

Igor Grigoriev

List of Publications by Year in Descending Order

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

323
papers

44,560
citations

90
h-index

209
g-index

371
ext. papers

54,716
ext. citations

11.2
avg, IF

6.38
L-index

#	Paper	IF	Citations
323	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,	11.5	15
322	The ectomycorrhizal fungus encodes a microRNA involved in cross-kingdom gene silencing during symbiosis.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	4
321	Detailed analysis of the D-galactose catabolic pathways in <i>Aspergillus niger</i> reveals complexity at both metabolic and regulatory level.. <i>Fungal Genetics and Biology</i> , 2022 , 159, 103670	3.9	0
320	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus .. <i>Journal of Advanced Research</i> , 2022 , 38, 91-106	13	2
319	Sequencing and Analysis of the Entire Genome of the Mycoparasitic Bioeffector Fungus <i>Trichoderma asperelloides</i> Strain T 203 (Hypocreales).. <i>Microbiology Resource Announcements</i> , 2022 , 11, e0099521	1.3	0
318	Genome Sequence and Analysis of the Flavinogenic Yeast IST 626.. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8,	5.6	1
317	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus .. <i>IScience</i> , 2022 , 25, 104065	6.1	1
316	Near-Complete Genome Sequence of <i>Zygosaccharomyces rouxii</i> NRRL Y-64007, a Yeast Capable of Growing on Lignocellulosic Hydrolysates.. <i>Microbiology Resource Announcements</i> , 2022 , e0005022	1.3	
315	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans.. <i>Microbiome</i> , 2022 , 10, 67	16.6	2
314	High-Quality Draft Nuclear and Mitochondrial Genome Sequence of <i>f. sp.</i> strain 9, the Causal Agent of Bayoud Disease on Date Palm.. <i>Plant Disease</i> , 2022 , PDIS01220245A	1.5	0
313	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. <i>Nature Communications</i> , 2021 , 12, 7227	17.4	8
312	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021 , 12, 680267	5.7	
311	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2021 ,	9.8	3
310	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyper-diverse lineage of mushroom-forming fungi. <i>New Phytologist</i> , 2021 ,	9.8	0
309	Revisiting a Simple Fungal metabolic pathway reveals redundancy, complexity and diversity. <i>Microbial Biotechnology</i> , 2021 , 14, 2525-2537	6.3	5
308	A multi-omic characterization of temperature stress in a halotolerant <i>Scenedesmus</i> strain for algal biotechnology. <i>Communications Biology</i> , 2021 , 4, 333	6.7	6
307	DNA affinity purification sequencing and transcriptional profiling reveal new aspects of nitrogen regulation in a filamentous fungus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	7

306	Niche differentiation of bacteria and fungi in carbon and nitrogen cycling of different habitats in a temperate coniferous forest: A metaproteomic approach. <i>Soil Biology and Biochemistry</i> , 2021 , 155, 108170	7.5	5
305	Anaerobic gut fungi are an untapped reservoir of natural products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	11
304	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021 , 24, 102290	6.1	3
303	A Multiomic Approach to Understand How Transforms Non-Woody Lignocellulosic Material. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	3
302	Annotated Genome Sequence of the High-Biomass-Producing Yellow-Green Alga <i>Tribonema minus</i> . <i>Microbiology Resource Announcements</i> , 2021 , 10, e0032721	1.3	0
301	Omics analyses and biochemical study of <i>Phlebiopsis gigantea</i> elucidate its degradation strategy of wood extractives. <i>Scientific Reports</i> , 2021 , 11, 12528	4.9	0
300	Chromosome assembled and annotated genome sequence of <i>Aspergillus flavus</i> NRRL 3357. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	2
299	Unique genomic traits for cold adaptation in <i>Naganishia vishniacii</i> , a polyextremophile yeast isolated from Antarctica. <i>FEMS Yeast Research</i> , 2021 , 21,	3.1	3
298	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1428-1446	8.3	22
297	Intra-species genetic variability drives carbon metabolism and symbiotic host interactions in the ectomycorrhizal fungus <i>Pisolithus microcarpus</i> . <i>Environmental Microbiology</i> , 2021 , 23, 2004-2020	5.2	2
296	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021 , 230, 774-792	9.8	9
295	Desert truffle genomes reveal their reproductive modes and new insights into plant-fungal interaction and ectendomycorrhizal lifestyle. <i>New Phytologist</i> , 2021 , 229, 2917-2932	9.8	6
294	Comparative genomics of pyrophilous fungi reveals a link between fire events and developmental genes. <i>Environmental Microbiology</i> , 2021 , 23, 99-109	5.2	3
293	PhycoCosm, a comparative algal genomics resource. <i>Nucleic Acids Research</i> , 2021 , 49, D1004-D1011	20.1	24
292	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021 , 15, 421-434	11.9	17
291	IMITATION SWITCH is required for normal chromatin structure and gene repression in PRC2 target domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	4
290	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021 , 23, 5716-5732	5.2	15
289	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi. <i>Scientific Reports</i> , 2021 , 11, 3217	4.9	9

288	Genome-wide role of codon usage on transcription and identification of potential regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	9
287	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	26.6	23
286	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. <i>MSystems</i> , 2021 , 6,	7.6	10
285	Retracted and Republished from: "Substrate-Specific Differential Gene Expression and RNA Editing in the Brown Rot Fungus ". <i>Applied and Environmental Microbiology</i> , 2021 , 87, e0032921	4.8	2
284	Genomic characterization of three marine fungi, including <i>Emericellopsis atlantica</i> sp. nov. with signatures of a generalist lifestyle and marine biomass degradation. <i>IMA Fungus</i> , 2021 , 12, 21	6.8	5
283	Genome, transcriptome and secretome analyses of the antagonistic, yeast-like fungus to identify potential biocontrol genes. <i>Microbial Cell</i> , 2021 , 8, 184-202	3.9	4
282	Diploid genomic architecture of <i>Nitzschia inconspicua</i> , an elite biomass production diatom. <i>Scientific Reports</i> , 2021 , 11, 15592	4.9	4
281	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. <i>MBio</i> , 2021 , 12, e0144221	7.8	0
280	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , 2021 , 31, 3905-3914.e6	6.3	3
279	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021 , 12, 5483	17.4	3
278	Cryptic genetic structure and copy-number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . <i>Environmental Microbiology</i> , 2021 , 23, 6536-6556	5.2	0
277	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. <i>Cell Surface</i> , 2021 , 7, 100050	4.8	5
276	Co-cultivation of the anaerobic fungus <i>Caecomyces churrovii</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. <i>Biotechnology for Biofuels</i> , 2021 , 14, 234	7.8	3
275	The Architecture of Metabolism Maximizes Biosynthetic Diversity in the Largest Class of Fungi. <i>Molecular Biology and Evolution</i> , 2020 , 37, 2838-2856	8.3	11
274	Draft Genome Assemblies of Ionic Liquid-Resistant <i>Yarrowia lipolytica</i> PO1f and Its Superior Evolved Strain, YLCW001. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	6
273	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020 , 27,	4.5	13
272	Genome sequencing of <i>Rigidoporus microporus</i> provides insights on genes important for wood decay, latex tolerance and interspecific fungal interactions. <i>Scientific Reports</i> , 2020 , 10, 5250	4.9	7
271	Genome Sequence of the Chestnut Blight Fungus EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 2020 , 110, 1180-1188	3.8	17

270	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020 , 11, 1106	17.4	54
269	Identification of a gene encoding the last step of the L-rhamnose catabolic pathway in <i>Aspergillus niger</i> revealed the inducer of the pathway regulator. <i>Microbiological Research</i> , 2020 , 234, 126426	5.3	6
268	101 genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020 , 96, 141-153	22.2	63
267	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	11.5	25
266	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	5.2	27
265	Inorganic nitrogen availability alters <i>Eucalyptus grandis</i> receptivity to the ectomycorrhizal fungus <i>Pisolithus albus</i> but not symbiotic nitrogen transfer. <i>New Phytologist</i> , 2020 , 226, 221-231	9.8	6
264	Genomic and proteomic biases inform metabolic engineering strategies for anaerobic fungi. <i>Metabolic Engineering Communications</i> , 2020 , 10, e00107	6.5	10
263	An ectomycorrhizal fungus alters sensitivity to jasmonate, salicylate, gibberellin, and ethylene in host roots. <i>Plant, Cell and Environment</i> , 2020 , 43, 1047-1068	8.4	12
262	Fungal ecological strategies reflected in gene transcription - a case study of two litter decomposers. <i>Environmental Microbiology</i> , 2020 , 22, 1089-1103	5.2	9
261	Defining the eco-enzymological role of the fungal strain <i>Coniochaeta</i> sp. 2T2.1 in a tripartite lignocellulolytic microbial consortium. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	6
260	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus <i>Dichomitus squalens</i> . <i>Journal of Biotechnology</i> , 2020 , 308, 35-39	3.7	4
259	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020 , 11, 5125	17.4	86
258	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020 , 50, 101990	5	5
257	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
256	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , 2020 , 104, 267-289	17.6	18
255	Survey of Early-Diverging Lineages of Fungi Reveals Abundant and Diverse Mycoviruses. <i>MBio</i> , 2020 , 11,	7.8	9
254	Shed Light in the DaRk LineagES of the Fungal Tree of Life-STRES. <i>Life</i> , 2020 , 10,	3	4
253	Succession of physiological stages hallmarks the transcriptomic response of the fungus to lignocellulose. <i>Biotechnology for Biofuels</i> , 2020 , 13, 69	7.8	2

252	Comprehensive genomic and transcriptomic analysis of polycyclic aromatic hydrocarbon degradation by a mycoremediation fungus, <i>Dentipellis</i> sp. KUC8613. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 8145-8155	5.7	23
251	Insights into an unusual Auxiliary Activity 9 family member lacking the histidine brace motif of lytic polysaccharide monoxygenases. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17117-17130	5.4	19
250	Genome expansion by allopolyploidization in the fungal strain 2T2.1 and its exceptional lignocellulolytic machinery. <i>Biotechnology for Biofuels</i> , 2019 , 12, 229	7.8	5
249	Fungal Endophytes of Alter Host Phenotype, Gene Expression, and Rhizobiome Composition. <i>Molecular Plant-Microbe Interactions</i> , 2019 , 32, 853-864	3.6	33
248	The Influence of Contrasting Microbial Lifestyles on the Pre-symbiotic Metabolite Responses of <i>Eucalyptus grandis</i> Roots. <i>Frontiers in Ecology and Evolution</i> , 2019 , 7,	3.7	7
247	Evolution of substrate-specific gene expression and RNA editing in brown rot wood-decaying fungi. <i>ISME Journal</i> , 2019 , 13, 1391-1403	11.9	10
246	Evolution and comparative genomics of the most common <i>Trichoderma</i> species. <i>BMC Genomics</i> , 2019 , 20, 485	4.5	93
245	Mitovirus and Mitochondrial Coding Sequences from Basal Fungus. <i>Viruses</i> , 2019 , 11,	6.2	13
244	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	8
243	Deletion of either the regulatory gene or metabolic gene in leads to increased CAZyme gene expression on crude plant biomass. <i>Biotechnology for Biofuels</i> , 2019 , 12, 81	7.8	7
242	Broad-specificity GH131 β glucanases are a hallmark of fungi and oomycetes that colonize plants. <i>Environmental Microbiology</i> , 2019 , 21, 2724-2739	5.2	8
241	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	11.5	62
240	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019 , 3, 668-678	12.3	98
239	Tracking of enzymatic biomass deconstruction by fungal secretomes highlights markers of lignocellulose recalcitrance. <i>Biotechnology for Biofuels</i> , 2019 , 12, 76	7.8	14
238	Multi-omic analyses of exogenous nutrient bag decomposition by the black morel <i>Morchella importuna</i> reveal sustained carbon acquisition and transferring. <i>Environmental Microbiology</i> , 2019 , 21, 3909-3926	5.2	27
237	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	4.5	54
236	Comparative genomics reveals unique wood-decay strategies and fruiting body development in the Schizophyllaceae. <i>New Phytologist</i> , 2019 , 224, 902-915	9.8	30
235	Cinnamic Acid and Sorbic acid Conversion Are Mediated by the Same Transcriptional Regulator in. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 249	5.8	13

234	The White-Rot Basidiomycete Shows Highly Specific Transcriptional Response to Lignocellulose-Related Aromatic Compounds. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 229	5.8	14
233	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	6.3	48
232	<i>Phyllosticta citricarpa</i> and sister species of global importance to Citrus. <i>Molecular Plant Pathology</i> , 2019 , 20, 1619-1635	5.7	26
231	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , 2019 , 3, 479-490	12.3	57
230	Draft Genome Sequence of the Ectomycorrhizal Ascomycete. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
229	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	10
228	Transcriptome analysis of <i>Aspergillus niger</i> xlnR and xkiA mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. <i>BMC Genomics</i> , 2019 , 20, 853	4.5	4
227	Genome sequencing of evolved aspergilli populations reveals robust genomes, transversions in <i>A. flavus</i> , and sexual aberrancy in non-homologous end-joining mutants. <i>BMC Biology</i> , 2019 , 17, 88	7.3	9
226	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. <i>Genetics</i> , 2019 , 213, 1545-1563	4	5
225	Enzymatic Adaptation of <i>Podospora anserina</i> to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. <i>Biotechnology Journal</i> , 2019 , 14, e1800185	5.6	8
224	Comparative genomics of <i>Rhizophagus irregularis</i> , <i>R. terrebriforme</i> , <i>R. diaphanus</i> and <i>Gigaspora rosea</i> highlights specific genetic features in Glomeromycotina. <i>New Phytologist</i> , 2019 , 222, 1584-1598	9.8	58
223	Genome-scale phylogenetics reveals a monophyletic Zoopagales (Zoopagomycota, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2019 , 133, 152-163	4.1	13
222	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019 , 222, 511-525	9.8	37
221	An analysis of codon bias in six red yeast species. <i>Yeast</i> , 2019 , 36, 53-64	3.4	6
220	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018 , 28, 569-580	9.7	71
219	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018 , 8, 6321	4.9	84
218	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	11.5	334
217	<i>Talaromyces borbonicus</i> , sp. nov., a novel fungus from biodegraded <i>Arundo donax</i> with potential abilities in lignocellulose conversion. <i>Mycologia</i> , 2018 , 110, 316-324	2.4	8

216	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018 , 6,		4
215	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2018 , 220, 1161-1171	9.8	107
214	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018 , 217, 1213-1229	9.8	99
213	Linking secondary metabolites to gene clusters through genome sequencing of six diverse species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E753-E761	11.5	78
212	The fungus that came in from the cold: dry rot's pre-adapted ability to invade buildings. <i>ISME Journal</i> , 2018 , 12, 791-801	11.9	12
211	<i>Coniella lustricola</i> , a new species from submerged detritus. <i>Mycological Progress</i> , 2018 , 17, 191-203	1.9	3
210	Draft Genome Sequence of <i>Tuber borchii</i> Vittad., a Whitish Edible Truffle. <i>Genome Announcements</i> , 2018 , 6,		14
209	Genome-wide analysis of cytochrome P450s of spp.: annotation and evolutionary relationships. <i>Fungal Biology and Biotechnology</i> , 2018 , 5, 12	7.5	19
208	Integrative visual omics of the white-rot fungus exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. <i>Biotechnology for Biofuels</i> , 2018 , 11, 201	7.8	18
207	Secretome Analysis from the Ectomycorrhizal Ascomycete. <i>Frontiers in Microbiology</i> , 2018 , 9, 141	5.7	16
206	Genome-Wide Analysis of Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018 , 9, 276	5.7	32
205	Multi-omic Analyses of Extensively Decayed <i>Pinus contorta</i> Reveal Expression of a Diverse Array of Lignocellulose-Degrading Enzymes. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	16
204	Fungal Genome Annotation. <i>Methods in Molecular Biology</i> , 2018 , 1775, 171-184	1.4	10
203	Substrate-Specific Differential Gene Expression and RNA Editing in the Brown Rot Fungus <i>Fomitopsis pinicola</i> . <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	17
202	Introduction: Overview of Fungal Genomics. <i>Methods in Molecular Biology</i> , 2018 , 1775, 1-7	1.4	
201	Genome Sequence of the Plant Growth Promoting Fungus <i>Serendipita vermifera</i> subsp. <i>bescii</i> : The First Native Strain from North America. <i>Phytobiomes Journal</i> , 2018 , 2, 62-63	4.8	11
200	Genomics and Development of <i>Lentinus tigrinus</i> : A White-Rot Wood-Decaying Mushroom with Dimorphic Fruiting Bodies. <i>Genome Biology and Evolution</i> , 2018 , 10, 3250-3261	3.9	20
199	The gold-standard genome of NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. <i>Studies in Mycology</i> , 2018 , 91, 61-78	22.2	33

198	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1956-1965	12.3	52
197	Genomic and exoproteomic diversity in plant biomass degradation approaches among <i>Aspergilli</i> . <i>Studies in Mycology</i> , 2018 , 91, 79-99	22.2	12
196	Draft Genome Assemblies of Five Robust <i>Yarrowia lipolytica</i> Strains Exhibiting High Lipid Production, Pentose Sugar Utilization, and Sugar Alcohol Secretion from Undetoxified Lignocellulosic Biomass Hydrolysates. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	7
195	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018 , 3,	5	20
194	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). <i>Frontiers in Microbiology</i> , 2018 , 9, 3058	5.7	23
193	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018 , 3, 1417-1428	6.6	60
192	Genetic dissection of interspecific differences in yeast thermotolerance. <i>Nature Genetics</i> , 2018 , 50, 1501-1504	17	
191	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018 , 20, 4141-4156	5.2	19
190	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
189	The obligate alkalophilic soda-lake fungus <i>Sodiomyces alkalinus</i> has shifted to a protein diet. <i>Molecular Ecology</i> , 2018 , 27, 4808-4819	5.7	10
188	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	36.3	100
187	Catabolic repression in early-diverging anaerobic fungi is partially mediated by natural antisense transcripts. <i>Fungal Genetics and Biology</i> , 2018 , 121, 1-9	3.9	6
186	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018 , 9, 1887	17.4	38
185	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade <i>Ustilaginomycotina</i> . <i>Molecular Biology and Evolution</i> , 2018 , 35, 1840-1854	8.3	28
184	Functional genomics of lipid metabolism in the oleaginous yeast. <i>ELife</i> , 2018 , 7,	8.9	49
183	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	6	71
182	Characterization of four endophytic fungi as potential consolidated bioprocessing hosts for conversion of lignocellulose into advanced biofuels. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 2603-2618	5.7	41
181	The ectomycorrhizal basidiomycete <i>Hebeloma cylindrosporum</i> undergoes early waves of transcriptional reprogramming prior to symbiotic structures differentiation. <i>Environmental Microbiology</i> , 2017 , 19, 1338-1354	5.2	12

180	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017 , 541, 536-540	50.4	226
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30	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . <i>Nature Biotechnology</i> , 2007 , 25, 319-26	44.5	393
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13	Genomes to Proteomes21-45		
12	The architecture of metabolism maximizes biosynthetic diversity in the largest class of fungi		1
11	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi		1
10	Early diverging insect pathogenic fungi of the order Entomophthorales possess diverse and unique subtilisin-like serine proteases		1
9	Genome-reconstruction for eukaryotes from complex natural microbial communities		5
8	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber		1
7	Metagenome-assembled genomes of phytoplankton communities across the Arctic Circle		6
6	Transcriptomic atlas of mushroom development highlights an independent origin of complex multicellularity		5
5	The genome of <i>Auriculariopsis ampla</i> sheds light on fruiting body development and wood-decay of bark-inhabiting fungi		2
4	Shallow Genome Sequencing for Phylogenomics of Mycorrhizal Fungi from Endangered Orchids		4
3	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome		1
2	Evolutionary priming and transition to the ectomycorrhizal habit in an iconic lineage of mushroom-forming fungi: is preadaptation a requirement?		2
1	Co-cultivation of the anaerobic fungus <i>Caecomyces churovis</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules		1

