

Bernard Henrissat

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4040272/publications.pdf>

Version: 2024-02-01

576
papers

117,933
citations

217

146
h-index

165

322
g-index

626
all docs

626
docs citations

626
times ranked

76132
citing authors

#	ARTICLE	IF	CITATIONS
1	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009, 457, 480-484.	13.7	6,819
2	The carbohydrate-active enzymes database (CAZy) in 2013. <i>Nucleic Acids Research</i> , 2014, 42, D490-D495.	6.5	5,443
3	The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. <i>Nucleic Acids Research</i> , 2009, 37, D233-D238.	6.5	4,854
4	The Genome of Black Cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006, 313, 1596-1604.	6.0	3,945
5	Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice. <i>Science</i> , 2013, 341, 1241-1244.	6.0	3,006
6	A classification of glycosyl hydrolases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1991, 280, 309-316.	1.7	2,901
7	New families in the classification of glycosyl hydrolases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1993, 293, 781-788.	1.7	1,939
8	A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility. <i>Cell</i> , 2016, 167, 1339-1353.e21.	13.5	1,882
9	Structures and mechanisms of glycosyl hydrolases. <i>Structure</i> , 1995, 3, 853-859.	1.6	1,803
10	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712
11	Glycosyltransferases: Structures, Functions, and Mechanisms. <i>Annual Review of Biochemistry</i> , 2008, 77, 521-555.	5.0	1,651
12	Structural and sequence-based classification of glycoside hydrolases. <i>Current Opinion in Structural Biology</i> , 1997, 7, 637-644.	2.6	1,494
13	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
14	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	6.0	1,424
15	Updating the sequence-based classification of glycosyl hydrolases. <i>Biochemical Journal</i> , 1996, 316, 695-696.	1.7	1,293
16	The abundance and variety of carbohydrate-active enzymes in the human gut microbiota. <i>Nature Reviews Microbiology</i> , 2013, 11, 497-504.	13.6	1,240
17	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq1 1 0.784314, 9.4 1,516	9.4	1,516
18	An Evolving Hierarchical Family Classification for Glycosyltransferases. <i>Journal of Molecular Biology</i> , 2003, 328, 307-317.	2.0	1,079

#	ARTICLE	IF	CITATIONS
19	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	9.4	1,047
20	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	9.4	1,012
21	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008, 452, 88-92.	13.7	1,003
22	Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. <i>Biotechnology for Biofuels</i> , 2013, 6, 41.	6.2	994
23	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002358.	1.5	939
24	Nomenclature for sugar-binding subsites in glycosyl hydrolases. <i>Biochemical Journal</i> , 1997, 321, 557-559.	1.7	934
25	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
26	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	9.4	870
27	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012, 44, 1060-1065.	9.4	840
28	The carbohydrate-active enzyme database: functions and literature. <i>Nucleic Acids Research</i> , 2022, 50, D571-D577.	6.5	813
29	Genome sequence of the lignocellulose degrading fungus <i>Phanerochaete chrysosporium</i> strain RP78. <i>Nature Biotechnology</i> , 2004, 22, 695-700.	9.4	805
30	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	1.4	804
31	A classification of nucleotide-diphospho-sugar glycosyltransferases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1997, 326, 929-939.	1.7	722
32	Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20117-20122.	3.3	717
33	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1948-1953.	3.3	669
34	Recognition and Degradation of Plant Cell Wall Polysaccharides by Two Human Gut Symbionts. <i>PLoS Biology</i> , 2011, 9, e1001221.	2.6	644
35	<i>Pezizomycotina</i> black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	13.7	641
36	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	3.3	640

#	ARTICLE	IF	CITATIONS
37	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5859-5864.	3.3	612
38	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	2.1	595
39	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9923-9928.	3.3	595
40	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011, 12, R40.	3.8	594
41	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	6.0	591
42	Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children. <i>Science</i> , 2016, 351, .	6.0	580
43	Conserved catalytic machinery and the prediction of a common fold for several families of glycosyl hydrolases.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7090-7094.	3.3	568
44	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	1.5	532
45	Dividing the large glycoside hydrolase family 13 into subfamilies: towards improved functional annotations of A-amylase-related proteins. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 555-562.	1.0	530
46	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
47	The Plant Cell Wallâ€™Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
48	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	2.6	490
49	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490
50	Comparative Genomics Yields Insights into Niche Adaptation of Plant Vascular Wilt Pathogens. <i>PLoS Pathogens</i> , 2011, 7, e1002137.	2.1	477
51	Deciphering protein sequence information through hydrophobic cluster analysis (HCA): current status and perspectives. <i>Cellular and Molecular Life Sciences</i> , 1997, 53, 621-645.	2.4	468
52	Multidomain architecture of beta-glycosyl transferases: implications for mechanism of action. <i>Journal of Bacteriology</i> , 1995, 177, 1419-1424.	1.0	466
53	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012, 3, 913.	5.8	458
54	The Impact of a Consortium of Fermented Milk Strains on the Gut Microbiome of Gnotobiotic Mice and Monozygotic Twins. <i>Science Translational Medicine</i> , 2011, 3, 106ra106.	5.8	456

#	ARTICLE	IF	CITATIONS
55	Endogenous cellulases in animals: Isolation of β -1,4-endoglucanase genes from two species of plant-parasitic cyst nematodes. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 4906-4911.	3.3	452
56	Genomic and metabolic adaptations of <i>Methanobrevibacter smithii</i> to the human gut. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10643-10648.	3.3	451
57	Synergism of Cellulases from <i>Trichoderma reesei</i> in the Degradation of Cellulose. Bio/technology, 1985, 3, 722-726.	1.9	450
58	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. Nature, 2017, 544, 65-70.	13.7	447
59	Cellulase families revealed by hydrophobic cluster analysis. Gene, 1989, 81, 83-95.	1.0	430
60	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . Nature Biotechnology, 2011, 29, 922-927.	9.4	428
61	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . Genome Biology, 2017, 18, 28.	3.8	417
62	Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7503-7508.	3.3	414
63	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	9.4	414
64	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. PLoS Genetics, 2009, 5, e1000618.	1.5	402
65	Glycoside hydrolases and glycosyltransferases: families and functional modules. Current Opinion in Structural Biology, 2001, 11, 593-600.	2.6	393
66	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	13.9	391
67	Evolution, substrate specificity and subfamily classification of glycoside hydrolase family 5 (GH5). BMC Evolutionary Biology, 2012, 12, 186.	3.2	389
68	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Nature, 2012, 492, 59-65.	13.7	377
69	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. ISME Journal, 2014, 8, 1566-1576.	4.4	377
70	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. PLoS ONE, 2012, 7, e49138.	1.1	374
71	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847.	6.0	371
72	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17501-17506.	3.3	359

#	ARTICLE	IF	CITATIONS
73	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	13.7	352
74	Stereochemistry of chitin hydrolysis by a plant chitinase/lysozyme and x-ray structure of a complex with allosamidin evidence for substrate assisted catalysis. <i>Biochemistry</i> , 1995, 34, 15619-15623.	1.2	349
75	Biosynthesis of cellulose-enriched tension wood in <i>Populus</i> : global analysis of transcripts and metabolites identifies biochemical and developmental regulators in secondary wall biosynthesis. <i>Plant Journal</i> , 2006, 45, 144-165.	2.8	347
76	Discovery and characterization of a new family of lytic polysaccharide monooxygenases. <i>Nature Chemical Biology</i> , 2014, 10, 122-126.	3.9	329
77	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015, 6, 7481.	5.8	328
78	Genome analysis of <i>Bifidobacterium bifidum</i> PRL2010 reveals metabolic pathways for host-derived glycan foraging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19514-19519.	3.3	324
79	Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. <i>Cell</i> , 2014, 159, 253-266.	13.5	324
80	Hydrophobic cluster analysis: procedures to derive structural and functional information from 2-D-representation of protein sequences. <i>Biochimie</i> , 1990, 72, 555-574.	1.3	322
81	Effects of microbiota-directed foods in gnotobiotic animals and undernourished children. <i>Science</i> , 2019, 365, .	6.0	305
82	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	13.9	301
83	Multiple lateral gene transfers and duplications have promoted plant parasitism ability in nematodes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17651-17656.	3.3	300
84	Comparative Genome Analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : Insights into Their Environmental Niche. <i>Microbial Ecology</i> , 2010, 60, 721-729.	1.4	293
85	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. <i>ISME Journal</i> , 2011, 5, 639-649.	4.4	292
86	Updates to the Symbol Nomenclature for Glycans guidelines. <i>Glycobiology</i> , 2019, 29, 620-624.	1.3	292
87	Complex Carbohydrate Utilization by the Healthy Human Microbiome. <i>PLoS ONE</i> , 2012, 7, e28742.	1.1	291
88	A hierarchical classification of polysaccharide lyases for glycogenomics. <i>Biochemical Journal</i> , 2010, 432, 437-444.	1.7	282
89	The crystal structures of <i>Sinapis alba</i> myrosinase and a covalent glycosyl enzyme intermediate provide insights into the substrate recognition and active-site machinery of an S-glycosidase. <i>Structure</i> , 1997, 5, 663-676.	1.6	280
90	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. <i>Environmental Microbiology</i> , 2015, 17, 4954-4964.	1.8	279

#	ARTICLE	IF	CITATIONS
91	Parallel-up structure evidences the molecular directionality during biosynthesis of bacterial cellulose. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 9091-9095.	3.3	273
92	Poplar Carbohydrate-Active Enzymes. Gene Identification and Expression Analyses. Plant Physiology, 2006, 140, 946-962.	2.3	271
93	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. Nature Chemical Biology, 2018, 14, 306-310.	3.9	269
94	A scheme for designating enzymes that hydrolyse the polysaccharides in the cell walls of plants. FEBS Letters, 1998, 425, 352-354.	1.3	267
95	Recent structural insights into the expanding world of carbohydrate-active enzymes. Current Opinion in Structural Biology, 2005, 15, 637-645.	2.6	264
96	Ectomycorrhizal fungi decompose soil organic matter using oxidative mechanisms adapted from saprotrophic ancestors. New Phytologist, 2016, 209, 1705-1719.	3.5	264
97	The molecular basis of polysaccharide cleavage by lytic polysaccharide monooxygenases. Nature Chemical Biology, 2016, 12, 298-303.	3.9	264
98	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic Bacteroides. Nature Microbiology, 2018, 3, 210-219.	5.9	263
99	Bacterial glycosidases for the production of universal red blood cells. Nature Biotechnology, 2007, 25, 454-464.	9.4	259
100	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5458-5463.	3.3	259
101	Starch- and glycogen-debranching and branching enzymes: Prediction of structural features of the catalytic (?/?)-barrel domain and evolutionary relationship to other amylolytic enzymes. The Protein Journal, 1993, 12, 791-805.	1.1	258
102	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. Nature Communications, 2020, 11, 5125.	5.8	258
103	Structure and boosting activity of a starch-degrading lytic polysaccharide monooxygenase. Nature Communications, 2015, 6, 5961.	5.8	254
104	Glycoside Hydrolases and Glycosyltransferases. Families, Modules, and Implications for Genomics. Plant Physiology, 2000, 124, 1515-1519.	2.3	251
105	Utilisation of Mucin Glycans by the Human Gut Symbiont Ruminococcus gnavus Is Strain-Dependent. PLoS ONE, 2013, 8, e76341.	1.1	250
106	Structure of the <i>Fusarium oxysporum</i> Endoglucanase I with a Nonhydrolyzable Substrate Analogue: A Substrate Distortion Gives Rise to the Preferred Axial Orientation for the Leaving Group. Biochemistry, 1996, 35, 15280-15287.	1.2	248
107	Effects of Diet on Resource Utilization by a Model Human Gut Microbiota Containing <i>Bacteroides cellulosilyticus</i> WH2, a Symbiont with an Extensive Glycobiome. PLoS Biology, 2013, 11, e1001637.	2.6	244
108	Bacteroidetes use thousands of enzyme combinations to break down glycans. Nature Communications, 2019, 10, 2043.	5.8	238

#	ARTICLE	IF	CITATIONS
109	Genetic determinants of in vivo fitness and diet responsiveness in multiple human gut <i>Bacteroides</i> . <i>Science</i> , 2015, 350, aac5992.	6.0	229
110	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	2.4	228
111	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	1.5	226
112	Interspecies Competition Impacts Targeted Manipulation of Human Gut Bacteria by Fiber-Derived Glycans. <i>Cell</i> , 2019, 179, 59-73.e13.	13.5	224
113	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2504-2509.	3.3	218
114	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.	1.6	215
115	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. <i>Nature Communications</i> , 2016, 7, 11362.	5.8	214
116	Novel Features of the Polysaccharide-Digesting Gliding Bacterium <i>Flavobacterium johnsoniae</i> as Revealed by Genome Sequence Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6864-6875.	1.4	212
117	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	3.5	210
118	Genome Sequence of the Cellulolytic Gliding Bacterium <i>Cytophaga hutchinsonii</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 3536-3546.	1.4	208
119	High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont <i>Rhizophagus irregularis</i> . <i>New Phytologist</i> , 2018, 220, 1161-1171.	3.5	206
120	Genome of the red alga <i>Porphyridium purpureum</i> . <i>Nature Communications</i> , 2013, 4, 1941.	5.8	204
121	Klotho Is a Novel β -Glucuronidase Capable of Hydrolyzing Steroid β -Glucuronides. <i>Journal of Biological Chemistry</i> , 2004, 279, 9777-9784.	1.6	201
122	Automatic prediction of polysaccharide utilization loci in Bacteroidetes species. <i>Bioinformatics</i> , 2015, 31, 647-655.	1.8	195
123	The β -carrageenase of <i>P. carrageenovora</i> Features a Tunnel-Shaped Active Site. <i>Structure</i> , 2001, 9, 513-525.	1.6	193
124	Imaging the Enzymatic Digestion of Bacterial Cellulose Ribbons Reveals the Endo Character of the Cellobiohydrolase Cel6A from <i>Humicola insolens</i> and Its Mode of Synergy with Cellobiohydrolase Cel7A. <i>Applied and Environmental Microbiology</i> , 2000, 66, 1444-1452.	1.4	192
125	An ancient family of lytic polysaccharide monooxygenases with roles in arthropod development and biomass digestion. <i>Nature Communications</i> , 2018, 9, 756.	5.8	192
126	PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , 2018, 46, D677-D683.	6.5	191

#	ARTICLE	IF	CITATIONS
127	A census of carbohydrate-active enzymes in the genome of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2001, 47, 55-72.	2.0	190
128	The Three-dimensional Structure of Invertase (β -Fructosidase) from <i>Thermotoga maritima</i> Reveals a Bimodular Arrangement and an Evolutionary Relationship between Retaining and Inverting Glycosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 18903-18910.	1.6	189
129	A modular family 19 chitinase found in the prokaryotic organism <i>Streptomyces griseus</i> HUT 6037. <i>Journal of Bacteriology</i> , 1996, 178, 5065-5070.	1.0	188
130	Mucopolidosis II is caused by mutations in GNPTA encoding the β -GlcNAc-1-phosphotransferase. <i>Nature Medicine</i> , 2005, 11, 1109-1112.	15.2	187
131	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	3.5	185
132	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017, 2, 17087.	5.9	183
133	Evolution and comparative genomics of the most common <i>Trichoderma</i> species. <i>BMC Genomics</i> , 2019, 20, 485.	1.2	181
134	Genome analyses highlight the different biological roles of cellulases. <i>Nature Reviews Microbiology</i> , 2012, 10, 227-234.	13.6	180
135	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
136	Ten years of CAZypedia: a living encyclopedia of carbohydrate-active enzymes. <i>Glycobiology</i> , 2018, 28, 3-8.	1.3	175
137	Carbohydrate-Active Enzymes Involved in the Secondary Cell Wall Biogenesis in Hybrid Aspen. <i>Plant Physiology</i> , 2005, 137, 983-997.	2.3	173
138	Dividing the Large Glycoside Hydrolase Family 43 into Subfamilies: a Motivation for Detailed Enzyme Characterization. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1686-1692.	1.4	173
139	The mechanism of substrate (aglycone) specificity in beta -glucosidases is revealed by crystal structures of mutant maize beta -glucosidase-DIMBOA, -DIMBOAGlc, and -dhurrin complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 13555-13560.	3.3	168
140	Comparative Genomics of a Plant-Pathogenic Fungus, <i>Pyrenophora tritici-repentis</i> , Reveals Transduplication and the Impact of Repeat Elements on Pathogenicity and Population Divergence. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 41-63.	0.8	167
141	Undirectional degradation of valonia cellulose microcrystals subjected to cellulase action. <i>FEBS Letters</i> , 1985, 184, 285-288.	1.3	166
142	High Resolution X-ray Crystallography Shows That Ascorbate Is a Cofactor for Myrosinase and Substitutes for the Function of the Catalytic Base. <i>Journal of Biological Chemistry</i> , 2000, 275, 39385-39393.	1.6	165
143	Glycosidase families. <i>Biochemical Society Transactions</i> , 1998, 26, 153-156.	1.6	160
144	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.	9.4	160

#	ARTICLE	IF	CITATIONS
145	Insights into Plant Cell Wall Degradation from the Genome Sequence of the Soil Bacterium <i>Cellvibrio japonicus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 5455-5463.	1.0	159
146	Influenza B virus neuraminidase can synthesize its own inhibitor. <i>Structure</i> , 1993, 1, 19-26.	1.6	158
147	Domain Evolution in the α -Amylase Family. <i>Journal of Molecular Evolution</i> , 1997, 45, 322-331.	0.8	157
148	Cellulases and their interaction with cellulose. <i>Cellulose</i> , 1994, 1, 169-196.	2.4	156
149	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	5.8	156
150	The genome of the yellow potato cyst nematode, <i>Globodera rostochiensis</i> , reveals insights into the basis of parasitism and virulence. <i>Genome Biology</i> , 2016, 17, 124.	3.8	156
151	A novel, small endoglucanase gene, <i>egl5</i> , from <i>Trichoderma reesei</i> isolated by expression in yeast. <i>Molecular Microbiology</i> , 1994, 13, 219-228.	1.2	154
152	Structures of Oligosaccharide-Bound Forms of the Endoglucanase V from <i>Humicola insolens</i> at 1.9 Å Resolution. <i>Biochemistry</i> , 1995, 34, 16210-16220.	1.2	154
153	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , 2017, 19, 2964-2983.	1.8	154
154	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.	3.3	154
155	Insights on the Evolution of Mycoparasitism from the Genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 465-480.	1.1	150
156	Cello-Oligosaccharide Oxidation Reveals Differences between Two Lytic Polysaccharide Monooxygenases (Family GH61) from <i>Podospira anserina</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 488-496.	1.4	149
157	Unique Organization of Extracellular Amylases into Amylosomes in the Resistant Starch-Utilizing Human Colonic <i>Firmicutes</i> Bacterium <i>Ruminococcus bromii</i> . <i>MBio</i> , 2015, 6, e01058-15.	1.8	145
158	Exploring the genomic diversity of black yeasts and relatives (<i>Chaetothyriales</i> , <i>Ascomycota</i>). <i>Studies in Mycology</i> , 2017, 86, 1-28.	4.5	144
159	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.	1.5	143
160	Complete Genome Sequence of the Complex Carbohydrate-Degrading Marine Bacterium, <i>Saccharophagus degradans</i> Strain 2-40T. <i>PLoS Genetics</i> , 2008, 4, e1000087.	1.5	142
161	Crystal Structure of <i>Thermotoga maritima</i> α -L-Fucosidase. <i>Journal of Biological Chemistry</i> , 2004, 279, 13119-13128.	1.6	141
162	The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	1.5	141

#	ARTICLE	IF	CITATIONS
163	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011, 12, R20.	13.9	141
164	Mimivirus shows dramatic genome reduction after intraamoebal culture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10296-10301.	3.3	138
165	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018, 8, 6321.	1.6	138
166	Detection of secondary structure elements in proteins by hydrophobic cluster analysis. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 629-635.	1.0	137
167	AA16, a new lytic polysaccharide monooxygenase family identified in fungal secretomes. <i>Biotechnology for Biofuels</i> , 2019, 12, 55.	6.2	137
168	Post-genomic analyses of fungal lignocellulosic biomass degradation reveal the unexpected potential of the plant pathogen <i>Ustilago maydis</i> . <i>BMC Genomics</i> , 2012, 13, 57.	1.2	135
169	Why are there so many carbohydrate-active enzyme-related genes in plants?. <i>Trends in Plant Science</i> , 2003, 8, 563-565.	4.3	134
170	Structural and electronic determinants of lytic polysaccharide monooxygenase reactivity on polysaccharide substrates. <i>Nature Communications</i> , 2017, 8, 1064.	5.8	134
171	Post-genomic insights into the plant polysaccharide degradation potential of <i>Aspergillus nidulans</i> and comparison to <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S161-S169.	0.9	133
172	Comparative genomics of <i>Rhizophagus irregularis</i> , <i>R. Âcerebriforme</i> , <i>R. Âdiaphanus</i> and <i>Gigaspora rosea</i> highlights specific genetic features in Glomeromycotina. <i>New Phytologist</i> , 2019, 222, 1584-1598.	3.5	133
173	Genomic and Proteomic Analyses of the Agarolytic System Expressed by <i>Saccharophagus degradans</i> 2-40. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3396-3405.	1.4	129
174	The mucin-degradation strategy of <i>Ruminococcus gnavus</i> : The importance of intramolecular <i>trans</i> -sialidases. <i>Gut Microbes</i> , 2016, 7, 302-312.	4.3	127
175	Complete Cellulase System in the Marine Bacterium <i>Saccharophagus degradans</i> Strain 2-40 T. <i>Journal of Bacteriology</i> , 2006, 188, 3849-3861.	1.0	126
176	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. <i>BMC Genomics</i> , 2012, 13, 444.	1.2	125
177	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
178	Diversity and Strain Specificity of Plant Cell Wall Degrading Enzymes Revealed by the Draft Genome of <i>Ruminococcus flavefaciens</i> FD-1. <i>PLoS ONE</i> , 2009, 4, e6650.	1.1	124
179	<i>Bifidobacterium asteroides</i> PRL2011 Genome Analysis Reveals Clues for Colonization of the Insect Gut. <i>PLoS ONE</i> , 2012, 7, e44229.	1.1	123
180	Comparative genomics of the major fungal agents of human and animal Sporotrichosis: <i>Sporothrix schenckii</i> and <i>Sporothrix brasiliensis</i> . <i>BMC Genomics</i> , 2014, 15, 943.	1.2	121

#	ARTICLE	IF	CITATIONS
181	Functional guild classification predicts the enzymatic role of fungi in litter and soil biogeochemistry. <i>Soil Biology and Biochemistry</i> , 2015, 88, 441-456.	4.2	121
182	Feed in summer, rest in winter: microbial carbon utilization in forest topsoil. <i>Microbiome</i> , 2017, 5, 122.	4.9	121
183	The Three-dimensional Structures of Two β -Agarases. <i>Journal of Biological Chemistry</i> , 2003, 278, 47171-47180.	1.6	120
184	The convergence of carbohydrate active gene repertoires in human gut microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15076-15081.	3.3	120
185	Ninety-nine <i>de novo</i> 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.	4.4	120
186	Functional Implications of Structure-Based Sequence Alignment of Proteins in the Extracellular Pectate Lyase Superfamily. <i>Plant Physiology</i> , 1995, 107, 963-976.	2.3	118
187	Structural Determinants of Substrate Specificity in Family 1 β -Glucosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 31796-31803.	1.6	118
188	FOLy: An integrated database for the classification and functional annotation of fungal oxidoreductases potentially involved in the degradation of lignin and related aromatic compounds. <i>Fungal Genetics and Biology</i> , 2008, 45, 638-645.	0.9	118
189	A subfamily roadmap of the evolutionarily diverse glycoside hydrolase family 16 (GH16). <i>Journal of Biological Chemistry</i> , 2019, 294, 15973-15986.	1.6	118
190	Comparison of three algorithms for the assignment of secondary structure in proteins: the advantages of a consensus assignment. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 377-382.	1.0	117
191	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.	3.3	115
192	Characteristics of an exochitinase from <i>Streptomyces olivaceoviridis</i> , its corresponding gene, putative protein domains and relationship to other chitinases. <i>FEBS Journal</i> , 1993, 214, 659-669.	0.2	114
193	β -Carrageenases Constitute a Novel Family of Glycoside Hydrolases, Unrelated to That of α -Carrageenases. <i>Journal of Biological Chemistry</i> , 2000, 275, 35499-35505.	1.6	113
194	Archaea: Essential inhabitants of the human digestive microbiota. <i>Human Microbiome Journal</i> , 2017, 3, 1-8.	3.8	113
195	Colloidal gold labelling of 1,4- β -D-glucan cellobiohydrolase adsorbed on cellulose substrates. <i>FEBS Letters</i> , 1984, 172, 193-197.	1.3	111
196	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111
197	Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , 2017, 18, 667.	1.2	111
198	Genomewide analysis of polysaccharides degrading enzymes in 11 white- and brown-rot Polyporales provides insight into mechanisms of wood decay. <i>Mycologia</i> , 2013, 105, 1412-1427.	0.8	110

#	ARTICLE	IF	CITATIONS
199	Plant chitinases use two different hydrolytic mechanisms. <i>FEBS Letters</i> , 1996, 382, 186-188.	1.3	109
200	Evidence for a general role for high-affinity non-catalytic cellulose binding domains in microbial plant cell wall hydrolases. <i>Molecular Microbiology</i> , 1994, 11, 375-382.	1.2	108
201	The kappa-carrageenase of the marine bacterium <i>Cytophaga drobachiensis</i> . Structural and phylogenetic relationships within family-16 glycoside hydrolases. <i>Molecular Biology and Evolution</i> , 1998, 15, 528-537.	3.5	107
202	Crystal structure of a monocotyledon (maize ZMGluc1) β -D-glucosidase and a model of its complex with p-nitrophenyl β -D-thioglucoside. <i>Biochemical Journal</i> , 2001, 354, 37-46.	1.7	107
203	Secreted pectin monooxygenases drive plant infection by pathogenic oomycetes. <i>Science</i> , 2021, 373, 774-779.	6.0	106
204	Carbohydrate-active enzymes from the zygomycete fungus <i>Rhizopus oryzae</i> : a highly specialized approach to carbohydrate degradation depicted at genome level. <i>BMC Genomics</i> , 2011, 12, 38.	1.2	105
205	The transcriptome of <i>Euglena gracilis</i> reveals unexpected metabolic capabilities for carbohydrate and natural product biochemistry. <i>Molecular BioSystems</i> , 2015, 11, 2808-2820.	2.9	104
206	Insights into plant biomass conversion from the genome of the anaerobic thermophilic bacterium <i>Caldicellulosiruptor bescii</i> DSM 6725. <i>Nucleic Acids Research</i> , 2011, 39, 3240-3254.	6.5	103
207	A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. <i>Nature Microbiology</i> , 2018, 3, 1314-1326.	5.9	103
208	Single-domain flavoenzymes trigger lytic polysaccharide monooxygenases for oxidative degradation of cellulose. <i>Scientific Reports</i> , 2016, 6, 28276.	1.6	102
209	Dimension, Shape, and Conformational Flexibility of a Two Domain Fungal Cellulase in Solution Probed by Small Angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2002, 277, 40887-40892.	1.6	101
210	A Metagenomic Investigation of the Duodenal Microbiota Reveals Links with Obesity. <i>PLoS ONE</i> , 2015, 10, e0137784.	1.1	101
211	Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018, 9, 310.	5.8	101
212	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018, 3, 1417-1428.	5.9	101
213	The Location of the Ligand-binding Site of Carbohydrate-binding Modules That Have Evolved from a Common Sequence Is Not Conserved. <i>Journal of Biological Chemistry</i> , 2001, 276, 48580-48587.	1.6	99
214	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	0.9	99
215	How members of the human gut microbiota overcome the sulfation problem posed by glycosaminoglycans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7037-7042.	3.3	99
216	Extreme genome diversity in the hyper-prevalent parasitic eukaryote <i>Blastocystis</i> . <i>PLoS Biology</i> , 2017, 15, e2003769.	2.6	99

#	ARTICLE	IF	CITATIONS
217	The action of 1,4-β-D-glucan cellobiohydrolase on Valoniacellulose microcrystals. FEBS Letters, 1983, 153, 113-118.	1.3	98
218	Glycogen metabolism loss: a common marker of parasitic behaviour in bacteria?. Trends in Genetics, 2002, 18, 437-440.	2.9	98
219	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5096-104.	3.3	98
220	Serratia marcescens chitobiase is a retaining glycosidase utilizing substrate acetamido group participation. Biochemical Journal, 1997, 328, 945-949.	1.7	97
221	How nature can exploit nonspecific catalytic and carbohydrate binding modules to create enzymatic specificity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20889-20894.	3.3	97
222	Deciphering Genome Content and Evolutionary Relationships of Isolates from the Fungus <i>Magnaporthe oryzae</i> Attacking Different Host Plants. Genome Biology and Evolution, 2015, 7, 2896-2912.	1.1	96
223	Optimized mixtures of recombinant <i>Humicola insolens</i> cellulases for the biodegradation of crystalline cellulose. Biotechnology and Bioengineering, 2001, 72, 339-345.	1.7	95
224	Comparative genomics analysis of <i>Lactobacillus</i> species associated with weight gain or weight protection. Nutrition and Diabetes, 2014, 4, e109-e109.	1.5	95
225	Peizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. Nature Ecology and Evolution, 2018, 2, 1956-1965.	3.4	95
226	Stereochemistry, specificity and kinetics of the hydrolysis of reduced cellodextrins by nine cellulases. FEBS Journal, 1993, 217, 947-953.	0.2	94
227	<i>Podospira anserina</i> Hemicellulases Potentiate the <i>Trichoderma reesei</i> Secretome for Saccharification of Lignocellulosic Biomass. Applied and Environmental Microbiology, 2011, 77, 237-246.	1.4	94
228	The Complete Genome of <i>Teredinibacter turnerae</i> T7901: An Intracellular Endosymbiont of Marine Wood-Boring Bivalves (Shipworms). PLoS ONE, 2009, 4, e6085.	1.1	93
229	Viral RNA-polymerases a predicted 2-O-ribose methyltransferase domain shared by all Mononegavirales. Trends in Biochemical Sciences, 2002, 27, 222-224.	3.7	92
230	Characterization of salt-adapted secreted lignocellulolytic enzymes from the mangrove fungus <i>Pestalotiopsis</i> sp.. Nature Communications, 2013, 4, 1810.	5.8	92
231	Crystal structures of human pancreatic α-amylase in complex with carbohydrate and proteinaceous inhibitors. Biochemical Journal, 2000, 346, 201-208.	1.7	91
232	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	1.2	91
233	Specificity mapping of cellulolytic enzymes: Classification into families of structurally related proteins confirmed by biochemical analysis. Protein Science, 1992, 1, 1293-1297.	3.1	90
234	Analysis of the <i>Phlebiopsis gigantea</i> Genome, Transcriptome and Secretome Provides Insight into Its Pioneer Colonization Strategies of Wood. PLoS Genetics, 2014, 10, e1004759.	1.5	90

#	ARTICLE	IF	CITATIONS
235	The continuing expansion of CAZymes and their families. <i>Current Opinion in Chemical Biology</i> , 2019, 53, 82-87.	2.8	90
236	Nucleotide sequences of the arb genes, which control beta-glucoside utilization in <i>Erwinia chrysanthemi</i> : comparison with the <i>Escherichia coli</i> bgl operon and evidence for a new beta-glycohydrolase family including enzymes from eubacteria, archeobacteria, and humans. <i>Journal of Bacteriology</i> , 1992, 174, 765-777.	1.0	89
237	<i>Streptococcus pyogenes</i> protein F promotes invasion of HeLa cells. <i>Microbiology (United Kingdom)</i> , 1998, 144, 3079-3086.	0.7	89
238	The Family 6 Carbohydrate Binding Module CmCBM6-2 Contains Two Ligand-binding Sites with Distinct Specificities. <i>Journal of Biological Chemistry</i> , 2004, 279, 21552-21559.	1.6	89
239	Microbial community function and biomarker discovery in the human microbiome. <i>Genome Biology</i> , 2011, 12, .	13.9	89
240	Solid-state ¹³ C-N.M.R. and electron microscopy study on the reversible cellulose I β 'cellulose III β transformation in <i>Valonia</i> . <i>Carbohydrate Research</i> , 1987, 160, 1-11.	1.1	86
241	Structural Organization and a Standardized Nomenclature for Plant Endo-1,4- β -Glucanases (Cellulases) of Glycosyl Hydrolase Family 9. <i>Plant Physiology</i> , 2007, 144, 1693-1696.	2.3	86
242	Degradation of different pectins by fungi: correlations and contrasts between the pectinolytic enzyme sets identified in genomes and the growth on pectins of different origin. <i>BMC Genomics</i> , 2012, 13, 321.	1.2	86
243	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.	1.8	84
244	Structural and functional relationships in two families of beta-1,4-glycanases. <i>FEBS Journal</i> , 1991, 202, 367-377.	0.2	83
245	Localization of Synthesis of β -1,6-Glucan in <i>Saccharomyces cerevisiae</i> . <i>Journal of Bacteriology</i> , 1999, 181, 7414-7420.	1.0	82
246	Families, superfamilies and subfamilies of glycosyl hydrolases. <i>Biochemical Journal</i> , 1995, 311, 350-351.	1.7	81
247	Towards a classification of glycosyltransferases based on amino acid sequence similarities: prokaryotic β -mannosyltransferases. <i>Biochemical Journal</i> , 1996, 318, 133-138.	1.7	81
248	Divergence of Catalytic Mechanism within a Glycosidase Family Provides Insight into Evolution of Carbohydrate Metabolism by Human Gut Flora. <i>Chemistry and Biology</i> , 2008, 15, 1058-1067.	6.2	81
249	Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production. <i>Journal of Bacteriology</i> , 2010, 192, 6494-6496.	1.0	81
250	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. <i>Fungal Genetics and Biology</i> , 2014, 72, 168-181.	0.9	81
251	Xylan degradation by the human gut <i>Bacteroides xylanisolvens</i> XB1AT involves two distinct gene clusters that are linked at the transcriptional level. <i>BMC Genomics</i> , 2016, 17, 326.	1.2	81
252	The third chitinase gene (chiC) of <i>Serratia marcescens</i> 2170 and the relationship of its product to other bacterial chitinases. <i>Biochemical Journal</i> , 1999, 343, 587.	1.7	80

#	ARTICLE	IF	CITATIONS
253	Enzyme-Catalyzed Condensation Reaction in a Mammalian Î±-Amylase. High-Resolution Structural Analysis of an Enzyme~Inhibitor Complex. <i>Biochemistry</i> , 2001, 40, 7700-7709.	1.2	80
254	Protein Disorder: Conformational Distribution of the Flexible Linker in a Chimeric Double Cellulase. <i>Biophysical Journal</i> , 2005, 88, 2823-2832.	0.2	80
255	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico ~Dead Zone. <i>MBio</i> , 2017, 8, .	1.8	80
256	A census of carbohydrate-active enzymes in the genome of <i>Arabidopsis thaliana</i> . , 2001, , 55-72.		80
257	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. <i>Journal of Proteome Research</i> , 2012, 11, 5924-5933.	1.8	79
258	Structure~function characterization reveals new catalytic diversity in the galactose oxidase and glyoxal oxidase family. <i>Nature Communications</i> , 2015, 6, 10197.	5.8	79
259	The gene encoding the kappa-carrageenase of <i>Alteromonas carrageenovora</i> is related to Î²-1,3-1,4-glucanases. <i>Gene</i> , 1994, 139, 105-109.	1.0	78
260	Comparative genomics, proteomics and transcriptomics give new insight into the exoproteome of the basidiomycete <i>Helveloma cylindrosporum</i> and its involvement in ectomycorrhizal symbiosis. <i>New Phytologist</i> , 2015, 208, 1169-1187.	3.5	78
261	Galactosaminogalactan activates the inflammasome to provide host protection. <i>Nature</i> , 2020, 588, 688-692.	13.7	78
262	Functional Metagenomics Reveals Novel Pathways of Prebiotic Breakdown by Human Gut Bacteria. <i>PLoS ONE</i> , 2013, 8, e72766.	1.1	78
263	Crystal structure of a monocotyledon (maize ZMGluc1) Î²-glucosidase and a model of its complex with p-nitrophenyl Î²-d-thioglycoside. <i>Biochemical Journal</i> , 2001, 354, 37.	1.7	76
264	Biochemical and Structural Characterization of the Intracellular Mannanase AaManA of <i>Alicyclobacillus acidocaldarius</i> Reveals a Novel Glycoside Hydrolase Family Belonging to Clan GH-A. <i>Journal of Biological Chemistry</i> , 2008, 283, 31551-31558.	1.6	76
265	Modulation of cellulosome composition in <i>Clostridium cellulolyticum</i> : Adaptation to the polysaccharide environment revealed by proteomic and carbohydrate~active enzyme analyses. <i>Proteomics</i> , 2010, 10, 541-554.	1.3	76
266	Emergence of a subfamily of xylanase inhibitors within glycoside hydrolase family 18. <i>FEBS Journal</i> , 2005, 272, 1745-1755.	2.2	74
267	A Bifunctionalized Fluorogenic Tetrasaccharide as a Substrate to Study Cellulases. <i>Journal of Biological Chemistry</i> , 1997, 272, 2709-2713.	1.6	73
268	A mutation in the GTP hydrolysis site of <i>Arabidopsis</i> dynamin-related protein 1E confers enhanced cell death in response to powdery mildew infection. <i>Plant Journal</i> , 2006, 47, 75-84.	2.8	73
269	Rumen Cellulosomics: Divergent Fiber-Degrading Strategies Revealed by Comparative Genome-Wide Analysis of Six Ruminococcal Strains. <i>PLoS ONE</i> , 2014, 9, e99221.	1.1	73
270	Classification of chitinases modules. , 1999, 87, 137-156.		73

#	ARTICLE	IF	CITATIONS
271	Stereochemical course of the hydrolysis reaction catalyzed by chitinases A1 and D from <i>Bacillus circulans</i> WL-12. <i>FEBS Letters</i> , 1994, 343, 177-180.	1.3	72
272	Digestion of crystalline cellulose substrates by the <i>Clostridium thermocellum</i> cellulosome: structural and morphological aspects. <i>Biochemical Journal</i> , 1999, 340, 829-835.	1.7	72
273	Three-Dimensional Structures of UDP-Sugar Glycosyltransferases Illuminate the Biosynthesis of Plant Polysaccharides. <i>Plant Physiology</i> , 2001, 125, 527-531.	2.3	72
274	The genome of <i>Xylona heveae</i> provides a window into fungal endophytism. <i>Fungal Biology</i> , 2016, 120, 26-42.	1.1	72
275	Genomic Analysis Enlightens Agaricales Lifestyle Evolution and Increasing Peroxidase Diversity. <i>Molecular Biology and Evolution</i> , 2021, 38, 1428-1446.	3.5	72
276	Electron microscopic investigation of the diffusion of <i>Bacillus licheniformis</i> α -amylase into corn starch granules. <i>International Journal of Biological Macromolecules</i> , 1996, 19, 165-169.	3.6	71
277	The β -Carrageenase of <i>Alteromonas fortis</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 40202-40209.	1.6	71
278	Mannanase A from <i>Pseudomonas fluorescens</i> ssp. <i>cellulosals</i> a Retaining Glycosyl Hydrolase in Which E212 and E320 Are the Putative Catalytic Residues. <i>Biochemistry</i> , 1996, 35, 16195-16204.	1.2	70
279	Identification of the Catalytic Nucleophile of the Family 29 β -L-Fucosidase from <i>Thermotoga maritima</i> through Trapping of a Covalent Glycosyl-Enzyme Intermediate and Mutagenesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 47394-47399.	1.6	70
280	Evaluating microbiome-directed fibre snacks in gnotobiotic mice and humans. <i>Nature</i> , 2021, 595, 91-95.	13.7	70
281	X4 Modules Represent a New Family of Carbohydrate-binding Modules That Display Novel Properties. <i>Journal of Biological Chemistry</i> , 2004, 279, 22953-22963.	1.6	69
282	Genomic insights from <i>Monoglobus pectinilyticus</i> : a pectin-degrading specialist bacterium in the human colon. <i>ISME Journal</i> , 2019, 13, 1437-1456.	4.4	69
283	The Crystal Structure of the Family 6 Carbohydrate Binding Module from <i>Cellvibrio mixtus</i> Endoglucanase 5A in Complex with Oligosaccharides Reveals Two Distinct Binding Sites with Different Ligand Specificities. <i>Journal of Biological Chemistry</i> , 2004, 279, 21560-21568.	1.6	68
284	Amino acid sequence similarities between low molecular weight endo-1,4- β -xylanases and family H cellulases revealed by clustering analysis. <i>FEBS Letters</i> , 1993, 321, 135-139.	1.3	67
285	Biochemical Analysis of Recombinant Fungal Mutanases. <i>Journal of Biological Chemistry</i> , 2000, 275, 2009-2018.	1.6	67
286	Enzyme-Substrate Complex Structures of a GH39 β -Xylosidase from <i>Geobacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 2005, 353, 838-846.	2.0	67
287	The Structure of a <i>Streptomyces avermitilis</i> β -L-Rhamnosidase Reveals a Novel Carbohydrate-binding Module CBM67 within the Six-domain Arrangement. <i>Journal of Biological Chemistry</i> , 2013, 288, 12376-12385.	1.6	67
288	Enhanced degradation of softwood versus hardwood by the white-rot fungus <i>Pycnoporus coccineus</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 216.	6.2	67

#	ARTICLE	IF	CITATIONS
289	Display of the human mucinome with defined O-glycans by gene engineered cells. <i>Nature Communications</i> , 2021, 12, 4070.	5.8	67
290	Identification of the catalytic residues of the first family of Î ² (1â€³)glucanotransferases identified in fungi. <i>Biochemical Journal</i> , 2000, 347, 741-747.	1.7	66
291	Comparative genomic analysis provides insights into the evolution and niche adaptation of marine <i>Magnetospira</i> sp. QH strain. <i>Environmental Microbiology</i> , 2014, 16, 525-544.	1.8	66
292	Active-site motifs of lysosomal acid hydrolases: invariant features of clan GH-A glycosyl hydrolases deduced from hydrophobic cluster analysis. <i>Glycobiology</i> , 1997, 7, 277-284.	1.3	65
293	The Gene <i>glvA</i> of <i>Bacillus subtilis</i> 168 Encodes a Metal-requiring, NAD(H)-dependent 6-Phospho-Î-glucosidase. <i>Journal of Biological Chemistry</i> , 1998, 273, 27347-27356.	1.6	65
294	Abundance and Diversity of Dockerin-Containing Proteins in the Fiber-Degrading Rumen Bacterium, <i>Ruminococcus flavefaciens</i> FD-1. <i>PLoS ONE</i> , 2010, 5, e12476.	1.1	65
295	Mining for hemicellulases in the fungus-growing termite <i>Pseudacanthotermes militaris</i> using functional metagenomics. <i>Biotechnology for Biofuels</i> , 2013, 6, 78.	6.2	65
296	Quantitative Trait Loci and Comparative Genomics of Cereal Cell Wall Composition. <i>Plant Physiology</i> , 2003, 132, 263-271.	2.3	64
297	Crystal structure of inactivated <i>Thermotoga maritima</i> invertase in complex with the trisaccharide substrate raffinose. <i>Biochemical Journal</i> , 2006, 395, 457-462.	1.7	64
298	Parallel Substrate Binding Sites in a Î ² -Agarase Suggest a Novel Mode of Action on Double-Helical Agarose. <i>Structure</i> , 2004, 12, 623-632.	1.6	63
299	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3451-3456.	3.3	63
300	Discovery of genes coding for carbohydrate-active enzyme by metagenomic analysis of lignocellulosic biomasses. <i>Scientific Reports</i> , 2017, 7, 42623.	1.6	63
301	A fungal family of lytic polysaccharide monooxygenase-like copper proteins. <i>Nature Chemical Biology</i> , 2020, 16, 345-350.	3.9	63
302	<i>Mycobacterium tuberculosis</i> Strains Possess Functional Cellulases. <i>Journal of Biological Chemistry</i> , 2005, 280, 20181-20184.	1.6	62
303	<i>Mycobacterium tuberculosis</i> Complex <i>Mycobacteria</i> as <i>Amoeba</i> -Resistant Organisms. <i>PLoS ONE</i> , 2011, 6, e20499.	1.1	62
304	Complete genome of a new <i>Firmicutes</i> species belonging to the dominant human colonic microbiota (<i>Ruminococcus bicirculans</i>) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014, 16, 2879-2890.	1.8	62
305	Docking of congo red to the surface of crystalline cellulose using molecular mechanics. <i>Biopolymers</i> , 1995, 36, 201-210.	1.2	61
306	A classification of nucleotide-diphospho-sugar glycosyltransferases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1998, 329, 719-719.	1.7	61

#	ARTICLE	IF	CITATIONS
307	Carbohydrate-related enzymes of important Phytophthora plant pathogens. Fungal Genetics and Biology, 2014, 72, 192-200.	0.9	61
308	The chimeric nature of the genomes of marine magnetotactic coccoid-rod bacteria defines a novel group of <i>Proteobacteria</i> . Environmental Microbiology, 2017, 19, 1103-1119.	1.8	60
309	Crystal structure of a cohesin module from <i>Clostridium cellulolyticum</i> : implications for dockerin recognition. Journal of Molecular Biology, 2000, 304, 189-200.	2.0	59
310	Glycosyltransferases, glycoside hydrolases: surprise, surprise!. Current Opinion in Structural Biology, 2008, 18, 527-533.	2.6	59
311	CelS: a novel endoglucanase identified from <i>Erwinia carotovora</i> subsp. <i>carotovora</i> . Gene, 1990, 90, 9-14.	1.0	58
312	The crystal structure of methyl β -D-cellobioside monohydrate 0.25 ethanolate and its relationship to cellulose II. Carbohydrate Research, 1995, 277, 209-229.	1.1	58
313	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus. BMC Genomics, 2015, 16, 461.	1.2	58
314	Complexity of the <i>Ruminococcus flavefaciens</i> cellulosome reflects an expansion in glycan recognition. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7136-7141.	3.3	58
315	Metabolism of multiple glycosaminoglycans by <i>Bacteroides thetaiotaomicron</i> is orchestrated by a versatile core genetic locus. Nature Communications, 2020, 11, 646.	5.8	58
316	Genetic determinants of endophytism in the <i>Arabidopsis</i> root mycobiome. Nature Communications, 2021, 12, 7227.	5.8	58
317	Visualization of the adsorption of a bacterial endo- β -1,4-glucanase and its isolated cellulose-binding domain to crystalline cellulose. International Journal of Biological Macromolecules, 1993, 15, 347-351.	3.6	57
318	Functional Annotation of the <i>Ophiostoma novo-ulmi</i> Genome: Insights into the Phytopathogenicity of the Fungal Agent of Dutch Elm Disease. Genome Biology and Evolution, 2015, 7, 410-430.	1.1	56
319	Are stool samples suitable for studying the link between gut microbiota and obesity?. European Journal of Epidemiology, 2014, 29, 307-309.	2.5	55
320	A bioinformatics analysis of 3400 lytic polysaccharide oxidases from family AA9. Carbohydrate Research, 2017, 448, 166-174.	1.1	55
321	Microbiota-directed fibre activates both targeted and secondary metabolic shifts in the distal gut. Nature Communications, 2020, 11, 5773.	5.8	55
322	Cloning and Characterization of a Xylanase Gene from Corn Strains of <i>Erwinia chrysanthemi</i> . Molecular Plant-Microbe Interactions, 1996, 9, 651.	1.4	55
323	Structural homology among the peroxidase enzyme family revealed by hydrophobic cluster analysis. Proteins: Structure, Function and Bioinformatics, 1990, 8, 251-257.	1.5	54
324	Detailed Kinetic Analysis of a Family 52 Glycoside Hydrolase: A β -Xylosidase from <i>Geobacillus stearothermophilus</i> . Biochemistry, 2003, 42, 10528-10536.	1.2	54

#	ARTICLE	IF	CITATIONS
325	Genome-wide analysis of <i>Acetivibrio cellulolyticus</i> provides a blueprint of an elaborate cellulosome system. <i>BMC Genomics</i> , 2012, 13, 210.	1.2	54
326	Globally distributed root endophyte <i>Phialocephala subalpina</i> links pathogenic and saprophytic lifestyles. <i>BMC Genomics</i> , 2016, 17, 1015.	1.2	54
327	Multi-omic analyses of exogenous nutrient bag decomposition by the black morel <i>Morchella importuna</i> reveal sustained carbon acquisition and transferring. <i>Environmental Microbiology</i> , 2019, 21, 3909-3926.	1.8	54
328	Identification of an essential glutamate residue in the active site of endoglucanase III from <i>Trichoderma reesei</i> . <i>FEBS Letters</i> , 1993, 316, 137-140.	1.3	53
329	Identification of the Catalytic Residues in Family 52 Glycoside Hydrolase, a β -Xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Journal of Biological Chemistry</i> , 2003, 278, 26742-26749.	1.6	53
330	Fast solubilization of recalcitrant cellulosic biomass by the basidiomycete fungus <i>Laetisaria arvalis</i> involves successive secretion of oxidative and hydrolytic enzymes. <i>Biotechnology for Biofuels</i> , 2014, 7, 143.	6.2	53
331	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.	1.7	53
332	Comparative genomics reveals unique wood decay strategies and fruiting body development in the Schizophyllaceae. <i>New Phytologist</i> , 2019, 224, 902-915.	3.5	53
333	Membrane association is a determinant for substrate recognition by PMT4 protein O-mannosyltransferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7827-7832.	3.3	52
334	Identification of a GH110 Subfamily of β -1,3-Galactosidases. <i>Journal of Biological Chemistry</i> , 2008, 283, 8545-8554.	1.6	52
335	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> . <i>New Phytologist</i> , 2014, 202, 554-564.	3.5	52
336	A glycogene mutation map for discovery of diseases of glycosylation. <i>Glycobiology</i> , 2015, 25, 211-224.	1.3	52
337	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.	1.2	51
338	A novel synthesis of 5-thio-D-glucose. <i>Tetrahedron Letters</i> , 1981, 22, 5061-5062.	0.7	50
339	Dispersion polymerization of styrene in polar solvents. <i>Journal of Colloid and Interface Science</i> , 1990, 138, 170-181.	5.0	50
340	Nucleotide sequence of the engXCA gene encoding the major endoglucanase of <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Gene</i> , 1990, 89, 53-59.	1.0	50
341	Role of Glycoside Phosphorylases in Mannose Foraging by Human Gut Bacteria. <i>Journal of Biological Chemistry</i> , 2013, 288, 32370-32383.	1.6	50
342	Differential gene retention as an evolutionary mechanism to generate biodiversity and adaptation in yeasts. <i>Scientific Reports</i> , 2015, 5, 11571.	1.6	50

#	ARTICLE	IF	CITATIONS
343	Glycans affect DNA extraction and induce substantial differences in gut metagenomic studies. <i>Scientific Reports</i> , 2016, 6, 26276.	1.6	50
344	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.	5.8	50
345	Mechanism-Based Inhibition and Stereochemistry of Glucosinolate Hydrolysis by Myrosinase. <i>Biochemistry</i> , 1996, 35, 15256-15259.	1.2	49
346	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a secreted β -1,4 endoglucanase that plays a key role in symbiosis development. <i>New Phytologist</i> , 2018, 220, 1309-1321.	3.5	49
347	Comparative Analysis of Secretome Profiles of Manganese(II)-Oxidizing Ascomycete Fungi. <i>PLoS ONE</i> , 2016, 11, e0157844.	1.1	49
348	Molecular Basis for Galactosylation of Core Fucose Residues in Invertebrates. <i>Journal of Biological Chemistry</i> , 2009, 284, 36223-36233.	1.6	48
349	Classification of glycoside hydrolases and glycosyltransferases from hyperthermophiles. <i>Methods in Enzymology</i> , 2001, 330, 183-201.	0.4	47
350	The Cyst-Dividing Bacterium <i>Ramlibacter tataouinensis</i> TTB310 Genome Reveals a Well-Stocked Toolbox for Adaptation to a Desert Environment. <i>PLoS ONE</i> , 2011, 6, e23784.	1.1	47
351	Solution structure of the module X2_1 of unknown function of the cellulosomal scaffolding protein CipC of <i>Clostridium cellulolyticum</i> . <i>Journal of Molecular Biology</i> , 2000, 304, 201-217.	2.0	46
352	Visual Comparative Omics of Fungi for Plant Biomass Deconstruction. <i>Frontiers in Microbiology</i> , 2016, 7, 1335.	1.5	46
353	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.	5.5	46
354	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	4.4	46
355	VaZyMolO: a tool to define and classify modularity in viral proteins. <i>Journal of General Virology</i> , 2005, 86, 743-749.	1.3	45
356	A New Archaeal β -Glycosidase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 20691-20703.	1.6	45
357	Insights into Exo- and Endoglucanase Activities of Family 6 Glycoside Hydrolases from <i>Podospira anserina</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 4220-4229.	1.4	45
358	First Structural Insights into β -L-Arabinofuranosidases from the Two GH62 Glycoside Hydrolase Subfamilies. <i>Journal of Biological Chemistry</i> , 2014, 289, 5261-5273.	1.6	45
359	Integrative visual omics of the white-rot fungus <i>Polyporus brumalis</i> exposes the biotechnological potential of its oxidative enzymes for delignifying raw plant biomass. <i>Biotechnology for Biofuels</i> , 2018, 11, 201.	6.2	45
360	Comparative Genomic Analysis of <i>Drechmeria coniospora</i> Reveals Core and Specific Genetic Requirements for Fungal Endoparasitism of Nematodes. <i>PLoS Genetics</i> , 2016, 12, e1006017.	1.5	45

#	ARTICLE	IF	CITATIONS
361	Euglena in time: Evolution, control of central metabolic processes and multi-domain proteins in carbohydrate and natural product biochemistry. <i>Perspectives in Science</i> , 2015, 6, 84-93.	0.6	44
362	The yeast <i>Geotrichum candidum</i> encodes functional lytic polysaccharide monoxygenases. <i>Biotechnology for Biofuels</i> , 2017, 10, 215.	6.2	44
363	Gene family expansions and transcriptome signatures uncover fungal adaptations to wood decay. <i>Environmental Microbiology</i> , 2021, 23, 5716-5732.	1.8	44
364	Identification of Candidate Active Site Residues in Lysosomal β -Hexosaminidase A. <i>Journal of Biological Chemistry</i> , 1997, 272, 814-820.	1.6	43
365	Functional Analysis of Family GH36 β -Galactosidases from <i>Ruminococcus gnavus</i> E1: Insights into the Metabolism of a Plant Oligosaccharide by a Human Gut Symbiont. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7720-7732.	1.4	43
366	Carbohydrate-active enzymes revealed in <i>Coptotermes formosanus</i> (Isoptera: Rhinotermitidae) transcriptome. <i>Insect Molecular Biology</i> , 2012, 21, 235-245.	1.0	43
367	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.	1.3	43
368	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. <i>Molecular Biology and Evolution</i> , 2018, 35, 1840-1854.	3.5	43
369	Structure-Based Multiple Alignment of Extracellular Pectate Lyase Sequences. <i>Molecular Plant-Microbe Interactions</i> , 1995, 8, 331.	1.4	43
370	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.	0.9	42
371	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.	1.7	42
372	Stereochemistry of the hydrolysis reaction catalyzed by endoglucanase Z from <i>Erwinia chrysanthemi</i> . <i>FEBS Letters</i> , 1992, 300, 145-148.	1.3	41
373	Evolutionary and mechanistic relationships between glycosidases acting on β - and α -bonds. <i>Carbohydrate Research</i> , 2005, 340, 2728-2734.	1.1	41
374	CAZyme content of <i>Pochonia chlamydosporia</i> reflects that chitin and chitosan modification are involved in nematode parasitism. <i>Environmental Microbiology</i> , 2016, 18, 4200-4215.	1.8	41
375	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.	1.7	41
376	Transcriptome analysis of <i>Stagonospora nodorum</i> : gene models, effectors, metabolism and pantothenate dispensability. <i>Molecular Plant Pathology</i> , 2012, 13, 531-545.	2.0	40
377	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <i>ISME Journal</i> , 2014, 8, 493-503.	4.4	40
378	Phenotypic and Genomic Diversification in Complex Carbohydrate-Degrading Human Gut Bacteria. <i>MSystems</i> , 2022, 7, e0094721.	1.7	40

#	ARTICLE	IF	CITATIONS
379	Recognition of the Helical Structure of β -1,4-Galactan by a New Family of Carbohydrate-binding Modules. <i>Journal of Biological Chemistry</i> , 2010, 285, 35999-36009.	1.6	39
380	The β -glucuronidase Agu1 from <i>Schizophyllum commune</i> is a member of a novel glycoside hydrolase family (GH115). <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 1323-1332.	1.7	39
381	Genomic Evaluation of <i>Thermoanaerobacter</i> spp. for the Construction of Designer Co-Cultures to Improve Lignocellulosic Biofuel Production. <i>PLoS ONE</i> , 2013, 8, e59362.	1.1	39
382	Comparative analyses of <i>Podospora anserina</i> secretomes reveal a large array of lignocellulose-active enzymes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7457-7469.	1.7	39
383	Genome sequence and transcriptome analyses of the thermophilic zygomycete fungus <i>Rhizomucor miehei</i> . <i>BMC Genomics</i> , 2014, 15, 294.	1.2	39
384	CAZyChip: dynamic assessment of exploration of glycoside hydrolases in microbial ecosystems. <i>BMC Genomics</i> , 2016, 17, 671.	1.2	39
385	A Metagenomics Investigation of Carbohydrate-Active Enzymes along the Gastrointestinal Tract of Saudi Sheep. <i>Frontiers in Microbiology</i> , 2017, 8, 666.	1.5	39
386	Poplar carbohydrate-active enzymes: whole-genome annotation and functional analyses based on <i>scRNA</i> expression data. <i>Plant Journal</i> , 2019, 99, 589-609.	2.8	39
387	Cloning and characterization of the <i>bgxA</i> gene from <i>Erwinia chrysanthemi</i> D1 which encodes a β -glucosidase/xylosidase enzyme. <i>Molecular Genetics and Genomics</i> , 1995, 246, 465-477.	2.4	38
388	Structure-Function Analysis of a Mixed-linkage β -Glucanase/Xyloglucanase from the Key Ruminant Bacteroidetes <i>Prevotella bryantii</i> B14. <i>Journal of Biological Chemistry</i> , 2016, 291, 1175-1197.	1.6	38
389	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. <i>Scientific Reports</i> , 2017, 7, 40248.	1.6	38
390	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.	3.3	38
391	Ancient acquisition of α -alginate utilization loci by human gut microbiota. <i>Scientific Reports</i> , 2018, 8, 8075.	1.6	38
392	Hydrophobic cluster analysis of the primary sequences of β -amylases. <i>International Journal of Biological Macromolecules</i> , 1989, 11, 217-225.	3.6	37
393	<i>Aspergillus aculeatus</i> β -1,4-Galactanase: Substrate Recognition and Relations to Other Glycoside Hydrolases in Clan GH-A. <i>Biochemistry</i> , 2002, 41, 15135-15143.	1.2	37
394	Development and characterization of stable anaerobic thermophilic methanogenic microbiomes fermenting switchgrass at decreasing residence times. <i>Biotechnology for Biofuels</i> , 2018, 11, 243.	6.2	37
395	Secreted Glycoside Hydrolase Proteins as Effectors and Invasion Patterns of Plant-Associated Fungi and Oomycetes. <i>Frontiers in Plant Science</i> , 2022, 13, 853106.	1.7	37
396	Possible adsorption sites of cellulases on crystalline cellulose. <i>FEBS Letters</i> , 1988, 231, 177-182.	1.3	36

#	ARTICLE	IF	CITATIONS
397	Analysis of the Structural and Functional Diversity of Plant Cell Wall Specific Family 6 Carbohydrate Binding Modules. <i>Biochemistry</i> , 2009, 48, 10395-10404.	1.2	36
398	Metagenomics unveils the attributes of the alginolytic guilds of sediments from four distant cold coastal environments. <i>Environmental Microbiology</i> , 2016, 18, 4471-4484.	1.8	36
399	Development and Validation of a Microarray for the Investigation of the CAZymes Encoded by the Human Gut Microbiome. <i>PLoS ONE</i> , 2013, 8, e84033.	1.1	36
400	Cloning, sequencing and overexpression in <i>Escherichia coli</i> of the alginatelyase-encoding <i>aly</i> gene of <i>Pseudomonas alginovora</i> : identification of three classes of alginate lyases. <i>Biochemical Journal</i> , 1996, 319, 575-583.	1.7	35
401	Signature Active Site Architectures Illuminate the Molecular Basis for Ligand Specificity in Family 35 Carbohydrate Binding Module,. <i>Biochemistry</i> , 2010, 49, 6193-6205.	1.2	35
402	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . <i>BMC Genomics</i> , 2013, 14, 663.	1.2	35
403	De novo assembly of the complex genome of <i>Nippostrongylus brasiliensis</i> using MinION long reads. <i>BMC Biology</i> , 2018, 16, 6.	1.7	35
404	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. <i>GigaScience</i> , 2020, 9, .	3.3	35
405	Hydrophobic-cluster analysis of plant protein sequences. A domain homology between storage and lipid-transfer proteins. <i>Biochemical Journal</i> , 1988, 255, 901-905.	1.7	34
406	<i>Tropheryma whipplei</i> Glycosylation in the Pathophysiologic Profile of Whipple's Disease. <i>Journal of Infectious Diseases</i> , 2009, 199, 1043-1052.	1.9	34
407	De Novo Assembly and Genome Analyses of the Marine-Derived <i>Scopulariopsis brevicaulis</i> Strain LF580 Unravels Life-Style Traits and Anticancerous Scopularide Biosynthetic Gene Cluster. <i>PLoS ONE</i> , 2015, 10, e0140398.	1.1	34
408	Functional Exploration of the Polysaccharide Lyase Family PL6. <i>PLoS ONE</i> , 2016, 11, e0159415.	1.1	34
409	The Mechanism by Which Arabinoxylanases Can Recognize Highly Decorated Xylans. <i>Journal of Biological Chemistry</i> , 2016, 291, 22149-22159.	1.6	34
410	Asymmetric acetalation of α , α -trehalose: Synthesis of α -d-galactopyranosyl α -d-glucopyranoside and 6-deoxy-6-fluoro- α -d-glucopyranosyl α -d-glucopyranoside. <i>Carbohydrate Research</i> , 1978, 63, 41-49.	1.1	33
411	Endoglucanase II (EGII) of <i>Penicillium janthinellum</i> : cDNA sequence, heterologous expression and promoter analysis. <i>Current Genetics</i> , 1996, 29, 490-495.	0.8	33
412	Evidence That Galactanase A from <i>Pseudomonas fluorescens</i> Subspecies <i>cellulosals</i> a Retaining Family 53 Glycosyl Hydrolase in Which E161 and E270 Are the Catalytic Residues. <i>Biochemistry</i> , 1997, 36, 15489-15500.	1.2	33
413	A Novel, Noncatalytic Carbohydrate-binding Module Displays Specificity for Galactose-containing Polysaccharides through Calcium-mediated Oligomerization. <i>Journal of Biological Chemistry</i> , 2011, 286, 22499-22509.	1.6	33
414	The identification and molecular characterization of the first archaeal bifunctional exo- β -glucosidase/N-acetyl- β -glucosaminidase demonstrate that family GH116 is made of three functionally distinct subfamilies. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 367-377.	1.1	33

#	ARTICLE	IF	CITATIONS
415	Unraveling the pectinolytic function of <i>Bacteroides xylophilus</i> using a RNA-seq approach and mutagenesis. <i>BMC Genomics</i> , 2016, 17, 147.	1.2	33
416	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.	1.9	33
417	Infection cushions of <i>Fusarium graminearum</i> are fungal arsenals for wheat infection. <i>Molecular Plant Pathology</i> , 2020, 21, 1070-1087.	2.0	33
418	Clinical evidence of the role of <i>Methanobrevibacter smithii</i> in severe acute malnutrition. <i>Scientific Reports</i> , 2021, 11, 5426.	1.6	33
419	Processing and Hydrolytic Mechanism of the <i>cgkA</i> -Encoded kappa-Carrageenase of <i>Alteromonas carrageenovora</i> . <i>FEBS Journal</i> , 1995, 228, 971-975.	0.2	33
420	Investigating host-microbiome interactions by droplet based microfluidics. <i>Microbiome</i> , 2020, 8, 141.	4.9	33
421	A family GH51 α -L-arabinofuranosidase from <i>Pleurotus ostreatus</i> : identification, recombinant expression and characterization. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 995-1006.	1.7	32
422	Broad phylogeny and functionality of cellulosomal components in the bovine rumen microbiome. <i>Environmental Microbiology</i> , 2017, 19, 185-197.	1.8	32
423	Discovery of hyperstable carbohydrate-active enzymes through metagenomics of extreme environments. <i>FEBS Journal</i> , 2020, 287, 1116-1137.	2.2	32
424	Fungal ecological strategies reflected in gene transcription – a case study of two litter decomposers. <i>Environmental Microbiology</i> , 2020, 22, 1089-1103.	1.8	32
425	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	1.5	32
426	Stereochemical Course and Reaction Products of the Action of beta-Xylosidase from <i>Thermoanaerobacterium saccharolyticum</i> Strain B6A-RI. <i>FEBS Journal</i> , 1996, 236, 706-713.	0.2	31
427	Human glucocerebrosidase: heterologous expression of active site mutants in murine null cells. <i>Glycobiology</i> , 2000, 10, 1217-1224.	1.3	31
428	The Enzymatic Synthesis of Glycosidic Bonds: "Glycosynthases" and Glycosyltransferases.. <i>Trends in Glycoscience and Glycotechnology</i> , 2001, 13, 105-120.	0.0	31
429	Identification of <i>Euglena gracilis</i> β -1,3-glucan phosphorylase and establishment of a new glycoside hydrolase (GH) family GH149. <i>Journal of Biological Chemistry</i> , 2018, 293, 2865-2876.	1.6	31
430	Stereochemistry of the hydrolysis of α , α -trehalose by trehalase, determined by using a labelled substrate. <i>Carbohydrate Research</i> , 1983, 124, 265-273.	1.1	30
431	The human gut microbe <i>Bacteroides thetaiotaomicron</i> encodes the founding member of a novel glycosaminoglycan-degrading polysaccharide lyase family PL29. <i>Journal of Biological Chemistry</i> , 2018, 293, 17906-17916.	1.6	30
432	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.	1.6	30

#	ARTICLE	IF	CITATIONS
433	Insights into an unusual Auxiliary Activity 9 family member lacking the histidine brace motif of lytic polysaccharide monoxygenases. <i>Journal of Biological Chemistry</i> , 2019, 294, 17117-17130.	1.6	30
434	From proteins to polysaccharides: lifestyle and genetic evolution of <i>Coprothermobacter proteolyticus</i> . <i>ISME Journal</i> , 2019, 13, 603-617.	4.4	30
435	Comparative Analysis of Carbohydrate Active Enzymes in <i>Clostridium termitidis</i> CT1112 Reveals Complex Carbohydrate Degradation Ability. <i>PLoS ONE</i> , 2014, 9, e104260.	1.1	29
436	Unique organization and unprecedented diversity of the Bacteroides (Pseudobacteroides) cellulolvens cellulosome system. <i>Biotechnology for Biofuels</i> , 2017, 10, 211.	6.2	29
437	Proteomic Dissection of the Cellulolytic Machineries Used by Soil-Dwelling Bacteroidetes. <i>MSystems</i> , 2018, 3, .	1.7	29
438	Glycosidase active site mutations in human \hat{A} -L-iduronidase. <i>Glycobiology</i> , 2001, 11, 741-750.	1.3	28
439	Genome and Transcriptome of <i>Clostridium phytofermentans</i> , Catalyst for the Direct Conversion of Plant Feedstocks to Fuels. <i>PLoS ONE</i> , 2015, 10, e0118285.	1.1	28
440	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.	3.5	28
441	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines. , 2017, , 117-131.		27
442	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.	5.1	27
443	4-Thiocellooligosaccharides : Their Synthesis and use as Inhibitors of Cellulases. <i>Journal of Carbohydrate Chemistry</i> , 1993, 12, 743-752.	0.4	26
444	Viewing the human microbiome through three-dimensional glasses: integrating structural and functional studies to better define the properties of myriad carbohydrate-active enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1261-1264.	0.7	26
445	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 13271-13283.	1.6	26
446	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides. <i>Nature Communications</i> , 2022, 13, 629.	5.8	26
447	Microbial liberation of N-methylserotonin from orange fiber in gnotobiotic mice and humans. <i>Cell</i> , 2022, 185, 2495-2509.e11.	13.5	26
448	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.	1.6	25
449	Substrate specificity, regiospecificity, and processivity in glycoside hydrolase family 74. <i>Journal of Biological Chemistry</i> , 2019, 294, 13233-13247.	1.6	25
450	Crystal structures of human pancreatic \hat{I} -amylase in complex with carbohydrate and proteinaceous inhibitors. <i>Biochemical Journal</i> , 2000, 346, 201.	1.7	25

#	ARTICLE	IF	CITATIONS
451	Digestion of crystalline cellulose substrates by the <i>Clostridium thermocellum</i> cellulosome: structural and morphological aspects. <i>Biochemical Journal</i> , 1999, 340, 829.	1.7	24
452	Paradoxical conservation of a set of three cellulose-targeting genes in <i>Mycobacterium tuberculosis</i> complex organisms. <i>Microbiology (United Kingdom)</i> , 2010, 156, 1468-1475.	0.7	24
453	Understanding plant cell-wall remodelling during the symbiotic interaction between <i>Tuber melanosporum</i> and <i>Corylus avellana</i> using a carbohydrate microarray. <i>Planta</i> , 2016, 244, 347-359.	1.6	24
454	Comparative Metagenomics of Cellulose- and Poplar Hydrolysate-Degrading Microcosms from Gut Microflora of the Canadian Beaver (<i>Castor canadensis</i>) and North American Moose (<i>Alces americanus</i>) after Long-Term Enrichment. <i>Frontiers in Microbiology</i> , 2017, 8, 2504.	1.5	24
455	Cellulosome-like sequences in <i>Archaeoglobus fulgidus</i> : an enigmatic vestige of cohesin and dockerin domains. <i>FEBS Letters</i> , 1999, 463, 277-280.	1.3	23
456	Carbohydrate-active enzymes from pigmented <i>Bacilli</i> : a genomic approach to assess carbohydrate utilization and degradation. <i>BMC Microbiology</i> , 2011, 11, 198.	1.3	23
457	Ecological generalism drives hyperdiversity of secondary metabolite gene clusters in xylarialean endophytes. <i>New Phytologist</i> , 2022, 233, 1317-1330.	3.5	23
458	Identification of the catalytic residues of the first family of β (1 \rightarrow 3)glucanosyltransferases identified in fungi. <i>Biochemical Journal</i> , 2000, 347, 741.	1.7	21
459	The <i>celA</i> Gene, Encoding a Glycosyl Hydrolase Family 3 β -Glucosidase in <i>Azospirillum irakense</i> , Is Required for Optimal Growth on Cellobiosides. <i>Applied and Environmental Microbiology</i> , 2001, 67, 2380-2383.	1.4	21
460	Dissection of Hexosyl- and Sialyltransferase Domains in the Bifunctional Capsule Polymerases from <i>Neisseria meningitidis</i> W and Y Defines a New Sialyltransferase Family. <i>Journal of Biological Chemistry</i> , 2014, 289, 33945-33957.	1.6	21
461	How do gut microbes break down dietary fiber?. <i>Trends in Biochemical Sciences</i> , 2014, 39, 156-158.	3.7	21
462	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.	3.5	21
463	Mechanistic insights into consumption of the food additive xanthan gum by the human gut microbiota. <i>Nature Microbiology</i> , 2022, 7, 556-569.	5.9	21
464	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
465	Structure of a polyisoprenoid binding domain from <i>Saccharophagus degradans</i> implicated in plant cell wall breakdown. <i>FEBS Letters</i> , 2010, 584, 1577-1584.	1.3	20
466	Characterization of a mycobacterial cellulase and its impact on biofilm- and drug-induced cellulose production. <i>Glycobiology</i> , 2017, 27, 392-399.	1.3	20
467	The obligate alkalophilic soda-lake fungus <i>Sodiomyces alkalinus</i> has shifted to a protein diet. <i>Molecular Ecology</i> , 2018, 27, 4808-4819.	2.0	20
468	The Cellulosome Paradigm in An Extreme Alkaline Environment. <i>Microorganisms</i> , 2019, 7, 347.	1.6	20

#	ARTICLE	IF	CITATIONS
469	Processing and Hydrolytic Mechanism of the <i>cgkA</i> -Encoded kappa-Carrageenase of <i>Alteromonas carrageenovora</i> . <i>FEBS Journal</i> , 1995, 228, 971-975.	0.2	19
470	Enhanced whole genome sequence and annotation of <i>Clostridium stercorarium</i> DSM8532T using RNA-seq transcriptomics and high-throughput proteomics. <i>BMC Genomics</i> , 2014, 15, 567.	1.2	19
471	Draft genome sequence of a monokaryotic model brown-rot fungus <i>Postia (Rhodonia) placenta</i> SB12. <i>Genomics Data</i> , 2017, 14, 21-23.	1.3	19
472	Identification of the molecular determinants driving the substrate specificity of fungal lytic polysaccharide monoxygenases (LPMOs). <i>Journal of Biological Chemistry</i> , 2021, 296, 100086.	1.6	19
473	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	3.5	19
474	Current perspectives on the families of glycoside hydrolases of <i>Mycobacterium tuberculosis</i> : their importance and prospects for assigning function to unknowns. <i>Glycobiology</i> , 2017, 27, 112-122.	1.3	18
475	Broad-specificity GH131 β -glucanases are a hallmark of fungi and oomycetes that colonize plants. <i>Environmental Microbiology</i> , 2019, 21, 2724-2739.	1.8	18
476	Utilization of Galectins by Pathogens for Infection. <i>Frontiers in Immunology</i> , 2020, 11, 1877.	2.2	18
477	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, .	3.3	18
478	Structural features of normal and mutant human lysosomal glycoside hydrolases deduced from bioinformatics analysis. <i>Human Molecular Genetics</i> , 2000, 9, 967-977.	1.4	17
479	<i>Mycobacterium tuberculosis</i> Rv1090 and Rv1987 encode functional β -glucan-targeting proteins. <i>Protein Expression and Purification</i> , 2011, 75, 172-176.	0.6	17
480	Pan-Cellulosomics of Mesophilic Clostridia: Variations on a Theme. <i>Microorganisms</i> , 2017, 5, 74.	1.6	17
481	Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. <i>Current Biology</i> , 2021, 31, 3905-3914.e6.	1.8	17
482	Growth of <i>Azospirillum irakense</i> KBC1 on the Aryl β -Glucoside Salicin Requires either <i>salA</i> or <i>salB</i> . <i>Journal of Bacteriology</i> , 1999, 181, 3003-3009.	1.0	17
483	Genome Assembly of the Fungus <i>Cochliobolus miyabeanus</i> , and Transcriptome Analysis during Early Stages of Infection on American Wildrice (<i>Zizania palustris</i> L.). <i>PLoS ONE</i> , 2016, 11, e0154122.	1.1	17
484	<i>Streptomyces matensis</i> laminaripentaose hydrolase is an "inverting" β -1,3-glucanase. <i>FEBS Letters</i> , 2001, 499, 187-190.	1.3	16
485	Intrinsic dynamic behavior of enzyme:substrate complexes govern the catalytic action of β -galactosidases across clan GH-A. <i>Scientific Reports</i> , 2019, 9, 10346.	1.6	16
486	Unraveling the subtleties of β -(1 \rightarrow 3)-glucan phosphorylase specificity in the GH94, GH149, and GH161 glycoside hydrolase families. <i>Journal of Biological Chemistry</i> , 2019, 294, 6483-6493.	1.6	16

#	ARTICLE	IF	CITATIONS
487	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.	1.6	16
488	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.	4.4	16
489	The ectomycorrhizal basidiomycete <i>Laccaria bicolor</i> releases a GH28 polygalacturonase that plays a key role in symbiosis establishment. <i>New Phytologist</i> , 2022, 233, 2534-2547.	3.5	16
490	Hidden domains and active site residues in β -glucanase-encoding gene sequences?. <i>Gene</i> , 1993, 125, 199-204.	1.0	15
491	Family a cellulases: two essential tryptophan residues in endoglucanase III from <i>Trichoderma reesei</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1995, 1245, 187-190.	1.1	15
492	Dynamic light scattering study of the two-domain structure of <i>Humicola insolens</i> endoglucanase V. <i>FEBS Letters</i> , 1995, 376, 49-52.	1.3	15
493	A new cellulase family. <i>Molecular Microbiology</i> , 1997, 23, 848-849.	1.2	15
494	Draft Genome Sequence of the Deep-Sea Ascomycetous Filamentous Fungus <i>Cadophora malorum</i> Mo12 from the Mid-Atlantic Ridge Reveals Its Biotechnological Potential. <i>Genome Announcements</i> , 2016, 4, .	0.8	15
495	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , 2016, 4, .	0.8	15
496	A metagenome-derived thermostable β -glucanase with an unusual module architecture which defines the new glycoside hydrolase family GH148. <i>Scientific Reports</i> , 2017, 7, 17306.	1.6	15
497	Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical <i>Elizabethkingia meningoseptica</i> strains. <i>PLoS ONE</i> , 2019, 14, e0222648.	1.1	15
498	Identification of Copper-Containing Oxidoreductases in the Secretomes of Three <i>Colletotrichum</i> Species with a Focus on Copper Radical Oxidases for the Biocatalytic Production of Fatty Aldehydes. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0152621.	1.4	15
499	Title is missing!. <i>Cellulose</i> , 1997, 4, 7-20.	2.4	14
500	Dynamic Light Scattering Evidence for a Ligand-Induced Motion between the Two Domains of Glucoamylase G1 of <i>Aspergillus niger</i> with Heterobivalent Substrate Analogues. <i>Angewandte Chemie - International Edition</i> , 1999, 38, 974-977.	7.2	14
501	Draft Genome Sequence of <i>Nonlabens ulvanivorans</i> , an Ulvan-Degrading Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	14
502	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico "Dead Zone". <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	14
503	Multimodularity of a GH10 Xylanase Found in the Termite Gut Metagenome. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	14
504	Sucrose 6F-phosphate phosphorylase: a novel insight in the human gut microbiome. <i>Microbial Genomics</i> , 2019, 5, .	1.0	14

#	ARTICLE	IF	CITATIONS
505	The Land-Sea Connection: Insights Into the Plant Lineage from a Green Algal Perspective. Annual Review of Plant Biology, 2022, 73, 585-616.	8.6	14
506	Comparative genomics reveals a dynamic genome evolution in the ectomycorrhizal milkcap (<i>Lactarius</i>) mushrooms. New Phytologist, 2022, 235, 306-319.	3.5	14
507	Peptidoglycan: a post-genomic analysis. BMC Microbiology, 2012, 12, 294.	1.3	13
508	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	1.5	13
509	The Quaternary Structure of a Glycoside Hydrolase Dictates Specificity toward Î ² -Glucans. Journal of Biological Chemistry, 2016, 291, 7183-7194.	1.6	13
510	<i>Talaromyces borbonicus</i> , sp. nov., a novel fungus from biodegraded <i>Arundo donax</i> with potential abilities in lignocellulose conversion. Mycologia, 2018, 110, 316-324.	0.8	13
511	Inverting family GH156 sialidases define an unusual catalytic motif for glycosidase action. Nature Communications, 2019, 10, 4816.	5.8	13
512	Investigating Host Microbiota Relationships Through Functional Metagenomics. Frontiers in Microbiology, 2019, 10, 1286.	1.5	13
513	A metagenomics investigation of carbohydrate-active enzymes along the goat and camel intestinal tract. International Microbiology, 2019, 22, 429-435.	1.1	13
514	Trichoderma reesei Dehydrogenase, a Pyrroloquinoline Quinone-Dependent Member of Auxiliary Activity Family 12 of the Carbohydrate-Active Enzymes Database: Functional and Structural Characterization. Applied and Environmental Microbiology, 2019, 85, .	1.4	13
515	Larvae of longhorned beetles (Coleoptera; Cerambycidae) have evolved a diverse and phylogenetically conserved array of plant cell wall degrading enzymes. Systematic Entomology, 2021, 46, 784-797.	1.7	13
516	Lytic Polysaccharide Monooxygenases as Chitin-Specific Virulence Factors in Crayfish Plague. Biomolecules, 2021, 11, 1180.	1.8	13
517	The Families of Carbohydrate-Active Enzymes in the Genomic Era. Journal of Applied Glycoscience (1999), 2003, 50, 241-244.	0.3	13
518	Eukaryote to gut bacteria transfer of a glycoside hydrolase gene essential for starch breakdown in plants. Mobile Genetic Elements, 2012, 2, 81-87.	1.8	12
519	Correction for Riley et al., Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14959-14959.	3.3	12
520	Structural Dynamics and Catalytic Properties of a Multimodular Xanthanase. ACS Catalysis, 2018, 8, 6021-6034.	5.5	12
521	The Cellulosome: A Natural Bacterial Strategy to Combat Biomass Recalcitrance. , 0, , 407-435.		12
522	An approach for evaluating the effects of dietary fiber polysaccharides on the human gut microbiome and plasma proteome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123411119.	3.3	12

#	ARTICLE	IF	CITATIONS
523	Draft Genome Sequences of Two Ulvan-Degrading Isolates, Strains LTR and LOR, That Belong to the <i>Alteromonas</i> Genus. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
524	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	11
525	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.	1.1	11
526	Composting-Like Conditions Are More Efficient for Enrichment and Diversity of Organisms Containing Cellulase-Encoding Genes than Submerged Cultures. <i>PLoS ONE</i> , 2016, 11, e0167216.	1.1	11
527	Reading-frame shift in <i>Saccharomyces glucoamylases</i> restores catalytic base, extends sequence and improves alignment with other glucoamylases. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1281-1282.	1.0	10
528	Structural basis for carbohydrate binding properties of a plant chitinase-like agglutinin with conserved catalytic machinery. <i>Journal of Structural Biology</i> , 2015, 190, 115-121.	1.3	10
529	Functional diversity of three tandem C-terminal carbohydrate-binding modules of a β -mannanase. <i>Journal of Biological Chemistry</i> , 2021, 296, 100638.	1.6	10
530	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.	1.9	10
531	Phylogenomics and Comparative Genomics Highlight Specific Genetic Features in <i>Ganoderma</i> Species. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 311.	1.5	10
532	Cracking the code, slowly: the state of carbohydrate-active enzymes in 2013. <i>Current Opinion in Structural Biology</i> , 2013, 23, 649-651.	2.6	9
533	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
534	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.	1.3	9
535	C-type cytochrome-initiated reduction of bacterial lytic polysaccharide monooxygenases. <i>Biochemical Journal</i> , 2021, 478, 2927-2944.	1.7	9
536	Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i> . <i>Science Advances</i> , 2022, 8, eabi5075.	4.7	9
537	Precipitation and crystallization of cellulose doped with dyes. <i>Die Makromolekulare Chemie Rapid Communications</i> , 1985, 6, 737-741.	1.1	8
538	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	1.4	8
539	Identification of the galactosyltransferase of <i>Cryptococcus neoformans</i> involved in the biosynthesis of basidiomycete-type glycosylinositolphosphoceramide. <i>Glycobiology</i> , 2013, 23, 1210-1219.	1.3	7
540	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain PLSV, an Ulvan-Degrading Bacterium. <i>Genome Announcements</i> , 2014, 2, .	0.8	7

#	ARTICLE	IF	CITATIONS
541	Mycobacterium ulcerans mycolactones-fungi crosstalk. Scientific Reports, 2019, 9, 3028.	1.6	7
542	Characterization of the CAZy Repertoire from the Marine-Derived Fungus Stemphylium lucomagnoense in Relation to Saline Conditions. Marine Drugs, 2020, 18, 461.	2.2	7
543	Sulfation of Arabinogalactan Proteins Confers Privileged Nutrient Status to Bacteroides plebeius. MBio, 2021, 12, e0136821.	1.8	7
544	Fungal secretomics of ascomycete fungi for biotechnological applications. Mycosphere, 2016, 7, 1546-1553.	1.9	7
545	National publication bias. Nature, 1991, 354, 427-427.	13.7	6
546	On the classification of modular proteins. Protein Engineering, Design and Selection, 1996, 9, 725-726.	1.0	6
547	Crystallization and preliminary crystallographic analysis of a thermostable family 52 β -D-xylosidase from Geobacillus stearothermophilus T-6. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1461-1463.	2.5	6
548	Draft Genome Sequence of the Deep-Sea Basidiomycetous Yeast Cryptococcus sp. Strain Mo29 Reveals Its Biotechnological Potential. Genome Announcements, 2016, 4, .	0.8	6
549	A mutation map for human glycoside hydrolase genes. Glycobiology, 2020, 30, 500-515.	1.3	6
550	SOME RECENT ASPECTS OF THE SPECIFICITY AND MECHANISM OF ACTION OF TREHALASES. , 1980, , 331-353.		6
551	Analysis of the diversity of the glycoside hydrolase family 130 in mammal gut microbiomes reveals a novel mannoside-phosphorylase function. Microbial Genomics, 2020, 6, .	1.0	6
552	Assembly and synthesis of the extracellular matrix in brown algae. Seminars in Cell and Developmental Biology, 2023, 134, 112-124.	2.3	6
553	Characterization of some mesogenic alkyl 1-thioglycosides. Canadian Journal of Chemistry, 2002, 80, 1162-1165.	0.6	5
554	Analysis of carbohydrate-active enzymes in <i>Thermogemmatispora</i> sp. strain T81 reveals carbohydrate degradation ability. Canadian Journal of Microbiology, 2018, 64, 992-1003.	0.8	5
555	Characterization of the β -glucuronidase Pn3Pase as the founding member of glycoside hydrolase family GH169. Glycobiology, 2021, 31, 266-274.	1.3	5
556	Endoglucanase II (EGII) of Penicillium janthinellum: cDNA sequence, heterologous expression and promoter analysis. Current Genetics, 1996, 29, 490-495.	0.8	5
557	Functional exploration of the glycoside hydrolase family GH113. PLoS ONE, 2022, 17, e0267509.	1.1	5
558	Assignment of the ^1H , ^{13}C , and ^{15}N resonances of the 22,5 kDa CBM28 module of the cellulase Cel5I of Clostridium cellulolyticum. Journal of Biomolecular NMR, 2002, 23, 157-158.	1.6	4

#	ARTICLE	IF	CITATIONS
559	Crystallization and preliminary X-ray analysis of family 39 β -D-xylosidase from <i>Geobacillus stearothermophilus</i> T-6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 583-585.	2.5	4
560	Plant proteinaceous inhibitors of carbohydrate-active enzymes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1696, 141.	1.1	3
561	Carbohydrate-Active Enzymes Database: Principles and Classification of Glycosyltransferases. , 0, , 89-118.		3
562	A novel β -N-acetylgalactosaminidase family with an NAD ⁺ -dependent catalytic mechanism suitable for enzymatic removal of blood group A antigens. <i>Biocatalysis and Biotransformation</i> , 2010, 28, 22-32.	1.1	3
563	Production of β -1,3-L-arabinofuranosidase active on substituted xylan does not improve compost degradation by <i>Agaricus bisporus</i> . <i>PLoS ONE</i> , 2018, 13, e0201090.	1.1	3
564	A corrective frameshift in the sequence of the β -glucosidase gene from <i>Cellvibrio gilvus</i> restores similarity with a large domain found in other β -glucosidases. <i>Journal of Bioscience and Bioengineering</i> , 1993, 76, 240-242.	0.9	2
565	Genome Features of <i>Asaia</i> sp. W12 Isolated from the Mosquito <i>Anopheles stephensi</i> Reveal Symbiotic Traits. <i>Genes</i> , 2021, 12, 752.	1.0	2
566	(Hemi-)Cellulose Degrading Enzymes and Their Encoding Genes from <i>Aspergillus</i> and <i>Trichoderma</i> . , 2011, , 341-355.		2
567	Molecular characterization of a cell wall-associated β (1-3)endoglucanase of <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2002, 40, 455-464.	0.3	2
568	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.	0.7	2
569	Generation of a Library of Carbohydrate-Active Enzymes for Plant Biomass Deconstruction. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4024.	1.8	2
570	Identification of Two Tryptophan Residues in Endoglucanase III from <i>Trichoderma reesei</i> Essential for Cellulose Binding and Catalytic Activity. <i>ACS Symposium Series</i> , 1996, , 164-173.	0.5	1
571	Carbohydrate-Active Enzymes Database, Metagenomic Expert Resource. , 2012, , 1-7.		1
572	Carbohydrate-active enzymes in completely sequenced genomes. <i>Special Publication - Royal Society of Chemistry</i> , 0, , 171-177.	0.0	1
573	Sequence Families and Modular Organization of Carbohydrate-Active Enzymes. , 2003, , .		1
574	Exploring biomass degrading communities for lignocellulolytic activities. <i>New Biotechnology</i> , 2014, 31, S169.	2.4	0
575	Erratum to : peptidoglycan: a post-genomic analysis. <i>BMC Microbiology</i> , 2014, 14, .	1.3	0
576	How a Glycoside Hydrolase Recognizes a Helical Polyglucan. <i>Structure</i> , 2017, 25, 1319-1321.	1.6	0