

# Kerrie Barry

## List of Publications by Citations

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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	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , <b>2010</b> , 463, 178-83	50.4	2997
197	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , <b>2014</b> , 345, 1251788	33.3	1129
196	The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. <i>Science</i> , <b>2012</b> , 336, 1715-9	33.3	1129
195	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , <b>2007</b> , 450, 560-5	50.4	990
194	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , <b>2014</b> , 46, 707-13	36.3	772
193	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
192	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , <b>2012</b> , 30, 555-61	44.5	573
191	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , <b>2006</b> , 24, 1263-9	44.5	541
190	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
189	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , <b>2014</b> , 510, 356-62	50.4	497
188	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , <b>2014</b> , 345, 1250092	33.3	419
187	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. <i>Science</i> , <b>2011</b> , 333, 762-5	33.3	417
186	Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1003037	7.6	387
185	Genomic islands and the ecology and evolution of <i>Prochlorococcus</i> . <i>Science</i> , <b>2006</b> , 311, 1768-70	33.3	362
184	Sequencing genomes from single cells by polymerase cloning. <i>Nature Biotechnology</i> , <b>2006</b> , 24, 680-6	44.5	353
183	Symbiosis insights through metagenomic analysis of a microbial consortium. <i>Nature</i> , <b>2006</b> , 443, 950-5	50.4	339
182	Insights into the maize pan-genome and pan-transcriptome. <i>Plant Cell</i> , <b>2014</b> , 26, 121-35	11.6	336

181	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , <b>2012</b> , 492, 59-65	50.4	304
180	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> , <b>2010</b> , 27, 1436-48	8.3	294
179	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
178	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , <b>2007</b> , 4, 495-500	21.6	257
177	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , <b>2010</b> , 4, 660-72	11.9	249
176	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , <b>2017</b> , 541, 536-540	50.4	226
175	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> , <b>2012</b> , 109, 5458-63	11.5	225
174	Horizontal transfer of entire genomes via mitochondrial fusion in the angiosperm <i>Amborella</i> . <i>Science</i> , <b>2013</b> , 342, 1468-73	33.3	219
173	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <i>Plant Journal</i> , <b>2013</b> , 76, 718-27	6.9	219
172	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> , <b>2008</b> , 105, 8102-7	11.5	214
171	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
170	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , <b>2014</b> , 15, 549	4.5	193
169	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
168	Origins and recombination of the bacterial-sized multichromosomal mitochondrial genome of cucumber. <i>Plant Cell</i> , <b>2011</b> , 23, 2499-513	11.6	189
167	An insect herbivore microbiome with high plant biomass-degrading capacity. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001129	11.29	172
166	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
165	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> , <b>2010</b> , 107, 14793-8	11.5	163
164	Comparative genome structure, secondary metabolite, and effector coding capacity across <i>Cochliobolus</i> pathogens. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003233	6	161

163	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
162	Insights into the red algae and eukaryotic evolution from the genome of (Bangioophyceae, 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
161	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> , <b>2011</b> , 108, 13212-7	11.5	131
160	Isolation of Succinivibrionaceae implicated in low methane emissions from Tammar wallabies. <i>Science</i> , <b>2011</b> , 333, 646-8	33.3	119
159	Comparative genomics of the social amoebae Dictyostelium discoideum and Dictyostelium purpureum. <i>Genome Biology</i> , <b>2011</b> , 12, R20	18.3	117
158	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17087	26.6	111
157	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
156	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , <b>2012</b> , 6, 1688-701	11.9	100
155	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. <i>Nature Genetics</i> , <b>2018</b> , 50, 1688-1695	36.3	100
154	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
153	Comparative genomics of Mortierella elongata and its bacterial endosymbiont Mycoavidus cysteinexigens. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 2964-2983	5.2	98
152	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 668-678	12.3	98
151	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus Cenococcum geophilum. <i>Nature Communications</i> , <b>2016</b> , 7, 12662	17.4	97
150	Comparative genomics of the white-rot fungi, Phanerochaete carnosa and P. chrysosporium, to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , <b>2012</b> , 13, 444	4.5	97
149	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , <b>2013</b> , 7, 1173-86	11.9	96
148	Analysis of clock-regulated genes in Neurospora reveals widespread posttranscriptional control of metabolic potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 16995-7002	11.5	94
147	Metagenomic profiling reveals lignocellulose degrading system in a microbial community associated with a wood-feeding beetle. <i>PLoS ONE</i> , <b>2013</b> , 8, e73827	3.7	87
146	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

145	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
144	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> , <b>2012</b> , 157, 202-9	5.8	85
143	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
142	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
141	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
140	Complete genome sequence of the filamentous anoxygenic phototrophic bacterium <i>Chloroflexus aurantiacus</i> . <i>BMC Genomics</i> , <b>2011</b> , 12, 334	4.5	77
139	<i>Leucoagaricus gongylophorus</i> produces diverse enzymes for the degradation of recalcitrant plant polymers in leaf-cutter ant fungus gardens. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3770-8	4.8	75
138	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
137	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
136	Analysis of the <i>Phlebiopsis gigantea</i> genome, transcriptome and secretome provides insight into its pioneer colonization strategies of wood. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004759	6	67
135	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
134	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
133	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
132	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
131	Genome diversity in <i>Brachypodium distachyon</i> : deep sequencing of highly diverse inbred lines. <i>Plant Journal</i> , <b>2014</b> , 79, 361-74	6.9	58
130	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
129	Strand-Specific RNA-Seq Analyses of Fruiting Body Development in <i>Coprinopsis cinerea</i> . <i>PLoS ONE</i> , <b>2015</b> , 10, e0141586	3.7	55
128	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

127	Comparative Genomics in Switchgrass Using 61,585 High-Quality Expressed Sequence Tags. <i>Plant Genome</i> , <b>2008</b> , 1,	4.4	53
126	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
125	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
124	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
123	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
122	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
121	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
120	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , <b>2021</b> , 590, 438-444	44.4	42
119	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
118	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
117	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
116	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
115	A willow sex chromosome reveals convergent evolution of complex palindromic repeats. <i>Genome Biology</i> , <b>2020</b> , 21, 38	18.3	39
114	Facile recovery of individual high-molecular-weight, low-copy-number natural plasmids for genomic sequencing. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 4899-906	4.8	39
113	Phylogenomics of Endogonaceae and evolution of mycorrhizas within Mucoromycota. <i>New Phytologist</i> , <b>2019</b> , 222, 511-525	9.8	37
112	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
111	Blueprint for a pop-up SARS-CoV-2 testing lab. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 791-797	44.5	36
110	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

109	Feathermoss and epiphytic Nostoc cooperate differently: expanding the spectrum of plant-cyanobacteria symbiosis. <i>ISME Journal</i> , <b>2017</b> , 11, 2821-2833	11.9	35
108	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
107	A new reference genome for Sorghum bicolor 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
106	Diversity and population structure of northern switchgrass as revealed through exome capture sequencing. <i>Plant Journal</i> , <b>2015</b> , 84, 800-15	6.9	33
105	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
104	Genome-Wide Analysis of Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 276	5.7	32
103	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , <b>2019</b> , 100, 1066-1082	6.9	32
102	Complete genome sequence of Rhodospirillum rubrum type strain (S1). <i>Standards in Genomic Sciences</i> , <b>2011</b> , 4, 293-302		31
101	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial Populus trichocarpa. <i>Genome Biology</i> , <b>2020</b> , 21, 259	18.3	31
100	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
99	Complete genome sequence of Methanoculleus marisnigri Romesser et al. 1981 type strain JR1. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 189-96		28
98	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
97	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
96	The complete genome sequence of Staphylothermus marinus reveals differences in sulfur metabolism among heterotrophic Crenarchaeota. <i>BMC Genomics</i> , <b>2009</b> , 10, 145	4.5	26
95	Complete genome sequence of Methanocorpusculum labreanum type strain Z. <i>Standards in Genomic Sciences</i> , <b>2009</b> , 1, 197-203		26
94	Insights into the effects of long-term artificial selection on seed size in maize. <i>Genetics</i> , <b>2014</b> , 198, 409-24		25
93	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
92	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 3058	5.7	23



91	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. <i>Biotechnology for Biofuels</i> , <b>2018</b> , 11, 170	7.8	22
90	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
89	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
88	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , <b>2019</b> , 20, 905	4.5	21
87	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , <b>2018</b> , 3,	5	20
86	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
85	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
84	Mediation of plant-mycorrhizal interaction by a lectin receptor-like kinase. <i>Nature Plants</i> , <b>2019</b> , 5, 676-680	11.5	18
83	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
82	Draft Nuclear Genome Sequence of the Liquid Hydrocarbon-Accumulating Green Microalga Race B (Showa). <i>Genome Announcements</i> , <b>2017</b> , 5,		16
81	Secretome Analysis from the Ectomycorrhizal Ascomycete. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 141	5.7	16
80	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
79	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
78	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , <b>2018</b> , 11, 170055	4.4	16
77	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
76	Genome Sequence of the ethene- and vinyl chloride-oxidizing actinomycete <i>Nocardioides</i> sp. strain JS614. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 3399-400	3.5	15
75	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	15
74	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



73	Draft Genome Sequence of Tuber borchii Vittad., a Whitish Edible Truffle. <i>Genome Announcements</i> , <b>2018</b> , 6,		14
72	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus Pycnoporus. <i>DNA Research</i> , <b>2020</b> , 27,	4.5	13
71	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
70	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
69	Complete genome sequence of Candidatus Ruthia magnifica. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 163-73		12
68	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
67	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
66	Comparative genomics of Coniophora olivacea reveals different patterns of genome expansion in Boletales. <i>BMC Genomics</i> , <b>2017</b> , 18, 883	4.5	11
65	Genome Sequence of the Plant Growth Promoting Fungus Serendipita vermifera subsp. bescii: The First Native Strain from North America. <i>Phytobiomes Journal</i> , <b>2018</b> , 2, 62-63	4.8	11
64	Complete Genome Sequence of Anaeromyxobacter sp. Fw109-5, an Anaerobic, Metal-Reducing Bacterium Isolated from a Contaminated Subsurface Environment. <i>Genome Announcements</i> , <b>2015</b> , 3,		10
63	Draft Genome Sequence of Coniochaeta ligniaria NRRL 30616, a Lignocellulolytic Fungus for Bioabatement of Inhibitors in Plant Biomass Hydrolysates. <i>Genome Announcements</i> , <b>2017</b> , 5,		10
62	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
61	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
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