

Bernard Henrissat

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.

579
papers

90,222
citations

132
h-index

291
g-index

624
ext. papers

106,972
ext. citations

9.3
avg, IF

7.9
L-index

#	Paper	IF	Citations
579	Fungal glycoside hydrolase family 44 xyloglucanases are restricted to the phylum Basidiomycota and show a distinct xyloglucan cleavage pattern.. <i>IScience</i> , 2022 , 25, 103666	6.1	0
578	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides.. <i>Nature Communications</i> , 2022 , 13, 629	17.4	3
577	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria.. <i>MSystems</i> , 2022 , e0094721	7.6	4
576	Secreted Glycoside Hydrolase Proteins as Effectors and Invasion Patterns of Plant-Associated Fungi and Oomycetes.. <i>Frontiers in Plant Science</i> , 2022 , 13, 853106	6.2	3
575	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota.. <i>Nature Microbiology</i> , 2022 , 7, 556-569	26.6	3
574	Functional exploration of the glycoside hydrolase family GH113.. <i>PLoS ONE</i> , 2022 , 17, e0267509	3.7	1
573	Genome evolution of a nonparasitic secondary heterotroph, the diatom .. <i>Science Advances</i> , 2022 , 8, eabi5075	14.75	2
572	An approach for evaluating the effects of dietary fiber polysaccharides on the human gut microbiome and plasma proteome.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2123411119	11.5	0
571	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a GH28 polygalacturonase that plays a key role in symbiosis establishment.. <i>New Phytologist</i> , 2021 ,	9.8	2
570	Genetic determinants of endophytism in the Arabidopsis root mycobiome. <i>Nature Communications</i> , 2021 , 12, 7227	17.4	8
569	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2021 ,	9.8	3
568	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
567	The carbohydrate-active enzyme database: functions and literature. <i>Nucleic Acids Research</i> , 2021 ,	20.1	81
566	Identification of Copper-Containing Oxidoreductases in the Secretomes of Three Species with a Focus on Copper Radical Oxidases for the Biocatalytic Production of Fatty Aldehydes. <i>Applied and Environmental Microbiology</i> , 2021 , 87, e0152621	4.8	2
565	Clinical evidence of the role of <i>Methanobrevibacter smithii</i> in severe acute malnutrition. <i>Scientific Reports</i> , 2021 , 11, 5426	4.9	9
564	Discovery of fungal oligosaccharide-oxidising flavo-enzymes with previously unknown substrates, redox-activity profiles and interplay with LPMOs. <i>Nature Communications</i> , 2021 , 12, 2132	17.4	15
563	Strain-level functional variation in the human gut microbiota based on bacterial binding to artificial food particles. <i>Cell Host and Microbe</i> , 2021 , 29, 664-673.e5	23.4	4

562	Characterization of three bacterial glycoside hydrolase family 9 endoglucanases with different modular architectures isolated from a compost metagenome. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021 , 1865, 129848	4	3
561	Larvae of longhorned beetles (Coleoptera; Cerambycidae) have evolved a diverse and phylogenetically conserved array of plant cell wall degrading enzymes. <i>Systematic Entomology</i> , 2021 , 46, 784-797	3.4	4
560	Gut microbiome contributions to altered metabolism in a pig model of undernutrition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
559	Evaluating microbiome-directed fibre snacks in gnotobiotic mice and humans. <i>Nature</i> , 2021 , 595, 91-95	50.4	13
558	Display of the human mucinome with defined O-glycans by gene engineered cells. <i>Nature Communications</i> , 2021 , 12, 4070	17.4	26
557	C-type cytochrome-initiated reduction of bacterial lytic polysaccharide monooxygenases. <i>Biochemical Journal</i> , 2021 , 478, 2927-2944	3.8	2
556	Multimodularity of a GH10 Xylanase Found in the Termite Gut Metagenome. <i>Applied and Environmental Microbiology</i> , 2021 , 87,	4.8	8
555	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021 , 38, 1428-1446	8.3	22
554	Identification of the molecular determinants driving the substrate specificity of fungal lytic polysaccharide monooxygenases (LPMOs). <i>Journal of Biological Chemistry</i> , 2021 , 296, 100086	5.4	7
553	Niche differentiation and evolution of the wood decay machinery in the invasive fungus <i>Serpula lacrymans</i> . <i>ISME Journal</i> , 2021 , 15, 592-604	11.9	6
552	Characterization of the β -glucuronidase Pn3Pase as the founding member of glycoside hydrolase family GH169. <i>Glycobiology</i> , 2021 , 31, 266-274	5.8	1
551	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021 , 15, 421-434	11.9	17
550	Functional diversity of three tandem C-terminal carbohydrate-binding modules of a β -mannanase. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100638	5.4	3
549	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021 , 23, 5716-5732	5.2	15
548	Lytic Polysaccharide Monooxygenases as Chitin-Specific Virulence Factors in Crayfish Plague. <i>Biomolecules</i> , 2021 , 11,	5.9	1
547	Secreted pectin monooxygenases drive plant infection by pathogenic oomycetes. <i>Science</i> , 2021 , 373, 774-779	33.3	29
546	Sulfation of Arabinogalactan Proteins Confers Privileged Nutrient Status to <i>Bacteroides plebeius</i> . <i>MBio</i> , 2021 , 12, e0136821	7.8	2
545	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , 2021 , 31, 3905-3914.e6	6.3	3

544	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
543	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , 2020 , 9,	7.6	21
542	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020 , 27,	4.5	13
541	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
540	Infection cushions of <i>Fusarium graminearum</i> are fungal arsenals for wheat infection. <i>Molecular Plant Pathology</i> , 2020 , 21, 1070-1087	5.7	14
539	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020 , 11, 1106	17.4	54
538	A mutation map for human glycoside hydrolase genes. <i>Glycobiology</i> , 2020 , 30, 500-515	5.8	2
537	Metabolism of multiple glycosaminoglycans by <i>Bacteroides thetaiotaomicron</i> is orchestrated by a versatile core genetic locus. <i>Nature Communications</i> , 2020 , 11, 646	17.4	27
536	Discovery of a Fungal Copper Radical Oxidase with High Catalytic Efficiency toward 5-Hydroxymethylfurfural and Benzyl Alcohols for Bioprocessing. <i>ACS Catalysis</i> , 2020 , 10, 3042-3058	13.1	21
535	Investigating host-microbiome interactions by droplet based microfluidics. <i>Microbiome</i> , 2020 , 8, 141	16.6	15
534	Revisiting Old Questions and New Approaches to Investigate the Fungal Cell Wall Construction. <i>Current Topics in Microbiology and Immunology</i> , 2020 , 425, 331-369	3.3	0
533	Analysis of the diversity of the glycoside hydrolase family 130 in mammal gut microbiomes reveals a novel mannoside-phosphorylase function. <i>Microbial Genomics</i> , 2020 , 6,	4.4	3
532	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
531	Discovery of hyperstable carbohydrate-active enzymes through metagenomics of extreme environments. <i>FEBS Journal</i> , 2020 , 287, 1116-1137	5.7	12
530	A fungal family of lytic polysaccharide monooxygenase-like copper proteins. <i>Nature Chemical Biology</i> , 2020 , 16, 345-350	11.7	33
529	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
528	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
527	Galactosaminogalactan activates the inflammasome to provide host protection. <i>Nature</i> , 2020 , 588, 688-692	17.4	28

526	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. <i>Nature Communications</i> , 2020 , 11, 5773	17.4	24
525	Utilization of Galectins by Pathogens for Infection. <i>Frontiers in Immunology</i> , 2020 , 11, 1877	8.4	7
524	Characterization of the CAZy Repertoire from the Marine-Derived Fungus in Relation to Saline Conditions. <i>Marine Drugs</i> , 2020 , 18,	6	6
523	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
522	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
521	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , 2019 , 294, 15973-15986	5.4	55
520	Interspecies Competition Impacts Targeted Manipulation of Human Gut Bacteria by Fiber-Derived Glycans. <i>Cell</i> , 2019 , 179, 59-73.e13	56.2	103
519	The Cellulosome Paradigm in An Extreme Alkaline Environment. <i>Microorganisms</i> , 2019 , 7,	4.9	5
518	The continuing expansion of CAZymes and their families. <i>Current Opinion in Chemical Biology</i> , 2019 , 53, 82-87	9.7	39
517	Investigating Host Microbiota Relationships Through Functional Metagenomics. <i>Frontiers in Microbiology</i> , 2019 , 10, 1286	5.7	9
516	Updates to the Symbol Nomenclature for Glycans guidelines. <i>Glycobiology</i> , 2019 , 29, 620-624	5.8	148
515	Evolution and comparative genomics of the most common <i>Trichoderma</i> species. <i>BMC Genomics</i> , 2019 , 20, 485	4.5	93
514	Poplar carbohydrate-active enzymes: whole-genome annotation and functional analyses based on RNA expression data. <i>Plant Journal</i> , 2019 , 99, 589-609	6.9	15
513	Bacteroidetes use thousands of enzyme combinations to break down glycans. <i>Nature Communications</i> , 2019 , 10, 2043	17.4	109
512	Broad-specificity GH131 β -glucanases are a hallmark of fungi and oomycetes that colonize plants. <i>Environmental Microbiology</i> , 2019 , 21, 2724-2739	5.2	8
511	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
510	A metagenomics investigation of carbohydrate-active enzymes along the goat and camel intestinal tract. <i>International Microbiology</i> , 2019 , 22, 429-435	3	9
509	Unraveling the subtleties of α (1-B)-glucan phosphorylase specificity in the GH94, GH149, and GH161 glycoside hydrolase families. <i>Journal of Biological Chemistry</i> , 2019 , 294, 6483-6493	5.4	9

508	AA16, a new lytic polysaccharide monooxygenase family identified in fungal secretomes. <i>Biotechnology for Biofuels</i> , 2019 , 12, 55	7.8	96
507	Discovery of novel carbohydrate-active enzymes through the rational exploration of the protein sequences space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 6063-6068	11.5	88
506	Mycobacterium ulcerans mycolactones-fungi crosstalking. <i>Scientific Reports</i> , 2019 , 9, 3028	4.9	6
505	Genomic insights from Monoglobus pectinilyticus: a pectin-degrading specialist bacterium in the human colon. <i>ISME Journal</i> , 2019 , 13, 1437-1456	11.9	25
504	Multi-omic analyses of exogenous nutrient bag decomposition by the black morel Morchella importuna reveal sustained carbon acquisition and transferring. <i>Environmental Microbiology</i> , 2019 , 21, 3909-3926	5.2	27
503	Effects of microbiota-directed foods in gnotobiotic animals and undernourished children. <i>Science</i> , 2019 , 365,	33.3	160
502	Substrate specificity, regiospecificity, and processivity in glycoside hydrolase family 74. <i>Journal of Biological Chemistry</i> , 2019 , 294, 13233-13247	5.4	15
501	Intrinsic dynamic behavior of enzyme:substrate complexes govern the catalytic action of EGalactosidases across clan GH-A. <i>Scientific Reports</i> , 2019 , 9, 10346	4.9	9
500	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
499	Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical Elizabethkingia meningoseptica strains. <i>PLoS ONE</i> , 2019 , 14, e0222648	3.7	9
498	Inverting family GH156 sialidases define an unusual catalytic motif for glycosidase action. <i>Nature Communications</i> , 2019 , 10, 4816	17.4	5
497	Sucrose 6-phosphate phosphorylase: a novel insight in the human gut microbiome. <i>Microbial Genomics</i> , 2019 , 5,	4.4	6
496	Dehydrogenase, a Pyrroloquinoline Quinone-Dependent Member of Auxiliary Activity Family 12 of the Carbohydrate-Active Enzymes Database: Functional and Structural Characterization. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	8
495	Comparative genomics of Rhizophagus irregularis, R. cerebriforme, R. diaphanus and Gigaspora rosea highlights specific genetic features in Glomeromycotina. <i>New Phytologist</i> , 2019 , 222, 1584-1598	9.8	58
494	From proteins to polysaccharides: lifestyle and genetic evolution of Coprothermobacter proteolyticus. <i>ISME Journal</i> , 2019 , 13, 603-617	11.9	19
493	An ancient family of lytic polysaccharide monooxygenases with roles in arthropod development and biomass digestion. <i>Nature Communications</i> , 2018 , 9, 756	17.4	135
492	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
491	Talaromyces borbonicus, sp. nov., a novel fungus from biodegraded Arundo donax with potential abilities in lignocellulose conversion. <i>Mycologia</i> , 2018 , 110, 316-324	2.4	8

490	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a secreted β ,4 endoglucanase that plays a key role in symbiosis development. <i>New Phytologist</i> , 2018 , 220, 1309-1321	9.8	26
489	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018 , 6,		4
488	Ten years of CAZypedia: a living encyclopedia of carbohydrate-active enzymes. <i>Glycobiology</i> , 2018 , 28, 3-8	5.8	104
487	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. <i>Nature Chemical Biology</i> , 2018 , 14, 306-310	11.7	183
486	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018 , 8, 1931	4.9	127
485	Identification of β ,3-glucan phosphorylase and establishment of a new glycoside hydrolase (GH) family GH149. <i>Journal of Biological Chemistry</i> , 2018 , 293, 2865-2876	5.4	26
484	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018 , 9, 310	17.4	55
483	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
482	PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , 2018 , 46, D6772-D6831	10.4	
481	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic <i>Bacteroides</i> . <i>Nature Microbiology</i> , 2018 , 3, 210-219	26.6	142
480	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
479	Glycosyltransferase genes that cause monogenic congenital disorders of glycosylation are distinct from glycosyltransferase genes associated with complex diseases. <i>Glycobiology</i> , 2018 , 28, 284-294	5.8	28
478	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018 , 36, 359-367	44.5	207
477	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
476	Production of β ,3-L-arabinofuranosidase active on substituted xylan does not improve compost degradation by <i>Agaricus bisporus</i> . <i>PLoS ONE</i> , 2018 , 13, e0201090	3.7	3
475	Genome Sequencing and analyses of Two Marine Fungi from the North Sea Unraveled a Plethora of Novel Biosynthetic Gene Clusters. <i>Scientific Reports</i> , 2018 , 8, 10187	4.9	14
474	Structural Dynamics and Catalytic Properties of a Multimodular Xanthanase. <i>ACS Catalysis</i> , 2018 , 8, 6021-6034	6.9	
473	De novo assembly of the complex genome of <i>Nippostrongylus brasiliensis</i> using MinION long reads. <i>BMC Biology</i> , 2018 , 16, 6	7.3	22

472	Novel carbohydrate binding modules in the surface anchored α -amylase of <i>Eubacterium rectale</i> provide a molecular rationale for the range of starches used by this organism in the human gut. <i>Molecular Microbiology</i> , 2018 , 107, 249-264	4.1	36
471	Comparative analysis of basidiomycete transcriptomes reveals a core set of expressed genes encoding plant biomass degrading enzymes. <i>Fungal Genetics and Biology</i> , 2018 , 112, 40-46	3.9	30
470	Annotating Carbohydrate-Active Enzymes in Plant Genomes: Present Challenges 2018 , 93-107		
469	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1956-1965	12.3	52
468	Proteomic Dissection of the Cellulolytic Machineries Used by Soil-Dwelling. <i>MSystems</i> , 2018 , 3,	7.6	19
467	Nuclear genome sequence of the plastid-lacking cryptomonad <i>Goniomonas avonlea</i> provides insights into the evolution of secondary plastids. <i>BMC Biology</i> , 2018 , 16, 137	7.3	19
466	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018 , 3, 1417-1428	26.6	60
465	The human gut microbe encodes the founding member of a novel glycosaminoglycan-degrading polysaccharide lyase family PL29. <i>Journal of Biological Chemistry</i> , 2018 , 293, 17906-17916	5.4	18
464	Functional metagenomics identifies an exosialidase with an inverting catalytic mechanism that defines a new glycoside hydrolase family (GH156). <i>Journal of Biological Chemistry</i> , 2018 , 293, 18138-18150	5.4	17
463	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
462	Analysis of carbohydrate-active enzymes in <i>Thermogemmatispora</i> sp. strain T81 reveals carbohydrate degradation ability. <i>Canadian Journal of Microbiology</i> , 2018 , 64, 992-1003	3.2	2
461	A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. <i>Nature Microbiology</i> , 2018 , 3, 1314-1326	26.6	57
460	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
459	Rapid Divergence of Genome Architectures Following the Origin of an Ectomycorrhizal Symbiosis in the Genus <i>Amanita</i> . <i>Molecular Biology and Evolution</i> , 2018 , 35, 2786-2804	8.3	17
458	Development and characterization of stable anaerobic thermophilic methanogenic microbiomes fermenting switchgrass at decreasing residence times. <i>Biotechnology for Biofuels</i> , 2018 , 11, 243	7.8	21
457	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico "Dead Zone". <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	7
456	Ancient acquisition of "alginate utilization loci" by human gut microbiota. <i>Scientific Reports</i> , 2018 , 8, 8075	4.9	28
455	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade <i>Ustilaginomycotina</i> . <i>Molecular Biology and Evolution</i> , 2018 , 35, 1840-1854	8.3	28

454	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
453	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. <i>Scientific Reports</i> , 2017 , 7, 40248	4.9	27
452	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
451	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , 2017 , 19, 2964-2983	5.2	98
450	Exploring the genomic diversity of black yeasts and relatives (,). <i>Studies in Mycology</i> , 2017 , 86, 1-28	22.2	93
449	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
448	Discovery of genes coding for carbohydrate-active enzyme by metagenomic analysis of lignocellulosic biomasses. <i>Scientific Reports</i> , 2017 , 7, 42623	4.9	38
447	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
446	Unusual active site location and catalytic apparatus in a glycoside hydrolase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 4936-4941	11.5	30
445	A bioinformatics analysis of 3400 lytic polysaccharide oxidases from family AA9. <i>Carbohydrate Research</i> , 2017 , 448, 166-174	2.9	41
444	The chimeric nature of the genomes of marine magnetotactic coccoid-ovoid bacteria defines a novel group of Proteobacteria. <i>Environmental Microbiology</i> , 2017 , 19, 1103-1119	5.2	36
443	Structural insights into a family 39 glycoside hydrolase from the gut symbiont <i>Bacteroides cellulosilyticus</i> WH2. <i>Journal of Structural Biology</i> , 2017 , 197, 227-235	3.4	5
442	Characterization of a mycobacterial cellulase and its impact on biofilm- and drug-induced cellulose production. <i>Glycobiology</i> , 2017 , 27, 392-399	5.8	8
441	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. <i>Journal of Biological Chemistry</i> , 2017 , 292, 13271-13283	5.4	20
440	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017 , 2, 17087	26.6	111
439	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , 2017 , 544, 65-70	50.4	291
438	Archaea: Essential inhabitants of the human digestive microbiota. <i>Human Microbiome Journal</i> , 2017 , 3, 1-8	5.6	59
437	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines 2017 , 117-131		18

436	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <i>MBio</i> , 2017 , 8,	7.8	46
435	Structural and electronic determinants of lytic polysaccharide monooxygenase reactivity on polysaccharide substrates. <i>Nature Communications</i> , 2017 , 8, 1064	17.4	101
434	Unique organization and unprecedented diversity of the cellulosome system. <i>Biotechnology for Biofuels</i> , 2017 , 10, 211	7.8	22
433	The yeast encodes functional lytic polysaccharide monooxygenases. <i>Biotechnology for Biofuels</i> , 2017 , 10, 215	7.8	33
432	Feed in summer, rest in winter: microbial carbon utilization in forest topsoil. <i>Microbiome</i> , 2017 , 5, 122	16.6	71
431	Pan-Cellulosomics of Mesophilic Clostridia: Variations on a Theme. <i>Microorganisms</i> , 2017 , 5,	4.9	12
430	Draft genome sequence of a monokaryotic model brown-rot fungus SB12. <i>Genomics Data</i> , 2017 , 14, 21-23		9
429	How a Glycoside Hydrolase Recognizes a Helical Polyglucan. <i>Structure</i> , 2017 , 25, 1319-1321	5.2	
428	Ninety-nine de novo assembled genomes from the moose (<i>Alces alces</i>) rumen microbiome provide new insights into microbial plant biomass degradation. <i>ISME Journal</i> , 2017 , 11, 2538-2551	11.9	70
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12	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae)		1
11	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber		1
10	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment		1
9	Transcriptomic atlas of mushroom development highlights an independent origin of complex multicellularity		5
8	The genome of <i>Auriculariopsis ampla</i> sheds light on fruiting body development and wood-decay of bark-inhabiting fungi		2
7	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut		1
6	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome		1
5	Global and temporal state of the human gut microbiome in health and disease		2

4	The Food Additive Xanthan Gum Drives Adaptation of the Human Gut Microbiota	1
3	Evolutionary priming and transition to the ectomycorrhizal habit in an iconic lineage of mushroom-forming fungi: is preadaptation a requirement?	2
2	Co-cultivation of the anaerobic fungus <i>Caecomyces churovis</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules	1
1	The Cellulosome: A Natural Bacterial Strategy to Combat Biomass Recalcitrance407-435	12