

Jacob L Steenwyk

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

2,497
citations

279487

23
h-index

264894

42
g-index

92
all docs

92
docs citations

92
times ranked

2423
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of gliotoxin biosynthesis and protection in <i>Aspergillus</i> species. <i>PLoS Genetics</i> , 2022, 18, e1009965.	1.5	16
2	Resistance-Guided Mining of Bacterial Genotoxins Defines a Family of DNA Glycosylases. <i>MBio</i> , 2022, 13, e0329721.	1.8	2
3	An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. <i>Science Advances</i> , 2022, 8, eabn0105.	4.7	10
4	BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. <i>Genetics</i> , 2022, 221, .	1.2	13
5	Examination of Genome-Wide Ortholog Variation in Clinical and Environmental Isolates of the Fungal Pathogen <i>Aspergillus fumigatus</i> . <i>MBio</i> , 2022, 13, .	1.8	8
6	A portrait of budding yeasts: A symbol of the arts, sciences and a whole greater than the sum of its parts. <i>Yeast</i> , 2021, 38, 54-56.	0.8	2
7	PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. <i>Bioinformatics</i> , 2021, 37, 2325-2331.	1.8	69
8	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. <i>Systematic Biology</i> , 2021, 70, 997-1014.	2.7	28
9	Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. <i>PLoS Biology</i> , 2021, 19, e3001185.	2.6	18
10	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021, 31, 1653-1665.e5.	1.8	170
11	Evolutionary Divergence in DNA Damage Responses among Fungi. <i>MBio</i> , 2021, 12, .	1.8	9
12	An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related <i>Aspergillus</i> fungi. <i>Genetics</i> , 2021, 218, .	1.2	18
13	orthofisher: a broadly applicable tool for automated gene identification and retrieval. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	12
14	<i>Aspergillus fumigatus</i> Acetate Utilization Impacts Virulence Traits and Pathogenicity. <i>MBio</i> , 2021, 12, e0168221.	1.8	10
15	Examining Signatures of Natural Selection in Antifungal Resistance Genes Across <i>Aspergillus</i> Fungi. <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	2
16	Genomic and Phenotypic Analysis of COVID-19-Associated Pulmonary <i>Aspergillus fumigatus</i> Isolates of <i>Aspergillus fumigatus</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0001021.	1.2	31
17	Examination of Gene Loss in the DNA Mismatch Repair Pathway and Its Mutational Consequences in a Fungal Phylum. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
18	ggpubfigs: Colorblind-Friendly Color Palettes and ggplot2 Graphic System Extensions for Publication-Quality Scientific Figures. <i>Microbiology Resource Announcements</i> , 2021, 10, e0087121.	0.3	19

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19	Biosynthetic gene clusters and the evolution of fungal chemodiversity. <i>Natural Product Reports</i> , 2020, 37, 868-878.	5.2	93
20	<i>Aspergillus fumigatus</i> G-Protein Coupled Receptors GprM and GprJ Are Important for the Regulation of the Cell Wall Integrity Pathway, Secondary Metabolite Production, and Virulence. <i>MBio</i> , 2020, 11, .	1.8	11
21	The <i>Aspergillus fumigatus</i> transcription factor RglT is important for gliotoxin biosynthesis and self-protection, and virulence. <i>PLoS Pathogens</i> , 2020, 16, e1008645.	2.1	27
22	Feature frequency profile-based phylogenies are inaccurate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31580-31581.	3.3	3
23	Draft Genome Sequences of Four <i>Aspergillus</i> Section <i>Fumigati</i> Clinical Strains. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
24	Variation Among Biosynthetic Gene Clusters, Secondary Metabolite Profiles, and Cards of Virulence Across <i>Aspergillus</i> Species. <i>Genetics</i> , 2020, 216, 481-497.	1.2	50
25	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. <i>Science Advances</i> , 2020, 6, .	4.7	84
26	Genomic and Phenotypic Heterogeneity of Clinical Isolates of the Human Pathogens <i>Aspergillus fumigatus</i> , <i>Aspergillus lentulus</i> , and <i>Aspergillus fumigatiaffinis</i> . <i>Frontiers in Genetics</i> , 2020, 11, 459.	1.1	44
27	Gliotoxin, a Known Virulence Factor in the Major Human Pathogen <i>Aspergillus fumigatus</i> , Is Also Biosynthesized by Its Nonpathogenic Relative <i>Aspergillus fischeri</i> . <i>MBio</i> , 2020, 11, .	1.8	32
28	Recurrent Loss of <i>abaA</i> , a Master Regulator of Asexual Development in Filamentous Fungi, Correlates with Changes in Genomic and Morphological Traits. <i>Genome Biology and Evolution</i> , 2020, 12, 1119-1130.	1.1	16
29	Evolving moldy murderers: <i>Aspergillus</i> section <i>Fumigati</i> as a model for studying the repeated evolution of fungal pathogenicity. <i>PLoS Pathogens</i> , 2020, 16, e1008315.	2.1	40
30	Pathogenic Allodiploid Hybrids of <i>Aspergillus</i> Fungi. <i>Current Biology</i> , 2020, 30, 2495-2507.e7.	1.8	39
31	Into the wild: new yeast genomes from natural environments and new tools for their analysis. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	29
32	Functional Characterization of Clinical Isolates of the Opportunistic Fungal Pathogen <i>Aspergillus nidulans</i> . <i>MSphere</i> , 2020, 5, .	1.3	32
33	ClipKIT: A multiple sequence alignment trimming software for accurate phylogenomic inference. <i>PLoS Biology</i> , 2020, 18, e3001007.	2.6	237
34	Title is missing!. , 2020, 16, e1008645.		0
35	Title is missing!. , 2020, 16, e1008645.		0
36	Title is missing!. , 2020, 16, e1008645.		0

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37	Title is missing!. , 2020, 16, e1008645.		0
38	Title is missing!. , 2020, 16, e1008645.		0
39	Variation and selection on codon usage bias across an entire subphylum. PLoS Genetics, 2019, 15, e1008304.	1.5	68
40	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
41	Treehouse: a user-friendly application to obtain subtrees from large phylogenies. BMC Research Notes, 2019, 12, 541.	0.6	14
42	Nutritional Heterogeneity Among <i>Aspergillus fumigatus</i> Strains Has Consequences for Virulence in a Strain- and Host-Dependent Manner. Frontiers in Microbiology, 2019, 10, 854.	1.5	52
43	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
44	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
45	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
46	Rapid Phenotypic and Metabolomic Domestication of Wild <i>Penicillium</i> Molds on Cheese. MBio, 2019, 10, .	1.8	43
47	Draft Genome Sequence of the Griseofulvin-Producing Fungus <i>Xylaria flabelliformis</i> Strain G536. Microbiology Resource Announcements, 2019, 8, .	0.3	14
48	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
49	Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. Cell, 2018, 175, 1533-1545.e20.	13.5	445
50	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
51	Copy Number Variation in Fungi and Its Implications for Wine Yeast Genetic Diversity and Adaptation. Frontiers in Microbiology, 2018, 9, 288.	1.5	63
52	Extensive Copy Number Variation in Fermentation-Related Genes Among <i>Saccharomyces cerevisiae</i> Wine Strains. G3: Genes, Genomes, Genetics, 2017, 7, 1475-1485.	0.8	77
53	Copy number variation contributes to cryptic genetic variation in outbreak lineages of <i>Cryptococcus gattii</i> from the North American Pacific Northwest. BMC Genomics, 2016, 17, 700.	1.2	36
54	Extensive Non-Coding Sequence Divergence Between the Major Human Pathogen <i>Aspergillus fumigatus</i> and its Relatives. Frontiers in Fungal Biology, 0, 3, .	0.9	3