

Bernard Henrissat

List of Publications by Citations

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579
papers

90,222
citations

132
h-index

291
g-index

624
ext. papers

106,972
ext. citations

9.3
avg, IF

7.9
L-index

#	Paper	IF	Citations
579	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009 , 457, 480-4	50.4	5429
578	The carbohydrate-active enzymes database (CAZy) in 2013. <i>Nucleic Acids Research</i> , 2014 , 42, D490-5	20.1	3918
577	The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. <i>Nucleic Acids Research</i> , 2009 , 37, D233-8	20.1	3914
576	The genome of black cottonwood, <i>Populus trichocarpa</i> (Torr. & Gray). <i>Science</i> , 2006 , 313, 1596-604	33.3	3205
575	A classification of glycosyl hydrolases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1991 , 280 (Pt 2), 309-16	3.8	2550
574	Gut microbiota from twins discordant for obesity modulate metabolism in mice. <i>Science</i> , 2013 , 341, 1241-1244	33.3	2251
573	New families in the classification of glycosyl hydrolases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1993 , 293 (Pt 3), 781-8	3.8	1729
572	Structures and mechanisms of glycosyl hydrolases. <i>Structure</i> , 1995 , 3, 853-9	5.2	1582
571	Structural and sequence-based classification of glycoside hydrolases. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 637-44	8.1	1373
570	Glycosyltransferases: structures, functions, and mechanisms. <i>Annual Review of Biochemistry</i> , 2008 , 77, 521-55	29.1	1240
569	Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. <i>Science</i> , 2011 , 332, 970-4	33.3	1215
568	Updating the sequence-based classification of glycosyl hydrolases. <i>Biochemical Journal</i> , 1996 , 316 (Pt 2), 695-6	3.8	1175
567	A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility. <i>Cell</i> , 2016 , 167, 1339-1353.e21	56.2	1149
566	The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. <i>Science</i> , 2012 , 336, 1715-9	33.3	1129
565	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010 , 464, 367-73	50.4	1085
564	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea jecorina</i>). <i>Nature Biotechnology</i> , 2008 , 26, 553-60	44.5	920
563	An evolving hierarchical family classification for glycosyltransferases. <i>Journal of Molecular Biology</i> , 2003 , 328, 307-17	6.5	912

562	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007 , 25, 221-31	44.5	889
561	Nomenclature for sugar-binding subsites in glycosyl hydrolases. <i>Biochemical Journal</i> , 1997 , 321 (Pt 2), 557-9	3.8	845
560	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis. <i>Nature</i> , 2008 , 452, 88-92	50.4	823
559	The abundance and variety of carbohydrate-active enzymes in the human gut microbiota. <i>Nature Reviews Microbiology</i> , 2013 , 11, 497-504	22.2	811
558	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008 , 26, 909-15	44.5	790
557	Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. <i>Biotechnology for Biofuels</i> , 2013 , 6, 41	7.8	734
556	Metabolic reconstruction for metagenomic data and its application to the human microbiome. <i>PLoS Computational Biology</i> , 2012 , 8, e1002358	5	730
555	Genome sequence of the lignocellulose degrading fungus <i>Phanerochaete chrysosporium</i> strain RP78. <i>Nature Biotechnology</i> , 2004 , 22, 695-700	44.5	710
554	Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011 , 7, e1002230	6	659
553	A classification of nucleotide-diphospho-sugar glycosyltransferases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1997 , 326 (Pt 3), 929-39	3.8	641
552	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015 , 47, 410-5	36.3	601
551	Three genomes from the phylum Acidobacteria provide insight into the lifestyles of these microorganisms in soils. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2046-56	4.8	590
550	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012 , 44, 1060-5	36.3	564
549	Piigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010 , 464, 1033-8	50.4	545
548	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, 7090-4	11.5	511
547	Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009 , 324, 268-72	33.3	503
546	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, 20117-22	11.5	499
545	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, 1948-53	11.5	495

544	Recognition and degradation of plant cell wall polysaccharides by two human gut symbionts. <i>PLoS Biology</i> , 2011 , 9, e1001221	9.7	480
543	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, 9166-71	11.5	479
542	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, 1954-9	11.5	479
541	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, 5859-64	11.5	478
540	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, 9923-8	11.5	461
539	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011 , 12, R40	18.3	448
538	Dividing the large glycoside hydrolase family 13 into subfamilies: towards improved functional annotations of alpha-amylase-related proteins. <i>Protein Engineering, Design and Selection</i> , 2006 , 19, 555-62	19	430
537	Deciphering protein sequence information through hydrophobic cluster analysis (HCA): current status and perspectives. <i>Cellular and Molecular Life Sciences</i> , 1997 , 53, 621-45	10.3	426
536	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. <i>Science</i> , 2011 , 333, 762-5	33.3	417
535	Multidomain architecture of beta-glycosyl transferases: implications for mechanism of action. <i>Journal of Bacteriology</i> , 1995 , 177, 1419-24	3.5	415
534	Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children. <i>Science</i> , 2016 , 351,	33.3	406
533	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	6	401
532	Evolution of symbiotic bacteria in the distal human intestine. <i>PLoS Biology</i> , 2007 , 5, e156	9.7	401
531	Endogenous cellulases in animals: isolation of beta-1, 4-endoglucanase genes from two species of plant-parasitic cyst nematodes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 4906-11	11.5	401
530	Synergism of Cellulases from <i>Trichoderma reesei</i> in the Degradation of Cellulose. <i>Bio/technology</i> , 1985 , 3, 722-726		395
529	Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. <i>PLoS Pathogens</i> , 2012 , 8, e1003037	7.6	387
528	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	17.5	384
527	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010 , 28, 957-63	44.5	381

526	Cellulase families revealed by hydrophobic cluster analysis. <i>Gene</i> , 1989 , 81, 83-95	3.8	376
525	Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7503-8	11.5	364
524	Genomic and metabolic adaptations of <i>Methanobrevibacter smithii</i> to the human gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 10643-8	11.5	360
523	Glycoside hydrolases and glycosyltransferases: families and functional modules. <i>Current Opinion in Structural Biology</i> , 2001 , 11, 593-600	8.1	344
522	Comparative genomics yields insights into niche adaptation of plant vascular wilt pathogens. <i>PLoS Pathogens</i> , 2011 , 7, e1002137	7.6	335
521	The genome of <i>Nectria haematococca</i> : contribution of supernumerary chromosomes to gene expansion. <i>PLoS Genetics</i> , 2009 , 5, e1000618	6	329
520	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011 , 29, 922-7	44.5	324
519	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, 15619-23	3.2	322
518	Integrated metagenomics/metaproteomics reveals human host-microbiota signatures of Crohn's disease. <i>PLoS ONE</i> , 2012 , 7, e49138	3.7	320
517	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . <i>Nature Communications</i> , 2012 , 3, 913	17.4	307
516	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, 144-65	6.9	306
515	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012 , 492, 59-65	50.4	304
514	<i>Cyanophora paradoxa</i> genome elucidates origin of photosynthesis in algae and plants. <i>Science</i> , 2012 , 335, 843-7	33.3	304
513	Hydrophobic cluster analysis: procedures to derive structural and functional information from 2-D-representation of protein sequences. <i>Biochimie</i> , 1990 , 72, 555-74	4.6	298
512	Evolution, substrate specificity and subfamily classification of glycoside hydrolase family 5 (GH5). <i>BMC Evolutionary Biology</i> , 2012 , 12, 186	3	296
511	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , 2017 , 544, 65-70	50.4	291
510	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010 , 11, R73	18.3	280
509	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 17501-6	11.5	277

508	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013 , 500, 453-7	50.4	274
507	Discovery and characterization of a new family of lytic polysaccharide monooxygenases. <i>Nature Chemical Biology</i> , 2014 , 10, 122-6	11.7	268
506	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, 19514-9	11.5	266
505	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017 , 18, 28	18.3	261
504	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, 663-75	5.2	260
503	Parallel-up structure evidences the molecular directionality during biosynthesis of bacterial cellulose. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 9091-5	11.5	245
502	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, 17651-6	11.5	244
501	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015 , 6, 7481	17.4	241
500	Recent structural insights into the expanding world of carbohydrate-active enzymes. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 637-45	8.1	238
499	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008 , 9, R77	18.3	237
498	Starch- and glycogen-debranching and branching enzymes: prediction of structural features of the catalytic (beta/alpha) ₈ -barrel domain and evolutionary relationship to other amylolytic enzymes. <i>The Protein Journal</i> , 1993 , 12, 791-805		233
497	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. <i>ISME Journal</i> , 2011 , 5, 639-49	11.9	229
496	Poplar carbohydrate-active enzymes. Gene identification and expression analyses. <i>Plant Physiology</i> , 2006 , 140, 946-62	6.6	229
495	Structure of the <i>Fusarium oxysporum</i> endoglucanase I with a nonhydrolyzable substrate analogue: substrate distortion gives rise to the preferred axial orientation for the leaving group. <i>Biochemistry</i> , 1996 , 35, 15280-7	3.2	227
494	Bacteria from diverse habitats colonize and compete in the mouse gut. <i>Cell</i> , 2014 , 159, 253-66	56.2	226
493	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 5458-63	11.5	225
492	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. <i>ISME Journal</i> , 2014 , 8, 1566-76	11.9	224
491	Glycoside hydrolases and glycosyltransferases. Families, modules, and implications for genomics. <i>Plant Physiology</i> , 2000 , 124, 1515-9	6.6	224

490	Complex carbohydrate utilization by the healthy human microbiome. <i>PLoS ONE</i> , 2012 , 7, e28742	3.7	219
489	A hierarchical classification of polysaccharide lyases for glycogenomics. <i>Biochemical Journal</i> , 2010 , 432, 437-44	3.8	218
488	A scheme for designating enzymes that hydrolyse the polysaccharides in the cell walls of plants. <i>FEBS Letters</i> , 1998 , 425, 352-4	3.8	212
487	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. <i>Nature Biotechnology</i> , 2018 , 36, 359-367	44.5	207
486	Structure and boosting activity of a starch-degrading lytic polysaccharide monooxygenase. <i>Nature Communications</i> , 2015 , 6, 5961	17.4	205
485	The molecular basis of polysaccharide cleavage by lytic polysaccharide monooxygenases. <i>Nature Chemical Biology</i> , 2016 , 12, 298-303	11.7	205
484	Bacterial glycosidases for the production of universal red blood cells. <i>Nature Biotechnology</i> , 2007 , 25, 454-64	44.5	199
483	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. <i>Environmental Microbiology</i> , 2015 , 17, 4954-64	5.2	193
482	Comparative genome analysis of <i>Prevotella ruminicola</i> and <i>Prevotella bryantii</i> : insights into their environmental niche. <i>Microbial Ecology</i> , 2010 , 60, 721-9	4.4	192
481	Ectomycorrhizal fungi decompose soil organic matter using oxidative mechanisms adapted from saprotrophic ancestors. <i>New Phytologist</i> , 2016 , 209, 1705-19	9.8	190
480	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	6	189
479	Effects of diet on resource utilization by a model human gut microbiota containing <i>Bacteroides cellulosilyticus</i> WH2, a symbiont with an extensive glycobiome. <i>PLoS Biology</i> , 2013 , 11, e1001637	9.7	184
478	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. <i>Nature Chemical Biology</i> , 2018 , 14, 306-310	11.7	183
477	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010 , 20, 1605-12	9.7	182
476	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, 6864-75	4.8	177
475	A census of carbohydrate-active enzymes in the genome of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2001 , 47, 55-72	4.6	176
474	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, 1444-52	4.8	176
473	Klotho is a novel beta-glucuronidase capable of hydrolyzing steroid beta-glucuronides. <i>Journal of Biological Chemistry</i> , 2004 , 279, 9777-84	5.4	172

472	Genome sequence of the cellulolytic gliding bacterium <i>Cytophaga hutchinsonii</i> . <i>Applied and Environmental Microbiology</i> , 2007 , 73, 3536-46	4.8	170
471	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	9.8	168
470	The three-dimensional structure of invertase (beta-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, 18903-10	5.4	168
469	Mucopolipidosis II is caused by mutations in GNPTA encoding the alpha/beta GlcNAc-1-phosphotransferase. <i>Nature Medicine</i> , 2005 , 11, 1109-12	50.5	167
468	The kappa-carrageenase of <i>P. carrageenovora</i> features a tunnel-shaped active site: a novel insight in the evolution of Clan-B glycoside hydrolases. <i>Structure</i> , 2001 , 9, 513-25	5.2	167
467	A modular family 19 chitinase found in the prokaryotic organism <i>Streptomyces griseus</i> HUT 6037. <i>Journal of Bacteriology</i> , 1996 , 178, 5065-70	3.5	166
466	Genome of the red alga <i>Porphyridium purpureum</i> . <i>Nature Communications</i> , 2013 , 4, 1941	17.4	165
465	Utilisation of mucin glycans by the human gut symbiont <i>Ruminococcus gnavus</i> is strain-dependent. <i>PLoS ONE</i> , 2013 , 8, e76341	3.7	165
464	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, 2504-9	11.5	161
463	Effects of microbiota-directed foods in gnotobiotic animals and undernourished children. <i>Science</i> , 2019 , 365,	33.3	160
462	Genome analyses highlight the different biological roles of cellulases. <i>Nature Reviews Microbiology</i> , 2012 , 10, 227-34	22.2	154
461	Glycosidase families. <i>Biochemical Society Transactions</i> , 1998 , 26, 153-6	5.1	152
460	Carbohydrate-active enzymes involved in the secondary cell wall biogenesis in hybrid aspen. <i>Plant Physiology</i> , 2005 , 137, 983-97	6.6	152
459	Updates to the Symbol Nomenclature for Glycans guidelines. <i>Glycobiology</i> , 2019 , 29, 620-624	5.8	148
458	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, 13555-60	11.5	148
457	Influenza B virus neuraminidase can synthesize its own inhibitor. <i>Structure</i> , 1993 , 1, 19-26	5.2	148
456	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic Bacteroides. <i>Nature Microbiology</i> , 2018 , 3, 210-219	26.6	142
455	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, 39385-93	5.4	142

454	Undirectional degradation of valonia cellulose microcrystals subjected to cellulase action. <i>FEBS Letters</i> , 1985 , 184, 285-288	3.8	142
453	Cellulases and their interaction with cellulose. <i>Cellulose</i> , 1994 , 1, 169-196	5.5	141
452	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, 5455-63	3.5	140
451	Genetic determinants of in vivo fitness and diet responsiveness in multiple human gut <i>Bacteroides</i> . <i>Science</i> , 2015 , 350, aac5992	33.3	138
450	Structures of oligosaccharide-bound forms of the endoglucanase V from <i>Humicola insolens</i> at 1.9 Å resolution. <i>Biochemistry</i> , 1995 , 34, 16210-20	3.2	136
449	An ancient family of lytic polysaccharide monoxygenases with roles in arthropod development and biomass digestion. <i>Nature Communications</i> , 2018 , 9, 756	17.4	135
448	Cello-oligosaccharide oxidation reveals differences between two lytic polysaccharide monoxygenases (Family GH61) from <i>Podospora anserina</i> . <i>Applied and Environmental Microbiology</i> , 2013 , 79, 488-96	4.8	132
447	Complete genome sequence of the complex carbohydrate-degrading marine bacterium, <i>Saccharophagus degradans</i> strain 2-40 T. <i>PLoS Genetics</i> , 2008 , 4, e1000087	6	132
446	Automatic prediction of polysaccharide utilization loci in <i>Bacteroidetes</i> species. <i>Bioinformatics</i> , 2015 , 31, 647-55	7.2	131
445	Domain evolution in the alpha-amylase family. <i>Journal of Molecular Evolution</i> , 1997 , 45, 322-31	3.1	131
444	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. <i>Nature Communications</i> , 2016 , 7, 11362	17.4	130
443	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, <i>Leptinotarsa decemlineata</i> (Coleoptera: Chrysomelidae). <i>Scientific Reports</i> , 2018 , 8, 1931	4.9	127
442	Crystal structure of <i>Thermotoga maritima</i> alpha-L-fucosidase. Insights into the catalytic mechanism and the molecular basis for fucosidosis. <i>Journal of Biological Chemistry</i> , 2004 , 279, 13119-28	5.4	124
441	A novel, small endoglucanase gene, <i>egl5</i> , from <i>Trichoderma reesei</i> isolated by expression in yeast. <i>Molecular Microbiology</i> , 1994 , 13, 219-28	4.1	122
440	The <i>Bifidobacterium dentium</i> Bd1 genome sequence reflects its genetic adaptation to the human oral cavity. <i>PLoS Genetics</i> , 2009 , 5, e1000785	6	120
439	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016 , 26, 1577-1584	6.3	119
438	Complete cellulase system in the marine bacterium <i>Saccharophagus degradans</i> strain 2-40T. <i>Journal of Bacteriology</i> , 2006 , 188, 3849-61	3.5	118
437	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	4.8	117

436	Comparative genomics of the social amoebae <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . <i>Genome Biology</i> , 2011 , 12, R20	18.3	117
435	Why are there so many carbohydrate-active enzyme-related genes in plants?. <i>Trends in Plant Science</i> , 2003 , 8, 563-5	13.1	117
434	Detection of secondary structure elements in proteins by hydrophobic cluster analysis. <i>Protein Engineering, Design and Selection</i> , 1992 , 5, 629-35	1.9	112
433	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017 , 2, 17087	26.6	111
432	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	3.2	111
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