Igor Grigoriev

List of Publications by Year
in descending order

327 papers	60,097 citations	2213 99 h-index	1113 231 g-index
371 all docs	371 docs citations	371 times ranked	47137 citing authors

#	Article	IF	Citations
1	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus Lentinula edodes. Journal of Advanced Research, 2022, 38, 91-106.	4.4	16
2	Abscisic acid supports colonization of Eucalyptus grandis roots by the mutualistic ectomycorrhizal fungus Pisolithus microcarpus. New Phytologist, 2022, 233, 966-982.	3.5	12
3	Draft genome sequences of strains CBS6241 and CBS6242 of the basidiomycetous yeastFilobasidium floriforme. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	0
4	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. New Phytologist, 2022, 233, 1317-1330.	3.5	23
5	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. New Phytologist, 2022, 233, 1383-1400.	3.5	19
6	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroomâ€forming fungi. New Phytologist, 2022, 233, 2294-2309.	3.5	21
7	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	124
8	Population genomics of a forest fungus reveals high gene flow and climate adaptation signatures. Molecular Ecology, 2022, 31, 1963-1979.	2.0	3
9	The ectomycorrhizal fungus Pisolithus microcarpus encodes a microRNA involved in cross-kingdom gene silencing during symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	53
10	Kingdom-Wide Analysis of FungalÂProtein-Coding and tRNA Genes Reveals Conserved Patterns of Adaptive Evolution. Molecular Biology and Evolution, 2022, 39, .	3.5	12
11	Detailed analysis of the D-galactose catabolic pathways in Aspergillus niger reveals complexity at both metabolic and regulatory level. Fungal Genetics and Biology, 2022, 159, 103670.	0.9	7
12	Sequencing and Analysis of the Entire Genome of the Mycoparasitic Bioeffector Fungus Trichoderma asperelloides Strain T 203 (Hypocreales). Microbiology Resource Announcements, 2022, 11, e0099521.	0.3	4
13	GalR, GalX and AraR coâ€regulate <scp>d</scp>â€galactose and <scp>l</scp>â€arabinose utilization in Aspergillus nidulans. Microbial Biotechnology, 2022, 15, 1839-1851.	2.0	4
14	Enemy or ally: a genomic approach to elucidate the lifestyle of Phyllosticta citrichinaensis. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	0
15	Genome Sequence and Analysis of the Flavinogenic Yeast Candida membranifaciens IST 626. Journal of Fungi (Basel, Switzerland), 2022, 8, 254.	1.5	1
16	Phylogenomics and Comparative Genomics Highlight Specific Genetic Features in Ganoderma Species. Journal of Fungi (Basel, Switzerland), 2022, 8, 311.	1.5	10
17	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus Aspergillus niger. IScience, 2022, 25, 104065.	1.9	5
18	Comparative genomics reveals a dynamic genome evolution in the ectomycorrhizal milkâ€cap (Lactarius) mushrooms. New Phytologist, 2022, 235, 306-319.	3.5	14

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19	Genomic Signatures of a Major Adaptive Event in the Pathogenic Fungus Melampsora larici-populina. Genome Biology and Evolution, 2022, 14, .	1.1	9
20	Near-Complete Genome Sequence of Zygosaccharomyces rouxii NRRL Y-64007, a Yeast Capable of Growing on Lignocellulosic Hydrolysates. Microbiology Resource Announcements, 2022, , e0005022.	0.3	0
21	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. Microbiome, 2022, 10, 67.	4.9	17
22	High-Quality Draft Nuclear and Mitochondrial Genome Sequence of Fusarium oxysporum f. sp. albedinis strain 9, the Causal Agent of Bayoud Disease on Date Palm. Plant Disease, 2022, 106, 1974-1976.	0.7	3
23	Salinity tolerance mechanisms of an Arctic Pelagophyte using comparative transcriptomic and gene expression analysis. Communications Biology, 2022, 5, .	2.0	7
24	The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom Schizophyllum commune. MBio, 2022, 13, .	1.8	10
25	The role of zinc in the adaptive evolution of polar phytoplankton. Nature Ecology and Evolution, 2022, 6, 965-978.	3.4	14
26	Unique genomic traits for cold adaptation inNaganishia vishniacii, a polyextremophile yeast isolated from Antarctica. FEMS Yeast Research, 2021, 21, .	1.1	14
27	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. Molecular Biology and Evolution, 2021, 38, 1428-1446.	3.5	72
28	Intraâ€species genetic variability drives carbon metabolism and symbiotic host interactions in the ectomycorrhizal fungus Pisolithus microcarpus. Environmental Microbiology, 2021, 23, 2004-2020.	1.8	14
29	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. New Phytologist, 2021, 230, 774-792.	3.5	37
30	Desert truffle genomes reveal their reproductive modes and new insights into plantâ€“fungal interaction and ectendomycorrhizal lifestyle. New Phytologist, 2021, 229, 2917-2932.	3.5	19
31	Comparative genomics of pyrophilous fungi reveals a link between fire events and developmental genes. Environmental Microbiology, 2021, 23, 99-109.	1.8	12
32	PhycoCosm, a comparative algal genomics resource. Nucleic Acids Research, 2021, 49, D1004-D1011.	6.5	98
33	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. ISME Journal, 2021, 15, 421-434.	4.4	46
34	IMITATION SWITCH is required for normal chromatin structure and gene repression in PRC2 target domains. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
35	Draft Genome Sequences of the Black Truffles Tuber brumale Vittad. and Tuber indicum Cook & Massee. Microbiology Resource Announcements, 2021, 10, .	0.3	7
36	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. Environmental Microbiology, 2021, 23, 5716-5732.	1.8	44

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37	Genome-scale phylogenetic analyses confirm Olpidium as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi. Scientific Reports, 2021, 11, 3217.	1.6	24
38	Genome-wide role of codon usage on transcription and identification of potential regulators. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	30
39	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	5.9	116
40	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. MSystems, 2021, 6, .	1.7	33
41	Revisiting a â€˜simpleâ€™ fungal metabolic pathway reveals redundancy, complexity and diversity. Microbial Biotechnology, 2021, 14, 2525-2537.	2.0	10
42	A multi-omic characterization of temperature stress in a halotolerant Scenedesmus strain for algal biotechnology. Communications Biology, 2021, 4, 333.	2.0	22
43	DNA affinity purification sequencing and transcriptional profiling reveal new aspects of nitrogen regulation in a filamentous fungus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
44	Niche differentiation of bacteria and fungi in carbon and nitrogen cycling of different habitats in a temperate coniferous forest: A metaproteomic approach. Soil Biology and Biochemistry, 2021, 155, 108170.	4.2	28
45	Anaerobic gut fungi are an untapped reservoir of natural products. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
46	A single-cell genomics pipeline for environmental microbial eukaryotes. IScience, 2021, 24, 102290.	1.9	7
47	A Multiomic Approach to Understand How Pleurotus eryngii Transforms Non-Woody Lignocellulosic Material. Journal of Fungi (Basel, Switzerland), 2021, 7, 426.	1.5	9
48	Annotated Genome Sequence of the High-Biomass-Producing Yellow-Green Alga Tribonema minus. Microbiology Resource Announcements, 2021, 10, e0032721.	0.3	4
49	Omics analyses and biochemical study of Phlebiopsis gigantea elucidate its degradation strategy of wood extractives. Scientific Reports, 2021, 11, 12528.	1.6	5
50	Chromosome assembled and annotated genome sequence of Aspergillus flavus NRRL 3357. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	19
51	Genomic characterization of three marine fungi, including Emericellopsis atlantica sp. nov. with signatures of a generalist lifestyle and marine biomass degradation. IMA Fungus, 2021, 12, 21.	1.7	23
52	Genome, transcriptome and secretome analyses of the antagonistic, yeast-like fungus Aureobasidium pullulans to identify potential biocontrol genes. Microbial Cell, 2021, 8, 184-202.	1.4	17
53	Diploid genomic architecture of Nitzschia inconspicua, an elite biomass production diatom. Scientific Reports, 2021, 11, 15592.	1.6	12
54	A Genomic Catalog of Stress Response Genes in Anaerobic Fungi for Applications in Bioproduction. Frontiers in Fungal Biology, 2021, 2, .	0.9	1

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55	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. MBio, 2021, 12, e0144221.	1.8	12
56	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. Current Biology, 2021, 31, 3905-3914.e6.	1.8	17
57	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature Communications, 2021, 12, 5483.	5.8	29
58	Cryptic genetic structure and copyâ€number variation in the ubiquitous forest symbiotic fungus <scp>Cenococcum geophilum</scp>. Environmental Microbiology, 2021, 23, 6536-6556.	1.8	5
59	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. Cell Surface, 2021, 7, 100050.	1.5	16
60	Evidence for Lignocellulose-Decomposing Enzymes in the Genome and Transcriptome of the Aquatic Hyphomycete Clavariopsis aquatica. Journal of Fungi (Basel, Switzerland), 2021, 7, 854.	1.5	6
61	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. Frontiers in Microbiology, 2021, 12, 680267.	1.5	3
62	RNA-editing in Basidiomycota, revisited. ISME Communications, 2021, 1, .	1.7	2
63	Genetic determinants of endophytism in the Arabidopsis root mycobiome. Nature Communications, 2021, 12, 7227.	5.8	58
64	Coâ€‘cultivation of the anaerobic fungus Caecomyces churrovis with Methanobacterium bryantii enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. Biotechnology for Biofuels, 2021, 14, 234.	6.2	21
65	At the nexus of three kingdoms: the genome of the mycorrhizal fungus Gigaspora margarita provides insights into plant, endobacterial and fungal interactions. Environmental Microbiology, 2020, 22, 122-141.	1.8	84
66	Inorganic nitrogen availability alters Eucalyptus grandis receptivity to the ectomycorrhizal fungus Pisolithus albus but not symbiotic nitrogen transfer. New Phytologist, 2020, 226, 221-231.	3.5	27
67	Genomic and proteomic biases inform metabolic engineering strategies for anaerobic fungi. Metabolic Engineering Communications, 2020, 10, e00107.	1.9	18
68	An ectomycorrhizal fungus alters sensitivity to jasmonate, salicylate, gibberellin, and ethylene in host roots. Plant, Cell and Environment, 2020, 43, 1047-1068.	2.8	30
69	Fungal ecological strategies reflected in gene transcription â€•a case study of two litter decomposers. Environmental Microbiology, 2020, 22, 1089-1103.	1.8	32
70	Defining the eco-enzymological role of the fungal strain Coniochaeta sp. 2T2.1 in a tripartite lignocellulolytic microbial consortium. FEMS Microbiology Ecology, 2020, 96, .	1.3	12
71	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus Dichomitus squalens. Journal of Biotechnology, 2020, 308, 35-39.	1.9	7
72	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. Nature Communications, 2020, 11, 5125.	5.8	258

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73	Genomic adaptations of the green alga Dunaliella salina to life under high salinity. Algal Research, 2020, 50, 101990.	2.4	18
74	Phylogenomic Analyses of Non-Dikarya Fungi Supports Horizontal Gene Transfer Driving Diversification of Secondary Metabolism in the Amphibian Gastrointestinal Symbiont, Basidiobolus. G3: Genes, Genomes, Genetics, 2020, 10, 3417-3433.	0.8	27
75	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. Fungal Diversity, 2020, 104, 267-289.	4.7	57
76	Survey of Early-Diverging Lineages of Fungi Reveals Abundant and Diverse Mycoviruses. MBio, 2020, 11, .	1.8	32
77	Shed Light in the DaRk LineagES of the Fungal Tree of Lifeâ€"STRES. Life, 2020, 10, 362.	1.1	16
78	The Architecture of Metabolism Maximizes Biosynthetic Diversity in the Largest Class of Fungi. Molecular Biology and Evolution, 2020, 37, 2838-2856.	3.5	33
79	Draft Genome Assemblies of Ionic Liquid-Resistant Yarrowia lipolytica PO1f and Its Superior Evolved Strain, YlCW001. Microbiology Resource Announcements, 2020, 9, .	0.3	11
80	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus Pycnoporus. DNA Research, 2020, 27, .	1.5	32
81	Genome sequencing of Rigidoporus microporus provides insights on genes important for wood decay, latex tolerance and interspecific fungal interactions. Scientific Reports, 2020, 10, 5250.	1.6	16
82	Genome Sequence of the Chestnut Blight Fungus Cryphonectria parasitica EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. Phytopathology, 2020, 110, 1180-1188.	1.1	34
83	A comparative genomics study of 23 Aspergillus species from section Flavi. Nature Communications, 2020, 11, 1106.	5.8	125
84	Identification of a gene encoding the last step of the L-rhamnose catabolic pathway in Aspergillus niger revealed the inducer of the pathway regulator. Microbiological Research, 2020, 234, 126426.	2.5	11
85	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. Studies in Mycology, 2020, 96, 141-153.	4.5	135
86	The regulatory and transcriptional landscape associated with carbon utilization in a filamentous fungus. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6003-6013.	3.3	75
87	Succession of physiological stages hallmarks the transcriptomic response of theÂfungus Aspergillus niger to lignocellulose. Biotechnology for Biofuels, 2020, 13, 69.	6.2	4
88	Multiâ€omic analyses of exogenous nutrient bag decomposition by the black morel Morchella importuna reveal sustained carbon acquisition and transferring. Environmental Microbiology, 2019, 21, 3909-3926.	1.8	54
89	The lichen symbiosis re-viewed through the genomes of Cladonia grayi and its algal partner Asterochloris glomerata. BMC Genomics, 2019, 20, 605.	1.2	98
90	Comparative genomics reveals unique woodâ€decay strategies and fruiting body development in the Schizophyllaceae. New Phytologist, 2019, 224, 902-915.	3.5	53

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91	Cinnamic Acid and Sorbic acid Conversion Are Mediated by the Same Transcriptional Regulator in Aspergillus niger. Frontiers in Bioengineering and Biotechnology, 2019, 7, 249.	2.0	19
92	The White-Rot Basidiomycete Dichomitus squalens Shows Highly Specific Transcriptional Response to Lignocellulose-Related Aromatic Compounds. Frontiers in Bioengineering and Biotechnology, 2019, 7, 229.	2.0	21
93	Early Diverging Fungus Mucor circinelloides Lacks Centromeric Histone CENP-A and Displays a Mosaic of Point and Regional Centromeres. Current Biology, 2019, 29, 3791-3802.e6.	1.8	77
94	Phyllosticta citricarpa and sister species of global importance to Citrus. Molecular Plant Pathology, 2019, 20, 1619-1635.	2.0	43
95	Comprehensive genomic and transcriptomic analysis of polycyclic aromatic hydrocarbon degradation by a mycoremediation fungus, Dentipellis sp. KUC8613. Applied Microbiology and Biotechnology, 2019, 103, 8145-8155.	1.7	41
96	Insights into an unusual Auxiliary Activity 9 family member lacking the histidine brace motif of lytic polysaccharide monooxygenases. Journal of Biological Chemistry, 2019, 294, 17117-17130.	1.6	30
97	Genome expansion by allopolyploidization in the fungal strain Coniochaeta 2T2.1 and its exceptional lignocellulolytic machinery. Biotechnology for Biofuels, 2019, 12, 229.	6.2	12
98	Fungal Endophytes ofPopulus trichocarpaAlter Host Phenotype, Gene Expression, and Rhizobiome Composition. Molecular Plant-Microbe Interactions, 2019, 32, 853-864.	1.4	52
99	The Influence of Contrasting Microbial Lifestyles on the Pre-symbiotic Metabolite Responses of Eucalyptus grandis Roots. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	17
100	Evolution and comparative genomics of the most common Trichoderma species. BMC Genomics, 2019, 20, 485.	1.2	181
101	Mitovirus and Mitochondrial Coding Sequences from Basal Fungus Entomophthora muscae. Viruses, 2019, 11, 351.	1.5	21
102	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus Dichomitus squalens. Microbiology Resource Announcements, 2019, 8, .	0.3	22
103	Deletion of either the regulatory gene ara1 or metabolic gene xki1 in Trichoderma reesei leads to increased CAZyme gene expression on crude plant biomass. Biotechnology for Biofuels, 2019, 12, 81.	6.2	10
104	Broadâ€specificity GH131 Î²â€glucanases are a hallmark of fungi and oomycetes that colonize plants. Environmental Microbiology, 2019, 21, 2724-2739.	1.8	18
105	Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7409-7418.	3.3	115
106	Megaphylogeny resolves global patterns of mushroom evolution. Nature Ecology and Evolution, 2019, 3, 668-678.	3.4	187
107	Tracking of enzymatic biomass deconstruction by fungal secretomes highlights markers of lignocellulose recalcitrance. Biotechnology for Biofuels, 2019, 12, 76.	6.2	25
108	Diversity of cytosine methylation across the fungal tree of life. Nature Ecology and Evolution, 2019, 3, 479-490.	3.4	98

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109	Draft Genome Sequence of the Ectomycorrhizal Ascomycete Sphaerosporella brunnea. Microbiology Resource Announcements, 2019, 8, .	0.3	3
110	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus Dichomitus squalens. Applied and Environmental Microbiology, 2019, 85, .	1.4	21
111	Transcriptome analysis of Aspergillus niger xlnR and xkiA mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. BMC Genomics, 2019, 20, 853.	1.2	5
112	Genome sequencing of evolved aspergilli populations reveals robust genomes, transversions in A. flavus, and sexual aberrancy in non-homologous end-joining mutants. BMC Biology, 2019, 17, 88.	1.7	18
113	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. Genetics, 2019, 213, 1545-1563.	1.2	14
114	Enzymatic Adaptation of Podospora anserina to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. Biotechnology Journal, 2019, 14, 1800185.	1.8	11
115	Comparative genomics of Rhizophagus irregularis, R.Âcerebriforme, R.Âdiaphanus and Gigaspora rosea highlights specific genetic features in Glomeromycotina. New Phytologist, 2019, 222, 1584-1598.	3.5	133
116	Genome-scale phylogenetics reveals a monophyletic Zoopagales (Zoopagomycota, Fungi). Molecular Phylogenetics and Evolution, 2019, 133, 152-163.	1.2	26
117	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. New Phytologist, 2019, 222, 511-525.	3.5	81
118	An analysis of codon bias in six red yeast species. Yeast, 2019, 36, 53-64.	0.8	8
119	Genome-reconstruction for eukaryotes from complex natural microbial communities. Genome Research, 2018, 28, 569-580.	2.4	163
120	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. Scientific Reports, 2018, 8, 6321.	1.6	138
121	Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4325-4333.	3.3	652
122	Talaromyces borbonicus, sp. nov., a novel fungus from biodegraded Arundo donax with potential abilities in lignocellulose conversion. Mycologia, 2018, 110, 316-324.	0.8	13
123	Draft Genome Sequence of the Basidiomycete White-Rot Fungus Phlebia centrifuga. Genome Announcements, 2018, 6, .	0.8	11
124	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont Rhizophagus irregularis. New Phytologist, 2018, 220, 1161-1171.	3.5	206
125	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. New Phytologist, 2018, 217, 1213-1229.	3.5	185
126	Linking secondary metabolites to gene clusters through genome sequencing of six diverse Aspergillus species. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E753-E761.	3.3	126

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127	The fungus that came in from the cold: dry rotâ€™s pre-adapted ability to invade buildings. ISME Journal, 2018, 12, 791-801.	4.4	23
128	Coniella lustricola, a new species from submerged detritus. Mycological Progress, 2018, 17, 191-203.	0.5	8
129	Genomics and Development ofLentinus tigrinus: A White-Rot Wood-Decaying Mushroom with Dimorphic Fruiting Bodies. Genome Biology and Evolution, 2018, 10, 3250-3261.	1.1	53
130	The gold-standard genome of Aspergillus niger NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. Studies in Mycology, 2018, 91, 61-78.	4.5	62
131	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. Nature Ecology and Evolution, 2018, 2, 1956-1965.	3.4	95
132	Genomic and exoproteomic diversity in plant biomass degradation approaches among Aspergilli. Studies in Mycology, 2018, 91, 79-99.	4.5	24
133	Draft Genome Assemblies of Five Robust Yarrowia lipolytica Strains Exhibiting High Lipid Production, Pentose Sugar Utilization, and Sugar Alcohol Secretion from Undetoxified Lignocellulosic Biomass Hydrolysates. Microbiology Resource Announcements, 2018, 7, .	0.3	11
134	Regulation of Yeast-to-Hyphae Transition in Yarrowia lipolytica. MSphere, 2018, 3, .	1.3	35
135	Genomic and Genetic Insights Into a Cosmopolitan Fungus, Paecilomyces variotii (Eurotiales). Frontiers in Microbiology, 2018, 9, 3058.	1.5	35
136	Leveraging single-cell genomics to expand the fungal tree of life. Nature Microbiology, 2018, 3, 1417-1428.	5.9	101
137	Genetic dissection of interspecific differences in yeast thermotolerance. Nature Genetics, 2018, 50, 1501-1504.	9.4	43
138	Dichomitus squalens partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	1.8	36
139	Early Diverging Insect-Pathogenic Fungi of the Order Entomophthorales Possess Diverse and Unique Subtilisin-Like Serine Proteases. G3: Genes, Genomes, Genetics, 2018, 8, 3311-3319.	0.8	20
140	The obligate alkalophilic sodaâ€lake fungus Sodiomyces alkalinus has shifted to a protein diet. Molecular Ecology, 2018, 27, 4808-4819.	2.0	20
141	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. Nature Genetics, 2018, 50, 1688-1695.	9.4	160
142	Catabolic repression in early-diverging anaerobic fungi is partially mediated by natural antisense transcripts. Fungal Genetics and Biology, 2018, 121, 1-9.	0.9	8
143	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. Nature Communications, 2018, 9, 1887.	5.8	70
144	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. Molecular Biology and Evolution, 2018, 35, 1840-1854.	3.5	43

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145	Functional genomics of lipid metabolism in the oleaginous yeast Rhodosporidium toruloides. ELife, 2018, 7, .	2.8	98
146	Massive lateral transfer of genes encoding plant cell wall-degrading enzymes to the mycoparasitic fungus Trichoderma from its plant-associated hosts. PLoS Genetics, 2018, 14, e1007322.	1.5	143
147	Draft Genome Sequence of Tuber borchii Vittad., a Whitish Edible Truffle. Genome Announcements, 2018, 6, .	0.8	20
148	Genome-wide analysis of cytochrome P450s of Trichoderma spp.: annotation and evolutionary relationships. Fungal Biology and Biotechnology, 2018, 5, 12.	2.5	36
149	Integrative visual omics of the white-rot fungus Polyporus brumalis exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. Biotechnology for Biofuels, 2018, 11, 201.	6.2	45
150	Secretome Analysis from the Ectomycorrhizal Ascomycete Cenococcum geophilum. Frontiers in Microbiology, 2018, 9, 141.	1.5	24
151	Genome-Wide Analysis of Corynespora cassiicola Leaf Fall Disease Putative Effectors. Frontiers in Microbiology, 2018, 9, 276.	1.5	58
152	Multi-omic Analyses of Extensively Decayed Pinus contorta Reveal Expression of a Diverse Array of Lignocellulose-Degrading Enzymes. Applied and Environmental Microbiology, 2018, 84, .	1.4	24
153	Fungal Genome Annotation. Methods in Molecular Biology, 2018, 1775, 171-184.	0.4	14
154	Substrate-Specific Differential Gene Expression and RNA Editing in the Brown Rot Fungus Fomitopsis pinicola. Applied and Environmental Microbiology, 2018, 84, .	1.4	22
155	Introduction: Overview of Fungal Genomics. Methods in Molecular Biology, 2018, 1775, 1-7.	0.4	0
156	Genome Sequence of the Plant Growth Promoting Fungus Serendipita vermifera subsp. bescii: The First Native Strain from North America. Phytobiomes Journal, 2018, 2, 62-63.	1.4	20
157	Characterization of four endophytic fungi as potential consolidated bioprocessing hosts for conversion of lignocellulose into advanced biofuels. Applied Microbiology and Biotechnology, 2017, 101, 2603-2618.	1.7	53
158	The ectomycorrhizal basidiomycete Hebeloma cylindrosporum undergoes early waves of transcriptional reprogramming prior to symbiotic structures differentiation. Environmental Microbiology, 2017, 19, 1338-1354.	1.8	22
159	Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540.	13.7	332
160	The draft genome sequence of the ascomycete fungus Penicillium subrubescens reveals a highly enriched content of plant biomass related CAZymes compared to related fungi. Journal of Biotechnology, 2017, 246, 1-3.	1.9	33
161	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
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