

Pedro M Coutinho

List of Publications by Year in descending order

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108
papers

37,234
citations

17776

65
h-index

37326

100
g-index

111
all docs

111
docs citations

111
times ranked

36102
citing authors

#	ARTICLE	IF	CITATIONS
1	The carbohydrate-active enzymes database (CAZy) in 2013. <i>Nucleic Acids Research</i> , 2014, 42, D490-D495.	6.5	5,443
2	The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. <i>Nucleic Acids Research</i> , 2009, 37, D233-D238.	6.5	4,854
3	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	13.7	1,442
4	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	6.0	1,424
5	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq1 10.784314. <i>Journal of Molecular Biology</i> , 2003, 328, 307-317.	9.4	1,116
6	An Evolving Hierarchical Family Classification for Glycosyltransferases. <i>Journal of Molecular Biology</i> , 2003, 328, 307-317.	2.0	1,079
7	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
8	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	9.4	1,012
9	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
10	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
11	Genome sequence of the lignocellulose degrading fungus <i>Phanerochaete chrysosporium</i> strain RP78. <i>Nature Biotechnology</i> , 2004, 22, 695-700.	9.4	805
12	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
13	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
14	<i>Pezizomycotina</i> black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	13.7	641
15	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
16	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
17	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
18	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispersome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	1.5	532

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19	Dividing the large glycoside hydrolase family 13 into subfamilies: towards improved functional annotations of α -amylase-related proteins. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 555-562.	1.0	530
20	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
21	The Plant Cell Wall "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
22	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	2.6	490
23	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490
24	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, 10643-10648.	3.3	451
25	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	9.4	428
26	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	1.5	402
27	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.	13.9	391
28	Evolution, substrate specificity and subfamily classification of glycoside hydrolase family 5 (GH5). <i>BMC Evolutionary Biology</i> , 2012, 12, 186.	3.2	389
29	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	6.0	371
30	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, 17501-17506.	3.3	359
31	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
32	The genome sequence of the model ascomycete fungus <i>Podospira anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	13.9	301
33	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
34	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
35	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
36	A hierarchical classification of polysaccharide lyases for glycogenomics. <i>Biochemical Journal</i> , 2010, 432, 437-444.	1.7	282

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37	Poplar Carbohydrate-Active Enzymes. Gene Identification and Expression Analyses. <i>Plant Physiology</i> , 2006, 140, 946-962.	2.3	271
38	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, 5458-5463.	3.3	259
39	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	2.4	228
40	Genome of the red alga <i>Porphyridium purpureum</i> . <i>Nature Communications</i> , 2013, 4, 1941.	5.8	204
41	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
42	Carbohydrate-Active Enzymes Involved in the Secondary Cell Wall Biogenesis in Hybrid Aspen. <i>Plant Physiology</i> , 2005, 137, 983-997.	2.3	173
43	Measuring semantic similarity between Gene Ontology terms. <i>Data and Knowledge Engineering</i> , 2007, 61, 137-152.	2.1	166
44	Cello-Oligosaccharide Oxidation Reveals Differences between Two Lytic Polysaccharide Monoxygenases (Family GH61) from <i>Podospira anserina</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 488-496.	1.4	149
45	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
46	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
47	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
48	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
49	Glucoamylase structural, functional, and evolutionary relationships. , 1997, 29, 334-347.		127
50	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
51	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
52	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
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. <i>Fungal Genetics and Biology</i> , 2008, 45, 638-645.	0.9	118
54	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111

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55	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
56	Glycogen metabolism loss: a common marker of parasitic behaviour in bacteria?. <i>Trends in Genetics</i> , 2002, 18, 437-440.	2.9	98
57	How nature can exploit nonspecific catalytic and carbohydrate binding modules to create enzymatic specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20889-20894.	3.3	97
58	<i>Podospora anserina</i> Hemicellulases Potentiate the <i>Trichoderma reesei</i> Secretome for Saccharification of Lignocellulosic Biomass. <i>Applied and Environmental Microbiology</i> , 2011, 77, 237-246.	1.4	94
59	The Complete Genome of <i>Teredinibacter turnerae</i> T7901: An Intracellular Endosymbiont of Marine Wood-Boring Bivalves (Shipworms). <i>PLoS ONE</i> , 2009, 4, e6085.	1.1	93
60	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. <i>BMC Genomics</i> , 2014, 15, 486.	1.2	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. <i>BMC Genomics</i> , 2012, 13, 321.	1.2	86
62	Secretome analysis of <i>Phanerochaete chrysosporium</i> strain CIRM-BRFM41 grown on softwood. <i>Applied Microbiology and Biotechnology</i> , 2008, 80, 719-33.	1.7	83
63	A census of carbohydrate-active enzymes in the genome of <i>Arabidopsis thaliana</i> . , 2001, , 55-72.		80
64	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. <i>Journal of Proteome Research</i> , 2012, 11, 5924-5933.	1.8	79
65	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
66	Structure-function relationships in the catalytic and starch binding domains of glucoamylase. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 393-400.	1.0	68
67	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
68	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
69	Crystal Structure of β -Galactosidase from <i>Lactobacillus acidophilus</i> NCFM: Insight into Tetramer Formation and Substrate Binding. <i>Journal of Molecular Biology</i> , 2011, 412, 466-480.	2.0	63
70	Semantic similarity over the gene ontology. , 2005, , .		61
71	Carbohydrate-related enzymes of important <i>Phytophthora</i> plant pathogens. <i>Fungal Genetics and Biology</i> , 2014, 72, 192-200.	0.9	61
72	Exploring the Natural Fungal Biodiversity of Tropical and Temperate Forests toward Improvement of Biomass Conversion. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6483-6490.	1.4	60

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73	The chimeric nature of the genomes of marine magnetotactic coccoid-rod bacteria defines a novel group of <i>Proteobacteria</i> . <i>Environmental Microbiology</i> , 2017, 19, 1103-1119.	1.8	60
74	Complexity of the <i>Ruminococcus flavefaciens</i> cellulosome reflects an expansion in glycan recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7136-7141.	3.3	58
75	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
76	Finding genomic ontology terms in text using evidence content. <i>BMC Bioinformatics</i> , 2005, 6, S21.	1.2	48
77	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
78	A Novel Unsaturated β -Glucuronidase Involved in Ulvan Degradation Unveils the Versatility of Stereochemistry Requirements in Family GH105. <i>Journal of Biological Chemistry</i> , 2014, 289, 6199-6211.	1.6	46
79	A New Archaeal β -Glycosidase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 20691-20703.	1.6	45
80	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
81	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
82	Evolutionary and mechanistic relationships between glycosidases acting on α - and β -bonds. <i>Carbohydrate Research</i> , 2005, 340, 2728-2734.	1.1	41
83	The β -glucuronidase <i>Agu1</i> 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
84	A thermostable GH45 endoglucanase from yeast: impact of its atypical multimodularity on activity. <i>Microbial Cell Factories</i> , 2011, 10, 103.	1.9	39
85	Comparative analyses of <i>Podospira anserina</i> secretomes reveal a large array of lignocellulose-active enzymes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7457-7469.	1.7	39
86	Structural similarities in glucoamylases by hydrophobic cluster analysis. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 749-760.	1.0	37
87	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
88	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
89	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . <i>BMC Genomics</i> , 2013, 14, 663.	1.2	35
90	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

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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.	1.4	32
92	Automated docking of monosaccharide substrates and analogues and methyl β -Acarviosinide in the glucoamylase active site. , 1997, 27, 235-248.		31
93	Automated docking of maltose, 2-deoxymaltose, and maltotetraose into the soybean β -amylase active site. , 1999, 37, 166-175.		30
94	Replacement and deletion mutations in the catalytic domain and belt region of <i>Aspergillus awamori</i> glucoamylase to enhance thermostability. Protein Engineering, Design and Selection, 2000, 13, 655-659.	1.0	29
95	Deletion analysis of the starch-binding domain of <i>Aspergillus glucoamylase</i> . Protein Engineering, Design and Selection, 1995, 8, 1049-1055.	1.0	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.	1.3	23
99	Automated docking of glucosyl disaccharides in the glucoamylase active site. Proteins: Structure, Function and Bioinformatics, 1997, 28, 162-173.	1.5	21
100	Automated docking of isomaltose analogues in the glucoamylase active site. Carbohydrate Research, 1997, 297, 309-324.	1.1	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.	2.6	16
102	Intrinsic dynamic behavior of enzyme:substrate complexes govern the catalytic action of β -galactosidases across clan GH-A. Scientific Reports, 2019, 9, 10346.	1.6	16
103	Automated Docking of β -(1,4)- and β -(1,6)-Linked Glucosyl Trisaccharides in the Glucoamylase Active Site. Industrial & Engineering Chemistry Research, 1998, 37, 2148-2157.	1.8	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.	1.1	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.	0.7	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 <i>Aspergillus</i> and <i>Trichoderma</i> . , 2011, , 341-355.		2
108	Automated Docking of Glucoamylase Substrates and Inhibitors. Annals of the New York Academy of Sciences, 1996, 799, 164-171.	1.8	0