Micheal J Wise

List of Publications by Year
in descending order

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	Small investments with big returns: environmental genomic bioprospecting of microbial life. Critical Reviews in Microbiology, 2022, 48, 641-655.	2.7	7
2	From rags to enriched: metagenomic insights into ammonia€oxidizing archaea following ammonia enrichment of a denuded oligotrophic soil ecosystem. Environmental Microbiology, 2022, 24, 3097-3110.	1.8	4
3	Deep learning models for RNA secondary structure prediction (probably) do not generalize across families. Bioinformatics, 2022, 38, 3892-3899.	1.8	31
4	Helicobacteriology update. Microbiology Australia, 2021, 42, 92-95.	0.1	1
5	Annotation Tool and Urban Dataset for 3D Point Cloud Semantic Segmentation. IEEE Access, 2021, 9, 35984-35996.	2.6	12
6	Developing Bioprospecting Strategies for Bioplastics Through the Large-Scale Mining of Microbial Genomes. Frontiers in Microbiology, 2021, 12, 697309.	1.5	4
7	Absence of BapA type III effector protein affects Burkholderia pseudomallei intracellular lifecycle in human host cells. Process Biochemistry, 2021, 108, 48-59.	1.8	1
8	Modelling evolutionary pathways for commensalism and hypervirulence in Neisseria meningitidis. Microbial Genomics, 2021, 7, .	1.0	1
9	High Definition LiDAR mapping of Perth CBD. , 2021, , .		4
10	A novel taxon selection method, aimed at minimizing recombination, clarifies the discovery of a new sub€population of <i>Helicobacter pylori</i> from Australia. Evolutionary Applications, 2020, 13, 278-289.	1.5	6
11	Recent progress in the structure of glycogen serving as a durable energy reserve in bacteria. World Journal of Microbiology and Biotechnology, 2020, 36, 14.	1.7	27
12	Mutations of Helicobacter pylori RdxA are mainly related to the phylogenetic origin of the strain and not to metronidazole resistance. Journal of Antimicrobial Chemotherapy, 2020, 75, 3152-3155.	1.3	13
13	Meningococcal Disease-Associated Prophage-Like Elements Are Present in Neisseria gonorrhoeae and Some Commensal Neisseria Species. Genome Biology and Evolution, 2020, 12, 3938-3950.	1.1	13
14	A Longitudinal, Population-Level, Big-Data Study of Helicobacter pylori-Related Disease across Western Australia. Journal of Clinical Medicine, 2019, 8, 1821.	1.0	6
15	Structural, biomechanical and hemodynamic assessment of the bladder wall in healthy subjects . Research and Reports in Urology, 2019, Volume 11, 233-245.	0.6	13
16	Molecular Structure of Glycogen in <i>Escherichia coli</i>. Biomacromolecules, 2019, 20, 2821-2829.	2.6	27
17	Systematic Analysis of Metabolic Pathway Distributions of Bacterial Energy Reserves. G3: Genes, Genomes, Genetics, 2019, 9, 2489-2496.	0.8	9
18	Determining parameters for non-linear models of multi-loop free energy change. Bioinformatics, 2019, 35, 4298-4306.	1.8	5

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19	Analysis of core protein clusters identifies candidate variable sites conferring metronidazole resistance in <i>Helicobacter pylori</i>. Gastroenterology Report, 2019, 7, 42-49.	0.6	18
20	Bioinformatics Analysis of Metabolism Pathways of Archaeal Energy Reserves. Scientific Reports, 2019, 9, 1034.	1.6	27
21	An updated view on bacterial glycogen structure. Microbiology Australia, 2019, , .	0.1	9
22	Gastric <i>Helicobacter pylori</i> infection perturbs human oral microbiota. PeerJ, 2019, 7, e6336.	0.9	9
23	Genomic epidemiology and population structure of Neisseria gonorrhoeae from remote highly endemic Western Australian populations. BMC Genomics, 2018, 19, 165.	1.2	22
24	Distribution Patterns of Polyphosphate Metabolism Pathway and Its Relationships With Bacterial Durability and Virulence. Frontiers in Microbiology, 2018, 9, 782.	1.5	34
25	Structure and Evolution of Glycogen Branching Enzyme N-Termini From Bacteria. Frontiers in Microbiology, 2018, 9, 3354.	1.5	23
26	Optimized M9 Minimal Salts Medium for Enhanced Growth Rate and Glycogen Accumulation of Escherichia coli DH5ï¿½ï¿½. Microbiology and Biotechnology Letters, 2018, 46, 194-200.	0.2	9
27	A Faster Algorithm for Maximum Induced Matchings on Circle Graphs. Journal of Graph Algorithms and Applications, 2018, 22, 389-396.	0.4	1
28	Quantum changes in <i>Helicobacter pylori</i> gene expression accompany host-adaptation. DNA Research, 2017, 24, dsw046.	1.5	8
29	Advanced multi-loop algorithms for RNA secondary structure prediction reveal that the simplest model is best. Nucleic Acids Research, 2017, 45, 8541-8550.	6.5	29
30	The Sit-and-Wait Hypothesis in Bacterial Pathogens: A Theoretical Study of Durability and Virulence. Frontiers in Microbiology, 2017, 8, 2167.	1.5	24
31	dCITE: Measuring Necessary Cladistic Information Can Help You Reduce Polytomy Artefacts in Trees. PLoS ONE, 2016, 11, e0166991.	1.1	2
32	Consistent gene expression profiles in MexTAg transgenic mouse and wild type mouse asbestos-induced mesothelioma. BMC Cancer, 2015, 15, 983.	1.1	13
33	Novel Moraxella catarrhalis prophages display hyperconserved non-structural genes despite their genomic diversity. BMC Genomics, 2015, 16, 860.	1.2	10
34	Influence of in situ progressive N-terminal is still controversial truncation of glycogen branching enzyme in Escherichia coli DH5Î± on glycogen structure, accumulation, and bacterial viability. BMC Microbiology, 2015, 15, 96.	1.3	26
35	Comparative Analysis of the Full Genome of Helicobacter pylori Isolate Sahul64 Identifies Genes of High Divergence. Journal of Bacteriology, 2014, 196, 1073-1083.	1.0	25
36	Mean Protein Evolutionary Distance: A Method for Comparative Protein Evolution and Its Application. PLoS ONE, 2013, 8, e61276.	1.1	4

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37	Predicting pseudoknotted structures across two RNA sequences. Bioinformatics, 2012, 28, 3058-3065.	1.8	4
38	Intrinsically disordered proteins as molecular shields. Molecular BioSystems, 2012, 8, 210-219.	2.9	158
39	Coexpression of Nuclear Receptors and Histone Methylation Modifying Genes in the Testis: Implications for Endocrine Disruptor Modes of Action. PLoS ONE, 2012, 7, e34158.	1.1	19
40	Heuristic RNA pseudoknot prediction including intramolecular kissing hairpins. Rna, 2011, 17, 27-38.	1.6	41
41	Glycogen with short average chain length enhances bacterial durability. Die Naturwissenschaften, 2011, 98, 719-729.	0.6	85
42	Welcome to Microbial Informatics and Experimentation. Microbial Informatics and Experimentation, 2011, 1, 1.	7.6	4
43	Role of Pro-oncogenic Protein Disulfide Isomerase (PDI) Family Member Anterior Gradient 2 (AGR2) in the Control of Endoplasmic Reticulum Homeostasis. Journal of Biological Chemistry, 2011, 286, 44855-44868.	1.6	95
44	Expression profiling and cross-species RNA interference (RNAi) of desiccation-induced transcripts in the anhydrobiotic nematode Aphelenchus avenae. BMC Molecular Biology, 2010, 11, 6.	3.0	35
45	No so HoT â€" heads or tails is not able to reliably compare multiple sequence alignments. Cladistics, 2010, 26, 438-443.	1.5	9
46	Bioinformatics and protein expression analyses implicate LEA proteins in the drought response of Collembola. Journal of Insect Physiology, 2009, 55, 210-217.	0.9	44
47	Mind the Gaps: Evidence of Bias in Estimates of Multiple Sequence Alignments. Molecular Biology and Evolution, 2007, 24, 2433-2442.	3.5	108
48	The continuing conundrum of the LEA proteins. Die Naturwissenschaften, 2007, 94, 791-812.	0.6	629
49	Analysis of High Throughput Protein Expression in Escherichia coli. Molecular and Cellular Proteomics, 2006, 5, 1567-1580.	2.5	14
50	Consideration of RNA Secondary Structure Significantly Improves Likelihood-Based Estimates of Phylogeny: Examples from the Bilateria. Molecular Biology and Evolution, 2005, 22, 1129-1136.	3.5	168
51	POPP the question: what do LEA proteins do?. Trends in Plant Science, 2004, 9, 13-17.	4.3	396
52	LEAping to conclusions: a computational reanalysis of late embryogenesis abundant proteins and their possible roles. BMC Bioinformatics, 2003, 4, 52.	1.2	211
53	DiMSim:â€‰ A Discrete-Event Simulator of Metabolic Networks. Journal of Chemical Information and Computer Sciences, 2003, 43, 1011-1019.	2.8	8
54	Regionalized GC content of template DNA as a predictor of PCR success. Nucleic Acids Research, 2003, 31, 99e-99.	6.5	68

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55	Alignment algorithms revisited: Alignment algorithms for low similarity protein sequence comparisons. , 2003, , .		1
56	The POPPs: clustering and searching using peptide probability profiles. Bioinformatics, 2002, 18, S38-S45.	1.8	20
57	Amyloidogenic nature of spider silk. FEBS Journal, 2002, 269, 4159-4163.	0.2	184
58	Protein annotators' assistant: A novel application of information retrieval techniques. Journal of the Association for Information Science and Technology, 2000, 51, 1131-1136.	1.2	3
59	Protein Annotatorsâ€™ Assistant. Trends in Biochemical Sciences, 2000, 25, 252-253.	3.7	6
60	Peptide-mass fingerprinting and the ideal covering set for protein characterisation. Electrophoresis, 1997, 18, 1399-1409.	1.3	26
61	Achieving Incremental Compilation through Fine-grained Builds. Software - Practice and Experience, 1997, 27, 497-517.	2.5	0
62	Plagiarism a la Mode: A Comparison of Automated Systems for Detecting Suspected Plagiarism. Computer Journal, 1996, 39, 741-750.	1.5	30
63	YAP3. SIGCSE Bulletin, 1996, 28, 130-134.	0.1	57
64	Experience with PMS-Prolog: A distributed, coarse-grain-parallel prolog with processes, modules and streams. Software - Practice and Experience, 1993, 23, 151-175.	2.5	4
65	Detection of similarities in student programs. SIGCSE Bulletin, 1992, 24, 268-271.	0.1	24
66	Message-brokers and communicating prolog processes. Lecture Notes in Computer Science, 1992, , 533-549.	1.0	2
67	EPILOG = PROLOG + Data Flow. ACM SIGPLAN Notices, 1982, 17, 80-86.	0.2	7
68	A parallel Prolog. , 1982, , .		18