

Kerrie Barry

List of Publications by Year in descending order

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Version: 2024-02-01

200
papers

31,509
citations

8180

76
h-index

5120

166
g-index

233
all docs

233
docs citations

233
times ranked

31693
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
2	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	12.6	1,479
3	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
4	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	27.8	1,181
5	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
6	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	28.9	973
7	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	21.4	870
8	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
9	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
10	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	17.5	634
11	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	12.6	629
12	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	4.7	595
13	The Plant Cell Wall's "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
14	Insights into the Maize Pan-Genome and Pan-Transcriptome. <i>Plant Cell</i> , 2014, 26, 121-135.	6.6	498
15	Genomic Islands and the Ecology and Evolution of <i>Prochlorococcus</i> . <i>Science</i> , 2006, 311, 1768-1770.	12.6	437
16	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.	8.8	417
17	Insights into the Evolution of Mitochondrial Genome Size from Complete Sequences of <i>Citrullus lanatus</i> and <i>Cucurbita pepo</i> (Cucurbitaceae). <i>Molecular Biology and Evolution</i> , 2010, 27, 1436-1448.	8.9	400
18	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , 2006, 443, 950-955.	27.8	396

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19	Sequencing genomes from single cells by polymerase cloning. <i>Nature Biotechnology</i> , 2006, 24, 680-686.	17.5	388
20	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377
21	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , 2010, 4, 660-672.	9.8	332
22	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	27.8	332
23	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	19.0	322
24	Horizontal Transfer of Entire Genomes via Mitochondrial Fusion in the Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1468-1473.	12.6	322
25	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	7.1	302
26	Extensive gene content variation in the <i>Brachypodium distachyon</i> pan-genome correlates with population structure. <i>Nature Communications</i> , 2017, 8, 2184.	12.8	269
27	Origins and Recombination of the Bacterial-Sized Multichromosomal Mitochondrial Genome of Cucumber. <i>Plant Cell</i> , 2011, 23, 2499-2513.	6.6	266
28	Anchoring and ordering <i>NGS</i> contig assemblies by population sequencing (<i>POPSEQ</i>). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
29	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.	2.8	262
30	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	7.1	259
31	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	12.8	258
32	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , 2015, 16, 26.	8.8	256
33	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	7.1	253
34	Adaptation to herbivory by the Tammar wallaby includes bacterial and glycoside hydrolase profiles different from other herbivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14793-14798.	7.1	234
35	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	7.1	233
36	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232

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37	An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.	3.5	213
38	Comparative Genomics of Early-Diverging Mushroom-Forming Fungi Provides Insights into the Origins of Lignocellulose Decay Capabilities. <i>Molecular Biology and Evolution</i> , 2016, 33, 959-970.	8.9	213
39	Marker-free carotenoid-enriched rice generated through targeted gene insertion using CRISPR-Cas9. <i>Nature Communications</i> , 2020, 11, 1178.	12.8	204
40	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	7.8	187
41	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	7.3	185
42	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017, 2, 17087.	13.3	183
43	Isolation of Succinivibrionaceae Implicated in Low Methane Emissions from Tammar Wallabies. <i>Science</i> , 2011, 333, 646-648.	12.6	179
44	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13212-13217.	7.1	163
45	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.	21.4	160
46	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	12.8	156
47	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , 2017, 19, 2964-2983.	3.8	154
48	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.	7.8	145
49	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
50	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.	3.5	143
51	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011, 12, R20.	9.6	141
52	The Sequences of 1504 Mutants in the Model Rice Variety Kitaake Facilitate Rapid Functional Genomic Studies. <i>Plant Cell</i> , 2017, 29, 1218-1231.	6.6	138
53	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018, 8, 6321.	3.3	138
54	101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , 2020, 96, 141-153.	7.2	135

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55	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16995-17002.	7.1	131
56	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. ISME Journal, 2012, 6, 1688-1701.	9.8	126
57	Linking secondary metabolites to gene clusters through genome sequencing of six diverse <i>Aspergillus</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E753-E761.	7.1	126
58	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnososa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444.	2.8	125
59	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. PLoS ONE, 2013, 8, e73827.	2.5	125
60	Fungal and plant gene expression in the <i>Tulasnella calospora</i> – <i>Serapias vomeracea</i> symbiosis provides clues about nitrogen pathways in orchid mycorrhizas. New Phytologist, 2017, 213, 365-379.	7.3	125
61	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. Nature Communications, 2020, 11, 1106.	12.8	125
62	Community-wide plasmid gene mobilization and selection. ISME Journal, 2013, 7, 1173-1186.	9.8	124
63	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. ELife, 2018, 7, .	6.0	120
64	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	13.3	116
65	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. Plant Journal, 2018, 95, 168-182.	5.7	115
66	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.	7.1	115
67	Construction and comparison of three reference-quality genome assemblies for soybean. Plant Journal, 2019, 100, 1066-1082.	5.7	113
68	Genome-wide association studies and expression-based quantitative trait loci analyses reveal roles of HCT2 in caffeoylquinic acid biosynthesis and its regulation by defense-responsive transcription factors in <i>Populus</i> . New Phytologist, 2018, 220, 502-516.	7.3	112
69	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. Nature Biotechnology, 2020, 38, 1203-1210.	17.5	103
70	The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. International Journal of Food Microbiology, 2012, 157, 202-209.	4.7	102
71	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . Nature Communications, 2018, 9, 5213.	12.8	101
72	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. Applied and Environmental Microbiology, 2013, 79, 3770-3778.	3.1	98

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73	Peizizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018, 2, 1956-1965.	7.8	95
74	Strand-Specific RNA-Seq Analyses of Fruiting Body Development in <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , 2015, 10, e0141586.	2.5	95
75	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	7.8	94
76	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , 2011, 12, 334.	2.8	90
77	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.	3.5	90
78	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga <i>Dunaliella salina</i> Strain CCAP19/18. <i>Genome Announcements</i> , 2017, 5, .	0.8	83
79	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , 2019, 222, 511-525.	7.3	81
80	Genome diversity in <i>Brachypodium distachyon</i> : deep sequencing of highly diverse inbred lines. <i>Plant Journal</i> , 2014, 79, 361-374.	5.7	80
81	Genome-Wide Sequencing of 41 Rice (<i>Oryza sativa</i> L.) Mutated Lines Reveals Diverse Mutations Induced by Fast-Neutron Irradiation. <i>Molecular Plant</i> , 2016, 9, 1078-1081.	8.3	78
82	Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. <i>PLoS Genetics</i> , 2018, 14, e1007267.	3.5	78
83	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , 2019, 19, 45.	3.6	77
84	A fungal transcription factor essential for starch degradation affects integration of carbon and nitrogen metabolism. <i>PLoS Genetics</i> , 2017, 13, e1006737.	3.5	76
85	QTL × environment interactions underlie adaptive divergence in switchgrass across a large latitudinal gradient. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12933-12941.	7.1	75
86	PEATmoss (<i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	5.7	74
87	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , 2020, 21, 38.	8.8	74
88	A new reference genome for <i>Sorghum bicolor</i> reveals high levels of sequence similarity between sweet and grain genotypes: implications for the genetics of sugar metabolism. <i>BMC Genomics</i> , 2019, 20, 420.	2.8	73
89	Feathermoss and epiphytic <i>Nostoc</i> cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. <i>ISME Journal</i> , 2017, 11, 2821-2833.	9.8	69
90	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68

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91	Gradual polyploid genome evolution revealed by pan-genomic analysis of <i>Brachypodium hybridum</i> and its diploid progenitors. <i>Nature Communications</i> , 2020, 11, 3670.	12.8	67
92	The genetics of divergence and reproductive isolation between ecotypes of <i>Panicum hallii</i> . <i>New Phytologist</i> , 2015, 205, 402-414.	7.3	65
93	A Genome-Wide Scan for Evidence of Selection in a Maize Population Under Long-Term Artificial Selection for Ear Number. <i>Genetics</i> , 2014, 196, 829-840.	2.9	63
94	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , 2017, 3, 17054.	9.3	63
95	Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant-pathogen interactions in a tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11573-11578.	7.1	61
96	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59
97	Genome-Wide Analysis of <i>Corynespora cassicola</i> Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018, 9, 276.	3.5	58
98	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. <i>Nature Communications</i> , 2021, 12, 7227.	12.8	58
99	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , 2020, 104, 267-289.	12.3	57
100	Comparative Genomics in Switchgrass Using 61,585 High-Quality Expressed Sequence Tags. <i>Plant Genome</i> , 2008, 1, .	2.8	57
101	Genome-wide associations with flowering time in switchgrass using exome capture sequencing data. <i>New Phytologist</i> , 2017, 213, 154-169.	7.3	56
102	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.	3.6	53
103	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
104	Blueprint for a pop-up SARS-CoV-2 testing lab. <i>Nature Biotechnology</i> , 2020, 38, 791-797.	17.5	50
105	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , 2015, 84, 800-815.	5.7	47
106	Facile Recovery of Individual High-Molecular-Weight, Low-Copy-Number Natural Plasmids for Genomic Sequencing. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4899-4906.	3.1	44
107	Complete genome sequence of <i>Rhodospirillum rubrum</i> type strain (S1T). <i>Standards in Genomic Sciences</i> , 2011, 4, 293-302.	1.5	44
108	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	3.8	44

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109	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. <i>Molecular Biology and Evolution</i> , 2018, 35, 1840-1854.	8.9	43
110	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , 2019, 5, 676-680.	9.3	42
111	Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. <i>Genetics</i> , 2014, 198, 409-421.	2.9	38
112	Shared Genomic Regions Between Derivatives of a Large Segregating Population of Maize Identified Using Bulk Segregant Analysis Sequencing and Traditional Linkage Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1593-1602.	1.8	37
113	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , 2019, 12, 180069.	2.8	37
114	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021, 230, 774-792.	7.3	37
115	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018, 3, .	2.9	35
116	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). <i>Frontiers in Microbiology</i> , 2018, 9, 3058.	3.5	35
117	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	2.8	35
118	Complete genome sequence of <i>Methanoculleus marisnigri</i> Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , 2009, 1, 189-196.	1.5	34
119	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic <i>Neocallimastigomycota</i> Fungus. <i>MSystems</i> , 2021, 6, .	3.8	33
120	Fungal ecological strategies reflected in gene transcription – a case study of two litter decomposers. <i>Environmental Microbiology</i> , 2020, 22, 1089-1103.	3.8	32
121	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	3.4	32
122	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , 2018, 11, 170.	6.2	30
123	Ancient polymorphisms contribute to genome-wide variation by long-term balancing selection and divergent sorting in <i>Boechera stricta</i> . <i>Genome Biology</i> , 2019, 20, 126.	8.8	30
124	An ectomycorrhizal fungus alters sensitivity to jasmonate, salicylate, gibberellin, and ethylene in host roots. <i>Plant, Cell and Environment</i> , 2020, 43, 1047-1068.	5.7	30
125	Complete genome sequence of <i>Methanocorpusculum labreanum</i> type strain Z. <i>Standards in Genomic Sciences</i> , 2009, 1, 197-203.	1.5	29
126	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	12.8	29

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127	Draft Genome Sequence of <i>Microdochium bolleyi</i> , a Dark Septate Fungal Endophyte of Beach Grass. <i>Genome Announcements</i> , 2016, 4, .	0.8	27
128	Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , 2019, 3, 195-207.	4.9	27
129	The complete genome sequence of <i>Staphylothermus marinus</i> reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. <i>BMC Genomics</i> , 2009, 10, 145.	2.8	26
130	Secretome Analysis from the Ectomycorrhizal Ascomycete <i>Cenococcum geophilum</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 141.	3.5	24
131	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, .	3.1	24
132	Genetic dissection of natural variation in oilseed traits of camelina by whole-genome resequencing and QTL mapping. <i>Plant Genome</i> , 2021, 14, e20110.	2.8	24
133	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.	9.8	23
134	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	22
135	Draft Nuclear Genome Sequence of the Liquid Hydrocarbon-Accumulating Green Microalga <i>Botryococcus braunii</i> Race B (Showa). <i>Genome Announcements</i> , 2017, 5, .	0.8	21
136	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	5.5	21
137	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
138	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroom-forming fungi. <i>New Phytologist</i> , 2022, 233, 2294-2309.	7.3	21
139	Cocultivation of the anaerobic fungus <i>Caecomyces churrovis</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.	6.2	21
140	Comparative genomics of <i>Coniophora olivacea</i> reveals different patterns of genome expansion in Boletales. <i>BMC Genomics</i> , 2017, 18, 883.	2.8	20
141	Draft Genome Sequence of <i>Tuber borchii</i> Vittad., a Whitish Edible Truffle. <i>Genome Announcements</i> , 2018, 6, .	0.8	20
142	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.	2.7	20
143	Draft genome sequence of a monokaryotic model brown-rot fungus <i>Postia</i> (<i>Rhodonia</i>) <i>placenta</i> SB12. <i>Genomics Data</i> , 2017, 14, 21-23.	1.3	19
144	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.	7.3	19

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145	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	7.3	19
146	Complete genome sequence of <i>Candidatus Ruthia magnifica</i> . <i>Standards in Genomic Sciences</i> , 2010, 3, 163-173.	1.5	18
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157	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , 2021, 31, 3905-3914.e6.	3.9	17
158	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. <i>Microbiome</i> , 2022, 10, 67.	11.1	17
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160	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , 2021, 105, 93-107.	5.7	16
161	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus <i>Lentinula edodes</i> . <i>Journal of Advanced Research</i> , 2022, 38, 91-106.	9.5	16
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