

Zheng Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6630311/publications.pdf>

Version: 2024-02-01

66
papers

10,246
citations

136740

32
h-index

110170

64
g-index

68
all docs

68
docs citations

68
times ranked

12484
citing authors

#	ARTICLE	IF	CITATIONS
1	A higher-level phylogenetic classification of the Fungi. <i>Mycological Research</i> , 2007, 111, 509-547.	2.5	1,994
2	Reconstructing the early evolution of Fungi using a six-gene phylogeny. <i>Nature</i> , 2006, 443, 818-822.	13.7	1,625
3	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. <i>Nature Biotechnology</i> , 2015, 33, 408-414.	9.4	1,023
4	Improved software detection and extraction of ITS1 and $\langle scp \rangle ITS \langle /scp \rangle 2$ from ribosomal $\langle scp \rangle ITS \langle /scp \rangle$ sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 914-919.	2.2	868
5	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. <i>Systematic Biology</i> , 2009, 58, 224-239.	2.7	581
6	Pan-Genome of Wild and Cultivated Soybeans. <i>Cell</i> , 2020, 182, 162-176.e13.	13.5	508
7	Projecting hospital utilization during the COVID-19 outbreaks in the United States. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9122-9126.	3.3	441
8	Impact of international travel and border control measures on the global spread of the novel 2019 coronavirus outbreak. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7504-7509.	3.3	429
9	Contributions of <i>rpb2</i> and <i>tef1</i> to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 430-451.	1.2	341
10	Preserving Accuracy in GenBank. <i>Science</i> , 2008, 319, 1616-1616.	6.0	198
11	Parallel selection on a dormancy gene during domestication of crops from multiple families. <i>Nature Genetics</i> , 2018, 50, 1435-1441.	9.4	168
12	Evolution of helotialean fungi (Leotiomycetes, Pezizomycotina): A nuclear rDNA phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 295-312.	1.2	165
13	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. <i>Lancet Microbe</i> , The, 2021, 2, e666-e675.	3.4	147
14	A multigene phylogeny toward a new phylogenetic classification of Leotiomycetes. <i>IMA Fungus</i> , 2019, 10, 1.	1.7	140
15	Toward a phylogenetic classification of the Leotiomycetes based on rDNA data. <i>Mycologia</i> , 2006, 98, 1065-1075.	0.8	128
16	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	4.7	123
17	Metaxa: a software tool for automated detection and discrimination among ribosomal small subunit (12S/16S/18S) sequences of archaea, bacteria, eukaryotes, mitochondria, and chloroplasts in metagenomes and environmental sequencing datasets. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 471-475.	0.7	88
18	Molecular phylogenetics of the Gloeophyllales and relative ages of clades of Agaricomycotina producing a brown rot. <i>Mycologia</i> , 2011, 103, 510-524.	0.8	69

#	ARTICLE	IF	CITATIONS
19	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in <i>Neurospora crassa</i> . <i>Eukaryotic Cell</i> , 2014, 13, 154-169.	3.4	66
20	Toward a phylogenetic classification of the Leotiomycetes based on rDNA data. <i>Mycologia</i> , 2006, 98, 1065-1075.	0.8	64
21	Evolutionary relationships of <i>Mycaureola dilseae</i> (Agaricales), a basidiomycete pathogen of a subtidal rhodophyte. <i>American Journal of Botany</i> , 2006, 93, 547-556.	0.8	58
22	Comparative Genomic and Transcriptomic Analysis of <i>Wangiella dermatitidis</i> , A Major Cause of Phaeohyphomycosis and a Model Black Yeast Human Pathogen. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 561-578.	0.8	58
23	<i>Geoglossomycetes</i> cl. nov., <i>Geoglossales</i> ord. nov. and taxa above class rank in the <i>Ascomycota</i> Tree of Life. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2009, 22, 129-138.	1.6	55
24	Life history and systematics of the aquatic discomycete <i>Mitrula</i> (Helotiales, Ascomycota) based on cultural, morphological, and molecular studies. <i>American Journal of Botany</i> , 2005, 92, 1565-1574.	0.8	51
25	Phylogenetic relationships of <i>Sparassis</i> inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. <i>Mycologia</i> , 2004, 96, 1015-1029.	0.8	48
26	The ancestral levels of transcription and the evolution of sexual phenotypes in filamentous fungi. <i>PLoS Genetics</i> , 2017, 13, e1006867.	1.5	46
27	Light sensing by opsins and fungal ecology: <i>NOP1</i> modulates entry into sexual reproduction in response to environmental cues. <i>Molecular Ecology</i> , 2018, 27, 216-232.	2.0	43
28	Gene Expression Differences among Three <i>Neurospora</i> Species Reveal Genes Required for Sexual Reproduction in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2014, 9, e110398.	1.1	39
29	Genomic Comparison Among Global Isolates of <i>L. interrogans</i> Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 193.	1.8	39
30	The Fast-Evolving <i>phy-2</i> Gene Modulates Sexual Development in Response to Light in the Model Fungus <i>Neurospora crassa</i> . <i>MBio</i> , 2016, 7, e02148.	1.8	37
31	Phylogenetic Relationships of <i>Sparassis</i> Inferred from Nuclear and Mitochondrial Ribosomal DNA and RNA Polymerase Sequences. <i>Mycologia</i> , 2004, 96, 1015.	0.8	35
32	Differential impact of nutrition on developmental and metabolic gene expression during fruiting body development in <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 405-413.	0.9	33
33	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SAT alignments for Environmental ITS Data. <i>PLoS ONE</i> , 2011, 6, e19039.	1.1	32
34	Evolution of Reproductive Morphology in Leaf Endophytes. <i>PLoS ONE</i> , 2009, 4, e4246.	1.1	31
35	Sex-specific gene expression during asexual development of <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 533-543.	0.9	31
36	Maximizing Power in Phylogenetics and Phylogenomics: A Perspective Illuminated by Fungal Big Data. <i>Advances in Genetics</i> , 2017, 100, 1-47.	0.8	28

#	ARTICLE	IF	CITATIONS
37	Another fossil agaric from Dominican amber. <i>Mycologia</i> , 2003, 95, 685-687.	0.8	27
38	New species and distinctive geographical divergences of the genus <i>Sparassis</i> (Basidiomycota): evidence from morphological and molecular data. <i>Mycological Progress</i> , 2013, 12, 445-454.	0.5	26
39	Sex-linked transcriptional divergence in the hermaphrodite fungus <i>Neurospora tetrasperma</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130862.	1.2	26
40	Phylogeny and a new species of <i>Sparassis</i> (Polyporales, Basidiomycota): evidence from mitochondrial <i>atp6</i> , nuclear rDNA and <i>rpb2</i> genes. <i>Mycologia</i> , 2006, 98, 584-592.	0.8	25
41	Phylogeny and a new species of <i>Sparassis</i> (Polyporales, Basidiomycota): evidence from mitochondrial <i>atp6</i> , nuclear rDNA and <i>rpb2</i> genes. <i>Mycologia</i> , 2006, 98, 584-592.	0.8	24
42	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. <i>Molecular Biology and Evolution</i> , 2020, 37, 2228-2240.	3.5	23
43	Using evolutionary genomics, transcriptomics, and systems biology to reveal gene networks underlying fungal development. <i>Fungal Biology Reviews</i> , 2018, 32, 249-264.	1.9	22
44	Metabolism and Development during Conidial Germination in Response to a Carbon-Nitrogen-Rich Synthetic or a Natural Source of Nutrition in <i>Neurospora crassa</i> . <i>MBio</i> , 2019, 10, .	1.8	21
45	3 Pezizomycotina: Sordariomycetes and Leotiomycetes. , 2015, , 57-88.		19
46	Lvr, a Signaling System That Controls Global Gene Regulation and Virulence in Pathogenic <i>Leptospira</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 45.	1.8	19
47	Solving the ecological puzzle of mycorrhizal associations using data from annotated collections and environmental samples – an example of saddle fungi. <i>Environmental Microbiology Reports</i> , 2015, 7, 658-667.	1.0	18
48	A new species of <i>Cudonia</i> based on morphological and molecular data. <i>Mycologia</i> , 2002, 94, 641-650.	0.8	16
49	<i>Sparassis cystidiosa</i> sp. nov. from Thailand is described using morphological and molecular data. <i>Mycologia</i> , 2004, 96, 1010-1014.	0.8	16
50	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. <i>Fungal Biology</i> , 2016, , 25-46.	0.3	16
51	<i>Sparassis cystidiosa</i> sp. nov. from Thailand Is Described Using Morphological and Molecular Data. <i>Mycologia</i> , 2004, 96, 1010.	0.8	15
52	Multi-targeted priming for genome-wide gene expression assays. <i>BMC Genomics</i> , 2010, 11, 477.	1.2	14
53	Northern species of earth tongue genus <i>Thuemenidium</i> revisited, considering morphology, ecology and molecular phylogeny. <i>Mycologia</i> , 2010, 102, 1089-1095.	0.8	11
54	Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of <i>Pseudomonas syringae</i> pathovar <i>phaseolicola</i> . <i>PLoS ONE</i> , 2015, 10, e0144514.	1.1	11

#	ARTICLE	IF	CITATIONS
55	Phylogenetic relationships of Sparassis inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. <i>Mycologia</i> , 2004, 96, 1015-29.	0.8	11
56	A New Species of <i>Cudonia</i> Based on Morphological and Molecular Data. <i>Mycologia</i> , 2002, 94, 641.	0.8	9
57	A note on the incidence of reverse complementary fungal ITS sequences in the public sequence databases and a software tool for their detection and reorientation. <i>Mycoscience</i> , 2011, 52, 278-282.	0.3	7
58	The impact of incorporating molecular evolutionary model into predictions of phylogenetic signal and noise. <i>Frontiers in Ecology and Evolution</i> , 2014, 2, .	1.1	7
59	Integrative Activity of Mating Loci, Environmentally Responsive Genes, and Secondary Metabolism Pathways during Sexual Development of <i>Chaetomium globosum</i> . <i>MBio</i> , 2019, 10, .	1.8	7
60	A new <i>Sparassis</i> species from Spain described using morphological and molecular data. <i>Mycological Research</i> , 2006, 110, 1227-1231.	2.5	6
61	Comparative Genomics within and across Bilaterians Illuminates the Evolutionary History of ALK and LTK Proto-Oncogene Origination and Diversification. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	6
62	The GUL-1 Protein Binds Multiple RNAs Involved in Cell Wall Remodeling and Affects the MAK-1 Pathway in <i>Neurospora crassa</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	4
63	Transcriptional Divergence Underpinning Sexual Development in the Fungal Class Sordariomycetes. <i>MBio</i> , 2022, 13, .	1.8	4
64	Secondary Metabolism Gene Clusters Exhibit Increasingly Dynamic and Differential Expression during Asexual Growth, Conidiation, and Sexual Development in <i>Neurospora crassa</i> . <i>MSystems</i> , 2022, 7, .	1.7	2
65	Article Commentary: Snapshots of Tree Space. <i>Evolutionary Bioinformatics</i> , 2009, 5, EBO.S3416.	0.6	1
66	197â€¦The benefits of integrating compensation data with survey data: the Prospective Outcomes of Injury Study experience. <i>Occupational and Environmental Medicine</i> , 2013, 70, A66.4-A67.	1.3	0