

Jason Eric Stajich

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6028018/jason-eric-stajich-publications-by-year.pdf>

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

213
papers

16,156
citations

55
h-index

125
g-index

280
ext. papers

19,570
ext. citations

7.7
avg, IF

6.2
L-index

#	Paper	IF	Citations
213	Decoding Transcription Regulatory Mechanisms Associated with Phase Transition Using Total RNA.. <i>MSystems</i> , 2022 , e0140421	7.6	0
212	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain "Silveira".. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	1
211	Fungi are key players in extreme ecosystems.. <i>Trends in Ecology and Evolution</i> , 2022 ,	10.9	2
210	Efficient CRISPR/Cas9-mediated genome modification of the glassy-winged sharpshooter <i>Homalodisca vitripennis</i> (Germar).. <i>Scientific Reports</i> , 2022 , 12, 6428	4.9	0
209	Host Lung Environment Limits <i>Aspergillus fumigatus</i> Germination through an SskA-Dependent Signaling Response. <i>MSphere</i> , 2021 , e0092221	5	3
208	Fungal biodiversity and conservation mycology in light of new technology, big data, and changing attitudes. <i>Current Biology</i> , 2021 , 31, R1312-R1325	6.3	1
207	Understudied, underrepresented, and unknown: Methodological biases that limit detection of early diverging fungi from environmental samples. <i>Molecular Ecology Resources</i> , 2021 ,	8.4	2
206	Genomic analyses of two Italian oyster mushroom <i>Pleurotus pulmonarius</i> strains. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	2
205	Genome sequence of the oyster mushroom <i>Pleurotus ostreatus</i> strain PC9. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	8
204	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic that Includes the Species Complex. <i>Phytopathology</i> , 2021 , 111, 1064-1079	3.8	39
203	Genomic insights into the host specific adaptation of the <i>Pneumocystis</i> genus. <i>Communications Biology</i> , 2021 , 4, 305	6.7	5
202	<i>Datura</i> genome reveals duplications of psychoactive alkaloid biosynthetic genes and high mutation rate following tissue culture. <i>BMC Genomics</i> , 2021 , 22, 201	4.5	2
201	Identification and phylogenetic analysis of RNA binding domain abundant in apicomplexans or RAP proteins. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
200	Pre-Cambrian roots of novel Antarctic cryptoendolithic bacterial lineages. <i>Microbiome</i> , 2021 , 9, 63	16.6	3
199	Culture-Dependent and Amplicon Sequencing Approaches Reveal Diversity and Distribution of Black Fungi in Antarctic Cryptoendolithic Communities. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	3
198	The mitochondrial genomes of the human pathogens <i>Coccidioides immitis</i> and <i>C. posadasii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021 ,	3.2	3
197	Balancing Positive and Negative Selection: Evolution of <i>Candida lusitanae</i> . <i>MBio</i> , 2021 , 12,	7.8	4

196	The genome of <i>Geosiphon pyriformis</i> reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. <i>Current Biology</i> , 2021 , 31, 1570-1577.e4	6.3	7
195	A genome-scale phylogeny of the kingdom Fungi. <i>Current Biology</i> , 2021 , 31, 1653-1665.e5	6.3	29
194	Transcriptional Analysis of Mycelia and Spherules by RNA Sequencing. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	3
193	High-Quality Reference Genome Sequence for the Oomycete Vegetable Pathogen <i>Phytophthora capsici</i> Strain LT1534. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0029521	1.3	1
192	Metagenome Sequencing to Explore Phylogenomics of Terrestrial Cyanobacteria. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0025821	1.3	3
191	Amplicon Sequencing of Rock-Inhabiting Microbial Communities from Joshua Tree National Park, USA. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0049421	1.3	0
190	Diploidy within a Haploid Genus of Entomopathogenic Fungi. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	1
189	Beyond the extremes: Rocks as ultimate refuge for fungi in drylands. <i>Mycologia</i> , 2021 , 113, 108-133	2.4	18
188	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021 , 230, 774-792	9.8	9
187	<i>Aspergillus fumigatus</i> Strain-Specific Conidia Lung Persistence Causes an Allergic Broncho-Pulmonary Aspergillosis-Like Disease Phenotype. <i>MSphere</i> , 2021 , 6,	5	3
186	A Heterogeneously Expressed Gene Family Modulates the Biofilm Architecture and Hypoxic Growth of. <i>MBio</i> , 2021 , 12,	7.8	3
185	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoospore-forming fungus to the non-flagellated, terrestrial fungi. <i>Scientific Reports</i> , 2021 , 11, 3217	4.9	9
184	Effects of Simulated Microgravity on the Proteome and Secretome of the Polyextremotolerant Black Fungus. <i>Frontiers in Genetics</i> , 2021 , 12, 638708	4.5	3
183	Improved draft reference genome for the Glassy-winged Sharpshooter (<i>Homalodisca vitripennis</i>), a vector for Pierce's disease. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	1
182	<i>Aspergillus fumigatus</i> In-Host HOG Pathway Mutation for Cystic Fibrosis Lung Microenvironment Persistence. <i>MBio</i> , 2021 , 12, e0215321	7.8	4
181	Crowdsourced analysis of fungal growth and branching on microfluidic platforms. <i>PLoS ONE</i> , 2021 , 16, e0257823	3.7	2
180	Seven Years at High Salinity-Experimental Evolution of the Extremely Halotolerant Black Yeast. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	4
179	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. <i>MBio</i> , 2020 , 11,	7.8	94

178	Evolutionary relationships among spp. (Entomophthorales), obligate pathogens of cicadas. <i>Mycologia</i> , 2020 , 112, 1060-1074	2.4	6
177	Behavioral betrayal: How select fungal parasites enlist living insects to do their bidding. <i>PLoS Pathogens</i> , 2020 , 16, e1008598	7.6	9
176	Natural diversity in the predatory behavior facilitates the establishment of a robust model strain for nematode-trapping fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 6762-6770	11.5	34
175	Uncovered Microbial Diversity in Antarctic Cryptoendolithic Communities Sampling three Representative Locations of the Victoria Land. <i>Microorganisms</i> , 2020 , 8,	4.9	8
174	Insights into dryland biocrust microbiome: geography, soil depth and crust type affect biocrust microbial communities and networks in Mojave Desert, USA. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	11
173	Sampling strategies to assess microbial diversity of Antarctic cryptoendolithic communities. <i>Polar Biology</i> , 2020 , 43, 225-235	2	5
172	Endolithic Fungal Species Markers for Harshest Conditions in the McMurdo Dry Valleys, Antarctica. <i>Life</i> , 2020 , 10,	3	10
171	Sun exposure drives Antarctic cryptoendolithic community structure and composition. <i>Polar Biology</i> , 2020 , 43, 607-615	2	3
170	Metagenomes in the Borderline Ecosystems of the Antarctic Cryptoendolithic Communities. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	3
169	Draft Genome Sequence of the Yeast sp. Strain CCFEE 5036, Isolated from McMurdo Dry Valleys, Antarctica. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
168	The monophyletic <i>Sarcogyne canadensis</i> – <i>wheeleri</i> clade, a newly recognized group sister to the European <i>Acarospora glaucocarpa</i> group. <i>Bryologist</i> , 2020 , 123, 11	0.7	0
167	Airborne fungi spores distribution in various locations in Lagos, Nigeria. <i>Environmental Monitoring and Assessment</i> , 2020 , 192, 87	3.1	8
166	Genomic diversity generated by a transposable element burst in a rice recombinant inbred population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 26288-26297	11.5	3
165	Toward a Fully Resolved Fungal Tree of Life. <i>Annual Review of Microbiology</i> , 2020 , 74, 291-313	17.5	61
164	A novel genomic variant in Midwestern Brazil: evidence for an older and wider sporotrichosis epidemic. <i>Emerging Microbes and Infections</i> , 2020 , 9, 2515-2525	18.9	7
163	Clustering analysis of large-scale phenotypic data in the model filamentous fungus <i>Neurospora crassa</i> . <i>BMC Genomics</i> , 2020 , 21, 755	4.5	1
162	Phylogenomic Analyses of Non-Dikarya Fungi Supports Horizontal Gene Transfer Driving Diversification of Secondary Metabolism in the Amphibian Gastrointestinal Symbiont. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3417-3433	3.2	10
161	Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus <i>Friedmanniomyces endolithicus</i> . <i>Fungal Biology</i> , 2020 , 124, 458-467	2.8	16

160	No to : Phylogenomic and Practical Reasons for Continued Inclusion of the <i>Fusarium solani</i> Species Complex in the Genus. <i>MSphere</i> , 2020 , 5,	5	32
159	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , 2020 , 104, 267-289	17.6	18
158	Belowground impacts of alpine woody encroachment are determined by plant traits, local climate, and soil conditions. <i>Global Change Biology</i> , 2020 , 26, 7112-7127	11.4	7
157	Survey of Early-Diverging Lineages of Fungi Reveals Abundant and Diverse Mycoviruses. <i>MBio</i> , 2020 , 11,	7.8	9
156	Shed Light in the DaRk LineagES of the Fungal Tree of Life-STRES. <i>Life</i> , 2020 , 10,	3	4
155	Probe-Based Multiplex Real-Time PCR as a Diagnostic Tool to Distinguish Distinct Fungal Symbionts Associated With and in California. <i>Plant Disease</i> , 2020 , 104, 227-238	1.5	7
154	Reproduction and Dispersal of Biological Soil Crust Organisms. <i>Frontiers in Ecology and Evolution</i> , 2019 , 7,	3.7	16
153	Fungal biofilm morphology impacts hypoxia fitness and disease progression. <i>Nature Microbiology</i> , 2019 , 4, 2430-2441	26.6	46
152	Draft Genome Sequence of an Antarctic Isolate of the Black Yeast Fungus. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	6
151	Horizontal Gene Transfer as an Indispensable Driver for Evolution of Neocallimastigomycota into a Distinct Gut-Dwelling Fungal Lineage. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	35
150	Psychoactive plant- and mushroom-associated alkaloids from two behavior modifying cicada pathogens. <i>Fungal Ecology</i> , 2019 , 41, 147-164	4.1	27
149	Proteomic and Metabolomic Characteristics of Extremophilic Fungi Under Simulated Mars Conditions. <i>Frontiers in Microbiology</i> , 2019 , 10, 1013	5.7	17
148	FGMP: assessing fungal genome completeness. <i>BMC Bioinformatics</i> , 2019 , 20, 184	3.6	14
147	Fungi in the Marine Environment: Open Questions and Unsolved Problems. <i>MBio</i> , 2019 , 10,	7.8	107
146	Genome Sequence of a Lethal Vascular Wilt Fungus, <i>Verticillium nonalfalfae</i> , a Biological Control Used Against the Invasive <i>Ailanthus altissima</i> . <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	4
145	Tracking the origin of two genetic components associated with transposable element bursts in domesticated rice. <i>Nature Communications</i> , 2019 , 10, 641	17.4	15
144	Altitude and fungal diversity influence the structure of Antarctic cryptoendolithic Bacteria communities. <i>Environmental Microbiology Reports</i> , 2019 , 11, 718-726	3.7	15
143	Diversity and function of fungi associated with the fungivorous millipede,. <i>Fungal Ecology</i> , 2019 , 41, 187-197	4.97	10

142	Microfluidics and Metabolomics Reveal Symbiotic Bacterial-Fungal Interactions Between and Include Metabolite Exchange. <i>Frontiers in Microbiology</i> , 2019 , 10, 2163	5.7	16
141	<i>Pyricularia graminis-tritici</i> is not the correct species name for the wheat blast fungus: response to Ceresini et al. (MPP 20:2). <i>Molecular Plant Pathology</i> , 2019 , 20, 173-179	5.7	25
140	Improved Reference Genome Sequence of Strain WA_211, Isolated in Washington State. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
139	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , 2019 , 3, 479-490	12.3	57
138	Molecular Dating of the Emergence of Anaerobic Rumen Fungi and the Impact of Laterally Acquired Genes. <i>MSystems</i> , 2019 , 4,	7.6	12
137	Members of the <i>Euwallacea fornicatus</i> species complex exhibit promiscuous mutualism with ambrosia fungi in Taiwan. <i>Fungal Genetics and Biology</i> , 2019 , 133, 103269	3.9	11
136	Genome-scale phylogenetics reveals a monophyletic Zoopagales (Zoopagomycota, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2019 , 133, 152-163	4.1	13
135	Parasitoid Jewel Wasp Mounts Multipronged Neurochemical Attack to Hijack a Host Brain. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 99-114	7.6	13
134	International Space Station conditions alter genomics, proteomics, and metabolomics in <i>Aspergillus nidulans</i> . <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 1363-1377	5.7	15
133	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019 , 222, 511-525	9.8	37
132	Shrub range expansion alters diversity and distribution of soil fungal communities across an alpine elevation gradient. <i>Molecular Ecology</i> , 2018 , 27, 2461-2476	5.7	25
131	Phylogenetic and Phylogenomic Definition of Species. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 2007-2018	3.2	27
130	Ultra-low input transcriptomics reveal the spore functional content and phylogenetic affiliations of poorly studied arbuscular mycorrhizal fungi. <i>DNA Research</i> , 2018 , 25, 217-227	4.5	19
129	Two Novel Fungal Symbionts <i>Fusarium kuroshium</i> sp. nov. and <i>Graphium kuroshium</i> sp. nov. of Kuroshio Shot Hole Borer (<i>Euwallacea</i> sp. nr. <i>fornicatus</i>) Cause <i>Fusarium</i> Dieback on Woody Host Species in California. <i>Plant Disease</i> , 2018 , 102, 1154-1164	1.5	41
128	Comparative genomic analysis of the 'pseudofungus'. <i>Open Biology</i> , 2018 , 8,	7	20
127	Genomic evidence for intraspecific hybridization in a clonal and extremely halotolerant yeast. <i>BMC Genomics</i> , 2018 , 19, 364	4.5	24
126	Antarctic Cryptoendolithic Fungal Communities Are Highly Adapted and Dominated by Lecanoromycetes and Dothideomycetes. <i>Frontiers in Microbiology</i> , 2018 , 9, 1392	5.7	36
125	Analysis of Transposable Elements in <i>Coccidioides</i> Species. <i>Journal of Fungi (Basel, Switzerland)</i> , 2018 , 4,	5.6	9

124	Sun Exposure Shapes Functional Grouping of Fungi in Cryptoendolithic Antarctic Communities. <i>Life</i> , 2018 , 8,	3	26
123	Comparative analysis reveals unexpected genome features of newly isolated Thraustochytrids strains: on ecological function and PUFAs biosynthesis. <i>BMC Genomics</i> , 2018 , 19, 541	4.5	20
122	Comparative Population Genomics Analysis of the Mammalian Fungal Pathogen. <i>MBio</i> , 2018 , 9,	7.8	19
121	Evolution of drug resistance in an antifungal-naïve chronic infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12040-12045	11.5	28
120	Early Diverging Insect-Pathogenic Fungi of the Order Entomophthorales Possess Diverse and Unique Subtilisin-Like Serine Proteases. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3311-3319	3.2	8
119	Characterization of <i>Aspergillus niger</i> Isolated from the International Space Station. <i>MSystems</i> , 2018 , 3,	7.6	27
118	Comparative Genomics Reveals the Core Gene Toolbox for the Fungus-Insect Symbiosis. <i>MBio</i> , 2018 , 9,	7.8	8
117	Innovation and constraint leading to complex multicellularity in the Ascomycota. <i>Nature Communications</i> , 2017 , 8, 14444	17.4	52
116	Insight into the Recent Genome Duplication of the Halophilic Yeast : Combining an Improved Genome with Gene Expression and Chromatin Structure. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2015-2022	3.2	31
115	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017 , 49, 964-968	36.3	181
114	PCR Multiplexes Discriminate <i>Fusarium</i> Symbionts of Invasive <i>Euwallacea</i> Ambrosia Beetles that Inflict Damage on Numerous Tree Species Throughout the United States. <i>Plant Disease</i> , 2017 , 101, 233-240	1.5	13
113	Fungal Genomes and Insights into the Evolution of the Kingdom. <i>Microbiology Spectrum</i> , 2017 , 5,	8.9	47
112	Microbial associates of the southern mole cricket (<i>Scapteriscus borellii</i>) are highly pathogenic. <i>Journal of Invertebrate Pathology</i> , 2017 , 150, 54-62	2.6	5
111	The Fungal Tree of Life: from Molecular Systematics to Genome-Scale Phylogenies. <i>Microbiology Spectrum</i> , 2017 , 5,	8.9	104
110	Draft Genome Sequences of the Antarctic Endolithic Fungi CCFEE 5527 and sp. CCFEE 5018. <i>Genome Announcements</i> , 2017 , 5,		15
109	<i>Bifiguratus adelaidae</i> , gen. et sp. nov., a new member of Mucoromycotina in endophytic and soil-dwelling habitats. <i>Mycologia</i> , 2017 , 109, 363-378	2.4	20
108	Tracking the genome-wide outcomes of a transposable element burst over decades of amplification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E10550-E10559	11.5	25
107	The Fungal Tree of Life: From Molecular Systematics to Genome-Scale Phylogenies 2017 , 1-34		16

106	Fungal Genomes and Insights into the Evolution of the Kingdom 2017 , 619-633		9
105	Chlorophyte aspartyl aminopeptidases: Ancient origins, expanded families, new locations, and secondary functions. <i>PLoS ONE</i> , 2017 , 12, e0185492	3.7	2
104	RelocaTE2: a high resolution transposable element insertion site mapping tool for population resequencing. <i>PeerJ</i> , 2017 , 5, e2942	3.1	18
103	Exploring the binding properties and structural stability of an opsin in the chytrid using comparative and molecular modeling. <i>PeerJ</i> , 2017 , 5, e3206	3.1	5
102	Deacetylation of Fungal Exopolysaccharide Mediates Adhesion and Biofilm Formation. <i>MBio</i> , 2016 , 7, e00252-16	7.8	65
101	Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). <i>Molecular Phylogenetics and Evolution</i> , 2016 , 98, 210-32	4.1	70
100	Small genome of the fungus <i>Escovopsis weberi</i> , a specialized disease agent of ant agriculture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 3567-72	11.5	49
99	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016 , 12, e1006108	6	103
98	Fungal Evolution: <i>Mucor</i> and <i>Phycomyces</i> See Double. <i>Current Biology</i> , 2016 , 26, R775-7	6.3	3
97	A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. <i>Mycologia</i> , 2016 , 108, 1028-1046	2.4	684
96	Characterization of the Carbohydrate Binding Module 18 gene family in the amphibian pathogen <i>Batrachochytrium dendrobatidis</i> . <i>Fungal Genetics and Biology</i> , 2015 , 77, 31-9	3.9	19
95	The low information content of <i>Neurospora</i> splicing signals: implications for RNA splicing and intron origin. <i>Rna</i> , 2015 , 21, 997-1004	5.8	2
94	Cellular Subcompartments through Cytoplasmic Streaming. <i>Developmental Cell</i> , 2015 , 34, 410-20	10.2	30
93	Deciphering the uniqueness of Mucoromycotina cell walls by combining biochemical and phylogenomic approaches. <i>Environmental Microbiology</i> , 2015 , 17, 1649-62	5.2	36
92	Analysis of the <i>Candida albicans</i> Phosphoproteome. <i>Eukaryotic Cell</i> , 2015 , 14, 474-85		31
91	Endogenous Small RNA Mediates Meiotic Silencing of a Novel DNA Transposon. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1949-60	3.2	28
90	11 Phylogenomics Enabling Genome-Based Mycology 2015 , 279-294		2
89	Evolutionary origins and diversification of proteobacterial mutualists. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014 , 281, 20132146	4.4	42

88	Evolutionary histories of soil fungi are reflected in their large-scale biogeography. <i>Ecology Letters</i> , 2014 , 17, 1086-93	10	60
87	MixS-BE: a MixS extension defining a minimum information standard for sequence data from the built environment. <i>ISME Journal</i> , 2014 , 8, 1-3	11.9	109
86	MicroRNAs suppress NB domain genes in tomato that confer resistance to <i>Fusarium oxysporum</i> . <i>PLoS Pathogens</i> , 2014 , 10, e1004464	7.6	111
85	Analysis of the genome and transcriptome of <i>Cryptococcus neoformans</i> var. <i>grubii</i> reveals complex RNA expression and microevolution leading to virulence attenuation. <i>PLoS Genetics</i> , 2014 , 10, e1004261 ⁶	6	260
84	Literature-based gene curation and proposed genetic nomenclature for cryptococcus. <i>Eukaryotic Cell</i> , 2014 , 13, 878-83		13
83	Comparative genomics of the major fungal agents of human and animal Sporotrichosis: <i>Sporothrix schenckii</i> and <i>Sporothrix brasiliensis</i> . <i>BMC Genomics</i> , 2014 , 15, 943	4.5	78
82	Toward genome-enabled mycology. <i>Mycologia</i> , 2013 , 105, 1339-49	2.4	29
81	Shared signatures of parasitism and phylogenomics unite Cryptomycota and microsporidia. <i>Current Biology</i> , 2013 , 23, 1548-53	6.3	227
80	5'-Serial Analysis of Gene Expression studies reveal a transcriptomic switch during fruiting body development in <i>Coprinopsis cinerea</i> . <i>BMC Genomics</i> , 2013 , 14, 195	4.5	46
79	Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 9385-90	11.5	202
78	Genomic insights into the atopic eczema-associated skin commensal yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013 , 4, e00572-12	7.8	89
77	The genome and development-dependent transcriptomes of <i>Pyronema confluens</i> : a window into fungal evolution. <i>PLoS Genetics</i> , 2013 , 9, e1003820	6	65
76	The use of RelocaTE and unassembled short reads to produce high-resolution snapshots of transposable element generated diversity in rice. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 949-57	3.2	32
75	Regional control of histone H3 lysine 27 methylation in <i>Neurospora</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 6027-32	11.5	103
74	Emergence of the Chytrid Fungus <i>Batrachochytrium Dendrobatidis</i> and Global Amphibian Declines 2013 , 461-472		1
73	Meeting report: fungal its workshop (october 2012). <i>Standards in Genomic Sciences</i> , 2013 , 8, 118-23		26
72	<i>Neurospora</i> and the dead-end hypothesis: genomic consequences of selfing in the model genus. <i>Evolution; International Journal of Organic Evolution</i> , 2013 , 67, 3600-16	3.8	24
71	Sequential utilization of hosts from different fly families by genetically distinct, sympatric populations within the <i>Entomophthora muscae</i> species complex. <i>PLoS ONE</i> , 2013 , 8, e71168	3.7	10

70	Analyses of expressed sequence tags in <i>Neurospora</i> reveal rapid evolution of genes associated with the early stages of sexual reproduction in fungi. <i>BMC Evolutionary Biology</i> , 2012 , 12, 229	3	9
69	Unidirectional evolutionary transitions in fungal mating systems and the role of transposable elements. <i>Molecular Biology and Evolution</i> , 2012 , 29, 3215-26	8.3	76
68	FungiDB: an integrated functional genomics database for fungi. <i>Nucleic Acids Research</i> , 2012 , 40, D675-81	10.1	235
67	Species-specific chitin-binding module 18 expansion in the amphibian pathogen <i>Batrachochytrium dendrobatidis</i> . <i>MBio</i> , 2012 , 3, e00150-12	7.8	33
66	Genome variation in <i>Cryptococcus gattii</i> , an emerging pathogen of immunocompetent hosts. <i>MBio</i> , 2011 , 2, e00342-10	7.8	137
65	Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus <i>Neurospora tetrasperma</i> . <i>Genetics</i> , 2011 , 189, 55-69	4	61
64	Genomic transition to pathogenicity in chytrid fungi. <i>PLoS Pathogens</i> , 2011 , 7, e1002338	7.6	83
63	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010 , 28, 957-63	44.5	381
62	Transcription factors in light and circadian clock signaling networks revealed by genomewide mapping of direct targets for <i>Neurospora</i> white collar complex. <i>Eukaryotic Cell</i> , 2010 , 9, 1549-56		160
61	Using the Generic Synteny Browser (GBrowse_syn). <i>Current Protocols in Bioinformatics</i> , 2010 , Chapter 9, Unit 9.12	24.2	47
60	The deadly chytrid fungus: a story of an emerging pathogen. <i>PLoS Pathogens</i> , 2010 , 6, e1000550	7.6	37
59	De novo assembly of a 40 Mb eukaryotic genome from short sequence reads: <i>Sordaria macrospora</i> , a model organism for fungal morphogenesis. <i>PLoS Genetics</i> , 2010 , 6, e1000891	6	152
58	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom <i>Coprinopsis cinerea</i> (<i>Coprinus cinereus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 11889-94	11.5	322
57	Conflict between reproductive gene trees and species phylogeny among heterothallic and pseudohomothallic members of the filamentous ascomycete genus <i>Neurospora</i> . <i>Fungal Genetics and Biology</i> , 2010 , 47, 869-78	3.9	28
56	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010 , 11, R73	18.3	280
55	Population genomic sequencing of <i>Coccidioides</i> fungi reveals recent hybridization and transposon control. <i>Genome Research</i> , 2010 , 20, 938-46	9.7	140
54	A molecular perspective: biology of the emerging pathogen <i>Batrachochytrium dendrobatidis</i> . <i>Diseases of Aquatic Organisms</i> , 2010 , 92, 131-47	1.7	22
53	Analysis of the Basidiomycete <i>Coprinopsis cinerea</i> reveals conservation of the core meiotic expression program over half a billion years of evolution. <i>PLoS Genetics</i> , 2010 , 6, e1001135	6	28

52	Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives. <i>Genome Research</i> , 2009 , 19, 1722-31	9.7	229
51	The fungi. <i>Current Biology</i> , 2009 , 19, R840-5	6.3	226
50	Proteomic and phenotypic profiling of the amphibian pathogen <i>Batrachochytrium dendrobatidis</i> shows that genotype is linked to virulence. <i>Molecular Ecology</i> , 2009 , 18, 415-29	5.7	120
49	DNA Sequence Databases 2009 , 1-11		3
48	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008 , 452, 88-92	50.4	823
47	An expanded family of fungicidal extracellular metallopeptidases of <i>Coprinopsis cinerea</i> . <i>Mycological Research</i> , 2008 , 112, 389-98		20
46	Comparative hybridization reveals extensive genome variation in the AIDS-associated pathogen <i>Cryptococcus neoformans</i> . <i>Genome Biology</i> , 2008 , 9, R41	18.3	52
45	Resolving arthropod phylogeny: exploring phylogenetic signal within 41 kb of protein-coding nuclear gene sequence. <i>Systematic Biology</i> , 2008 , 57, 920-38	8.4	162
44	Global gene expression profiles for life stages of the deadly amphibian pathogen <i>Batrachochytrium dendrobatidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17034-9	11.5	89
43	An Introduction to BioPerl. <i>Methods in Molecular Biology</i> , 2007 , 406, 535-48	1.4	35
42	Evolution of the mating type locus: insights gained from the dimorphic primary fungal pathogens <i>Histoplasma capsulatum</i> , <i>Coccidioides immitis</i> , and <i>Coccidioides posadasii</i> . <i>Eukaryotic Cell</i> , 2007 , 6, 622-9		82
41	BASC: an integrated bioinformatics system for Brassica research. <i>Nucleic Acids Research</i> , 2007 , 35, D870-30.1	30.1	17
40	Evolution of budding yeast prion-determinant sequences across diverse fungi. <i>Journal of Molecular Biology</i> , 2007 , 368, 273-82	6.5	55
39	Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. <i>Genome Biology</i> , 2007 , 8, R223	18.3	100
38	A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. <i>BMC Evolutionary Biology</i> , 2006 , 6, 99	3	371
37	Evidence of mRNA-mediated intron loss in the human-pathogenic fungus <i>Cryptococcus neoformans</i> . <i>Eukaryotic Cell</i> , 2006 , 5, 789-93		46
36	The <i>Cryptococcus neoformans</i> catalase gene family and its role in antioxidant defense. <i>Eukaryotic Cell</i> , 2006 , 5, 1447-59		76
35	Comparative analysis of <i>Saccharomyces cerevisiae</i> WW domains and their interacting proteins. <i>Genome Biology</i> , 2006 , 7, R30	18.3	48

34	Open source tools and toolkits for bioinformatics: significance, and where are we?. <i>Briefings in Bioinformatics</i> , 2006 , 7, 287-96	13.4	33
33	Phylogenomic analysis of non-ribosomal peptide synthetases in the genus <i>Aspergillus</i> . <i>Gene</i> , 2006 , 383, 24-32	3.8	60
32	The evolution of mammalian gene families. <i>PLoS ONE</i> , 2006 , 1, e85	3.7	228
31	Reconstructing the early evolution of Fungi using a six-gene phylogeny. <i>Nature</i> , 2006 , 443, 818-22	50.4	1392
30	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006 , 444, 97-101	50.4	867
29	Disentangling the effects of demography and selection in human history. <i>Molecular Biology and Evolution</i> , 2005 , 22, 63-73	8.3	165
28	Same-sex mating and the origin of the Vancouver Island <i>Cryptococcus gattii</i> outbreak. <i>Nature</i> , 2005 , 437, 1360-4	50.4	409
27	Investigating hookworm genomes by comparative analysis of two <i>Ancylostoma</i> species. <i>BMC Genomics</i> , 2005 , 6, 58	4.5	46
26	Likelihoods from summary statistics: recent divergence between species. <i>Genetics</i> , 2005 , 171, 1419-36	4	20
25	Estimating the tempo and mode of gene family evolution from comparative genomic data. <i>Genome Research</i> , 2005 , 15, 1153-60	9.7	193
24	Identification of <i>Cryptococcus neoformans</i> temperature-regulated genes with a genomic-DNA microarray. <i>Eukaryotic Cell</i> , 2004 , 3, 1249-60		89
23	The effects of selection against spurious transcription factor binding sites. <i>Molecular Biology and Evolution</i> , 2003 , 20, 901-6	8.3	66
22	The genome sequence of <i>Caenorhabditis briggsae</i> : a platform for comparative genomics. <i>PLoS Biology</i> , 2003 , 1, E45	9.7	677
21	Ganglioside-induced differentiation-associated protein-1 is mutant in Charcot-Marie-Tooth disease type 4A/8q21. <i>Nature Genetics</i> , 2002 , 30, 21-2	36.3	302
20	The generic genome browser: a building block for a model organism system database. <i>Genome Research</i> , 2002 , 12, 1599-610	9.7	929
19	The Bioperl toolkit: Perl modules for the life sciences. <i>Genome Research</i> , 2002 , 12, 1611-8	9.7	1234
18	Combined Pan-, Population-, and Phylo-Genomic Analysis of <i>Aspergillus fumigatus</i> Reveals Population Structure and Lineage-Specific Diversity		2
17	Fungal CTAB DNA Extraction v1		4

16	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi	1
15	Early diverging insect pathogenic fungi of the order Entomophthorales possess diverse and unique subtilisin-like serine proteases	1
14	Diversity and function of fungi associated with the fungivorous millipede, <i>Brachycybe lecontii</i>	1
13	Metagenomes in the borderline ecosystems of the Antarctic cryptoendolithic communities	1
12	Antarctic cryptoendolithic bacterial lineages of pre-Cambrian origin as proxy for Mars colonization	2
11	A genome-scale phylogeny of Fungi; insights into early evolution, radiations, and the relationship between taxonomy and phylogeny	6
10	Volatiles from <i>Serratia marcescens</i> , <i>S. proteamaculans</i> , and <i>Bacillus subtilis</i> inhibit Growth of <i>Rhizopus stolonifer</i> and Other Fungi	1
9	Structural characterization and evolutionary analyses of the <i>Coccidioides immitis</i> and <i>Coccidioides posadasii</i> mitochondrial genomes	1
8	Molecular dating of the emergence of anaerobic rumen fungi and the impact of laterally acquired genes	3
7	Sun exposure drives Antarctic cryptoendolithic community structure and composition	2
6	Insights into the desert living skin microbiome: geography, soil depth, and crust type affect biocrust microbial communities and networks in Mojave Desert, USA	1
5	Natural diversity in the predatory behavior facilitates the establishment of a new robust model strain for nematode-trapping fungi	1
4	Shallow Genome Sequencing for Phylogenomics of Mycorrhizal Fungi from Endangered Orchids	4
3	FGMP: assessing fungal genome completeness and gene content	1
2	Genomic Perspectives on the Fungal Kingdom 657-666	
1	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain <i>Silveira</i>	1