

# Kerrie Barry

## 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.

198 papers	21,500 citations	63 h-index	145 g-index
233 ext. papers	27,968 ext. citations	12.4 avg, IF	5.78 L-index

#	Paper	IF	Citations
198	Population genomics provides insights into the genetic basis of adaptive evolution in the mushroom-forming fungus .. <i>Journal of Advanced Research</i> , <b>2022</b> , 38, 91-106	13	2
197	A generalist-specialist trade-off between switchgrass cytotypes impacts climate adaptation and geographic range.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119, e2118879119	11.5	1
196	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans.. <i>Microbiome</i> , <b>2022</b> , 10, 67	16.6	2
195	High-Quality Draft Nuclear and Mitochondrial Genome Sequence of f. sp. strain 9, the Causal Agent of Bayoud Disease on Date Palm.. <i>Plant Disease</i> , <b>2022</b> , PDIS01220245A	1.5	0
194	Genetic determinants of endophytism in the Arabidopsis root mycobiome. <i>Nature Communications</i> , <b>2021</b> , 12, 7227	17.4	8
193	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 680267	5.7	
192	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyper-diverse lineage of mushroom-forming fungi. <i>New Phytologist</i> , <b>2021</b> ,	9.8	0
191	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , <b>2021</b> , 24, 102290	6.1	3
190	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , <b>2021</b> , 31, 799-810	9.7	4
189	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , <b>2021</b> , 4, 537	6.7	4
188	Launching a saliva-based SARS-CoV-2 surveillance testing program on a university campus. <i>PLoS ONE</i> , <b>2021</b> , 16, e0251296	3.7	7
187	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	15
186	Genetic dissection of natural variation in oilseed traits of camelina by whole-genome resequencing and QTL mapping. <i>Plant Genome</i> , <b>2021</b> , 14, e20110	4.4	7
185	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , <b>2021</b> , 14, e20114	4.4	1
184	Unique genomic traits for cold adaptation in <i>Naganishia vishniacii</i> , a polyextremophile yeast isolated from Antarctica. <i>FEMS Yeast Research</i> , <b>2021</b> , 21,	3.1	3
183	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , <b>2021</b> , 230, 774-792	9.8	9
182	Desert truffle genomes reveal their reproductive modes and new insights into plant-fungal interaction and ectomycorrhizal lifestyle. <i>New Phytologist</i> , <b>2021</b> , 229, 2917-2932	9.8	6

181	Single-parent expression drives dynamic gene expression complementation in maize hybrids. <i>Plant Journal</i> , <b>2021</b> , 105, 93-107	6.9	5
180	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , <b>2021</b> , 590, 438-444	5.4	42
179	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 5716-5732	5.2	15
178	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. <i>Nature Microbiology</i> , <b>2021</b> , 6, 499-511	26.6	23
177	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. <i>MSystems</i> , <b>2021</b> , 6,	7.6	10
176	Integrative genomics reveals paths to sex dimorphism in <i>Salix purpurea</i> L. <i>Horticulture Research</i> , <b>2021</b> , 8, 170	7.7	1
175	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. <i>MBio</i> , <b>2021</b> , 12, e0144221	7.8	0
174	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , <b>2021</b> , 31, 3905-3914.e6	6.3	3
173	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , <b>2021</b> , 12, 5483	17.4	3
172	Cryptic genetic structure and copy-number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . <i>Environmental Microbiology</i> , <b>2021</b> , 23, 6536-6556	5.2	0
171	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> , <b>2021</b> , 14, 234	7.8	3
170	Draft Genome Assemblies of Ionic Liquid-Resistant <i>Yarrowia lipolytica</i> PO1f and Its Superior Evolved Strain, YLCW001. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	6
169	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , <b>2020</b> , 27,	4.5	13
168	Blueprint for a pop-up SARS-CoV-2 testing lab. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 791-797	44.5	36
167	Modulation of Plant and Fungal Gene Expression Upon Cd Exposure and Symbiosis in Ericoid Mycorrhizal. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 341	5.7	7
166	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> , <b>2020</b> , 10, 5250	4.9	7
165	Marker-free carotenoid-enriched rice generated through targeted gene insertion using CRISPR-Cas9. <i>Nature Communications</i> , <b>2020</b> , 11, 1178	17.4	111
164	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , <b>2020</b> , 11, 1106	17.4	54

163	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , <b>2020</b> , 21, 38	18.3	39
162	Natural Variation in Lignin and Pectin Biosynthesis-Related Genes in Switchgrass ( <i>Panicum virgatum</i> L.) and Association of SNP Variants with Dry Matter Traits. <i>Bioenergy Research</i> , <b>2020</b> , 13, 79-99	3.1	0
161	101 genomes: A test case for predicting lifestyles and emergence of pathogens. <i>Studies in Mycology</i> , <b>2020</b> , 96, 141-153	22.2	63
160	Overexpression of a Prefoldin $\beta$ subunit gene reduces biomass recalcitrance in the bioenergy crop <i>Populus</i> . <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 859-871	11.6	9
159	An ectomycorrhizal fungus alters sensitivity to jasmonate, salicylate, gibberellin, and ethylene in host roots. <i>Plant, Cell and Environment</i> , <b>2020</b> , 43, 1047-1068	8.4	12
158	PEATmoss (Physcomitrella Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , <b>2020</b> , 102, 165-177	6.9	21
157	Fungal ecological strategies reflected in gene transcription - a case study of two litter decomposers. <i>Environmental Microbiology</i> , <b>2020</b> , 22, 1089-1103	5.2	9
156	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> , <b>2020</b> , 96,	4.3	6
155	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> , <b>2020</b> , 21, 259	18.3	31
154	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , <b>2020</b> , 11, 5125	17.4	86
153	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1203-1210	44.5	43
152	Genomic adaptations of the green alga <i>Dunaliella salina</i> to life under high salinity. <i>Algal Research</i> , <b>2020</b> , 50, 101990	5	5
151	Gradual polyploid genome evolution revealed by pan-genomic analysis of <i>Brachypodium hybridum</i> and its diploid progenitors. <i>Nature Communications</i> , <b>2020</b> , 11, 3670	17.4	22
150	Resolving the Mortierellaceae phylogeny through synthesis of multi-gene phylogenetics and phylogenomics. <i>Fungal Diversity</i> , <b>2020</b> , 104, 267-289	17.6	18
149	Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids. <i>Plant Physiology</i> , <b>2020</b> , 182, 318-331	6.6	8
148	Succession of physiological stages hallmarks the transcriptomic response of the fungus to lignocellulose. <i>Biotechnology for Biofuels</i> , <b>2020</b> , 13, 69	7.8	2
147	Genome expansion by allopolyploidization in the fungal strain 2T2.1 and its exceptional lignocellulolytic machinery. <i>Biotechnology for Biofuels</i> , <b>2019</b> , 12, 229	7.8	5
146	Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop <i>Populus</i> . <i>Sustainable Energy and Fuels</i> , <b>2019</b> , 3, 195-207	5.8	18

145	Genome-wide association analysis of stalk biomass and anatomical traits in maize. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 45	5.3	39
144	Ancient polymorphisms contribute to genome-wide variation by long-term balancing selection and divergent sorting in <i>Boechera stricta</i> . <i>Genome Biology</i> , <b>2019</b> , 20, 126	18.3	15
143	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> , <b>2019</b> , 20, 420	4.5	33
142	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> , <b>2019</b> , 116, 12933-12941	11.5	36
141	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	8
140	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> , <b>2019</b> , 116, 7409-7418	11.5	62
139	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 668-678	12.3	98
138	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , <b>2019</b> , 100, 1066-1082	6.9	32
137	Multiple Maize Reference Genomes Impact the Identification of Variants by Genome-Wide Association Study in a Diverse Inbred Panel. <i>Plant Genome</i> , <b>2019</b> , 12, 180069	4.4	10
136	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , <b>2019</b> , 5, 676-680	11.5	18
135	Draft Genome Sequence of the Ectomycorrhizal Ascomycete. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1
134	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> , <b>2019</b> , 17, 88	7.3	9
133	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , <b>2019</b> , 20, 905	4.5	21
132	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. <i>Genetics</i> , <b>2019</b> , 213, 1545-1563	4	5
131	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , <b>2019</b> , 222, 511-525	9.8	37
130	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , <b>2018</b> , 8, 6321	4.9	84
129	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , <b>2018</b> , 95, 168-182	6.9	40
128	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , <b>2018</b> , 217, 1213-1229	9.8	99

127	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> , <b>2018</b> , 115, E753-E761	11.5	78
126	The fungus that came in from the cold: dry rot's pre-adapted ability to invade buildings. <i>ISME Journal</i> , <b>2018</b> , 12, 791-801	11.9	12
125	Annotation of the Corymbia terpene synthase gene family shows broad conservation but dynamic evolution of physical clusters relative to Eucalyptus. <i>Heredity</i> , <b>2018</b> , 121, 87-104	3.6	10
124	Draft Genome Sequence of <i>Tuber borchii</i> Vittad., a Whitish Edible Truffle. <i>Genome Announcements</i> , <b>2018</b> , 6,		14
123	A Variable Polyglutamine Repeat Affects Subcellular Localization and Regulatory Activity of a ANGUSTIFOLIA Protein. <i>G3: Genes, Genomes, Genetics</i> , <b>2018</b> , 8, 2631-2641	3.2	6
122	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 170	7.8	22
121	Secretome Analysis from the Ectomycorrhizal Ascomycete. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 141	5.7	16
120	Genome-Wide Analysis of Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 276	5.7	32
119	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> . <i>New Phytologist</i> , <b>2018</b> , 220, 502-516	9.8	51
118	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> , <b>2018</b> , 84,	4.8	16
117	Natural variation in genes potentially involved in plant architecture and adaptation in switchgrass ( <i>Panicum virgatum</i> L.). <i>BMC Evolutionary Biology</i> , <b>2018</b> , 18, 91	3	6
116	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> , <b>2018</b> , 14, e1007267	6	34
115	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> , <b>2018</b> , 2, 62-63	4.8	11
114	The genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , <b>2018</b> , 7,	8.9	63
113	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 1956-1965	12.3	52
112	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> , <b>2018</b> , 7,	1.3	7
111	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , <b>2018</b> , 9, 5213	17.4	51
110	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , <b>2018</b> , 3,	5	20

109	Population genomics and climate adaptation of a C4 perennial grass, <i>Panicum hallii</i> (Poaceae). <i>BMC Genomics</i> , <b>2018</b> , 19, 792	4.5	2
108	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 3058	5.7	23
107	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section Nigri. <i>Nature Genetics</i> , <b>2018</b> , 50, 1688-1695	36.3	100
106	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> , <b>2018</b> , 115, 11573-11578	11.5	33
105	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , <b>2018</b> , 11, 170055	4.4	16
104	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 1840-1854	8.3	28
103	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> , <b>2018</b> , 14, e1007322	6	71
102	Characterization of four endophytic fungi as potential consolidated bioprocessing hosts for conversion of lignocellulose into advanced biofuels. <i>Applied Microbiology and Biotechnology</i> , <b>2017</b> , 101, 2603-2618	5.7	41
101	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , <b>2017</b> , 19, 2964-2983	5.2	98
100	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , <b>2017</b> , 541, 536-540	50.4	226
99	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , <b>2017</b> , 18, 28	18.3	261
98	Sparse panicle1 is required for inflorescence development in <i>Setaria viridis</i> and maize. <i>Nature Plants</i> , <b>2017</b> , 3, 17054	11.5	35
97	Draft Nuclear Genome Sequence of the Liquid Hydrocarbon-Accumulating Green Microalga Race B (Showa). <i>Genome Announcements</i> , <b>2017</b> , 5,		16
96	Comparative Genomics of the Ectomycorrhizal Sister Species and (Basidiomycota: Boletales) Reveals a Divergence of the Mating Type Locus. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 1775-1789	3.2	11
95	The Sequences of 1504 Mutants in the Model Rice Variety Kitaake Facilitate Rapid Functional Genomic Studies. <i>Plant Cell</i> , <b>2017</b> , 29, 1218-1231	11.6	80
94	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17087	26.6	111
93	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , <b>2017</b> , 1, 119	12.3	59
92	Draft Nuclear Genome Sequence of the Halophilic and Beta-Carotene-Accumulating Green Alga Strain CCAP19/18. <i>Genome Announcements</i> , <b>2017</b> , 5,		49



91	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi <i>Armillaria</i> . <i>Nature Ecology and Evolution</i> , <b>2017</b> , 1, 1931-1941	12.3	85
90	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , <b>2017</b> , 171, 287-304.e15	56.2	538
89	Comparative genomics of <i>Coniophora olivacea</i> reveals different patterns of genome expansion in Boletales. <i>BMC Genomics</i> , <b>2017</b> , 18, 883	4.5	11
88	A fungal transcription factor essential for starch degradation affects integration of carbon and nitrogen metabolism. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006737	6	26
87	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> , <b>2017</b> , 5,		10
86	Draft genome sequence of a monokaryotic model brown-rot fungus SB12. <i>Genomics Data</i> , <b>2017</b> , 14, 21-23		9
85	Insights into the red algae and eukaryotic evolution from the genome of (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6361-E6370	11.5	131
84	Feathermoss and epiphytic <i>Nostoc</i> cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. <i>ISME Journal</i> , <b>2017</b> , 11, 2821-2833	11.9	35
83	Expression of CAZymes is determined by compositional changes in wheat straw generated by hydrothermal or ionic liquid pretreatments. <i>Biotechnology for Biofuels</i> , <b>2017</b> , 10, 35	7.8	13
82	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> , <b>2017</b> , 213, 365-379	9.8	69
81	Genome-wide associations with flowering time in switchgrass using exome-capture sequencing data. <i>New Phytologist</i> , <b>2017</b> , 213, 154-169	9.8	29
80	Extensive gene content variation in the <i>Brachypodium distachyon</i> pan-genome correlates with population structure. <i>Nature Communications</i> , <b>2017</b> , 8, 2184	17.4	168
79	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 9882-7	11.5	212
78	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , <b>2016</b> , 4,		9
77	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , <b>2016</b> , 7, 12662	17.4	97
76	Complete Genome Sequence of <i>Alkaliphilus metalliredigens</i> Strain QYMF, an Alkaliphilic and Metal-Reducing Bacterium Isolated from Borax-Contaminated Leachate Ponds. <i>Genome Announcements</i> , <b>2016</b> , 4,		5
75	Comparative Genomics of Early-Diverging Mushroom-Forming Fungi Provides Insights into the Origins of Lignocellulose Decay Capabilities. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 959-70	8.3	131
74	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> , <b>2016</b> , 9, 1078-81	14.4	57



73	Draft Genome Sequence of <i>Microdochium bolleyi</i> , a Dark Septate Fungal Endophyte of Beach Grass. <i>Genome Announcements</i> , <b>2016</b> , 4,		16
72	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> , <b>2016</b> , 86, 9-19	3.9	10
71	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , <b>2015</b> , 47, 410-5	36.3	601
70	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> , <b>2015</b> , 5, 1593-602	3.2	18
69	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. <i>Genome Biology</i> , <b>2015</b> , 16, 26	18.3	190
68	The genetics of divergence and reproductive isolation between ecotypes of <i>Panicum hallii</i> . <i>New Phytologist</i> , <b>2015</b> , 205, 402-14	9.8	39
67	Complete Genome Sequence of <i>Anaeromyxobacter</i> sp. Fw109-5, an Anaerobic, Metal-Reducing Bacterium Isolated from a Contaminated Subsurface Environment. <i>Genome Announcements</i> , <b>2015</b> , 3,		10
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57	A genome-wide scan for evidence of selection in a maize population under long-term artificial selection for ear number. <i>Genetics</i> , <b>2014</b> , 196, 829-40	4	47
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9	Metagenome-assembled genomes of phytoplankton communities across the Arctic Circle		6
8	The <i>Ceratodon purpureus</i> genome uncovers structurally complex, gene rich sex chromosomes		5
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1	Evolutionary priming and transition to the ectomycorrhizal habit in an iconic lineage of mushroom-forming fungi: is preadaptation a requirement?	2
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