

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	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.	3.3	16
2	Tracking of enzymatic biomass deconstruction by fungal secretomes highlights markers of lignocellulose recalcitrance. <i>Biotechnology for Biofuels</i> , 2019, 12, 76.	6.2	25
3	The chimeric nature of the genomes of marine magnetotactic coccoid ϵ -proteobacteria defines a novel group of <i>Proteobacteria</i> . <i>Environmental Microbiology</i> , 2017, 19, 1103-1119.	3.8	60
4	The CAZy Database/the Carbohydrate-Active Enzyme (CAZy) Database: Principles and Usage Guidelines. , 2017, , 117-131.		27
5	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.	7.1	58
6	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.	2.5	11
7	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111
8	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.	3.4	46
9	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
10	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.	3.6	39
11	First Structural Insights into α -L-Arabinofuranosidases from the Two GH62 Glycoside Hydrolase Subfamilies. <i>Journal of Biological Chemistry</i> , 2014, 289, 5261-5273.	3.4	45
12	The carbohydrate-active enzymes database (CAZy) in 2013. <i>Nucleic Acids Research</i> , 2014, 42, D490-D495.	14.5	5,443
13	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.	2.8	91
14	Carbohydrate-related enzymes of important <i>Phytophthora</i> plant pathogens. <i>Fungal Genetics and Biology</i> , 2014, 72, 192-200.	2.1	61
15	Comparative genomic analysis provides insights into the evolution and niche adaptation of marine <i>Magnetospira</i> sp. <i>QH-2</i> strain. <i>Environmental Microbiology</i> , 2014, 16, 525-544.	3.8	66
16	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
17	Multiple rewards from a treasure trove of novel glycoside hydrolase and polysaccharide lyase structures: new folds, mechanistic details, and evolutionary relationships. <i>Current Opinion in Structural Biology</i> , 2013, 23, 652-659.	5.7	16
18	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.	3.1	45

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19	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . <i>BMC Genomics</i> , 2013, 14, 663.	2.8	35
20	Genome of the red alga <i>Porphyridium purpureum</i> . <i>Nature Communications</i> , 2013, 4, 1941.	12.8	204
21	Cello-Oligosaccharide Oxidation Reveals Differences between Two Lytic Polysaccharide Monooxygenases (Family GH61) from <i>Podospora anserina</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 488-496.	3.1	149
22	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.	7.1	359
23	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. <i>Science</i> , 2012, 335, 843-847.	12.6	371
24	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.	7.1	97
25	Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome. <i>Journal of Proteome Research</i> , 2012, 11, 5924-5933.	3.7	79
26	Evolution, substrate specificity and subfamily classification of glycoside hydrolase family 5 (GH5). <i>BMC Evolutionary Biology</i> , 2012, 12, 186.	3.2	389
27	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.	2.8	86
28	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.	2.8	135
29	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.	3.1	60
30	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.	7.1	259
31	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
32	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	3.5	902
33	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.	7.1	640
34	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011, 12, R40.	8.8	594
35	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.	4.2	63
36	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.	17.5	428

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37	Phylogenetic and gene-centric metagenomics of the canine intestinal microbiome reveals similarities with humans and mice. <i>ISME Journal</i> , 2011, 5, 639-649.	9.8	292
38	The Î±-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.	3.6	39
39	A thermostable GH45 endoglucanase from yeast: impact of its atypical multimodularity on activity. <i>Microbial Cell Factories</i> , 2011, 10, 103.	4.0	39
40	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.	2.8	105
41	Carbohydrate-active enzymes from pigmented <i>Bacilli</i> : a genomic approach to assess carbohydrate utilization and degradation. <i>BMC Microbiology</i> , 2011, 11, 198.	3.3	23
42	<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.	3.1	94
43	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.	3.4	33
44	The Plant Cell Wallâ€œDecomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	12.6	512
45	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.	3.5	532
46	(Hemi-)Cellulose Degrading Enzymes and Their Encoding Genes from <i>Aspergillus</i> and <i>Trichoderma</i> . , 2011, , 341-355.		2
47	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.	2.5	47
48	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.	2.8	293
49	Modulation of cellulosome composition in <i>Clostridium cellulolyticum</i> : Adaptation to the polysaccharide environment revealed by proteomic and carbohydrate-â€œactive enzyme analyses. <i>Proteomics</i> , 2010, 10, 541-554.	2.2	76
50	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
51	PÃ©rigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. <i>Nature</i> , 2010, 464, 1033-1038.	27.8	641
52	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	17.5	490
53	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.	2.5	65
54	A New Archaeal Î²-Glycosidase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 20691-20703.	3.4	45

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55	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	5.5	228
56	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.	7.1	300
57	A hierarchical classification of polysaccharide lyases for glycogenomics. <i>Biochemical Journal</i> , 2010, 432, 437-444.	3.7	282
58	Signature Active Site Architectures Illuminate the Molecular Basis for Ligand Specificity in Family 35 Carbohydrate Binding Module,. <i>Biochemistry</i> , 2010, 49, 6193-6205.	2.5	35
59	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.	9.6	391
60	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.	2.5	93
61	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.	7.1	612
62	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
63	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.	7.1	530
64	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.	3.1	804
65	Analysis of the Structural and Functional Diversity of Plant Cell Wall Specific Family 6 Carbohydrate Binding Modules. <i>Biochemistry</i> , 2009, 48, 10395-10404.	2.5	36
66	The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. <i>Nucleic Acids Research</i> , 2009, 37, D233-D238.	14.5	4,854
67	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.	2.1	133
68	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.	7.1	669
69	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.	2.5	124
70	Secretome analysis of <i>Phanerochaete chrysosporium</i> strain CIRM-BRFM41 grown on softwood. <i>Applied Microbiology and Biotechnology</i> , 2008, 80, 719-33.	3.6	83
71	Genome sequence of the metazoan plant-parasitic nematode <i>Meloidogyne incognita</i> . <i>Nature Biotechnology</i> , 2008, 26, 909-915.	17.5	1,012
72	Genome sequencing and analysis of the biomass-degrading fungus <i>Trichoderma reesei</i> (syn. <i>Hypocrea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	17.8	1,116

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73	The genome sequence of the model ascomycete fungus <i>Podospora anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	9.6	301
74	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.	2.1	118
75	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.	7.1	120
76	Complete Genome Sequence of the Complex Carbohydrate-Degrading Marine Bacterium, <i>Saccharophagus degradans</i> Strain 2-40T. <i>PLoS Genetics</i> , 2008, 4, e1000087.	3.5	142
77	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.	7.1	451
78	Gene Overexpression and Biochemical Characterization of the Biotechnologically Relevant Chlorogenic Acid Hydrolase from <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 5624-5632.	3.1	32
79	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	5.6	490
80	Measuring semantic similarity between Gene Ontology terms. <i>Data and Knowledge Engineering</i> , 2007, 61, 137-152.	3.4	166
81	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	17.5	1,047
82	Complete Cellulase System in the Marine Bacterium <i>Saccharophagus degradans</i> Strain 2-40 T. <i>Journal of Bacteriology</i> , 2006, 188, 3849-3861.	2.2	126
83	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.	5.7	347
84	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.	2.1	530
85	Poplar Carbohydrate-Active Enzymes. Gene Identification and Expression Analyses. <i>Plant Physiology</i> , 2006, 140, 946-962.	4.8	271
86	Evolutionary and mechanistic relationships between glycosidases acting on β - and β -bonds. <i>Carbohydrate Research</i> , 2005, 340, 2728-2734.	2.3	41
87	Finding genomic ontology terms in text using evidence content. <i>BMC Bioinformatics</i> , 2005, 6, S21.	2.6	48
88	Semantic similarity over the gene ontology. , 2005, , .		61
89	Carbohydrate-Active Enzymes Involved in the Secondary Cell Wall Biogenesis in Hybrid Aspen. <i>Plant Physiology</i> , 2005, 137, 983-997.	4.8	173
90	Genome sequence of the lignocellulose degrading fungus <i>Phanerochaete chrysosporium</i> strain RP78. <i>Nature Biotechnology</i> , 2004, 22, 695-700.	17.5	805

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91	Why are there so many carbohydrate-active enzyme-related genes in plants?. Trends in Plant Science, 2003, 8, 563-565.	8.8	134
92	An Evolving Hierarchical Family Classification for Glycosyltransferases. Journal of Molecular Biology, 2003, 328, 307-317.	4.2	1,079
93	Glycogen metabolism loss: a common marker of parasitic behaviour in bacteria?. Trends in Genetics, 2002, 18, 437-440.	6.7	98
94	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
95	A census of carbohydrate-active enzymes in the genome of Arabidopsis thaliana. Plant Molecular Biology, 2001, 47, 55-72.	3.9	190
96	A census of carbohydrate-active enzymes in the genome of Arabidopsis thaliana. , 2001, , 55-72.		80
97	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
98	Automated docking of maltose, 2-deoxymaltose, and maltotetraose into the soybean Î²-amylase active site. , 1999, 37, 166-175.		30
99	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
100	Automated docking of isomaltose analogues in the glucoamylase active site. Carbohydrate Research, 1997, 297, 309-324.	2.3	17
101	Automated docking of monosaccharide substrates and analogues and methyl Î±-Acarviosinide in the glucoamylase active site. , 1997, 27, 235-248.		31
102	Automated docking of glucosyl disaccharides in the glucoamylase active site. Proteins: Structure, Function and Bioinformatics, 1997, 28, 162-173.	2.6	21
103	Glucoamylase structural, functional, and evolutionary relationships. , 1997, 29, 334-347.		127
104	Automated Docking of Glucoamylase Substrates and Inhibitors. Annals of the New York Academy of Sciences, 1996, 799, 164-171.	3.8	0
105	Deletion analysis of the starch-binding domain of Aspergillus glucoamylase. Protein Engineering, Design and Selection, 1995, 8, 1049-1055.	2.1	27
106	Structural similarities in glucoamylases by hydrophobic cluster analysis. Protein Engineering, Design and Selection, 1994, 7, 749-760.	2.1	37
107	Structureâ€“function relationships in the catalytic and starch binding domains of glucoamylase. Protein Engineering, Design and Selection, 1994, 7, 393-400.	2.1	68
108	Carbohydrate-Active Enzymes Database: Principles and Classification of Glycosyltransferases. , 0, , 89-118.		3