## Zheng Wang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transcriptional Divergence Underpinning Sexual Development in the Fungal Class Sordariomycetes. MBio, 2022, 13, .	1.8	4
2	Secondary Metabolism Gene Clusters Exhibit Increasingly Dynamic and Differential Expression during Asexual Growth, Conidiation, and Sexual Development in Neurospora crassa. MSystems, 2022, 7, .	1.7	2
3	The GUL-1 Protein Binds Multiple RNAs Involved in Cell Wall Remodeling and Affects the MAK-1 Pathway in Neurospora crassa. Frontiers in Fungal Biology, 2021, 2, .	0.9	4
4	Comparative Genomics within and across Bilaterians Illuminates the Evolutionary History of ALK and LTK Proto-Oncogene Origination and Diversification. Genome Biology and Evolution, 2021, 13, .	1.1	6
5	The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study. Lancet Microbe, The, 2021, 2, e666-e675.	3.4	147
6	Pan-Genome of Wild and Cultivated Soybeans. Cell, 2020, 182, 162-176.e13.	13.5	508
7	Unmatched Level of Molecular Convergence among Deeply Divergent Complex Multicellular Fungi. Molecular Biology and Evolution, 2020, 37, 2228-2240.	3.5	23
8	Impact of international travel and border control measures on the global spread of the novel 2019 coronavirus outbreak. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7504-7509.	3.3	429
9	Projecting hospital utilization during the COVID-19 outbreaks in the United States. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9122-9126.	3.3	441
10	A multigene phylogeny toward a new phylogenetic classification of Leotiomycetes. IMA Fungus, 2019, 10, 1.	1.7	140
11	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> . MBio, 2019, 10, .	1.8	21
12	Integrative Activity of Mating Loci, Environmentally Responsive Genes, and Secondary Metabolism Pathways during Sexual Development of Chaetomium globosum. MBio, 2019, 10, .	1.8	7
13	Using evolutionary genomics, transcriptomics, and systems biology to reveal gene networks underlying fungal development. Fungal Biology Reviews, 2018, 32, 249-264.	1.9	22
14	Light sensing by opsins and fungal ecology: NOPâ€4 modulates entry into sexual reproduction in response to environmental cues. Molecular Ecology, 2018, 27, 216-232.	2.0	43
15	Parallel selection on a dormancy gene during domestication of crops from multiple families. Nature Genetics, 2018, 50, 1435-1441.	9.4	168
16	Lvr, a Signaling System That Controls Global Gene Regulation and Virulence in Pathogenic Leptospira. Frontiers in Cellular and Infection Microbiology, 2018, 8, 45.	1.8	19
17	Genomic Comparison Among Global Isolates of L. interrogans Serovars Copenhageni and Icterohaemorrhagiae Identified Natural Genetic Variation Caused by an Indel. Frontiers in Cellular and Infection Microbiology, 2018, 8, 193.	1.8	39
18	Maximizing Power in Phylogenetics and Phylogenomics: A Perspective Illuminated by Fungal Big Data. Advances in Genetics, 2017, 100, 1-47.	0.8	28

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19	The ancestral levels of transcription and the evolution of sexual phenotypes in filamentous fungi. PLoS Genetics, 2017, 13, e1006867.	1.5	46
20	The Fast-Evolving <i>phy-2</i> Gene Modulates Sexual Development in Response to Light in the Model Fungus Neurospora crassa. MBio, 2016, 7, e02148.	1.8	37
21	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. Fungal Biology, 2016, , 25-46.	0.3	16
22	Solving the ecological puzzle of mycorrhizal associations using data from annotated collections and environmental samples – an example of saddle fungi. Environmental Microbiology Reports, 2015, 7, 658-667.	1.0	18
23	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. Nature Biotechnology, 2015, 33, 408-414.	9.4	1,023
24	3 Pezizomycotina: Sordariomycetes and Leotiomycetes. , 2015, , 57-88.		19
25	Genomic and Gene-Expression Comparisons among Phage-Resistant Type-IV Pilus Mutants of Pseudomonas syringae pathovar phaseolicola. PLoS ONE, 2015, 10, e0144514.	1.1	11
26	Gene Expression Differences among Three Neurospora Species Reveal Genes Required for Sexual Reproduction in Neurospora crassa. PLoS ONE, 2014, 9, e110398.	1.1	39
27	The impact of incorporating molecular evolutionary model into predictions of phylogenetic signal and noise. Frontiers in Ecology and Evolution, 2014, 2, .	1.1	7
28	Comparative Genomic and Transcriptomic Analysis of <i>Wangiella dermatitidis</i> , A Major Cause of Phaeohyphomycosis and a Model Black Yeast Human Pathogen. G3: Genes, Genomes, Genetics, 2014, 4, 561-578.	0.8	58
29	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in Neurospora crassa. Eukaryotic Cell, 2014, 13, 154-169.	3.4	66
30	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	4.7	123
31	Improved software detection and extraction of ITS1 and <scp>ITS</scp> 2 from ribosomal <scp>ITS</scp> sequences of fungi and other eukaryotes for analysis of environmental sequencing data. Methods in Ecology and Evolution, 2013, 4, 914-919.	2.2	868
32	New species and distinctive geographical divergences of the genus Sparassis (Basidiomycota): evidence from morphological and molecular data. Mycological Progress, 2013, 12, 445-454.	0.5	26
33	Sex-linked transcriptional divergence in the hermaphrodite fungus Neurospora tetrasperma. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20130862.	1.2	26
34	197â€The benefits of integrating compensation data with survey data: the Prospective Outcomes of Injury Study experience. Occupational and Environmental Medicine, 2013, 70, A66.4-A67.	1.3	0
35	Differential impact of nutrition on developmental and metabolic gene expression during fruiting body development in Neurospora crassa. Fungal Genetics and Biology, 2012, 49, 405-413.	0.9	33
36	Sex-specific gene expression during asexual development of Neurospora crassa. Fungal Genetics and Biology, 2012, 49, 533-543.	0.9	31

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37	Molecular phylogenetics of the Gloeophyllales and relative ages of clades of Agaricomycotina producing a brown rot. Mycologia, 2011, 103, 510-524.	0.8	69
38	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SATé Alignments for Environmental ITS Data. PLoS ONE, 2011, 6, e19039.	1.1	32
39	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. Mycoscience, 2011, 52, 278-282.	0.3	7
40	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. Antonie Van Leeuwenhoek, 2011, 100, 471-475.	0.7	88
41	Multi-targeted priming for genome-wide gene expression assays. BMC Genomics, 2010, 11, 477.	1.2	14
42	Northern species of earth tongue genus <i>Thuemenidium</i> revisited, considering morphology, ecology and molecular phylogeny. Mycologia, 2010, 102, 1089-1095.	0.8	11
43	Evolution of Reproductive Morphology in Leaf Endophytes. PLoS ONE, 2009, 4, e4246.	1.1	31
44	The Ascomycota Tree of Life: A Phylum-wide Phylogeny Clarifies the Origin and Evolution of Fundamental Reproductive and Ecological Traits. Systematic Biology, 2009, 58, 224-239.	2.7	581
45	Article Commentary: Snapshots of Tree Space. Evolutionary Bioinformatics, 2009, 5, EBO.S3416.	0.6	1
46	<i>Geoglossomycetes</i> cl. nov., <i>Geoglossales</i> ord. nov. and taxa above class rank in the <i>Ascomycota</i> Tree of Life. Persoonia: Molecular Phylogeny and Evolution of Fungi, 2009, 22, 129-138.	1.6	55
47	Preserving Accuracy in GenBank. Science, 2008, 319, 1616-1616.	6.0	198
48	Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). Molecular Phylogenetics and Evolution, 2007, 43, 430-451.	1.2	341
49	A higher-level phylogenetic classification of the Fungi. Mycological Research, 2007, 111, 509-547.	2.5	1,994
50	Phylogeny and a new species of Sparassis (Polyporales, Basidiomycota): evidence from mitochondrial atp6, nuclear rDNA and rpb2 genes. Mycologia, 2006, 98, 584-592.	0.8	24
51	Toward a phylogenetic classification of the Leotiomycetes based on rDNA data. Mycologia, 2006, 98, 1065-1075.	0.8	64
52	Phylogeny and a new species of Sparassis (Polyporales, Basidiomycota): evidence from mitochondrial atp6, nuclear rDNA and rpb2 genes. Mycologia, 2006, 98, 584-592.	0.8	25
53	Reconstructing the early evolution of Fungi using a six-gene phylogeny. Nature, 2006, 443, 818-822.	13.7	1,625
54	Evolution of helotialean fungi (Leotiomycetes, Pezizomycotina): A nuclear rDNA phylogeny. Molecular Phylogenetics and Evolution, 2006, 41, 295-312.	1.2	165

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55	Toward a phylogenetic classification of the Leotiomycetes based on rDNA data. Mycologia, 2006, 98, 1065-1075.	0.8	128
56	A new Sparassis species from Spain described using morphological and molecular data. Mycological Research, 2006, 110, 1227-1231.	2.5	6
57	Evolutionary relationships of <i>Mycaureola dilseae</i> (Agaricales), a basidiomycete pathogen of a subtidal rhodophyte. American Journal of Botany, 2006, 93, 547-556.	0.8	58
58	Life history and systematics of the aquatic discomycete <i>Mitrula</i> (Helotiales, Ascomycota) based on cultural, morphological, and molecular studies. American Journal of Botany, 2005, 92, 1565-1574.	0.8	51
59	Phylogenetic Relationships of Sparassis Inferred from Nuclear and Mitochondrial Ribosomal DNA and RNA Polymerase Sequences. Mycologia, 2004, 96, 1015.	0.8	35
60	Sparassis cystidiosa sp. nov. from Thailand Is Described Using Morphological and Molecular Data. Mycologia, 2004, 96, 1010.	0.8	15
61	Phylogenetic relationships of <i>Sparassis</i> inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. Mycologia, 2004, 96, 1015-1029.	0.8	48
62	<i>Sparassis cystidiosa</i> sp. nov. from Thailand is described using morphological and molecular data. Mycologia, 2004, 96, 1010-1014.	0.8	16
63	Phylogenetic relationships of Sparassis inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. Mycologia, 2004, 96, 1015-29.	0.8	11
64	Another fossil agaric from Dominican amber. Mycologia, 2003, 95, 685-687.	0.8	27
65	A New Species of Cudonia Based on Morphological and Molecular Data. Mycologia, 2002, 94, 641.	0.8	9
66	A new species ofCudoniabased on morphological and molecular data. Mycologia, 2002, 94, 641-650.	0.8	16