

Carlos M G A Fontes

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

146
papers

4,389
citations

36
h-index

61
g-index

150
ext. papers

4,880
ext. citations

4.7
avg, IF

5.07
L-index

#	Paper	IF	Citations
146	Impact of <i>Chlorella vulgaris</i> as feed ingredient and carbohydrases on the health status and hepatic lipid metabolism of finishing pigs.. <i>Research in Veterinary Science</i> , 2022 , 144, 44-53	2.5	0
145	Influence of <i>Chlorella vulgaris</i> on growth, digestibility and gut morphology and microbiota of weaned piglet.. <i>Scientific Reports</i> , 2022 , 12, 6012	4.9	1
144	Mapping Molecular Recognition of β ,3-1,4-Glucans by a Surface Glycan-Binding Protein from the Human Gut Symbiont <i>Bacteroides ovatus</i> . <i>Microbiology Spectrum</i> , 2021 , e0182621	8.9	1
143	Cellulosomes: Highly Efficient Cellulolytic Complexes. <i>Sub-Cellular Biochemistry</i> , 2021 , 96, 323-354	5.5	5
142	An individual alginate lyase is effective in the disruption of <i>Laminaria digitata</i> recalcitrant cell wall. <i>Scientific Reports</i> , 2021 , 11, 9706	4.9	3
141	A trimodular family 16 glycoside hydrolase from the cellulosome of displays highly specific licheninase (EC 3.2.1.73) activity. <i>Microbiology (United Kingdom)</i> , 2021 , 167,	2.9	1
140	Small angle X-ray scattering based structure, modeling and molecular dynamics analyses of family 43 glycoside hydrolase β -L-arabinofuranosidase from. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 209-218	3.6	1
139	A dual cohesin-dockerin complex binding mode in <i>Bacteroides cellulosolvans</i> contributes to the size and complexity of its cellulosome. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100552	5.4	2
138	A Venomics Approach Coupled to High-Throughput Toxin Production Strategies Identifies the First Venom-Derived Melanocortin Receptor Agonists. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 8250-8264	8.3	10
137	A two-enzyme constituted mixture to improve the degradation of <i>Arthrospira platensis</i> microalga cell wall for monogastric diets. <i>Journal of Animal Physiology and Animal Nutrition</i> , 2020 , 104, 310-321	2.6	17
136	Discovery of hyperstable carbohydrate-active enzymes through metagenomics of extreme environments. <i>FEBS Journal</i> , 2020 , 287, 1116-1137	5.7	12
135	Molecular basis for the preferential recognition of β ,3-1,4-glucans by the family 11 carbohydrate-binding module from <i>Clostridium thermocellum</i> . <i>FEBS Journal</i> , 2020 , 287, 2723-2743	5.7	5
134	A High Dietary Incorporation Level of Improves the Nutritional Value of Pork Fat without Impairing the Performance of Finishing Pigs. <i>Animals</i> , 2020 , 10,	3.1	6
133	Immobilization of bacterial feruloyl esterase on mesoporous silica particles and enhancement of synthetic activity by hydrophobic-modified surface. <i>Bioresource Technology</i> , 2019 , 293, 122009	11	10
132	Directed evolution of the type C feruloyl esterase from <i>Fusarium oxysporum</i> FoFaeC and molecular docking analysis of its improved variants. <i>New Biotechnology</i> , 2019 , 51, 14-20	6.4	2
131	Molecular organization and protein stability of the <i>Clostridium thermocellum</i> glucuronoxylan endo- β ,4-xylanase of family 30 glycoside hydrolase in solution. <i>Journal of Structural Biology</i> , 2019 , 206, 335-344	3.4	3
130	Novel combination of feed enzymes to improve the degradation of <i>Chlorella vulgaris</i> recalcitrant cell wall. <i>Scientific Reports</i> , 2019 , 9, 5382	4.9	25

129	Molecular Cloning, Expression and Biochemical Characterization of a Family 5 Glycoside Hydrolase First Endo-Mannanase (RfGH5_7) from Ruminococcus flavefaciens FD-1 v3. <i>Molecular Biotechnology</i> , 2019 , 61, 826-835	3	5
128	High-Throughput Production of a New Library of Human Single and Tandem PDZ Domains Allows Quantitative PDZ-Peptide Interaction Screening Through High-Throughput Holdup Assay. <i>Methods in Molecular Biology</i> , 2019 , 2025, 439-476	1.4	15
127	High-Throughput Production of Oxidized Animal Toxins in Escherichia coli. <i>Methods in Molecular Biology</i> , 2019 , 2025, 165-190	1.4	2
126	Evolution of the feruloyl esterase MtFae1a from Myceliophthora thermophila towards improved catalysts for antioxidants synthesis. <i>Applied Microbiology and Biotechnology</i> , 2018 , 102, 5185-5196	5.7	8
125	Structure-function analyses generate novel specificities to assemble the components of multienzyme bacterial cellulosome complexes. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4201-4212	5.4	7
124	Cellulosome assembly: paradigms are meant to be broken!. <i>Current Opinion in Structural Biology</i> , 2018 , 49, 154-161	8.1	16
123	Target highlights from the first post-PSI CASP experiment (CASP12, May-August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 27-50	4.2	5
122	Higher order scaffoldin assembly in Ruminococcus flavefaciens cellulosome is coordinated by a discrete cohesin-dockerin interaction. <i>Scientific Reports</i> , 2018 , 8, 6987	4.9	4
121	Novel insights into the degradation of β 1,3-glucans by the cellulosome of Clostridium thermocellum revealed by structure and function studies of a family 81 glycoside hydrolase. <i>International Journal of Biological Macromolecules</i> , 2018 , 117, 890-901	7.9	11
120	Gene design, fusion technology and TEV cleavage conditions influence the purification of oxidized disulphide-rich venom peptides in Escherichia coli. <i>Microbial Cell Factories</i> , 2017 , 16, 4	6.4	19
119	Stability and Ligand Promiscuity of Type A Carbohydrate-binding Modules Are Illustrated by the Structure of CBM64C. <i>Journal of Biological Chemistry</i> , 2017 , 292, 4847-4860	5.4	13
118	Complexity of the Ruminococcus flavefaciens FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. <i>Scientific Reports</i> , 2017 , 7, 42355	4.9	20
117	Carbohydrate Depolymerization by Intricate Cellulosomal Systems. <i>Methods in Molecular Biology</i> , 2017 , 1588, 93-116	1.4	6
116	High-throughput expression of animal venom toxins in Escherichia coli to generate a large library of oxidized disulphide-reticulated peptides for drug discovery. <i>Microbial Cell Factories</i> , 2017 , 16, 6	6.4	33
115	A Novel Platform for High-Throughput Gene Synthesis to Maximize Recombinant Expression in Escherichia coli. <i>Methods in Molecular Biology</i> , 2017 , 1620, 113-128	1.4	4
114	Assembly of Ruminococcus flavefaciens cellulosome revealed by structures of two cohesin-dockerin complexes. <i>Scientific Reports</i> , 2017 , 7, 759	4.9	16
113	Single versus dual-binding conformations in cellulosomal cohesin-dockerin complexes. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 89-96	8.1	26
112	Single Binding Mode Integration of Hemicellulose-degrading Enzymes via Adaptor Scaffoldins in Ruminococcus flavefaciens Cellulosome. <i>Journal of Biological Chemistry</i> , 2016 , 291, 26658-26669	5.4	11

111	The Mechanism by Which Arabinoxylanases Can Recognize Highly Decorated Xylans. <i>Journal of Biological Chemistry</i> , 2016 , 291, 22149-22159	5.4	21
110	Conservation in the mechanism of glucuronoxylan hydrolysis revealed by the structure of glucuronoxylan xylanohydrolase (CtXyn30A) from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 1162-1173	5.5	6
109	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, 7136-41	11.5	40
108	T7 Endonuclease I Mediates Error Correction in Artificial Gene Synthesis. <i>Molecular Biotechnology</i> , 2016 , 58, 573-84	3	7
107	A New Member of Family 11 Polysaccharide Lyase, Rhamnogalacturonan Lyase (CtRGLF) from <i>Clostridium thermocellum</i> . <i>Molecular Biotechnology</i> , 2016 , 58, 232-40	3	12
106	Molecular determinants of substrate specificity revealed by the structure of <i>Clostridium thermocellum</i> arabinofuranosidase 43A from glycosyl hydrolase family 43 subfamily 16. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 1281-1289	5.5	8
105	Diverse specificity of cellulosome attachment to the bacterial cell surface. <i>Scientific Reports</i> , 2016 , 6, 38292	4.9	19
104	Development of a gene synthesis platform for the efficient large scale production of small genes encoding animal toxins. <i>BMC Biotechnology</i> , 2016 , 16, 86	3.5	2
103	Development of synthetic light-chain antibodies as novel and potent HIV fusion inhibitors. <i>Aids</i> , 2016 , 30, 1691-701	3.5	10
102	Recognition of xyloglucan by the crystalline cellulose-binding site of a family 3a carbohydrate-binding module. <i>FEBS Letters</i> , 2015 , 589, 2297-303	3.8	39
101	Combined Crystal Structure of a Type I Cohesin: MUTATION AND AFFINITY BINDING STUDIES REVEAL STRUCTURAL DETERMINANTS OF COHESIN-DOCKERIN SPECIFICITIES. <i>Journal of Biological Chemistry</i> , 2015 , 290, 16215-25	5.4	9
100	Cell-surface Attachment of Bacterial Multienzyme Complexes Involves Highly Dynamic Protein-Protein Anchors. <i>Journal of Biological Chemistry</i> , 2015 , 290, 13578-90	5.4	21
99	The family 6 Carbohydrate Binding Module (CtCBM6) of glucuronoxylanase (CtXynGH30) of <i>Clostridium thermocellum</i> binds decorated and undecorated xylans through cleft A. <i>Archives of Biochemistry and Biophysics</i> , 2015 , 575, 8-21	4.1	7
98	Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of Xyloglucan and β 1,3-1,4-Glucans through Distinct Mechanisms. <i>Journal of Biological Chemistry</i> , 2015 , 290, 10572-86	5.4	31
97	Unravelling glucan recognition systems by glycome microarrays using the designer approach and mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 974-88	7.6	42
96	Purification and crystallographic studies of a putative carbohydrate-binding module from the <i>Ruminococcus flavefaciens</i> FD-1 endoglucanase Cel5A. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 958-61	1.1	
95	Role of pectinolytic enzymes identified in <i>Clostridium thermocellum</i> cellulosome. <i>PLoS ONE</i> , 2015 , 10, e0116787	3.7	21
94	Expression, purification, crystallization and preliminary X-ray analysis of CttA, a putative cellulose-binding protein from <i>Ruminococcus flavefaciens</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 784-9	1.1	1

93	Crystallization and preliminary crystallographic studies of a novel noncatalytic carbohydrate-binding module from the <i>Ruminococcus flavefaciens</i> cellulosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 45-8	1.1	1
92	Overproduction, purification, crystallization and preliminary X-ray characterization of the family 46 carbohydrate-binding module (CBM46) of endo- β -1,4-glucanase B (CelB) from <i>Bacillus halodurans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 754-7	1.1	4
91	Construction of GH16 β -glucanase mini-cellulosomes to improve the nutritive value of barley-based diets for broilers. <i>Journal of Agricultural and Food Chemistry</i> , 2014 , 62, 7496-506	5.7	7
90	Crystallization and preliminary X-ray crystallographic analysis of a novel β -L-arabinofuranosidase (CtGH43) from <i>Clostridium thermocellum</i> ATCC 27405. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 616-8	1.1	2
89	Overexpression, crystallization and preliminary X-ray characterization of <i>Ruminococcus flavefaciens</i> scaffoldin C cohesin in complex with a dockerin from an uncharacterized CBM-containing protein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1061-4	1.1	2
88	Purification, crystallization and preliminary X-ray characterization of the third ScaB cohesin in complex with an ScaA X-dockerin from <i>Acetivibrio cellulolyticus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 656-8	1.1	1
87	Overexpression, purification, crystallization and preliminary X-ray characterization of the fourth scaffoldin A cohesin from <i>Acetivibrio cellulolyticus</i> in complex with a dockerin from a family 5 glycoside hydrolase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1065-7	1.1	4
86	Crystallization and preliminary X-ray diffraction analysis of a trimodular endo- β -1,4-glucanase (Cel5B) from <i>Bacillus halodurans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1628-30	1.1	4
85	Expression, purification and crystallization of a novel carbohydrate-binding module from the <i>Ruminococcus flavefaciens</i> cellulosome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1653-6	1.1	
84	Elaborate cellulosome architecture of <i>Acetivibrio cellulolyticus</i> revealed by selective screening of cohesin-dockerin interactions. <i>PeerJ</i> , 2014 , 2, e636	3.1	24
83	NMR solution structure and SRP54M predicted interaction of the N-terminal sequence (1-30) of the ovine Doppel protein. <i>Peptides</i> , 2013 , 49, 32-40	3.8	17
82	Genetic background and diet impact beef fatty acid composition and stearoyl-CoA desaturase mRNA expression. <i>Lipids</i> , 2013 , 48, 369-81	1.6	12
81	Efficient pretreatment for bioethanol production from water hyacinth (<i>Eichhornia crassipes</i>) involving naturally isolated and recombinant enzymes and its recovery. <i>Environmental Progress and Sustainable Energy</i> , 2013 , 33, n/a-n/a	2.5	4
80	The family 6 carbohydrate-binding module (CtCBM6B) of <i>Clostridium thermocellum</i> α -L-arabinofuranosidase binds xylans and thermally stabilized by Ca^{2+} ions. <i>Biocatalysis and Biotransformation</i> , 2013 , 31, 217-225	2.5	3
79	Understanding how noncatalytic carbohydrate binding modules can display specificity for xyloglucan. <i>Journal of Biological Chemistry</i> , 2013 , 288, 4799-809	5.4	29
78	Solution structure, dynamics and binding studies of a family 11 carbohydrate-binding module from <i>Clostridium thermocellum</i> (CtCBM11). <i>Biochemical Journal</i> , 2013 , 451, 289-300	3.8	15
77	Carcass fat partitioning and meat quality of Alentejana and Barrosã young bulls fed high or low maize silage diets. <i>Meat Science</i> , 2013 , 93, 405-12	6.4	10
76	Thermostable recombinant β (1-4)-mannanase from <i>C. thermocellum</i> : biochemical characterization and manno-oligosaccharides production. <i>Journal of Agricultural and Food Chemistry</i> , 2013 , 61, 12333-44	5.7	41

75	Small angle X-ray scattering analysis of Clostridium thermocellum cellulosome N-terminal complexes reveals a highly dynamic structure. <i>Journal of Biological Chemistry</i> , 2013 , 288, 7978-7985	5.4	18
74	Overproduction, purification, crystallization and preliminary X-ray characterization of the C-terminal family 65 carbohydrate-binding module (CBM65B) of endoglucanase Cel5A from Eubacterium cellulosolvens. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 9, 1430-1434		
73	Overexpression, crystallization and preliminary X-ray crystallographic analysis of glucuronoxylan xylanohydrolase (Xyn30A) from Clostridium thermocellum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 9, 1440-2		3
72	A novel β -arabinofuranosidase of family 43 glycoside hydrolase (Ct43Araf) from Clostridium thermocellum. <i>PLoS ONE</i> , 2013 , 8, e73575	3.7	27
71	Deciphering ligand specificity of a Clostridium thermocellum family 35 carbohydrate binding module (CtCBM35) for gluco- and galacto- substituted mannans and its calcium induced stability. <i>PLoS ONE</i> , 2013 , 8, e80415	3.7	6
70	Purification, crystallization and preliminary X-ray characterization of the Acetivibrio cellulolyticus type I cohesin ScaC in complex with the ScaB dockerin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 1030-3		3
69	Escherichia coli expression, purification, crystallization, and structure determination of bacterial cohesin-dockerin complexes. <i>Methods in Enzymology</i> , 2012 , 510, 395-415	1.7	4
68	Contrasting cellularity and fatty acid composition in fat depots from Alentejana and Barros Bovine breeds fed high and low forage diets. <i>International Journal of Biological Sciences</i> , 2012 , 8, 214-27	11.2	8
67	Bioethanol production involving recombinant C. thermocellum hydrolytic hemicellulase and fermentative microbes. <i>Applied Biochemistry and Biotechnology</i> , 2012 , 167, 1475-88	3.2	31
66	Novel Clostridium thermocellum type I cohesin-dockerin complexes reveal a single binding mode. <i>Journal of Biological Chemistry</i> , 2012 , 287, 44394-405	5.4	25
65	Influence of a mannan binding family 32 carbohydrate binding module on the activity of the appended mannanase. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 4781-7	4.8	22
64	Overproduction, purification, crystallization and preliminary X-ray characterization of a novel carbohydrate-binding module of endoglucanase Cel5A from Eubacterium cellulosolvens. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 491-3		2
63	Molecular architecture and structural transitions of a Clostridium thermocellum mini-cellulosome. <i>Journal of Molecular Biology</i> , 2011 , 407, 571-80	6.5	25
62	Purification, crystallization and preliminary X-ray characterization of the pentamodular arabinoxylanase CtXyl5A from Clostridium thermocellum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 833-6		2
61	Structural insights into a unique cellulase fold and mechanism of cellulose hydrolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5237-42	11.5	76
60	Structure and function of an arabinoxylan-specific xylanase. <i>Journal of Biological Chemistry</i> , 2011 , 286, 22510-20	5.4	69
59	A novel, noncatalytic carbohydrate-binding module displays specificity for galactose-containing polysaccharides through calcium-mediated oligomerization. <i>Journal of Biological Chemistry</i> , 2011 , 286, 22499-509	5.4	31
58	Signature active site architectures illuminate the molecular basis for ligand specificity in family 35 carbohydrate binding module. <i>Biochemistry</i> , 2010 , 49, 6193-205	3.2	32

57	Putting an N-terminal end to the <i>Clostridium thermocellum</i> xylanase Xyn10B story: crystal structure of the CBM22-1-GH10 modules complexed with xylohexaose. <i>Journal of Structural Biology</i> , 2010 , 172, 353-62	3.4	46
56	Effect of cooking methods on fatty acids, conjugated isomers of linoleic acid and nutritional quality of beef intramuscular fat. <i>Meat Science</i> , 2010 , 84, 769-77	6.4	119
55	Cellulosomes: highly efficient nanomachines designed to deconstruct plant cell wall complex carbohydrates. <i>Annual Review of Biochemistry</i> , 2010 , 79, 655-81	29.1	427
54	Family 42 carbohydrate-binding modules display multiple arabinoxylan-binding interfaces presenting different ligand affinities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2010 , 1804, 2054-62	4	7
53	Evidence that family 35 carbohydrate binding modules display conserved specificity but divergent function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 3065-70	11.5	89
52	Structural and biochemical properties of lichenase from <i>Clostridium thermocellum</i> . <i>Indian Journal of Microbiology</i> , 2009 , 49, 72-6	3.7	3
51	Family 6 carbohydrate-binding modules display multiple beta1,3-linked glucan-specific binding interfaces. <i>FEMS Microbiology Letters</i> , 2009 , 300, 48-57	2.9	8
50	Effect of the feeding system on intramuscular fatty acids and conjugated linoleic acid isomers of beef cattle, with emphasis on their nutritional value and discriminatory ability. <i>Food Chemistry</i> , 2009 , 114, 939-946	8.5	135
49	Functional insights into the role of novel type I cohesin and dockerin domains from <i>Clostridium thermocellum</i> . <i>Biochemical Journal</i> , 2009 , 424, 375-84	3.8	31
48	The active site of a carbohydrate esterase displays divergent catalytic and noncatalytic binding functions. <i>PLoS Biology</i> , 2009 , 7, e71	9.7	49
47	Crystal structure of a cellulosomal family 3 carbohydrate esterase from <i>Clostridium thermocellum</i> provides insights into the mechanism of substrate recognition. <i>Journal of Molecular Biology</i> , 2008 , 379, 64-72	6.5	37
46	Diet supplementation with the cis-9,trans-11 conjugated linoleic acid isomer affects the size of adipocytes in Wistar rats. <i>Nutrition Research</i> , 2008 , 28, 480-6	4	13
45	<i>Escherichia coli</i> expression and purification of four antimicrobial peptides fused to a family 3 carbohydrate-binding module (CBM) from <i>Clostridium thermocellum</i> . <i>Protein Expression and Purification</i> , 2008 , 59, 161-8	2	29
44	Probing the beta-1,3:1,4 glucanase, CtLic26A, with a thio-oligosaccharide and enzyme variants. <i>Organic and Biomolecular Chemistry</i> , 2008 , 6, 851-3	3.9	5
43	The <i>Clostridium cellulolyticum</i> dockerin displays a dual binding mode for its cohesin partner. <i>Journal of Biological Chemistry</i> , 2008 , 283, 18422-30	5.4	66
42	Recombinant lichenase from <i>Clostridium thermocellum</i> binds glucomannan but not to lichenan: Analysis by affinity electrophoresis. <i>Annals of Microbiology</i> , 2008 , 58, 723-725	3.2	
41	Purification, crystallization and crystallographic analysis of <i>Clostridium thermocellum</i> endo-1,4-beta-D-xylanase 10B in complex with xylohexaose. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 715-8		3
40	Molecular determinants of ligand specificity in family 11 carbohydrate binding modules: an NMR, X-ray crystallography and computational chemistry approach. <i>FEBS Journal</i> , 2008 , 275, 2524-35	5.7	27

39	Evidence for a dual binding mode of dockerin modules to cohesins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3089-94	11.5	110
38	Contents of conjugated linoleic acid isomers in ruminant-derived foods and estimation of their contribution to daily intake in Portugal. <i>British Journal of Nutrition</i> , 2007 , 98, 1206-13	3.6	44
37	Effect of slaughter season on fatty acid composition, conjugated linoleic acid isomers and nutritional value of intramuscular fat in BarrosPDO veal. <i>Meat Science</i> , 2007 , 75, 44-52	6.4	45
36	Influence of slaughter season and muscle type on fatty acid composition, conjugated linoleic acid isomeric distribution and nutritional quality of intramuscular fat in Arouquesa-PDO veal. <i>Meat Science</i> , 2007 , 76, 787-95	6.4	21
35	Irradiation effect on fatty acid composition and conjugated linoleic acid isomers in frozen lamb meat. <i>Meat Science</i> , 2007 , 77, 689-95	6.4	33
34	Fatty acid composition, including isomeric profile of conjugated linoleic acid, and cholesterol in Mertolenga-PDO beef. <i>Journal of the Science of Food and Agriculture</i> , 2006 , 86, 2196-2205	4.3	15
33	Crystal structures of Clostridium thermocellum xyloglucanase, XGH74A, reveal the structural basis for xyloglucan recognition and degradation. <i>Journal of Biological Chemistry</i> , 2006 , 281, 24922-33	5.4	75
32	Structure and activity of two metal ion-dependent acetylxylan esterases involved in plant cell wall degradation reveals a close similarity to peptidoglycan deacetylases. <i>Journal of Biological Chemistry</i> , 2006 , 281, 10968-75	5.4	86
31	Xyloglucan is recognized by carbohydrate-binding modules that interact with beta-glucan chains. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8815-28	5.4	87
30	Galactanases and Mannanases Improve the Nutritive Value of Maize and Soybean Meal Based Diets for Broiler Chicks. <i>Journal of Poultry Science</i> , 2006 , 43, 344-350	1.6	9
29	Galactomannan hydrolysis and mannose metabolism in Cellvibrio mixtus. <i>FEMS Microbiology Letters</i> , 2006 , 261, 123-32	2.9	22
28	Novel modular enzymes encoded by a cellulase gene cluster in Cellvibrio mixtus. <i>FEMS Microbiology Letters</i> , 2006 , 265, 26-34	2.9	8
27	Insights into the structural determinants of cohesin-dockerin specificity revealed by the crystal structure of the type II cohesin from Clostridium thermocellum SdbA. <i>Journal of Molecular Biology</i> , 2005 , 349, 909-15	6.5	30
26	Molecular determinants of substrate specificity in the feruloyl esterase module of xylanase 10B from Clostridium thermocellum. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 194-7		18
25	Overexpression, purification and crystallization of the two C-terminal domains of the bifunctional cellulase ctCel9D-Cel44A from Clostridium thermocellum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 1043-5		8
24	How family 26 glycoside hydrolases orchestrate catalysis on different polysaccharides: structure and activity of a Clostridium thermocellum lichenase, CtLic26A. <i>Journal of Biological Chemistry</i> , 2005 , 280, 32761-7	5.4	53
23	The crystal structure of the family 6 carbohydrate binding module from Cellvibrio mixtus endoglucanase 5a in complex with oligosaccharides reveals two distinct binding sites with different ligand specificities. <i>Journal of Biological Chemistry</i> , 2004 , 279, 21560-8	5.4	58
22	The mechanisms by which family 10 glycoside hydrolases bind decorated substrates. <i>Journal of Biological Chemistry</i> , 2004 , 279, 9597-605	5.4	135

21	The family 6 carbohydrate binding module CmCBM6-2 contains two ligand-binding sites with distinct specificities. <i>Journal of Biological Chemistry</i> , 2004 , 279, 21552-9	5.4	83
20	The family 11 carbohydrate-binding module of <i>Clostridium thermocellum</i> Lic26A-Cel5E accommodates beta-1,4- and beta-1,3-1,4-mixed linked glucans at a single binding site. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34785-93	5.4	85
19	Insights into the molecular determinants of substrate specificity in glycoside hydrolase family 5 revealed by the crystal structure and kinetics of <i>Cellvibrio mixtus</i> mannosidase 5A. <i>Journal of Biological Chemistry</i> , 2004 , 279, 25517-26	5.4	79
18	The N-terminal family 22 carbohydrate-binding module of xylanase 10B of <i>Clostridium thermocellum</i> is not a thermostabilizing domain. <i>FEMS Microbiology Letters</i> , 2004 , 238, 71-78	2.9	16
17	Common inhibition of both beta-glucosidases and beta-mannosidases by isofagomine lactam reflects different conformational itineraries for pyranoside hydrolysis. <i>ChemBioChem</i> , 2004 , 5, 1596-9	3.8	37
16	The N-terminal family 22 carbohydrate-binding module of xylanase 10B of <i>Clostridium thermocellum</i> is not a thermostabilizing domain. <i>FEMS Microbiology Letters</i> , 2004 , 238, 71-8	2.9	15
15	Cellulosome assembly revealed by the crystal structure of the cohesin-dockerin complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13809-14	11.5	210
14	Evidence for temporal regulation of the two <i>Pseudomonas cellulosa</i> xylanases belonging to glycoside hydrolase family 11. <i>Journal of Bacteriology</i> , 2002 , 184, 4124-33	3.5	34
13	The membrane-bound alpha-glucuronidase from <i>Pseudomonas cellulosa</i> hydrolyzes 4-O-methyl-D-glucuronoxyloligosaccharides but not 4-O-methyl-D-glucuronoxylan. <i>Journal of Bacteriology</i> , 2002 , 184, 4925-9	3.5	42
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10	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, 48580-7	5.4	93
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