.5	34
16	Deep learning models for RNA secondary structure prediction (probably) do not generalize across families. <i>Bioinformatics</i> , 2022, 38, 3892-3899.	1.8	31
17	Plagiarism a la Mode: A Comparison of Automated Systems for Detecting Suspected Plagiarism. <i>Computer Journal</i> , 1996, 39, 741-750.	1.5	30
18	Advanced multi-loop algorithms for RNA secondary structure prediction reveal that the simplest model is best. <i>Nucleic Acids Research</i> , 2017, 45, 8541-8550.	6.5	29

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19	Molecular Structure of Glycogen in <i>Escherichia coli</i> . <i>Biomacromolecules</i> , 2019, 20, 2821-2829.	2.6	27
20	Bioinformatics Analysis of Metabolism Pathways of Archaeal Energy Reserves. <i>Scientific Reports</i> , 2019, 9, 1034.	1.6	27
21	Recent progress in the structure of glycogen serving as a durable energy reserve in bacteria. <i>World Journal of Microbiology and Biotechnology</i> , 2020, 36, 14.	1.7	27
22	Peptide-mass fingerprinting and the ideal covering set for protein characterisation. <i>Electrophoresis</i> , 1997, 18, 1399-1409.	1.3	26
23	Influence of in situ progressive N-terminal is still controversial truncation of glycogen branching enzyme in <i>Escherichia coli</i> DH5 α on glycogen structure, accumulation, and bacterial viability. <i>BMC Microbiology</i> , 2015, 15, 96.	1.3	26
24	Comparative Analysis of the Full Genome of <i>Helicobacter pylori</i> Isolate Sahul64 Identifies Genes of High Divergence. <i>Journal of Bacteriology</i> , 2014, 196, 1073-1083.	1.0	25
25	Detection of similarities in student programs. <i>SIGCSE Bulletin</i> , 1992, 24, 268-271.	0.1	24
26	The Sit-and-Wait Hypothesis in Bacterial Pathogens: A Theoretical Study of Durability and Virulence. <i>Frontiers in Microbiology</i> , 2017, 8, 2167.	1.5	24
27	Structure and Evolution of Glycogen Branching Enzyme N-Termini From Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 3354.	1.5	23
28	Genomic epidemiology and population structure of <i>Neisseria gonorrhoeae</i> from remote highly endemic Western Australian populations. <i>BMC Genomics</i> , 2018, 19, 165.	1.2	22
29	The POPPs: clustering and searching using peptide probability profiles. <i>Bioinformatics</i> , 2002, 18, S38-S45.	1.8	20
30	Coexpression of Nuclear Receptors and Histone Methylation Modifying Genes in the Testis: Implications for Endocrine Disruptor Modes of Action. <i>PLoS ONE</i> , 2012, 7, e34158.	1.1	19
31	A parallel Prolog. , 1982, , .		18
32	Analysis of core protein clusters identifies candidate variable sites conferring metronidazole resistance in <i>Helicobacter pylori</i> . <i>Gastroenterology Report</i> , 2019, 7, 42-49.	0.6	18
33	Analysis of High Throughput Protein Expression in <i>Escherichia coli</i> . <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1567-1580.	2.5	14
34	Consistent gene expression profiles in MexTag transgenic mouse and wild type mouse asbestos-induced mesothelioma. <i>BMC Cancer</i> , 2015, 15, 983.	1.1	13
35	<p>Structural, biomechanical and hemodynamic assessment of the bladder wall in healthy subjects</p>. <i>Research and Reports in Urology</i> , 2019, Volume 11, 233-245.	0.6	13
36	Mutations of <i>Helicobacter pylori</i> RdxA are mainly related to the phylogenetic origin of the strain and not to metronidazole resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3152-3155.	1.3	13

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37	Meningococcal Disease-Associated Prophage-Like Elements Are Present in <i>Neisseria gonorrhoeae</i> and Some Commensal <i>Neisseria</i> Species. <i>Genome Biology and Evolution</i> , 2020, 12, 3938-3950.	1.1	13
38	Annotation Tool and Urban Dataset for 3D Point Cloud Semantic Segmentation. <i>IEEE Access</i> , 2021, 9, 35984-35996.	2.6	12
39	Novel <i>Moraxella catarrhalis</i> prophages display hyperconserved non-structural genes despite their genomic diversity. <i>BMC Genomics</i> , 2015, 16, 860.	1.2	10
40	No so HoT "heads or tails" is not able to reliably compare multiple sequence alignments. <i>Cladistics</i> , 2010, 26, 438-443.	1.5	9
41	Systematic Analysis of Metabolic Pathway Distributions of Bacterial Energy Reserves. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2489-2496.	0.8	9
42	An updated view on bacterial glycogen structure. <i>Microbiology Australia</i> , 2019, , .	0.1	9
43	Optimized M9 Minimal Salts Medium for Enhanced Growth Rate and Glycogen Accumulation of <i>Escherichia coli</i> DH5 α . <i>Microbiology and Biotechnology Letters</i> , 2018, 46, 194-200.	0.2	9
44	Gastric <i>Helicobacter pylori</i> infection perturbs human oral microbiota. <i>PeerJ</i> , 2019, 7, e6336.	0.9	9
45	DiMSim: A Discrete-Event Simulator of Metabolic Networks. <i>Journal of Chemical Information and Computer Sciences</i> , 2003, 43, 1011-1019.	2.8	8
46	Quantum changes in <i>Helicobacter pylori</i> gene expression accompany host-adaptation. <i>DNA Research</i> , 2017, 24, dsw046.	1.5	8
47	EPILOG = PROLOG + Data Flow. <i>ACM SIGPLAN Notices</i> , 1982, 17, 80-86.	0.2	7
48	Small investments with big returns: environmental genomic bioprospecting of microbial life. <i>Critical Reviews in Microbiology</i> , 2022, 48, 641-655.	2.7	7
49	Protein Annotators™ Assistant. <i>Trends in Biochemical Sciences</i> , 2000, 25, 252-253.	3.7	6
50	A Longitudinal, Population-Level, Big-Data Study of <i>Helicobacter pylori</i> -Related Disease across Western Australia. <i>Journal of Clinical Medicine</i> , 2019, 8, 1821.	1.0	6
51	A novel taxon selection method, aimed at minimizing recombination, clarifies the discovery of a new subpopulation of <i>Helicobacter pylori</i> from Australia. <i>Evolutionary Applications</i> , 2020, 13, 278-289.	1.5	6
52	Determining parameters for non-linear models of multi-loop free energy change. <i>Bioinformatics</i> , 2019, 35, 4298-4306.	1.8	5
53	Experience with PMS-Prolog: A distributed, coarse-grain-parallel prolog with processes, modules and streams. <i>Software - Practice and Experience</i> , 1993, 23, 151-175.	2.5	4
54	Welcome to Microbial Informatics and Experimentation. <i>Microbial Informatics and Experimentation</i> , 2011, 1, 1.	7.6	4

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55	Predicting pseudoknotted structures across two RNA sequences. <i>Bioinformatics</i> , 2012, 28, 3058-3065.	1.8	4
56	Mean Protein Evolutionary Distance: A Method for Comparative Protein Evolution and Its Application. <i>PLoS ONE</i> , 2013, 8, e61276.	1.1	4
57	Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 697309.	1.5	4
58	From rags to enriched: metagenomic insights into ammonia-oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. <i>Environmental Microbiology</i> , 2022, 24, 3097-3110.	1.8	4
59	High Definition LiDAR mapping of Perth CBD. , 2021, , .		4
60	Protein annotators' assistant: A novel application of information retrieval techniques. <i>Journal of the Association for Information Science and Technology</i> , 2000, 51, 1131-1136.	1.2	3
61	Message-brokers and communicating prolog processes. <i>Lecture Notes in Computer Science</i> , 1992, , 533-549.	1.0	2
62	dCITE: Measuring Necessary Cladistic Information Can Help You Reduce Polytoamy Artefacts in Trees. <i>PLoS ONE</i> , 2016, 11, e0166991.	1.1	2
63	Alignment algorithms revisited: Alignment algorithms for low similarity protein sequence comparisons. , 2003, , .		1
64	Helicobacteriology update. <i>Microbiology Australia</i> , 2021, 42, 92-95.	0.1	1
65	Absence of BapA type III effector protein affects <i>Burkholderia pseudomallei</i> intracellular lifecycle in human host cells. <i>Process Biochemistry</i> , 2021, 108, 48-59.	1.8	1
66	A Faster Algorithm for Maximum Induced Matchings on Circle Graphs. <i>Journal of Graph Algorithms and Applications</i> , 2018, 22, 389-396.	0.4	1
67	Modelling evolutionary pathways for commensalism and hypervirulence in <i>Neisseria meningitidis</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
68	Achieving Incremental Compilation through Fine-grained Builds. <i>Software - Practice and Experience</i> , 1997, 27, 497-517.	2.5	0