

Igor Grigoriev

List of Publications by Year in descending order

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papers

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2213

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371
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371
times ranked

47137
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#	ARTICLE	IF	CITATIONS
1	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
2	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
3	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	6.0	2,354
4	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	6.0	1,712
5	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	13.7	1,496
6	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	13.7	1,458
7	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	6.0	1,424
8	Sea Anemone Genome Reveals Ancestral Eumetazoan Gene Repertoire and Genomic Organization. <i>Science</i> , 2007, 317, 86-94.	6.0	1,423
9	MycCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014, 42, D699-D704.	6.5	1,187
10	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	9.4	1,116
11	A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. <i>Mycologia</i> , 2016, 108, 1028-1046.	0.8	1,092
12	The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011, 331, 555-561.	6.0	1,086
13	<i>Phytophthora</i> Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 2006, 313, 1261-1266.	6.0	1,059
14	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008, 451, 783-788.	13.7	1,006
15	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
16	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	9.4	870
17	<i>Trichoderma</i> : the genomics of opportunistic success. <i>Nature Reviews Microbiology</i> , 2011, 9, 749-759.	13.6	814
18	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	9.4	814

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19	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008, 454, 955-960.	13.7	801
20	The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	794
21	Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20117-20122.	3.3	717
22	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	6.0	708
23	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	3.3	652
24	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	3.3	640
25	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	2.1	595
26	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	3.3	595
27	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011, 12, R40.	3.8	594
28	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	6.0	591
29	The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. <i>Nucleic Acids Research</i> , 2014, 42, D26-D31.	6.5	590
30	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	13.7	564
31	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	3.3	563
32	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . <i>Science</i> , 2010, 329, 223-226.	6.0	536
33	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	1.5	532
34	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
35	The Plant Cell Wall "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
36	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490

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37	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . <i>Nature Biotechnology</i> , 2007, 25, 319-326.	9.4	449
38	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	13.7	448
39	The <i>Chlorella variabilis</i> NC64A Genome Reveals Adaptation to Photosymbiosis, Coevolution with Viruses, and Cryptic Sex. <i>Plant Cell</i> , 2010, 22, 2943-2955.	3.1	441
40	The Genome Portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012, 40, D26-D32.	6.5	439
41	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	9.4	428
42	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	3.8	417
43	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	1.5	402
44	The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. <i>Cell</i> , 2010, 140, 631-642.	13.5	399
45	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	13.7	377
46	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	3.3	359
47	Widespread Polycistronic Transcripts in Fungi Revealed by Single-Molecule mRNA Sequencing. <i>PLoS ONE</i> , 2015, 10, e0132628.	1.1	340
48	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
49	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	2.4	329
50	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	9.0	322
51	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	3.3	302
52	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017, 49, 964-968.	9.4	292
53	The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. <i>Genome Biology</i> , 2012, 13, R39.	13.9	289
54	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. <i>Science</i> , 2016, 351, 1192-1195.	6.0	266

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55	Genome Sequencing and Mapping Reveal Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen <i>Phytophthora capsici</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 1350-1360.	1.4	264
56	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	1.2	262
57	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	3.3	259
58	Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 2013, 105, 1350-1373.	0.8	259
59	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	5.8	258
60	Niche of harmful alga <i>Aureococcus anophagefferens</i> revealed through ecogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4352-4357.	3.3	256
61	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	9.4	254
62	Comparative Transcriptome and Secretome Analysis of Wood Decay Fungi <i>Postia placenta</i> and <i>Phanerochaete chrysosporium</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 3599-3610.	1.4	237
63	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	1.5	232
64	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	1.5	226
65	Comparative Genomics of Early-Diverging Mushroom-Forming Fungi Provides Insights into the Origins of Lignocellulose Decay Capabilities. <i>Molecular Biology and Evolution</i> , 2016, 33, 959-970.	3.5	213
66	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	3.5	210
67	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2018, 220, 1161-1171.	3.5	206
68	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	3.4	187
69	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	3.5	185
70	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017, 2, 17087.	5.9	183
71	Evolution and comparative genomics of the most common <i>Trichoderma</i> species. <i>BMC Genomics</i> , 2019, 20, 485.	1.2	181
72	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	1.5	177

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73	Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. <i>Genome Biology and Evolution</i> , 2015, 7, 1590-1601.	1.1	175
74	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
75	The ectomycorrhizal fungus <i>Paxillus involutus</i> converts organic matter in plant litter using a trimmed brown-rot mechanism involving Fenton chemistry. <i>Environmental Microbiology</i> , 2012, 14, 1477-1487.	1.8	173
76	Structural Characterization of the Reaction Pathway in Phosphoserine Phosphatase: Crystallographic Snapshots of Intermediate States. <i>Journal of Molecular Biology</i> , 2002, 319, 421-431.	2.0	170
77	The Fungal Tree of Life: from Molecular Systematics to Genome-Scale Phylogenies. <i>Microbiology Spectrum</i> , 2017, 5, .	1.2	169
78	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	0.8	167
79	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13212-13217.	3.3	163
80	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018, 28, 569-580.	2.4	163
81	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018, 50, 1688-1695.	9.4	160
82	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	13.7	156
83	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	5.8	156
84	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi <i>Armillaria</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1931-1941.	3.4	145
85	Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus <i>Trichoderma</i> from its plant-associated hosts. <i>PLoS Genetics</i> , 2018, 14, e1007322.	1.5	143
86	Transcriptomic response of the mycoparasitic fungus <i>Trichoderma atroviride</i> to the presence of a fungal prey. <i>BMC Genomics</i> , 2009, 10, 567.	1.2	141
87	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011, 12, R20.	13.9	141
88	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	0.9	141
89	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018, 8, 6321.	1.6	138
90	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020, 96, 141-153.	4.5	135

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91	Computational analysis of the <i>Phanerochaete chrysosporium</i> v2.0 genome database and mass spectrometry identification of peptides in ligninolytic cultures reveal complex mixtures of secreted proteins. <i>Fungal Genetics and Biology</i> , 2006, 43, 343-356.	0.9	134
92	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. <i>Nature Communications</i> , 2014, 5, 4471.	5.8	133
93	Comparative genomics of <i>Rhizoglyphus irregularis</i> , <i>R. Âcerebriforme</i> , <i>R. Âdiaphanus</i> and <i>Gigaspora rosea</i> highlights specific genetic features in Glomeromycotina. <i>New Phytologist</i> , 2019, 222, 1584-1598.	3.5	133
94	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16995-17002.	3.3	131
95	Linking secondary metabolites to gene clusters through genome sequencing of six diverse <i>Aspergillus</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E753-E761.	3.3	126
96	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnososa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , 2012, 13, 444.	1.2	125
97	Fungal and plant gene expression in the <i>Tulasnella calospora</i> – <i>Serapias vomeracea</i> symbiosis provides clues about nitrogen pathways in orchid mycorrhizas. <i>New Phytologist</i> , 2017, 213, 365-379.	3.5	125
98	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
99	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
100	Single-cell RNA sequencing reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. <i>PLoS Biology</i> , 2017, 15, e2004050.	2.6	118
101	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. <i>Nature Microbiology</i> , 2021, 6, 499-511.	5.9	116
102	Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7409-7418.	3.3	115
103	Sequencing the fungal tree of life. <i>New Phytologist</i> , 2011, 190, 818-821.	3.5	107
104	Significant Alteration of Gene Expression in Wood Decay Fungi <i>Postia placenta</i> and <i>Phanerochaete chrysosporium</i> by Plant Species. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4499-4507.	1.4	106
105	Endogenous short RNAs generated by Dicer 2 and RNA-dependent RNA polymerase 1 regulate mRNAs in the basal fungus <i>Mucor circinelloides</i> . <i>Nucleic Acids Research</i> , 2010, 38, 5535-5541.	6.5	104
106	The genome of the xerotolerant mold <i>Wallemia sebi</i> reveals adaptations to osmotic stress and suggests cryptic sexual reproduction. <i>Fungal Genetics and Biology</i> , 2012, 49, 217-226.	0.9	103
107	Genomics of wood-degrading fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 82-90.	0.9	103
108	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004, 431, 268-274.	13.7	102

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109	The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. <i>International Journal of Food Microbiology</i> , 2012, 157, 202-209.	2.1	102
110	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018, 3, 1417-1428.	5.9	101
111	Genetic isolation between two recently diverged populations of a symbiotic fungus. <i>Molecular Ecology</i> , 2015, 24, 2747-2758.	2.0	100
112	Functional genomics of lipid metabolism in the oleaginous yeast <i>Rhodospiridium toruloides</i> . <i>ELife</i> , 2018, 7, .	2.8	98
113	The lichen symbiosis re-viewed through the genomes of <i>Cladonia grayi</i> and its algal partner <i>Asterochloris glomerata</i> . <i>BMC Genomics</i> , 2019, 20, 605.	1.2	98
114	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , 2019, 3, 479-490.	3.4	98
115	PhycoCosm, a comparative algal genomics resource. <i>Nucleic Acids Research</i> , 2021, 49, D1004-D1011.	6.5	98
116	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	3.4	95
117	Strand-Specific RNA-Seq Analyses of Fruiting Body Development in <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0141586.	1.1	95
118	Transcription Factor Amr1 Induces Melanin Biosynthesis and Suppresses Virulence in <i>Alternaria brassicicola</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002974.	2.1	91
119	Analysis of the <i>Phlebiopsis gigantea</i> Genome, Transcriptome and Secretome Provides Insight into Its Pioneer Colonization Strategies of Wood. <i>PLoS Genetics</i> , 2014, 10, e1004759.	1.5	90
120	Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. <i>Nature Communications</i> , 2017, 8, 1843.	5.8	85
121	At the nexus of three kingdoms: the genome of the mycorrhizal fungus <i>Gigaspora margarita</i> provides insights into plant, endobacterial and fungal interactions. <i>Environmental Microbiology</i> , 2020, 22, 122-141.	1.8	84
122	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Frontiers in Microbiology</i> , 2015, 6, 978.	1.5	83
123	The Mutualist <i>Laccaria bicolor</i> Expresses a Core Gene Regulon During the Colonization of Diverse Host Plants and a Variable Regulon to Counteract Host-Specific Defenses. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 261-273.	1.4	82
124	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019, 222, 511-525.	3.5	81
125	Comparative genomics, proteomics and transcriptomics give new insight into the exoproteome of the basidiomycete <i>Habelementha cylindrosporum</i> and its involvement in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2015, 208, 1169-1187.	3.5	78
126	Comparative and transcriptional analysis of the predicted secretome in the lignocellulose-degrading basidiomycete fungus <i>Pleurotus ostreatus</i> . <i>Environmental Microbiology</i> , 2016, 18, 4710-4726.	1.8	77

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127	Early Diverging Fungus <i>Mucor circinelloides</i> Lacks Centromeric Histone CENP-A and Displays a Mosaic of Point and Regional Centromeres. <i>Current Biology</i> , 2019, 29, 3791-3802.e6.	1.8	77
128	Combating a Global Threat to a Clonal Crop: Banana Black Sigatoka Pathogen <i>Pseudocercospora fijiensis</i> (Synonym <i>Mycosphaerella fijiensis</i>) Genomes Reveal Clues for Disease Control. <i>PLoS Genetics</i> , 2016, 12, e1005876.	1.5	77
129	A fungal transcription factor essential for starch degradation affects integration of carbon and nitrogen metabolism. <i>PLoS Genetics</i> , 2017, 13, e1006737.	1.5	76
130	The regulatory and transcriptional landscape associated with carbon utilization in a filamentous fungus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6003-6013.	3.3	75
131	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016, 17, 267.	1.2	74
132	Population genomics of picophytoplankton unveils novel chromosome hypervariability. <i>Science Advances</i> , 2017, 3, e1700239.	4.7	73
133	The genome of <i>Xylona heveae</i> provides a window into fungal endophytism. <i>Fungal Biology</i> , 2016, 120, 26-42.	1.1	72
134	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	3.5	72
135	FunGAP: Fungal Genome Annotation Pipeline using evidence-based gene model evaluation. <i>Bioinformatics</i> , 2017, 33, 2936-2937.	1.8	70
136	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887.	5.8	70
137	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.	1.2	69
138	Rediscovery by Whole Genome Sequencing: Classical Mutations and Genome Polymorphisms in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 303-316.	0.8	68
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