Carlos M G A Fontes

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Cellulosomes: Highly Efficient Nanomachines Designed to Deconstruct Plant Cell Wall Complex Carbohydrates. Annual Review of Biochemistry, 2010, 79, 655-681.	5.0	498
2	Cellulosome assembly revealed by the crystal structure of the cohesin-dockerin complex. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13809-13814.	3.3	230
3	Effect of cooking methods on fatty acids, conjugated isomers of linoleic acid and nutritional quality of beef intramuscular fat. Meat Science, 2010, 84, 769-777.	2.7	162
4	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. Food Chemistry, 2009, 114, 939-946.	4.2	158
5	The X6 "Thermostabilizing―Domains of Xylanases Are Carbohydrate-Binding Modules:  Structure and Biochemistry of the Clostridium thermocellum X6b Domain,. Biochemistry, 2000, 39, 5013-5021.	1.2	154
6	The Mechanisms by Which Family 10 Glycoside Hydrolases Bind Decorated Substrates. Journal of Biological Chemistry, 2004, 279, 9597-9605.	1.6	151
7	Evidence for a dual binding mode of dockerin modules to cohesins. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3089-3094.	3.3	124
8	The Structure of the Feruloyl Esterase Module of Xylanase 10B from Clostridium thermocellum Provides Insights into Substrate Recognition. Structure, 2001, 9, 1183-1190.	1.6	112
9	Evidence that family 35 carbohydrate binding modules display conserved specificity but divergent function. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3065-3070.	3.3	109
10	Xyloglucan Is Recognized by Carbohydrate-binding Modules That Interact with β-Glucan Chains. Journal of Biological Chemistry, 2006, 281, 8815-8828.	1.6	102
11	The Location of the Ligand-binding Site of Carbohydrate-binding Modules That Have Evolved from a Common Sequence Is Not Conserved. Journal of Biological Chemistry, 2001, 276, 48580-48587.	1.6	99
12	Structure and Activity of Two Metal Ion-dependent Acetylxylan Esterases Involved in Plant Cell Wall Degradation Reveals a Close Similarity to Peptidoglycan Deacetylases. Journal of Biological Chemistry, 2006, 281, 10968-10975.	1.6	99
13	Homologous xylanases from <i>Clostridium thermocellum</i> : evidence for bi-functional activity, synergism between xylanase catalytic modules and the presence of xylan-binding domains in enzyme complexes. Biochemical Journal, 1999, 342, 105-110.	1.7	97
14	The Family 11 Carbohydrate-binding Module of Clostridium thermocellum Lic26A-Cel5E Accommodates β-1,4- and β-1,3–1,4-Mixed Linked Glucans at a Single Binding Site. Journal of Biological Chemistry, 2004, 279, 34785-34793.	1.6	95
15	Insights into the Molecular Determinants of Substrate Specificity in Glycoside Hydrolase Family 5 Revealed by the Crystal Structure and Kinetics of Cellvibrio mixtus Mannosidase 5A. Journal of Biological Chemistry, 2004, 279, 25517-25526.	1.6	91
16	The Family 6 Carbohydrate Binding Module CmCBM6-2 Contains Two Ligand-binding Sites with Distinct Specificities. Journal of Biological Chemistry, 2004, 279, 21552-21559.	1.6	89
17	Structure and Function of an Arabinoxylan-specific Xylanase. Journal of Biological Chemistry, 2011, 286, 22510-22520.	1.6	89
18	Structural insights into a unique cellulase fold and mechanism of cellulose hydrolysis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5237-5242.	3.3	88

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19	Clostridium thermocellum Xyn10B Carbohydrate-Binding Module 22-2:  The Role of Conserved Amino Acids in Ligand Binding,. Biochemistry, 2001, 40, 9167-9176.	1.2	80
20	Crystal Structures of Clostridium thermocellum Xyloglucanase, XGH74A, Reveal the Structural Basis for Xyloglucan Recognition and Degradation. Journal of Biological Chemistry, 2006, 281, 24922-24933.	1.6	79
21	The Clostridium cellulolyticum Dockerin Displays a Dual Binding Mode for Its Cohesin Partner. Journal of Biological Chemistry, 2008, 283, 18422-18430.	1.6	71
22	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. Journal of Biological Chemistry, 2004, 279, 21560-21568.	1.6	68
23	How Family 26 Glycoside Hydrolases Orchestrate Catalysis on Different Polysaccharides. Journal of Biological Chemistry, 2005, 280, 32761-32767.	1.6	60
24	Unravelling Glucan Recognition Systems by Glycome Microarrays Using the Designer Approach and Mass Spectrometry. Molecular and Cellular Proteomics, 2015, 14, 974-988.	2.5	58
25	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.	3.3	58
26	A modular xylanase from mesophilicCellulomonas fimicontains the same cellulose-binding and thermostabilizing domains as xylanases from thermophilic bacteria. FEMS Microbiology Letters, 1996, 139, 27-35.	0.7	56
27	The Active Site of a Carbohydrate Esterase Displays Divergent Catalytic and Noncatalytic Binding Functions. PLoS Biology, 2009, 7, e1000071.	2.6	56
28	Effect of slaughter season on fatty acid composition, conjugated linoleic acid isomers and nutritional value of intramuscular fat in Barrosã-PDO veal. Meat Science, 2007, 75, 44-52.	2.7	54
29	Putting an N-terminal end to the Clostridium thermocellum xylanase Xyn10B story: Crystal structure of the CBM22-1–GH10 modules complexed with xylohexaose. Journal of Structural Biology, 2010, 172, 353-362.	1.3	52
30	Contents of conjugated linoleic acid isomers in ruminant-derived foods and estimation of their contribution to daily intake in Portugal. British Journal of Nutrition, 2007, 98, 1206-1213.	1.2	50
31	The Membrane-Bound α-Glucuronidase from Pseudomonas cellulosa Hydrolyzes 4- O- Methyl- d -Glucuronoxylooligosaccharides but Not 4- O- Methyl- d -Glucuronoxylan. Journal of Bacteriology, 2002, 184, 4925-4929.	1.0	49
32	Novel combination of feed enzymes to improve the degradation of Chlorella vulgaris recalcitrant cell wall. Scientific Reports, 2019, 9, 5382.	1.6	47
33	Thermostable Recombinant β-(1→4)-Mannanase from C. thermocellum: Biochemical Characterization and Manno-Oligosaccharides Production. Journal of Agricultural and Food Chemistry, 2013, 61, 12333-12344.	2.4	46
34	Recognition of xyloglucan by the crystalline celluloseâ€binding site of a family 3a carbohydrateâ€binding module. FEBS Letters, 2015, 589, 2297-2303.	1.3	46
35	High-throughput expression of animal venom toxins in Escherichia coli to generate a large library of oxidized disulphide-reticulated peptides for drug discovery. Microbial Cell Factories, 2017, 16, 6.	1.9	43
36	Crystal Structure of a Cellulosomal Family 3 Carbohydrate Esterase from Clostridium thermocellum Provides Insights into the Mechanism of Substrate Recognition. Journal of Molecular Biology, 2008, 379, 64-72.	2.0	41

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37	Homologous xylanases from Clostridium thermocellum: evidence for bi-functional activity, synergism between xylanase catalytic modules and the presence of xylan-binding domains in enzyme complexes. Biochemical Journal, 1999, 342, 105.	1.7	41
38	Common Inhibition of Both β-Glucosidases and β-Mannosidases by Isofagomine Lactam Reflects Different Conformational Itineraries for Pyranoside Hydrolysis. ChemBioChem, 2004, 5, 1596-1599.	1.3	38
39	Irradiation effect on fatty acid composition and conjugated linoleic acid isomers in frozen lamb meat. Meat Science, 2007, 77, 689-695.	2.7	37
40	A Novel Î \pm -L-Arabinofuranosidase of Family 43 Glycoside Hydrolase (Ct43Araf) from Clostridium thermocellum. PLoS ONE, 2013, 8, e73575.	1.1	37
41	Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of Xyloglucan and β-1,3–1,4-Glucans through Distinct Mechanisms. Journal of Biological Chemistry, 2015, 290, 10572-10586.	1.6	36
42	Evidence for Temporal Regulation of the Two Pseudomonas cellulosa Xylanases Belonging to Glycoside Hydrolase Family 11. Journal of Bacteriology, 2002, 184, 4124-4133.	1.0	35
43	Signature Active Site Architectures Illuminate the Molecular Basis for Ligand Specificity in Family 35 Carbohydrate Binding Module,. Biochemistry, 2010, 49, 6193-6205.	1.2	35
44	Bioethanol Production Involving Recombinant C. thermocellum Hydrolytic Hemicellulase and Fermentative Microbes. Applied Biochemistry and Biotechnology, 2012, 167, 1475-1488.	1.4	35
45	Insights into the Structural Determinants of Cohesin—Dockerin Specificity Revealed by the Crystal Structure of the Type II Cohesin from Clostridium thermocellum SdbA. Journal of Molecular Biology, 2005, 349, 909-915.	2.0	34
46	Functional insights into the role of novel typeÂl cohesin and dockerin domains from <i>Clostridium thermocellum</i> . Biochemical Journal, 2009, 424, 375-384.	1.7	34
47	Single versus dual-binding conformations in cellulosomal cohesin–dockerin complexes. Current Opinion in Structural Biology, 2016, 40, 89-96.	2.6	34
48	The Mechanism by Which Arabinoxylanases Can Recognize Highly Decorated Xylans. Journal of Biological Chemistry, 2016, 291, 22149-22159.	1.6	34
49	A Novel, Noncatalytic Carbohydrate-binding Module Displays Specificity for Galactose-containing Polysaccharides through Calcium-mediated Oligomerization. Journal of Biological Chemistry, 2011, 286, 22499-22509.	1.6	33
50	Discovery of hyperstable carbohydrateâ€active enzymes through metagenomics of extreme environments. FEBS Journal, 2020, 287, 1116-1137.	2.2	32
51	Understanding How Noncatalytic Carbohydrate Binding Modules Can Display Specificity for Xyloglucan. Journal of Biological Chemistry, 2013, 288, 4799-4809.	1.6	31
52	Complexity of the Ruminococcus flavefaciens FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. Scientific Reports, 2017, 7, 42355.	1.6	31
53	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. Methods in Molecular Biology, 2019, 2025, 439-476.	0.4	31
54	Escherichia coli expression and purification of four antimicrobial peptides fused to a family 3 carbohydrate-binding module (CBM) from Clostridium thermocellum. Protein Expression and Purification, 2008, 59, 161-168.	0.6	30

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55	Gene design, fusion technology and TEV cleavage conditions influence the purification of oxidized disulphide-rich venom peptides in Escherichia coli. Microbial Cell Factories, 2017, 16, 4.	1.9	30
56	Molecular determinants of ligand specificity in family 11 carbohydrate binding modules – an NMR, Xâ€ray crystallography and computational chemistry approach. FEBS Journal, 2008, 275, 2524-2535.	2.2	29
57	A twoâ€enzyme constituted mixture to improve the degradation of <i>Arthrospira platensis</i> microalga cell wall for monogastric diets. Journal of Animal Physiology and Animal Nutrition, 2020, 104, 310-321.	1.0	29
58	Elaborate cellulosome architecture of <i>Acetivibrio cellulolyticus</i> revealed by selective screening of cohesin–dockerin interactions. PeerJ, 2014, 2, e636.	0.9	29
59	Molecular Architecture and Structural Transitions of a Clostridium thermocellum Mini-Cellulosome. Journal of Molecular Biology, 2011, 407, 571-580.	2.0	28
60	Possible roles for a non-modular, thermostable and proteinase-resistant cellulase from the mesophilic aerobic soil bacterium Cellvibrio mixtus. Applied Microbiology and Biotechnology, 1997, 48, 473-479.	1.7	27
61	Novel Clostridium thermocellum Type I Cohesin-Dockerin Complexes Reveal a Single Binding Mode. Journal of Biological Chemistry, 2012, 287, 44394-44405.	1.6	27
62	Influence of a Mannan Binding Family 32 Carbohydrate Binding Module on the Activity of the Appended Mannanase. Applied and Environmental Microbiology, 2012, 78, 4781-4787.	1.4	27
63	Cellulosome assembly: paradigms are meant to be broken!. Current Opinion in Structural Biology, 2018, 49, 154-161.	2.6	27
64	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. International Journal of Biological Macromolecules, 2018, 117, 890-901.	3.6	26
65	Galactomannan hydrolysis and mannose metabolism inCellvibrio mixtus. FEMS Microbiology Letters, 2006, 261, 123-132.	0.7	24
66	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. Meat Science, 2007, 76, 787-795.	2.7	24
67	Role of Pectinolytic Enzymes Identified in Clostridium thermocellum Cellulosome. PLoS ONE, 2015, 10, e0116787.	1.1	24
68	Molecular determinants of substrate specificity in the feruloyl esterase module of xylanase 10B fromClostridium thermocellum. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 194-197.	2.5	22
69	Small Angle X-ray Scattering Analysis of Clostridium thermocellum Cellulosome N-terminal Complexes Reveals a Highly Dynamic Structure. Journal of Biological Chemistry, 2013, 288, 7978-7985.	1.6	22
70	Cell-surface Attachment of Bacterial Multienzyme Complexes Involves Highly Dynamic Protein-Protein Anchors. Journal of Biological Chemistry, 2015, 290, 13578-13590.	1.6	22
71	Diverse specificity of cellulosome attachment to the bacterial cell surface. Scientific Reports, 2016, 6, 38292.	1.6	20
72	Assembly of Ruminococcus flavefaciens cellulosome revealed by structures of two cohesin-dockerin complexes. Scientific Reports, 2017, 7, 759.	1.6	20

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73	Single Binding Mode Integration of Hemicellulose-degrading Enzymes via Adaptor Scaffoldins in Ruminococcus flavefaciens Cellulosome. Journal of Biological Chemistry, 2016, 291, 26658-26669.	1.6	19
74	Stability and Ligand Promiscuity of Type A Carbohydrate-binding Modules Are Illustrated by the Structure of Spirochaeta thermophila StCBM64C. Journal of Biological Chemistry, 2017, 292, 4847-4860.	1.6	19
75	Identification of tandemly repeated type VI cellulose-binding domains in an endoglucanase from the aerobic soil bacterium Cellvibrio mixtus. Applied Microbiology and Biotechnology, 1998, 49, 552-559.	1.7	18
76	Bacterial xylanase expression in mammalian cells and transgenic mice. Journal of Biotechnology, 1999, 72, 95-101.	1.9	18
77	The N-terminal family 22 carbohydrate-binding module of xylanase 10B ofClostridium themocellumis not a thermostabilizing domain. FEMS Microbiology Letters, 2004, 238, 71-78.	0.7	18
78	NMR solution structure and SRP54M predicted interaction of the N-terminal sequence (1-30) of the ovine Doppel protein. Peptides, 2013, 49, 32-40.	1.2	18
79	Solution structure, dynamics and binding studies of a family 11 carbohydrate-binding module from <i>Clostridium thermocellum</i> (<i>Ct</i> CBM11). Biochemical Journal, 2013, 451, 289-300.	1.7	18
80	Immobilization of bacterial feruloyl esterase on mesoporous silica particles and enhancement of synthetic activity by hydrophobic-modified surface. Bioresource Technology, 2019, 293, 122009.	4.8	18
81	A High Dietary Incorporation Level of Chlorella vulgaris Improves the Nutritional Value of Pork Fat without Impairing the Performance of Finishing Pigs. Animals, 2020, 10, 2384.	1.0	17
82	The N-terminal family 22 carbohydrate-binding module of xylanase 10B of is not a thermostabilizing domain. FEMS Microbiology Letters, 2004, 238, 71-78.	0.7	16
83	Fatty acid composition, including isomeric profile of conjugated linoleic acid, and cholesterol in Mertolenga-PDO beef. Journal of the Science of Food and Agriculture, 2006, 86, 2196-2205.	1.7	15
84	Diet supplementation with the cis-9,trans-11 conjugated linoleic acid isomer affects the size of adipocytes in Wistar rats. Nutrition Research, 2008, 28, 480-486.	1.3	15
85	Genetic Background and Diet Impact Beef Fatty Acid Composition and Stearoylâ€CoA Desaturase mRNA Expression. Lipids, 2013, 48, 369-381.	0.7	15
86	A New Member of Family 11 Polysaccharide Lyase, Rhamnogalacturonan Lyase (CtRGLf) from Clostridium thermocellum. Molecular Biotechnology, 2016, 58, 232-240.	1.3	15
87	Carcass fat partitioning and meat quality of Alentejana and Barrosã young bulls fed high or low maize silage diets. Meat Science, 2013, 93, 405-412.	2.7	14
88	Galactanases and Mannanases Improve the Nutritive Value of Maize and Soybean Meal Based Diets for Broiler Chicks. Journal of Poultry Science, 2006, 43, 344-350.	0.7	13
89	Evolution of the feruloyl esterase MtFae1a from Myceliophthora thermophila towards improved catalysts for antioxidants synthesis. Applied Microbiology and Biotechnology, 2018, 102, 5185-5196.	1.7	13
90	A Venomics Approach Coupled to High-Throughput Toxin Production Strategies Identifies the First Venom-Derived Melanocortin Receptor Agonists. Journal of Medicinal Chemistry, 2020, 63, 8250-8264.	2.9	13

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91	An individual alginate lyase is effective in the disruption of Laminaria digitata recalcitrant cell wall. Scientific Reports, 2021, 11, 9706.	1.6	13
92	Influence of Chlorella vulgaris on growth, digestibility and gut morphology and microbiota of weaned piglet. Scientific Reports, 2022, 12, 6012.	1.6	13
93	Contrasting Cellularity and Fatty Acid Composition in Fat Depots from Alentejana and Barros£ Bovine Breeds Fed High and Low Forage Diets. International Journal of Biological Sciences, 2012, 8, 214-227.	2.6	12
94	Development of synthetic light-chain antibodies as novel and potent HIV fusion inhibitors. Aids, 2016, 30, 1691-1701.	1.0	12
95	Structure–function analyses generate novel specificities to assemble the components of multienzyme bacterial cellulosome complexes. Journal of Biological Chemistry, 2018, 293, 4201-4212.	1.6	12
96	Recalcitrant cell wall of Ulva lactuca seaweed is degraded by a single ulvan lyase from family 25 of polysaccharide lyases. Animal Nutrition, 2022, 9, 184-192.	2.1	12
97	Target highlights from the first postâ€PSI CASP experiment (CASP12, May–August 2016). Proteins: Structure, Function and Bioinformatics, 2018, 86, 27-50.	1.5	11
98	Cellulosomes: Highly Efficient Cellulolytic Complexes. Sub-Cellular Biochemistry, 2021, 96, 323-354.	1.0	11
99	Overexpression, purification and crystallization of the two C-terminal domains of the bifunctional cellulasectCel9D-Cel44A fromClostridium thermocellum. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1043-1045.	0.7	10
100	Construction of GH16 β-Glucanase Mini-cellulosomes To Improve the Nutritive Value of Barley-Based Diets for Broilers. Journal of Agricultural and Food Chemistry, 2014, 62, 7496-7506.	2.4	10
101	Combined Crystal Structure of a Type I Cohesin. Journal of Biological Chemistry, 2015, 290, 16215-16225.	1.6	10
102	The family 6 Carbohydrate Binding Module (CtCBM6) of glucuronoxylanase (CtXynGH30) of Clostridium thermocellum binds decorated and undecorated xylans through cleft A. Archives of Biochemistry and Biophysics, 2015, 575, 8-21.	1.4	10
103	Molecular Cloning, Expression and Biochemical Characterization of a Family 5 Glycoside Hydrolase First Endo-Mannanase (RfGH5_7) from Ruminococcus flavefaciens FD-1 v3. Molecular Biotechnology, 2019, 61, 826-835.	1.3	10
104	Novel modular enzymes encoded by a cellulase gene cluster in Cellvibrio mixtus. FEMS Microbiology Letters, 2006, 265, 26-34.	0.7	9
105	Family 42 carbohydrate-binding modules display multiple arabinoxylan-binding interfaces presenting different ligand affinities. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 2054-2062.	1.1	9
106	Molecular determinants of substrate specificity revealed by the structure of <i>Clostridium thermocellum</i> arabinofuranosidase 43A from glycosyl hydrolase family 43 subfamily 16. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1281-1289.	1.1	9
107	Conservation in the mechanism of glucuronoxylan hydrolysis revealed by the structure of glucuronoxylan xylanohydrolase (<i>Ct</i> Xyn30A) from <i>Clostridium thermocellum</i> . Acta Crystallographica Section D: Structural Biology, 2016, 72, 1162-1173.	1.1	9
108	Molecular basis for the preferential recognition of β1,3â€1,4â€glucans by the family 11 carbohydrateâ€binding module from <i>ClostridiumÂthermocellum</i> . FEBS Journal, 2020, 287, 2723-2743.	2.2	9

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109	Family 6 carbohydrate-binding modules display multiple β1,3-linked glucan-specific binding interfaces. FEMS Microbiology Letters, 2009, 300, 48-57.	0.7	8
110	T7 Endonuclease I Mediates Error Correction in Artificial Gene Synthesis. Molecular Biotechnology, 2016, 58, 573-584.	1.3	8
111	Carbohydrate Depolymerization by Intricate Cellulosomal Systems. Methods in Molecular Biology, 2017, 1588, 93-116.	0.4	8
112	A dual cohesin–dockerin complex binding mode in Bacteroides cellulosolvens contributes to the size and complexity of its cellulosome. Journal of Biological Chemistry, 2021, 296, 100552.	1.6	8
113	Deciphering Ligand Specificity of a Clostridium thermocellum Family 35 Carbohydrate Binding Module (CtCBM35) for Gluco- and Galacto- Substituted Mannans and Its Calcium Induced Stability. PLoS ONE, 2013, 8, e80415.	1.1	7
114	Impact of Chlorella vulgaris as feed ingredient and carbohydrases on the health status and hepatic lipid metabolism of finishing pigs. Research in Veterinary Science, 2022, 144, 44-53.	0.9	7
115	Highly efficient, processive and multifunctional recombinant endoglucanase RfGH5_4 from Ruminococcus flavefaciens FD-1 v3 for recycling lignocellulosic plant biomasses. International Journal of Biological Macromolecules, 2022, 209, 801-813.	3.6	7
116	Escherichia coli Expression, Purification, Crystallization, and Structure Determination of Bacterial Cohesin–Dockerin Complexes. Methods in Enzymology, 2012, 510, 395-415.	0.4	6
117	Efficient pretreatment for bioethanol production from water hyacinth (<i>eichhornia crassipes</i>) involving naturally isolated and recombinant enzymes and its recovery. Environmental Progress and Sustainable Energy, 2014, 33, 1396-1404.	1.3	6
118	Higher order scaffoldin assembly in Ruminococcus flavefaciens cellulosome is coordinated by a discrete cohesin-dockerin interaction. Scientific Reports, 2018, 8, 6987.	1.6	6
119	Targeted expression of microbial cellulases in transgenic animals. Progress in Biotechnology, 1995, 10, 279-293.	0.2	5
120	Co-integration and expression of bacterial and genomic transgenes in the pancreatic and intestinal tissues of transgenic mice. Gene, 1997, 202, 203-208.	1.0	5
121	Probing the β-1,3:1,4 glucanase, CtLic26A, with a thio-oligosaccharide and enzyme variants. Organic and Biomolecular Chemistry, 2008, 6, 851.	1.5	5
122	A Novel Platform for High-Throughput Gene Synthesis to Maximize Recombinant Expression in Escherichia coli. Methods in Molecular Biology, 2017, 1620, 113-128.	0.4	5
123	Directed evolution of the type C feruloyl esterase from Fusarium oxysporum FoFaeC and molecular docking analysis of its improved variants. New Biotechnology, 2019, 51, 14-20.	2.4	5
124	Molecular organization and protein stability of the Clostridium thermocellum glucuronoxylan endo-1²-1,4-xylanase of family 30 glycoside hydrolase in solution. Journal of Structural Biology, 2019, 206, 335-344.	1.3	5
125	Purification, crystallization and preliminary X-ray characterization of the pentamodular arabinoxylanase <i>Ct</i> Xyl5A from <i>Clostridium thermocellum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 833-836.	0.7	4
126	Overexpression, crystallization and preliminary X-ray crystallographic analysis of glucuronoxylan xylanohydrolase (Xyn30A) from <i>Clostridium thermocellum</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1440-1442.	0.7	4

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127	Overexpression, purification, crystallization and preliminary X-ray characterization of the fourth scaffoldin A cohesin fromAcetivibrio cellulolyticusin complex with a dockerin from a family 5 glycoside hydrolase. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1065-1067.	0.4	4
128	Crystallization and preliminary X-ray diffraction analysis of a trimodular endo-β-1,4-glucanase (Cel5B) fromBacillus halodurans. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1628-1630.	0.4	4
129	Overproduction, purification, crystallization and preliminary X-ray characterization of the family 46 carbohydrate-binding module (CBM46) of endo-β-1,4-glucanase B (CelB) fromBacillus halodurans. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 754-757.	0.4	4
130	High-Throughput Production of Oxidized Animal Toxins in Escherichia coli. Methods in Molecular Biology, 2019, 2025, 165-190.	0.4	4
131	Purification, crystallization and crystallographic analysis ofClostridium thermocellumendo-1,4-β-D-xylanase 10B in complex with xylohexaose. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 715-718.	0.7	3
132	Structural and biochemical properties of lichenase from Clostridium thermocellum. Indian Journal of Microbiology, 2009, 49, 72-76.	1.5	3
133	Purification, crystallization and preliminary X-ray characterization of theAcetivibrio cellulolyticustype I cohesin ScaC in complex with the ScaB dockerin. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1030-1033.	0.7	3
134	The family 6 carbohydrate-binding module (CtCBM6B) ofClostridium thermocellumalpha-L-arabinofuranosidase binds xylans and thermally stabilized by Ca2+ions. Biocatalysis and Biotransformation, 2013, 31, 217-225.	1.1	3
135	Crystallization and preliminary X-ray crystallographic analysis of a novel α- <scp>L</scp> -arabinofuranosidase (<i>Ct</i> GH43) from <i>Clostridium thermocellum</i> ATCC 27405. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 616-618.	0.4	3
136	Development of a gene synthesis platform for the efficient large scale production of small genes encoding animal toxins. BMC Biotechnology, 2016, 16, 86.	1.7	3
137	Small angle X-ray scattering based structure, modeling and molecular dynamics analyses of family 43 glycoside hydrolase α-L-arabinofuranosidase from <i>Clostridium thermocellum</i> . Journal of Biomolecular Structure and Dynamics, 2021, 39, 209-218.	2.0	3
138	Mapping Molecular Recognition of β1,3-1,4-Glucans by a Surface Glycan-Binding Protein from the Human Gut Symbiont Bacteroides ovatus. Microbiology Spectrum, 2021, 9, e0182621.	1.2	3
139	Overproduction, purification, crystallization and preliminary X-ray characterization of a novel carbohydrate-binding module of endoglucanase Cel5A fromEubacterium cellulosolvens. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 491-493.	0.7	2
140	Overexpression, crystallization and preliminary X-ray characterization ofRuminococcus flavefaciensscaffoldin C cohesin in complex with a dockerin from an uncharacterized CBM-containing protein. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1061-1064.	0.4	2
141	Expression, purification, crystallization and preliminary X-ray analysis of CttA, a putative cellulose-binding protein from <i>Ruminococcus flavefaciens</i> . Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 784-789.	0.4	2
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