Pedro M Coutinho

List of Publications by Year
in descending order

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108 papers	37,234 citations	15504 65 h-index	32842 100 g-index
111 all docs	111 docs citations	111 times ranked	32710 citing authors

#	ARTICLE	IF	CITATIONS
1	The carbohydrate-active enzymes database (CAZy) in 2013. Nucleic Acids Research, 2014, 42, D490-D495.	14.5	5,443
2	The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. Nucleic Acids Research, 2009, 37, D233-D238.	14.5	4,854
3	Comparative genomics reveals mobile pathogenicity chromosomes in Fusarium. Nature, 2010, 464, 367-373.	27.8	1,442
4	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. Science, 2012, 336, 1715-1719.	12.6	1,424
5	Genome sequencing and analysis of the biomass-degrading fungus Trichoderma reesei (syn. Hypocrea) Tj ETQq1 1 0.784314 rgBT /Over	17.5	1,116
6	An Evolving Hierarchical Family Classification for Glycosyltransferases. Journal of Molecular Biology, 2003, 328, 307-317.	4.2	1,079
7	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	17.5	1,047
8	Genome sequence of the metazoan plant-parasitic nematode Meloidogyne incognita. Nature Biotechnology, 2008, 26, 909-915.	17.5	1,012
9	Expansion of the enzymatic repertoire of the CAZy database to integrate auxiliary redox enzymes. Biotechnology for Biofuels, 2013, 6, 41.	6.2	994
10	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS Genetics, 2011, 7, e1002230.	3.5	902
11	Genome sequence of the lignocellulose degrading fungus Phanerochaete chrysosporium strain RP78. Nature Biotechnology, 2004, 22, 695-700.	17.5	805
12	Three Genomes from the Phylum<i>Acidobacteria</i>Provide Insight into the Lifestyles of These Microorganisms in Soils. Applied and Environmental Microbiology, 2009, 75, 2046-2056.	3.1	804
13	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1948-1953.	7.1	669
14	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature, 2010, 464, 1033-1038.	27.8	641
15	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9166-9171.	7.1	640
16	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5859-5864.	7.1	612
17	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of Trichoderma. Genome Biology, 2011, 12, R40.	8.8	594
18	Finished Genome of the Fungal Wheat Pathogen Mycosphaerella graminicola Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. PLoS Genetics, 2011, 7, e1002070.	3.5	532

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19	Dividing the large glycoside hydrolase family 13 into subfamilies: towards improved functional annotations of Α-amylase-related proteins. Protein Engineering, Design and Selection, 2006, 19, 555-562.	2.1	530
20	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1954-1959.	7.1	530
21	The Plant Cell Wallâ€"Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	12.6	512
22	Evolution of Symbiotic Bacteria in the Distal Human Intestine. PLoS Biology, 2007, 5, e156.	5.6	490
23	Genome sequence of the model mushroom Schizophyllum commune. Nature Biotechnology, 2010, 28, 957-963.	17.5	490
24	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.	7.1	451
25	Comparative genomic analysis of the thermophilic biomass-degrading fungi Myceliophthora thermophila and Thielavia terrestris. Nature Biotechnology, 2011, 29, 922-927.	17.5	428
26	The Genome of Nectria haematococca: Contribution of Supernumerary Chromosomes to Gene Expansion. PLoS Genetics, 2009, 5, e1000618.	3.5	402
27	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	9.6	391
28	Evolution, substrate specificity and subfamily classification of glycoside hydrolase family 5 (GH5). BMC Evolutionary Biology, 2012, 12, 186.	3.2	389
29	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847.	12.6	371
30	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.	7.1	359
31	Biosynthesis of cellulose-enriched tension wood inPopulus: global analysis of transcripts and metabolites identifies biochemical and developmental regulators in secondary wall biosynthesis. Plant Journal, 2006, 45, 144-165.	5.7	347
32	The genome sequence of the model ascomycete fungus Podospora anserina. Genome Biology, 2008, 9, R77.	9.6	301
33	Multiple lateral gene transfers and duplications have promoted plant parasitism ability in nematodes. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17651-17656.	7.1	300
34	Comparative Genome Analysis of Prevotella ruminicola and Prevotella bryantii: Insights into Their Environmental Niche. Microbial Ecology, 2010, 60, 721-729.	2.8	293
35	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. ISME Journal, 2011, 5, 639-649.	9.8	292
36	A hierarchical classification of polysaccharide lyases for glycogenomics. Biochemical Journal, 2010, 432, 437-444.	3.7	282

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37	Poplar Carbohydrate-Active Enzymes. Gene Identification and Expression Analyses. Plant Physiology, 2006, 140, 946-962.	4.8	271
38	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.	7.1	259
39	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. Genome Research, 2010, 20, 1605-1612.	5.5	228
40	Genome of the red alga Porphyridium purpureum. Nature Communications, 2013, 4, 1941.	12.8	204
41	A census of carbohydrate-active enzymes in the genome of Arabidopsis thaliana. Plant Molecular Biology, 2001, 47, 55-72.	3.9	190
42	Carbohydrate-Active Enzymes Involved in the Secondary Cell Wall Biogenesis in Hybrid Aspen. Plant Physiology, 2005, 137, 983-997.	4.8	173
43	Measuring semantic similarity between Gene Ontology terms. Data and Knowledge Engineering, 2007, 61, 137-152.	3.4	166
44	Cello-Oligosaccharide Oxidation Reveals Differences between Two Lytic Polysaccharide Monooxygenases (Family GH61) from Podospora anserina. Applied and Environmental Microbiology, 2013, 79, 488-496.	3.1	149
45	Complete Genome Sequence of the Complex Carbohydrate-Degrading Marine Bacterium, Saccharophagus degradans Strain 2-40T. PLoS Genetics, 2008, 4, e1000087.	3.5	142
46	Post-genomic analyses of fungal lignocellulosic biomass degradation reveal the unexpected potential of the plant pathogen Ustilago maydis. BMC Genomics, 2012, 13, 57.	2.8	135
47	Why are there so many carbohydrate-active enzyme-related genes in plants?. Trends in Plant Science, 2003, 8, 563-565.	8.8	134
48	Post-genomic insights into the plant polysaccharide degradation potential of Aspergillus nidulans and comparison to Aspergillus niger and Aspergillus oryzae. Fungal Genetics and Biology, 2009, 46, S161-S169.	2.1	133
49	Glucoamylase structural, functional, and evolutionary relationships. , 1997, 29, 334-347.		127
50	Complete Cellulase System in the Marine Bacterium Saccharophagus degradans Strain 2-40 T. Journal of Bacteriology, 2006, 188, 3849-3861.	2.2	126
51	Diversity and Strain Specificity of Plant Cell Wall Degrading Enzymes Revealed by the Draft Genome of Ruminococcus flavefaciens FD-1. PLoS ONE, 2009, 4, e6650.	2.5	124
52	The convergence of carbohydrate active gene repertoires in human gut microbes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15076-15081.	7.1	120
53	FOLy: An integrated database for the classification and functional annotation of fungal oxidoreductases potentially involved in the degradation of lignin and related aromatic compounds. Fungal Genetics and Biology, 2008, 45, 638-645.	2.1	118
54	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. Biotechnology for Biofuels, 2015, 8, 107.	6.2	111

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55	Carbohydrate-active enzymes from the zygomycete fungus Rhizopus oryzae: a highly specialized approach to carbohydrate degradation depicted at genome level. BMC Genomics, 2011, 12, 38.	2.8	105
56	Glycogen metabolism loss: a common marker of parasitic behaviour in bacteria?. Trends in Genetics, 2002, 18, 437-440.	6.7	98
57	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.	7.1	97
58	<i>Podospora anserina</i> Hemicellulases Potentiate the <i>Trichoderma reesei</i> Secretome for Saccharification of Lignocellulosic Biomass. Applied and Environmental Microbiology, 2011, 77, 237-246.	3.1	94
59	The Complete Genome of Teredinibacter turnerae T7901: An Intracellular Endosymbiont of Marine Wood-Boring Bivalves (Shipworms). PLoS ONE, 2009, 4, e6085.	2.5	93
60	The genome of the white-rot fungus Pycnoporus cinnabarinus: a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	2.8	91
61	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. BMC Genomics, 2012, 13, 321.	2.8	86
62	Secretome analysis of Phanerochaete chrysosporium strain CIRM-BRFM41 grown on softwood. Applied Microbiology and Biotechnology, 2008, 80, 719-33.	3.6	83
63	A census of carbohydrate-active enzymes in the genome of Arabidopsis thaliana. , 2001, , 55-72.		80
64	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. Journal of Proteome Research, 2012, 11, 5924-5933.	3.7	79
65	Modulation of cellulosome composition in <i>Clostridium cellulolyticum</i>: Adaptation to the polysaccharide environment revealed by proteomic and carbohydrateâ€active enzyme analyses. Proteomics, 2010, 10, 541-554.	2.2	76
66	Structureâ€“function relationships in the catalytic and starch binding domains of glucoamylase. Protein Engineering, Design and Selection, 1994, 7, 393-400.	2.1	68
67	Comparative genomic analysis provides insights into the evolution and niche adaptation of marine <i><scp>M</scp>agnetospira</i> sp. <scp>QH</scp>â€2 strain. Environmental Microbiology, 2014, 16, 525-544.	3.8	66
68	Abundance and Diversity of Dockerin-Containing Proteins in the Fiber-Degrading Rumen Bacterium, Ruminococcus flavefaciens FD-1. PLoS ONE, 2010, 5, e12476.	2.5	65
69	Crystal Structure of Î±-Galactosidase from Lactobacillus acidophilus NCFM: Insight into Tetramer Formation and Substrate Binding. Journal of Molecular Biology, 2011, 412, 466-480.	4.2	63
70	Semantic similarity over the gene ontology. , 2005, , .		61
71	Carbohydrate-related enzymes of important Phytophthora plant pathogens. Fungal Genetics and Biology, 2014, 72, 192-200.	2.1	61
72	Exploring the Natural Fungal Biodiversity of Tropical and Temperate Forests toward Improvement of Biomass Conversion. Applied and Environmental Microbiology, 2012, 78, 6483-6490.	3.1	60

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73	The chimeric nature of the genomes of marine magnetotactic coccoidâ€ovoid bacteria defines a novel group of <scp><i>P</i></scp><i>roteobacteria</i>. Environmental Microbiology, 2017, 19, 1103-1119.	3.8	60
74	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.	7.1	58
75	Fast solubilization of recalcitrant cellulosic biomass by the basidiomycete fungus Laetisaria arvalisinvolves successive secretion of oxidative and hydrolytic enzymes. Biotechnology for Biofuels, 2014, 7, 143.	6.2	53
76	Finding genomic ontology terms in text using evidence content. BMC Bioinformatics, 2005, 6, S21.	2.6	48
77	The Cyst-Dividing Bacterium Ramlibacter tataouinensis TTB310 Genome Reveals a Well-Stocked Toolbox for Adaptation to a Desert Environment. PLoS ONE, 2011, 6, e23784.	2.5	47
78	A Novel Unsaturated Î²-Glucuronyl Hydrolase Involved in Ulvan Degradation Unveils the Versatility of Stereochemistry Requirements in Family GH105. Journal of Biological Chemistry, 2014, 289, 6199-6211.	3.4	46
79	A New Archaeal Î²-Glycosidase from Sulfolobus solfataricus. Journal of Biological Chemistry, 2010, 285, 20691-20703.	3.4	45
80	Insights into Exo- and Endoglucanase Activities of Family 6 Glycoside Hydrolases from Podospora anserina. Applied and Environmental Microbiology, 2013, 79, 4220-4229.	3.1	45
81	First Structural Insights into Î±-l-Arabinofuranosidases from the Two GH62 Glycoside Hydrolase Subfamilies. Journal of Biological Chemistry, 2014, 289, 5261-5273.	3.4	45
82	Evolutionary and mechanistic relationships between glycosidases acting on Î±- and Î²-bonds. Carbohydrate Research, 2005, 340, 2728-2734.	2.3	41
83	The Î±-glucuronidase Agu1 from Schizophyllum commune is a member of a novel glycoside hydrolase family (GH115). Applied Microbiology and Biotechnology, 2011, 90, 1323-1332.	3.6	39
84	A thermostable GH45 endoglucanase from yeast: impact of its atypical multimodularity on activity. Microbial Cell Factories, 2011, 10, 103.	4.0	39
85	Comparative analyses of Podospora anserina secretomes reveal a large array of lignocellulose-active enzymes. Applied Microbiology and Biotechnology, 2014, 98, 7457-7469.	3.6	39
86	Structural similarities in glucoamylases by hydrophobic cluster analysis. Protein Engineering, Design and Selection, 1994, 7, 749-760.	2.1	37
87	Analysis of the Structural and Functional Diversity of Plant Cell Wall Specific Family 6 Carbohydrate Binding Modules. Biochemistry, 2009, 48, 10395-10404.	2.5	36
88	Signature Active Site Architectures Illuminate the Molecular Basis for Ligand Specificity in Family 35 Carbohydrate Binding Module,. Biochemistry, 2010, 49, 6193-6205.	2.5	35
89	Carbohydrate utilization and metabolism is highly differentiated in Agaricus bisporus. BMC Genomics, 2013, 14, 663.	2.8	35
90	A Novel, Noncatalytic Carbohydrate-binding Module Displays Specificity for Galactose-containing Polysaccharides through Calcium-mediated Oligomerization. Journal of Biological Chemistry, 2011, 286, 22499-22509.	3.4	33

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91	Gene Overexpression and Biochemical Characterization of the Biotechnologically Relevant Chlorogenic Acid Hydrolase from<i>Aspergillus niger</i>. Applied and Environmental Microbiology, 2007, 73, 5624-5632.	3.1	32
92	Automated docking of monosaccharide substrates and analogues and methyl Î±-Acarviosinide in the glucoamylase active site. , 1997, 27, 235-248.		31
93	Automated docking of maltose, 2-deoxymaltose, and maltotetraose into the soybean Î²-amylase active site. , 1999, 37, 166-175.		30
94	Replacement and deletion mutations in the catalytic domain and belt region of Aspergillus awamori glucoamylase to enhance thermostability. Protein Engineering, Design and Selection, 2000, 13, 655-659.	2.1	29
95	Deletion analysis of the starch-binding domain of Aspergillus glucoamylase. Protein Engineering, Design and Selection, 1995, 8, 1049-1055.	2.1	27
96	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines. , 2017, , 117-131.		27
97	Tracking of enzymatic biomass deconstruction by fungal secretomes highlights markers of lignocellulose recalcitrance. Biotechnology for Biofuels, 2019, 12, 76.	6.2	25
98	Carbohydrate-active enzymes from pigmented Bacilli: a genomic approach to assess carbohydrate utilization and degradation. BMC Microbiology, 2011, 11, 198.	3.3	23
99	Automated docking of glucosyl disaccharides in the glucoamylase active site. Proteins: Structure, Function and Bioinformatics, 1997, 28, 162-173.	2.6	21
100	Automated docking of isomaltose analogues in the glucoamylase active site. Carbohydrate Research, 1997, 297, 309-324.	2.3	17
101	Multiple rewards from a treasure trove of novel glycoside hydrolase and polysaccharide lyase structures: new folds, mechanistic details, and evolutionary relationships. Current Opinion in Structural Biology, 2013, 23, 652-659.	5.7	16
102	Intrinsic dynamic behavior of enzyme:substrate complexes govern the catalytic action of Î²-galactosidases across clan GH-A. Scientific Reports, 2019, 9, 10346.	3.3	16
103	Automated Docking of Î±-(1,4)- and Î±-(1,6)-Linked Glucosyl Trisaccharides in the Glucoamylase Active Site. Industrial & Engineering Chemistry Research, 1998, 37, 2148-2157.	3.7	15
104	Composting-Like Conditions Are More Efficient for Enrichment and Diversity of Organisms Containing Cellulase-Encoding Genes than Submerged Cultures. PLoS ONE, 2016, 11, e0167216.	2.5	11
105	The rational design of an iminosugar inhibitor able to mimic substrate distortion occurring during retaining-cellulase hydrolysis. Tetrahedron Letters, 2001, 42, 3443-3446.	1.4	6
106	Carbohydrate-Active Enzymes Database: Principles and Classification of Glycosyltransferases. , 0, , 89-118.		3
107	(Hemi-)Cellulose Degrading Enzymes and Their Encoding Genes from Aspergillus and Trichoderma. , 2011, , 341-355.		2
108	Automated Docking of Glucoamylase Substrates and Inhibitors. Annals of the New York Academy of Sciences, 1996, 799, 164-171.	3.8	0