Jacob L Steenwyk

List of Publications by Year in descending order

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279487 264894 2,497 54 23 42 citations g-index h-index papers 92 92 92 2423 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. Cell, 2018, 175, 1533-1545.e20.	13.5	445
2	ClipKIT: A multiple sequence alignment trimming software for accurate phylogenomic inference. PLoS Biology, 2020, 18, e3001007.	2.6	237
3	A genome-scale phylogeny of the kingdom Fungi. Current Biology, 2021, 31, 1653-1665.e5.	1.8	170
4	Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. PLoS Biology, 2019, 17, e3000255.	2.6	116
5	Gene Essentiality Analyzed by <i>In Vivo</i> Transposon Mutagenesis and Machine Learning in a Stable Haploid Isolate of <i>Candida albicans</i> MBio, 2018, 9, .	1.8	110
6	A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera <i>Aspergillus</i> and <i>Penicillium</i> MBio, 2019, 10, .	1.8	106
7	Biosynthetic gene clusters and the evolution of fungal chemodiversity. Natural Product Reports, 2020, 37, 868-878.	5.2	93
8	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. Science Advances, 2020, 6, .	4.7	84
9	Extensive Copy Number Variation in Fermentation-Related Genes Among <i>Saccharomyces cerevisiae </i> Vine Strains. G3: Genes, Genomes, Genetics, 2017, 7, 1475-1485.	0.8	77
10	PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. Bioinformatics, 2021, 37, 2325-2331.	1.8	69
11	Variation and selection on codon usage bias across an entire subphylum. PLoS Genetics, 2019, 15, e1008304.	1.5	68
12	Copy Number Variation in Fungi and Its Implications for Wine Yeast Genetic Diversity and Adaptation. Frontiers in Microbiology, 2018, 9, 288.	1.5	63
13	Nutritional Heterogeneity Among Aspergillus fumigatus Strains Has Consequences for Virulence in a Strain- and Host-Dependent Manner. Frontiers in Microbiology, 2019, 10, 854.	1.5	52
14	Variation Among Biosynthetic Gene Clusters, Secondary Metabolite Profiles, and Cards of Virulence Across <i>Aspergillus</i> Species. Genetics, 2020, 216, 481-497.	1.2	50
15	Genomic and Phenotypic Heterogeneity of Clinical Isolates of the Human Pathogens Aspergillus fumigatus, Aspergillus lentulus, and Aspergillus fumigatiaffinis. Frontiers in Genetics, 2020, 11, 459.	1.1	44
16	Rapid Phenotypic and Metabolomic Domestication of Wild <i>Penicillium</i> Molds on Cheese. MBio, 2019, 10, .	1.8	43
17	Characterizing the Pathogenic, Genomic, and Chemical Traits of <i>Aspergillus fischeri</i> , a Close Relative of the Major Human Fungal Pathogen <i>Aspergillus fumigatus</i> . MSphere, 2019, 4, .	1.3	42
18	Evolving moldy murderers: Aspergillus section Fumigati as a model for studying the repeated evolution of fungal pathogenicity. PLoS Pathogens, 2020, 16, e1008315.	2.1	40

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19	Pathogenic Allodiploid Hybrids of Aspergillus Fungi. Current Biology, 2020, 30, 2495-2507.e7.	1.8	39
20	Copy number variation contributes to cryptic genetic variation in outbreak lineages of Cryptococcus gattii from the North American Pacific Northwest. BMC Genomics, 2016, 17, 700.	1.2	36
21	Mapping the Fungal Battlefield: Using in situ Chemistry and Deletion Mutants to Monitor Interspecific Chemical Interactions Between Fungi. Frontiers in Microbiology, 2019, 10, 285.	1.5	35
22	Gliotoxin, a Known Virulence Factor in the Major Human Pathogen Aspergillus fumigatus, Is Also Biosynthesized by Its Nonpathogenic Relative <i>Aspergillus fischeri</i> . MBio, 2020, 11, .	1.8	32
23	Functional Characterization of Clinical Isolates of the Opportunistic Fungal Pathogen Aspergillus nidulans. MSphere, 2020, 5, .	1.3	32
24	Genomic and Phenotypic Analysis of COVID-19-Associated Pulmonary Aspergillosis Isolates of Aspergillus fumigatus. Microbiology Spectrum, 2021, 9, e0001021.	1.2	31
25	Into the wild: new yeast genomes from natural environments and new tools for their analysis. FEMS Yeast Research, 2020, 20, .	1.1	29
26	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. Systematic Biology, 2021, 70, 997-1014.	2.7	28
27	The Aspergillus fumigatus transcription factor RgIT is important for gliotoxin biosynthesis and self-protection, and virulence. PLoS Pathogens, 2020, 16, e1008645.	2.1	27
28	ggpubfigs: Colorblind-Friendly Color Palettes and ggplot2 Graphic System Extensions for Publication-Quality Scientific Figures. Microbiology Resource Announcements, 2021, 10, e0087121.	0.3	19
29	Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. PLoS Biology, 2021, 19, e3001185.	2.6	18
30	An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related <i>Aspergillus</i> fungi. Genetics, 2021, 218, .	1.2	18
31	Recurrent Loss of abaA, a Master Regulator of Asexual Development in Filamentous Fungi, Correlates with Changes in Genomic and Morphological Traits. Genome Biology and Evolution, 2020, 12, 1119-1130.	1.1	16
32	Regulation of gliotoxin biosynthesis and protection in Aspergillus species. PLoS Genetics, 2022, 18, e1009965.	1.5	16
33	Treehouse: a user-friendly application to obtain subtrees from large phylogenies. BMC Research Notes, 2019, 12, 541.	0.6	14
34	Draft Genome Sequence of the Griseofulvin-Producing Fungus Xylaria flabelliformis Strain G536. Microbiology Resource Announcements, 2019, 8, .	0.3	14
35	BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. Genetics, 2022, 221, .	1.2	13
36	orthofisher: a broadly applicable tool for automated gene identification and retrieval. G3: Genes, Genomes, Genetics, $2021,11,$.	0.8	12

#	Article	IF	Citations
37	Aspergillus fumigatus G-Protein Coupled Receptors GprM and GprJ Are Important for the Regulation of the Cell Wall Integrity Pathway, Secondary Metabolite Production, and Virulence. MBio, 2020, 11, .	1.8	11
38	Aspergillus fumigatus Acetate Utilization Impacts Virulence Traits and Pathogenicity. MBio, 2021, 12, e0168221.	1.8	10
39	Examination of Gene Loss in the DNA Mismatch Repair Pathway and Its Mutational Consequences in a Fungal Phylum. Genome Biology and Evolution, 2021, 13, .	1.1	10
40	An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. Science Advances, 2022, 8, eabn0105.	4.7	10
41	Evolutionary Divergence in DNA Damage Responses among Fungi. MBio, 2021, 12, .	1.8	9
42	Examination of Genome-Wide Ortholog Variation in Clinical and Environmental Isolates of the Fungal Pathogen Aspergillus fumigatus. MBio, 2022, 13 , .	1.8	8
43	Draft Genome Sequences of Four <i>Aspergillus</i> Section <i>Fumigati</i> Clinical Strains. Microbiology Resource Announcements, 2020, 9, .	0.3	4
44	Feature frequency profile-based phylogenies are inaccurate. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31580-31581.	3.3	3
45	Extensive Non-Coding Sequence Divergence Between the Major Human Pathogen Aspergillus fumigatus and its Relatives. Frontiers in Fungal Biology, 0, 3, .	0.9	3
46	integRATE: a desirability-based data integration framework for the prioritization of candidate genes across heterogeneous omics and its application to preterm birth. BMC Medical Genomics, 2018, 11, 107.	0.7	2
47	A portrait of budding yeasts: A symbol of the arts, sciences and a whole greater than the sum of its parts. Yeast, 2021, 38, 54-56.	0.8	2
48	Examining Signatures of Natural Selection in Antifungal Resistance Genes Across Aspergillus Fungi. Frontiers in Fungal Biology, 2021, 2, .	0.9	2
49	Resistance-Guided Mining of Bacterial Genotoxins Defines a Family of DNA Glycosylases. MBio, 2022, 13, e0329721.	1.8	2
50	Title is missing!. , 2020, 16, e1008645.		0
51	Title is missing!. , 2020, 16, e1008645.		0
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