

Jennifer H Wisecaver

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,273
citations

218381

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253896

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times ranked

4564
citing authors

#	ARTICLE	IF	CITATIONS
1	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2022, 233, 1317-1330.	3.5	23
2	Integrative analysis of the shikonin metabolic network identifies new gene connections and reveals evolutionary insight into shikonin biosynthesis. <i>Horticulture Research</i> , 2022, 9, .	2.9	13
3	CHD Chromatin Remodeling Protein Diversification Yields Novel Clades and Domains Absent in Classic Model Organisms. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
4	A De Novo Transcriptome Assembly of <i>Ceratopteris richardii</i> Provides Insights into the Evolutionary Dynamics of Complex Gene Families in Land Plants. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	34
5	Conservation and diversification of <i>HAIRY MERISTEM</i> gene family in land plants. <i>Plant Journal</i> , 2021, 106, 366-378.	2.8	26
6	Beyond the Biosynthetic Gene Cluster Paradigm: Genome-Wide Coexpression Networks Connect Clustered and Unclustered Transcription Factors to Secondary Metabolic Pathways. <i>Microbiology Spectrum</i> , 2021, 9, e0089821.	1.2	17
7	Conservation of Cdc14 phosphatase specificity in plant fungal pathogens: implications for antifungal development. <i>Scientific Reports</i> , 2020, 10, 12073.	1.6	6
8	Reference Genome for the Highly Transformable <i>Setaria viridis</i> ME034V. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3467-3478.	0.8	36
9	Hybrid de novo genome assembly of red gromwell (<i>Lithospermum erythrorhizon</i>) reveals evolutionary insight into shikonin biosynthesis. <i>Horticulture Research</i> , 2020, 7, 82.	2.9	31
10	The "Geddes" Composable Platform - An Evolution of Community Clusters for a Composable World. , 2020, , .		1
11	Horizontal Transfer of Bacterial Cytolethal Distending Toxin B Genes to Insects. <i>Molecular Biology and Evolution</i> , 2019, 36, 2105-2110.	3.5	36
12	The renaissance of comparative biochemistry. <i>American Journal of Botany</i> , 2019, 106, 3-13.	0.8	5
13	Genome-wide analysis of <i>Fusarium verticillioides</i> reveals inter-kingdom contribution of horizontal gene transfer to the expansion of metabolism. <i>Fungal Genetics and Biology</i> , 2019, 128, 60-73.	0.9	8
14	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. <i>GigaScience</i> , 2019, 8, .	3.3	167
15	Genome wide analysis of the transition to pathogenic lifestyles in Magnaporthales fungi. <i>Scientific Reports</i> , 2018, 8, 5862.	1.6	28
16	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. <i>Cell</i> , 2018, 175, 1533-1545.e20.	13.5	445
17	integRATE: a desirability-based data integration framework for the prioritization of candidate genes across heterogeneous omics and its application to preterm birth. <i>BMC Medical Genomics</i> , 2018, 11, 107.	0.7	2
18	The birth, evolution and death of metabolic gene clusters in fungi. <i>Nature Reviews Microbiology</i> , 2018, 16, 731-744.	13.6	155

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19	Fungal Isocyanide Synthases and Xanthocillin Biosynthesis in <i>Aspergillus fumigatus</i> . <i>MBio</i> , 2018, 9, .	1.8	44
20	Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. <i>ELife</i> , 2018, 7, .	2.8	67
21	A Global Coexpression Network Approach for Connecting Genes to Specialized Metabolic Pathways in Plants. <i>Plant Cell</i> , 2017, 29, 944-959.	3.1	225
22	<i>Chlamydomonas reinhardtii</i> LFO1 Is an IsdG Family Heme Oxygenase. <i>MSphere</i> , 2017, 2, .	1.3	15
23	Genome Sequence of <i>Ophidiomyces ophiodiicola</i> , an Emerging Fungal Pathogen of Snakes. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
24	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , 2017, 15, e2003583.	2.6	187
25	Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4116-4121.	3.3	70
26	Dynamic Evolution of Nitric Oxide Detoxifying Flavohemoglobins, a Family of Single-Protein Metabolic Modules in Bacteria and Eukaryotes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1979-1987.	3.5	46
27	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	3.3	302
28	<i>SICLE</i> : a high-throughput tool for extracting evolutionary relationships from phylogenetic trees. <i>PeerJ</i> , 2016, 4, e2359.	0.9	4
29	Insights into transcriptional changes that accompany organelle sequestration from the stolen nucleus of <i>Mesodinium rubrum</i> . <i>BMC Genomics</i> , 2015, 16, 805.	1.2	30
30	Draft Genome Sequence of the Ale-Fermenting <i>Saccharomyces cerevisiae</i> Strain GSY2239. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
31	Fungal metabolic gene clusters—caravans traveling across genomes and environments. <i>Frontiers in Microbiology</i> , 2015, 6, 161.	1.5	136
32	Clustering of Two Genes Putatively Involved in Cyanate Detoxification Evolved Recently and Independently in Multiple Fungal Lineages. <i>Genome Biology and Evolution</i> , 2015, 7, 789-800.	1.1	32
33	Examining the Evolution of the Regulatory Circuit Controlling Secondary Metabolism and Development in the Fungal Genus <i>Aspergillus</i> . <i>PLoS Genetics</i> , 2015, 11, e1005096.	1.5	70
34	The Evolution of Fungal Metabolic Pathways. <i>PLoS Genetics</i> , 2014, 10, e1004816.	1.5	183
35	The impact of automated filtering of BLAST-determined homologs in the phylogenetic detection of horizontal gene transfer from a transcriptome assembly. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 184-192.	1.2	8
36	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. <i>Nature Communications</i> , 2014, 5, 4784.	5.8	118

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37	Evolution of Saxitoxin Synthesis in Cyanobacteria and Dinoflagellates. <i>Molecular Biology and Evolution</i> , 2013, 30, 70-78.	3.5	152
38	Horizontal Gene Transfer is a Significant Driver of Gene Innovation in Dinoflagellates. <i>Genome Biology and Evolution</i> , 2013, 5, 2368-2381.	1.1	37
39	Bio-crude transcriptomics: Gene discovery and metabolic network reconstruction for the biosynthesis of the terpenome of the hydrocarbon oil-producing green alga, <i>Botryococcus braunii</i> race B (Showa)*. <i>BMC Genomics</i> , 2012, 13, 576.	1.2	52
40	ANALYSIS OF <i>ALEXANDRIUM TAMARENSE</i> (DINOPHYCEAE) GENES REVEALS THE COMPLEX EVOLUTIONARY HISTORY OF A MICROBIAL EUKARYOTE. <i>Journal of Phycology</i> , 2012, 48, 1130-1142.	1.0	29
41	Dinoflagellate Genome Evolution. <i>Annual Review of Microbiology</i> , 2011, 65, 369-387.	2.9	171
42	Transcriptome analysis reveals nuclear-encoded proteins for the maintenance of temporary plastids in the dinoflagellate <i>Dinophysis acuminata</i> . <i>BMC Genomics</i> , 2010, 11, 366.	1.2	94
43	The genome and structural proteome of an ocean siphovirus: a new window into the cyanobacterial "mobilome". <i>Environmental Microbiology</i> , 2009, 11, 2935-2951.	1.8	118