

Igor Grigoriev

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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 genome of black cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006 , 313, 1596-604	33.3	3205
322	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009 , 457, 551-6	50.4	2200
321	The <i>Chlamydomonas</i> genome reveals the evolution of key animal and plant functions. <i>Science</i> , 2007 , 318, 245-50	33.3	1969
320	The <i>Physcomitrella</i> genome reveals evolutionary insights into the conquest of land by plants. <i>Science</i> , 2008 , 319, 64-9	33.3	1419
319	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008 , 453, 1064-71	50.4	1266
318	Sea anemone genome reveals ancestral eumetazoan gene repertoire and genomic organization. <i>Science</i> , 2007 , 317, 86-94	33.3	1204
317	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008 , 456, 239-44	50.4	1200
316	The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. <i>Science</i> , 2012 , 336, 1715-9	33.3	1129
315	The ecoresponsive genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011 , 331, 555-61	33.3	924
314	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea jecorina</i>). <i>Nature Biotechnology</i> , 2008 , 26, 553-60	44.5	920
313	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008 , 451, 783-8	50.4	850
312	<i>Phytophthora</i> genome sequences uncover evolutionary origins and mechanisms of pathogenesis. <i>Science</i> , 2006 , 313, 1261-6	33.3	827
311	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008 , 452, 88-92	50.4	823
310	MycCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014 , 42, D699-704	20.1	768
309	A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data. <i>Mycologia</i> , 2016 , 108, 1028-1046	2.4	684
308	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008 , 454, 955-60	50.4	681
307	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011 , 43, 476-81	36.3	638

306	The Selaginella genome identifies genetic changes associated with the evolution of vascular plants. <i>Science</i> , 2011 , 332, 960-3	33.3	622
305	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015 , 47, 410-5	36.3	601
304	Trichoderma: the genomics of opportunistic success. <i>Nature Reviews Microbiology</i> , 2011 , 9, 749-59	22.2	595
303	The genome of the Western clawed frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010 , 328, 633-6	33.3	579
302	Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009 , 324, 268-72	33.3	503
301	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, 20117-22	11.5	499
300	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, 7705-10	11.5	482
299	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, 9166-71	11.5	479
298	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, 1954-9	11.5	479
297	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, 9923-8	11.5	461
296	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011 , 12, R40	18.3	448
295	Genomic analysis of organismal complexity in the multicellular green alga <i>Volvox carteri</i> . <i>Science</i> , 2010 , 329, 223-6	33.3	446
294	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013 , 493, 526-31	50.4	424
293	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. <i>Science</i> , 2011 , 333, 762-5	33.3	417
292	The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. <i>Nucleic Acids Research</i> , 2014 , 42, D26-31	20.1	401
291	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	6	401
290	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
289	Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. <i>PLoS Pathogens</i> , 2012 , 8, e1003037	7.6	387

288	The <i>Chlorella variabilis</i> NC64A genome reveals adaptation to photosymbiosis, coevolution with viruses, and cryptic sex. <i>Plant Cell</i> , 2010 , 22, 2943-55	11.6	384
287	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010 , 28, 957-63	44.5	381
286	The genome portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012 , 40, D26-32	20.1	359
285	Pan genome of the phytoplankton <i>Emiliania underpins</i> its global distribution. <i>Nature</i> , 2013 , 499, 209-13	50.4	356
284	The genome of <i>Naegleria gruberi</i> illuminates early eukaryotic versatility. <i>Cell</i> , 2010 , 140, 631-42	56.2	346
283	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
282	The genome of <i>Nectria haematococca</i> : contribution of supernumerary chromosomes to gene expansion. <i>PLoS Genetics</i> , 2009 , 5, e1000618	6	329
281	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011 , 29, 922-7	44.5	324
280	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012 , 492, 59-65	50.4	304
279	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, 17501-6	11.5	277
278	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011 , 21, 885-97	9.7	266
277	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	18.3	261
276	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007 , 4, 495-500	21.6	257
275	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017 , 541, 536-540	50.4	226
274	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008 , 26, 1029-34	44.5	226
273	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, 5458-63	11.5	225
272	Widespread Polycistronic Transcripts in Fungi Revealed by Single-Molecule mRNA Sequencing. <i>PLoS ONE</i> , 2015 , 10, e0132628	3.7	218
271	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, 3599-610	4.8	213

270	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9882-7	11.5	212
269	The genome of the polar eukaryotic microalga <i>Coccomyxa subellipsoidea</i> reveals traits of cold adaptation. <i>Genome Biology</i> , 2012 , 13, R39	18.3	211
268	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, 4352-7	11.5	205
267	Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 2013 , 105, 1350-73	2.4	199
266	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	4.5	193
265	The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporium</i> reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. <i>PLoS Genetics</i> , 2012 , 8, e1003088	6	189
264	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, 1350-60	3.6	183
263	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017 , 49, 964-968	36.3	181
262	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. <i>Science</i> , 2016 , 351, 1192-5	33.3	179
261	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	9.8	168
260	Comparative genome structure, secondary metabolite, and effector coding capacity across <i>Cochliobolus</i> pathogens. <i>PLoS Genetics</i> , 2013 , 9, e1003233	6	161
259	Structural characterization of the reaction pathway in phosphoserine phosphatase: crystallographic "snapshots" of intermediate states. <i>Journal of Molecular Biology</i> , 2002 , 319, 421-31	6.5	157
258	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, 1477-87	5.2	149
257	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, 959-70	8.3	131
256	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, 13212-7	11.5	131
255	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004 , 432, 988-94	50.4	129
254	Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. <i>Genome Biology and Evolution</i> , 2015 , 7, 1590-601	3.9	126
253	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, 343-56	3.9	125

252	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016 , 26, 1577-1584	6.3	119
251	Transcriptomic response of the mycoparasitic fungus <i>Trichoderma atroviride</i> to the presence of a fungal prey. <i>BMC Genomics</i> , 2009 , 10, 567	4.5	118
250	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011 , 12, R20	18.3	117
249	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017 , 2, 17087	26.6	111
248	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	3.2	111
247	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
246	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	3.9	107
245	The Fungal Tree of Life: from Molecular Systematics to Genome-Scale Phylogenies. <i>Microbiology Spectrum</i> , 2017 , 5,	8.9	104
244	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016 , 12, e1006108	6	103
243	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
242	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
241	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019 , 3, 668-678	12.3	98
240	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016 , 7, 12662	17.4	97
239	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosae</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	4.5	97
238	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, 4499-507	4.8	96
237	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, 16995-7002	11.5	94
236	Evolution and comparative genomics of the most common <i>Trichoderma</i> species. <i>BMC Genomics</i> , 2019 , 20, 485	4.5	93
235	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. <i>Nature Communications</i> , 2014 , 5, 4471	17.4	92

234	Sequencing the fungal tree of life. <i>New Phytologist</i> , 2011 , 190, 818-821	9.8	91
233	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004 , 431, 268-74	50.4	86
232	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
231	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	12.3	85
230	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, 202-9	5.8	85
229	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
228	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, 217-26	3.9	83
227	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
226	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, 5535-41	20.1	77
225	Genetic isolation between two recently diverged populations of a symbiotic fungus. <i>Molecular Ecology</i> , 2015 , 24, 2747-58	5.7	75
224	Genomics of wood-degrading fungi. <i>Fungal Genetics and Biology</i> , 2014 , 72, 82-90	3.9	74
223	Single-cell RNA sequencing reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. <i>PLoS Biology</i> , 2017 , 15, e2004050	9.7	72
222	Genome-reconstruction for eukaryotes from complex natural microbial communities. <i>Genome Research</i> , 2018 , 28, 569-580	9.7	71
221	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
220	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	9.8	69
219	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	6	67
218	101 genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020 , 96, 141-153	22.2	63
217	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

216	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
215	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018 , 3, 1417-1428	6.6	60
214	Comparative genomics of <i>Rhizophagus irregularis</i> , <i>R. cerebriforme</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
213	Transcription factor Amr1 induces melanin biosynthesis and suppresses virulence in <i>Alternaria brassicicola</i> . <i>PLoS Pathogens</i> , 2012 , 8, e1002974	7.6	57
212	Diversity of cytosine methylation across the fungal tree of life. <i>Nature Ecology and Evolution</i> , 2019 , 3, 479-490	12.3	57
211	The genome of <i>Xylona heveae</i> provides a window into fungal endophytism. <i>Fungal Biology</i> , 2016 , 120, 26-42	2.8	55
210	Strand-Specific RNA-Seq Analyses of Fruiting Body Development in <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , 2015 , 10, e0141586	3.7	55
209	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020 , 11, 1106	17.4	54
208	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
207	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Frontiers in Microbiology</i> , 2015 , 6, 978	5.7	54
206	Rediscovery by Whole Genome Sequencing: Classical Mutations and Genome Polymorphisms in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2011 , 1, 303-16	3.2	54
205	Genomics and Transcriptomics Analyses of the Oil-Accumulating Basidiomycete Yeast <i>Trichosporon oleaginosus</i> : Insights into Substrate Utilization and Alternative Evolutionary Trajectories of Fungal Mating Systems. <i>MBio</i> , 2015 , 6, e00918	7.8	52
204	Enhanced degradation of softwood versus hardwood by the white-rot fungus <i>Pycnoporus coccineus</i> . <i>Biotechnology for Biofuels</i> , 2015 , 8, 216	7.8	52
203	Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. <i>BMC Genomics</i> , 2016 , 17, 267	4.5	52
202	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1956-1965	12.3	52
201	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	5.2	50
200	Functional genomics of lipid metabolism in the oleaginous yeast. <i>ELife</i> , 2018 , 7,	8.9	49
199	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

198	Genetic Bases of Fungal White Rot Wood Decay Predicted by Phylogenomic Analysis of Correlated Gene-Phenotype Evolution. <i>Molecular Biology and Evolution</i> , 2017 , 34, 35-44	8.3	48
197	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 3451-6	11.5	47
196	Population genomics of picophytoplankton unveils novel chromosome hypervariability. <i>Science Advances</i> , 2017 , 3, e1700239	14.3	46
195	Genomic adaptations of the halophilic Dead Sea filamentous fungus <i>Eurotium rubrum</i> . <i>Nature Communications</i> , 2014 , 5, 3745	17.4	45
194	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, 261-73	3.6	44
193	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	6	44
192	Comparative genomics, proteomics and transcriptomics give new insight into the exoproteome of the basidiomycete <i>Hebeloma cylindrosporum</i> and its involvement in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2015 , 208, 1169-87	9.8	43
191	The GC-rich mitochondrial and plastid genomes of the green alga <i>Coccomyxa</i> give insight into the evolution of organelle DNA nucleotide landscape. <i>PLoS ONE</i> , 2011 , 6, e23624	3.7	43
190	Lipid metabolic changes in an early divergent fungus govern the establishment of a mutualistic symbiosis with endobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 15102-15107	11.5	43
189	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
188	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> . <i>New Phytologist</i> , 2014 , 202, 554-564	9.8	41
187	Phylogenetic, genomic organization and expression analysis of hydrophobin genes in the ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> . <i>Fungal Genetics and Biology</i> , 2012 , 49, 199-209	3.9	40
186	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016 , 7, 238	5.7	40
185	Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. <i>Nature Communications</i> , 2017 , 8, 1843	17.4	38
184	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018 , 9, 1887	17.4	38
183	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019 , 222, 511-525	9.8	37
182	Transposable element dynamics among asymptomatic and ectomycorrhizal <i>Amanita</i> fungi. <i>Genome Biology and Evolution</i> , 2014 , 6, 1564-78	3.9	35
181	Fungal-specific transcription factor AbPf2 activates pathogenicity in <i>Alternaria brassicicola</i> . <i>Plant Journal</i> , 2013 , 75, 498-514	6.9	35

180	Fungal Endophytes of Alter Host Phenotype, Gene Expression, and Rhizobiome Composition. <i>Molecular Plant-Microbe Interactions</i> , 2019 , 32, 853-864	3.6	33
179	The central role of selenium in the biochemistry and ecology of the harmful pelagophyte, <i>Aureococcus anophagefferens</i> . <i>ISME Journal</i> , 2013 , 7, 1333-43	11.9	33
178	Comparative Analysis of Secretome Profiles of Manganese(II)-Oxidizing Ascomycete Fungi. <i>PLoS ONE</i> , 2016 , 11, e0157844	3.7	33
177	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
176	FunGAP: Fungal Genome Annotation Pipeline using evidence-based gene model evaluation. <i>Bioinformatics</i> , 2017 , 33, 2936-2937	7.2	32
175	Genome-Wide Analysis of Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018 , 9, 276	5.7	32
174	Duplications and losses in gene families of rust pathogens highlight putative effectors. <i>Frontiers in Plant Science</i> , 2014 , 5, 299	6.2	32
173	Exploiting proteomic data for genome annotation and gene model validation in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2009 , 10, 61	4.5	32
172	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
171	Degradation of Bunker C Fuel Oil by White-Rot Fungi in Sawdust Cultures Suggests Potential Applications in Bioremediation. <i>PLoS ONE</i> , 2015 , 10, e0130381	3.7	30
170	Detection of protein fold similarity based on correlation of amino acid properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 14318-23	11.5	29
169	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1840-1854	8.3	28
168	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
167	Comparative Genomics Analysis of <i>Trichoderma reesei</i> Strains. <i>Industrial Biotechnology</i> , 2013 , 9, 352-367	1.3	27
166	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
165	A fungal transcription factor essential for starch degradation affects integration of carbon and nitrogen metabolism. <i>PLoS Genetics</i> , 2017 , 13, e1006737	6	26
164	<i>Phyllosticta citricarpa</i> and sister species of global importance to Citrus. <i>Molecular Plant Pathology</i> , 2019 , 20, 1619-1635	5.7	26
163	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

162	Genome sequencing of the <i>Trichoderma reesei</i> QM9136 mutant identifies a truncation of the transcriptional regulator XYR1 as the cause for its cellulase-negative phenotype. <i>BMC Genomics</i> , 2015 , 16, 326	4.5	25
161	A zinc-finger-family transcription factor, AbVf19, is required for the induction of a gene subset important for virulence in <i>Alternaria brassicicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012 , 25, 443-52	3.6	24
160	Visual Comparative Omics of Fungi for Plant Biomass Deconstruction. <i>Frontiers in Microbiology</i> , 2016 , 7, 1335	5.7	24
159	PhycoCosm, a comparative algal genomics resource. <i>Nucleic Acids Research</i> , 2021 , 49, D1004-D1011	20.1	24
158	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
157	Expanding genomics of mycorrhizal symbiosis. <i>Frontiers in Microbiology</i> , 2014 , 5, 582	5.7	23
156	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
155	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). <i>Frontiers in Microbiology</i> , 2018 , 9, 3058	5.7	23
154	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1428-1446	8.3	22
153	The draft genome sequence of the ascomycete fungus <i>Penicillium subrubescens</i> reveals a highly enriched content of plant biomass related CAZymes compared to related fungi. <i>Journal of Biotechnology</i> , 2017 , 246, 1-3	3.7	21
152	Conserved genomic collinearity as a source of broadly applicable, fast evolving, markers to resolve species complexes: A case study using the lichen-forming genus <i>Peltigera</i> section <i>Polydactylon</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017 , 117, 10-29	4.1	21
151	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
150	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018 , 3,	5	20
149	Insights into an unusual Auxiliary Activity 9 family member lacking the histidine brace motif of lytic polysaccharide monooxygenases. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17117-17130	5.4	19
148	Genome-wide analysis of cytochrome P450s of spp.: annotation and evolutionary relationships. <i>Fungal Biology and Biotechnology</i> , 2018 , 5, 12	7.5	19
147	<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
146	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
145	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , 2020 , 104, 267-289	17.6	18

144	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
143	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
142	Full Genome of <i>Phialocephala scopiformis</i> DAOMC 229536, a Fungal Endophyte of Spruce Producing the Potent Anti-Insectan Compound Rugulosin. <i>Genome Announcements</i> , 2016 , 4,		17
141	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021 , 15, 421-434	11.9	17
140	Genetic dissection of interspecific differences in yeast thermotolerance. <i>Nature Genetics</i> , 2018 , 50, 1501-1504	16.0	17
139	Secretome Analysis from the Ectomycorrhizal Ascomycete. <i>Frontiers in Microbiology</i> , 2018 , 9, 141	5.7	16
138	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
137	The Fungal Tree of Life: From Molecular Systematics to Genome-Scale Phylogenies 2017 , 1-34		16
136	Fungal Genomic Annotation. <i>Applied Mycology and Biotechnology</i> , 2006 , 123-142		16
135	Draft Genome Sequence of <i>Microdochium bolleyi</i> , a Dark Septate Fungal Endophyte of Beach Grass. <i>Genome Announcements</i> , 2016 , 4,		16
134	Improved High-Quality Draft Genome Sequence of the Eurypsychrophile <i>Rhodotorula</i> sp. JG1b, Isolated from Permafrost in the Hyperarid Upper-Elevation McMurdo Dry Valleys, Antarctica. <i>Genome Announcements</i> , 2016 , 4,		16
133	The transcription factor PDR-1 is a multi-functional regulator and key component of pectin deconstruction and catabolism in. <i>Biotechnology for Biofuels</i> , 2017 , 10, 149	7.8	15
132	Fungal Genomics. <i>Advances in Botanical Research</i> , 2014 , 1-52	2.2	15
131	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
130	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021 , 23, 5716-5732	5.2	15
129	Tracking of enzymatic biomass deconstruction by fungal secretomes highlights markers of lignocellulose recalcitrance. <i>Biotechnology for Biofuels</i> , 2019 , 12, 76	7.8	14
128	Draft Genome Sequence of <i>Tuber borchii</i> Vittad., a Whitish Edible Truffle. <i>Genome Announcements</i> , 2018 , 6,		14
127	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

126	Mitovirus and Mitochondrial Coding Sequences from Basal Fungus. <i>Viruses</i> , 2019 , 11,	6.2	13
125	Genome sequence of a white rot fungus <i>Schizophora paradoxa</i> KUC8140 for wood decay and mycoremediation. <i>Journal of Biotechnology</i> , 2015 , 211, 42-3	3.7	13
124	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020 , 27,	4.5	13
123	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
122	Expression of CAZymes is determined by compositional changes in wheat straw generated by hydrothermal or ionic liquid pretreatments. <i>Biotechnology for Biofuels</i> , 2017 , 10, 35	7.8	13
121	Genome-scale phylogenetics reveals a monophyletic Zoopagales (Zoopagomycota, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2019 , 133, 152-163	4.1	13
120	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
119	Draft Genome Sequence of <i>Neurospora crassa</i> Strain FGSC 73. <i>Genome Announcements</i> , 2015 , 3,		12
118	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
117	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
116	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
115	Comparative Genomics of the Ectomycorrhizal Sister Species and (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type Locus. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1775-1789	3.2	11
114	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
113	Comparative genomics of <i>Coniophora olivacea</i> reveals different patterns of genome expansion in Boletales. <i>BMC Genomics</i> , 2017 , 18, 883	4.5	11
112	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
111	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
110	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
109	Draft Genome Sequence of <i>Coniochaeta ligniaria</i> NRRL 30616, a Lignocellulolytic Fungus for Bioabatement of Inhibitors in Plant Biomass Hydrolysates. <i>Genome Announcements</i> , 2017 , 5,		10

108	Fungal Genome Annotation. <i>Methods in Molecular Biology</i> , 2018 , 1775, 171-184	1.4	10
107	Horizontal transfer of carbohydrate metabolism genes into ectomycorrhizal <i>Amanita</i> . <i>New Phytologist</i> , 2015 , 205, 1552-1564	9.8	10
106	Genomic and proteomic biases inform metabolic engineering strategies for anaerobic fungi. <i>Metabolic Engineering Communications</i> , 2020 , 10, e00107	6.5	10
105	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
104	Genetics of mating in members of the Chaetomiaceae as revealed by experimental and genomic characterization of reproduction in <i>Myceliophthora heterothallica</i> . <i>Fungal Genetics and Biology</i> , 2016 , 86, 9-19	3.9	10
103	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	10
102	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. <i>MSystems</i> , 2021 , 6,	7.6	10
101	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
100	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , 2016 , 4,		9
99	Draft genome sequence of a monokaryotic model brown-rot fungus SB12. <i>Genomics Data</i> , 2017 , 14, 21-23		9
98	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951. <i>Genome Announcements</i> , 2014 , 2,		9
97	Interhelical contacts determining the architecture of alpha-helical globular proteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 1994 , 12, 559-72	3.6	9
96	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
95	Survey of Early-Diverging Lineages of Fungi Reveals Abundant and Diverse Mycoviruses. <i>MBio</i> , 2020 , 11,	7.8	9
94	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
93	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021 , 230, 774-792	9.8	9
92	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
91	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

90	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
89	Broad-specificity GH131 Eglucanases are a hallmark of fungi and oomycetes that colonize plants. <i>Environmental Microbiology</i> , 2019 , 21, 2724-2739	5.2	8
88	<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
87	Transcriptional responses of the <i>Bdtf1</i> -deletion mutant to the phytoalexin brassinin in the necrotrophic fungus <i>Alternaria brassicicola</i> . <i>Molecules</i> , 2014 , 19, 10717-32	4.8	8
86	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. <i>Nature Communications</i> , 2021 , 12, 7227	17.4	8
85	The mitochondrial genome of the ethanol-metabolizing, wine cellar mold <i>Zasmidium cellare</i> is the smallest for a filamentous ascomycete. <i>Fungal Biology</i> , 2016 , 120, 961-974	2.8	8
84	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
83	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
82	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
81	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
80	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
79	Genome Sequences of Industrially Relevant <i>Saccharomyces cerevisiae</i> Strain M3707, Isolated from a Sample of Distillers Yeast and Four Haploid Derivatives. <i>Genome Announcements</i> , 2013 , 1,		7
78	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
77	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
76	The complete mitochondrial genome of the conifer needle endophyte, <i>Phialocephala scopiformis</i> DAOMC 229536 confirms evolutionary division within the fungal <i>Phialocephala fortinii</i> s.l. <i>Phialocephala appalanata</i> species complex. <i>Fungal Biology</i> , 2017 , 121, 212-221	2.8	6
75	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
74	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
73	Metagenome-assembled genomes of phytoplankton communities across the Arctic Circle		6

72	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
71	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
70	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
69	An analysis of codon bias in six red yeast species. <i>Yeast</i> , 2019 , 36, 53-64	3.4	6
68	Desert truffle genomes reveal their reproductive modes and new insights into plant-fungal interaction and ectomycorrhizal lifestyle. <i>New Phytologist</i> , 2021 , 229, 2917-2932	9.8	6
67	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
66	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
65	Sequence-based detection of distantly related proteins with the same fold. <i>Protein Engineering, Design and Selection</i> , 2001 , 14, 455-8	1.9	5
64	Genome-reconstruction for eukaryotes from complex natural microbial communities		5
63	Transcriptomic atlas of mushroom development highlights an independent origin of complex multicellularity		5
62	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , 2020 , 50, 101990	5	5
61	Revisiting a simple fungal metabolic pathway reveals redundancy, complexity and diversity. <i>Microbial Biotechnology</i> , 2021 , 14, 2525-2537	6.3	5
60	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
59	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. <i>Genetics</i> , 2019 , 213, 1545-1563	4	5
58	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
57	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
56	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018 , 6,		4
55	Simulated annealing for alpha-helical protein folding: searches in vicinity of the "molten globule" state. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998 , 16, 115-22	3.6	4

54	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
53	Reverse transcriptase and intron number evolution. <i>Stem Cell Investigation</i> , 2014 , 1, 17	5.1	4
52	Fungal Genomics for Energy and Environment. <i>Soil Biology</i> , 2013 , 11-27	1	4
51	Shallow Genome Sequencing for Phylogenomics of Mycorrhizal Fungi from Endangered Orchids		4
50	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
49	Shed Light in the DaRk LineagES of the Fungal Tree of Life-STRES. <i>Life</i> , 2020 , 10,	3	4
48	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
47	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
46	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
45	Diploid genomic architecture of <i>Nitzschia inconspicua</i> , an elite biomass production diatom. <i>Scientific Reports</i> , 2021 , 11, 15592	4.9	4
44	<i>Coniella lustricola</i> , a new species from submerged detritus. <i>Mycological Progress</i> , 2018 , 17, 191-203	1.9	3
43	The homothallic mating-type locus of the conifer needle endophyte <i>Phialocephala scopiformis</i> DAOMC 229536 (order Helotiales). <i>Fungal Biology</i> , 2017 , 121, 1011-1024	2.8	3
42	Target selection for structural genomics: a single genome approach. <i>OMICS A Journal of Integrative Biology</i> , 2002 , 6, 349-62	3.8	3
41	Alternative splicing acting as a bridge in evolution. <i>Stem Cell Investigation</i> , 2015 , 2, 19	5.1	3
40	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2021 ,	9.8	3
39	Proteomics for validation of automated gene model predictions. <i>Methods in Molecular Biology</i> , 2009 , 492, 447-52	1.4	3
38	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021 , 24, 102290	6.1	3
37	A Multiomic Approach to Understand How Transforms Non-Woody Lignocellulosic Material. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	3

36	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
35	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
34	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , 2021 , 31, 3905-3914.e6	6.3	3
33	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021 , 12, 5483	17.4	3
32	Co-cultivation of the anaerobic fungus <i>Caecomyces churovis</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
31	A Changing Landscape of Fungal Genomics 2013 , 1-20		2
30	The genome of <i>Auriculariopsis ampla</i> sheds light on fruiting body development and wood-decay of bark-inhabiting fungi		2
29	Chromosome assembled and annotated genome sequence of <i>Aspergillus flavus</i> NRRL 3357. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	2
28	Succession of physiological stages hallmarks the transcriptomic response of the fungus to lignocellulose. <i>Biotechnology for Biofuels</i> , 2020 , 13, 69	7.8	2
27	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
26	Evolutionary priming and transition to the ectomycorrhizal habit in an iconic lineage of mushroom-forming fungi: is preadaptation a requirement?		2
25	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
24	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
23	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans.. <i>Microbiome</i> , 2022 , 10, 67	16.6	2
22	The architecture of metabolism maximizes biosynthetic diversity in the largest class of fungi		1
21	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi		1
20	Early diverging insect pathogenic fungi of the order Entomophthorales possess diverse and unique subtilisin-like serine proteases		1
19	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber		1

18	Genetic determinants of endophytism in the Arabidopsis root mycobiome		1
17	Draft Genome Sequence of the Ectomycorrhizal Ascomycete. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
16	Co-cultivation of the anaerobic fungus <i>Caecomyces churrovis</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules		1
15	Genome Sequence and Analysis of the Flavinogenic Yeast IST 626.. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8,	5.6	1
14	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus .. <i>IScience</i> , 2022 , 25, 104065	6.1	1
13	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
12	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
11	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
10	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
9	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. <i>MBio</i> , 2021 , 12, e0144221	7.8	0
8	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
7	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
6	High-Quality Draft Nuclear and Mitochondrial Genome Sequence of <i>f. sp. strain 9</i> , the Causal Agent of Bayoud Disease on Date Palm.. <i>Plant Disease</i> , 2022 , PDIS01220245A	1.5	0
5	Introduction: Overview of Fungal Genomics. <i>Methods in Molecular Biology</i> , 2018 , 1775, 1-7	1.4	
4	Genomes to Proteomes21-45		
3	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , 2021 , 12, 680267	5.7	
2	Genome Portal, Joint Genome Institute 2013 , 1-10		
1	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	

