

Jennifer H Wisecaver

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,273
citations

218677

26
h-index

254184

43
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53
all docs

53
docs citations

53
times ranked

4564
citing authors

#	ARTICLE	IF	CITATIONS
1	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. <i>Cell</i> , 2018, 175, 1533-1545.e20.	28.9	445
2	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.	7.1	302
3	A Global Coexpression Network Approach for Connecting Genes to Specialized Metabolic Pathways in Plants. <i>Plant Cell</i> , 2017, 29, 944-959.	6.6	225
4	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , 2017, 15, e2003583.	5.6	187
5	The Evolution of Fungal Metabolic Pathways. <i>PLoS Genetics</i> , 2014, 10, e1004816.	3.5	183
6	Dinoflagellate Genome Evolution. <i>Annual Review of Microbiology</i> , 2011, 65, 369-387.	7.3	171
7	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. <i>GigaScience</i> , 2019, 8, .	6.4	167
8	The birth, evolution and death of metabolic gene clusters in fungi. <i>Nature Reviews Microbiology</i> , 2018, 16, 731-744.	28.6	155
9	Evolution of Saxitoxin Synthesis in Cyanobacteria and Dinoflagellates. <i>Molecular Biology and Evolution</i> , 2013, 30, 70-78.	8.9	152
10	Fungal metabolic gene clusters—caravans traveling across genomes and environments. <i>Frontiers in Microbiology</i> , 2015, 6, 161.	3.5	136
11	The genome and structural proteome of an ocean siphovirus: a new window into the cyanobacterial “mobilome”™. <i>Environmental Microbiology</i> , 2009, 11, 2935-2951.	3.8	118
12	Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge. <i>Nature Communications</i> , 2014, 5, 4784.	12.8	118
13	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.	2.8	94
14	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.	3.5	70
15	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.	7.1	70
16	Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. <i>ELife</i> , 2018, 7, .	6.0	67
17	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.	2.8	52
18	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.	8.9	46

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19	Fungal Isocyanide Synthases and Xanthocillin Biosynthesis in <i>Aspergillus fumigatus</i> . <i>MBio</i> , 2018, 9, .	4.1	44
20	Horizontal Gene Transfer is a Significant Driver of Gene Innovation in Dinoflagellates. <i>Genome Biology and Evolution</i> , 2013, 5, 2368-2381.	2.5	37
21	Horizontal Transfer of Bacterial Cytolethal Distending Toxin B Genes to Insects. <i>Molecular Biology and Evolution</i> , 2019, 36, 2105-2110.	8.9	36
22	Reference Genome for the Highly Transformable <i>Setaria viridis</i> ME034V. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3467-3478.	1.8	36
23	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, .	2.5	34
24	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.	2.5	32
25	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.	6.3	31
26	Insights into transcriptional changes that accompany organelle sequestration from the stolen nucleus of <i>Mesodinium rubrum</i> . <i>BMC Genomics</i> , 2015, 16, 805.	2.8	30
27	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.	2.3	29
28	Genome wide analysis of the transition to pathogenic lifestyles in Magnaporthales fungi. <i>Scientific Reports</i> , 2018, 8, 5862.	3.3	28
29	Conservation and diversification of <i>HAIRY MERISTEM</i> gene family in land plants. <i>Plant Journal</i> , 2021, 106, 366-378.	5.7	26
30	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2022, 233, 1317-1330.	7.3	23
31	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.	3.0	17
32	<i>Chlamydomonas reinhardtii</i> LFO1 Is an IsdG Family Heme Oxygenase. <i>MSphere</i> , 2017, 2, .	2.9	15
33	Integrative analysis of the shikonin metabolic network identifies new gene connections and reveals evolutionary insight into shikonin biosynthesis. <i>Horticulture Research</i> , 2022, 9, .	6.3	13
34	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.	2.7	8
35	Genome Sequence of <i>Ophidiomyces ophiodiicola</i> , an Emerging Fungal Pathogen of Snakes. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
36	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.	2.1	8

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37	Conservation of Cdc14 phosphatase specificity in plant fungal pathogens: implications for antifungal development. <i>Scientific Reports</i> , 2020, 10, 12073.	3.3	6
38	Draft Genome Sequence of the Ale-Fermenting <i>Saccharomyces cerevisiae</i> Strain GSY2239. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
39	The renaissance of comparative biochemistry. <i>American Journal of Botany</i> , 2019, 106, 3-13.	1.7	5
40	<tt>SICLE</tt>: a high-throughput tool for extracting evolutionary relationships from phylogenetic trees. <i>PeerJ</i> , 2016, 4, e2359.	2.0	4
41	CHD Chromatin Remodeling Protein Diversification Yields Novel Clades and Domains Absent in Classic Model Organisms. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
42	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.	1.5	2
43	The "Geddes" Composable Platform - An Evolution of Community Clusters for a Composable World. , 2020, , .		1