

Gideon Davies

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5909967/publications.pdf>

Version: 2024-02-01

401
papers

37,597
citations

3149

92
h-index

3815

178
g-index

441
all docs

441
docs citations

441
times ranked

23487
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures and mechanisms of glycosyl hydrolases. <i>Structure</i> , 1995, 3, 853-859.	1.6	1,803
2	Carbohydrate-binding modules: fine-tuning polysaccharide recognition. <i>Biochemical Journal</i> , 2004, 382, 769-781.	1.7	1,720
3	Glycosyltransferases: Structures, Functions, and Mechanisms. <i>Annual Review of Biochemistry</i> , 2008, 77, 521-555.	5.0	1,651
4	Structural and sequence-based classification of glycoside hydrolases. <i>Current Opinion in Structural Biology</i> , 1997, 7, 637-644.	2.6	1,494
5	An Evolving Hierarchical Family Classification for Glycosyltransferases. <i>Journal of Molecular Biology</i> , 2003, 328, 307-317.	2.0	1,079
6	Nomenclature for sugar-binding subsites in glycosyl hydrolases. <i>Biochemical Journal</i> , 1997, 321, 557-559.	1.7	934
7	Insights into the oxidative degradation of cellulose by a copper metalloenzyme that exploits biomass components. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15079-15084.	3.3	861
8	A classification of nucleotide-diphospho-sugar glycosyltransferases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1997, 326, 929-939.	1.7	722
9	Catalysis by hen egg-white lysozyme proceeds via a covalent intermediate. <i>Nature</i> , 2001, 412, 835-838.	13.7	588
10	A potent mechanism-inspired O-GlcNAcase inhibitor that blocks phosphorylation of tau in vivo. <i>Nature Chemical Biology</i> , 2008, 4, 483-490.	3.9	576
11	Conserved catalytic machinery and the prediction of a common fold for several families of glycosyl hydrolases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 7090-7094.	3.3	568
12	Crystal structure of an N-terminal fragment of the DNA gyrase B protein. <i>Nature</i> , 1991, 351, 624-629.	13.7	551
13	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , 2017, 544, 65-70.	13.7	447
14	Human gut Bacteroidetes can utilize yeast mannan through a selfish mechanism. <i>Nature</i> , 2015, 517, 165-169.	13.7	427
15	A discrete genetic locus confers xyloglucan metabolism in select human gut Bacteroidetes. <i>Nature</i> , 2014, 506, 498-502.	13.7	400
16	Structure of a flavonoid glucosyltransferase reveals the basis for plant natural product modification. <i>EMBO Journal</i> , 2006, 25, 1396-1405.	3.5	389
17	Mechanistic insights into glycosidase chemistry. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 539-555.	2.8	363
18	Glycosidase mechanisms. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 619-629.	2.8	349

#	ARTICLE	IF	CITATIONS
19	Structure of the Nucleotide-Diphospho-Sugar Transferase, SpsA from <i>Bacillus subtilis</i> , in Native and Nucleotide-Complexed Forms., <i>Biochemistry</i> , 1999, 38, 6380-6385.	1.2	329
20	Discovery and characterization of a new family of lytic polysaccharide monoxygenases. <i>Nature Chemical Biology</i> , 2014, 10, 122-126.	3.9	329
21	Crystal structure of the type-2 Cu depleted laccase from <i>Coprinus dnerus</i> at 2.2 Å... resolution. <i>Nature Structural Biology</i> , 1998, 5, 310-316.	9.7	325
22	Privateer: software for the conformational validation of carbohydrate structures. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 833-834.	3.6	301
23	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. <i>Nature Chemical Biology</i> , 2018, 14, 306-310.	3.9	269
24	Characterization and engineering of the bifunctional <i>N</i> - and <i>O</i> -glucosyltransferase involved in xenobiotic metabolism in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20238-20243.	3.3	267
25	Recent structural insights into the expanding world of carbohydrate-active enzymes. <i>Current Opinion in Structural Biology</i> , 2005, 15, 637-645.	2.6	264
26	The molecular basis of polysaccharide cleavage by lytic polysaccharide monoxygenases. <i>Nature Chemical Biology</i> , 2016, 12, 298-303.	3.9	264
27	Snapshots along an Enzymatic Reaction Coordinate:Â Analysis of a Retaining Î ² -Glycoside Hydrolaseâ€â€. <i>Biochemistry</i> , 1998, 37, 11707-11713.	1.2	255
28	Structure and boosting activity of a starch-degrading lytic polysaccharide monoxygenase. <i>Nature Communications</i> , 2015, 6, 5961.	5.8	254
29	Glycoside Hydrolases and Glycosyltransferases. Families, Modules, and Implications for Genomics. <i>Plant Physiology</i> , 2000, 124, 1515-1519.	2.3	251
30	Structure of the <i>Fusarium oxysporum</i> Endoglucanase I with a Nonhydrolyzable Substrate Analogue:Â Substrate Distortion Gives Rise to the Preferred Axial Orientation for the Leaving Groupâ€â€. <i>Biochemistry</i> , 1996, 35, 15280-15287.	1.2	248
31	The crystal structure of the catalytic core domain of endoglucanase I from <i>Trichoderma reesei</i> at 3.6 Å... resolution, and a comparison with related enzymes 1 1 Edited by K.Nagai. <i>Journal of Molecular Biology</i> , 1997, 272, 383-397.	2.0	238
32	Lytic Polysaccharide Monoxygenases in Biomass Conversion. <i>Trends in Biotechnology</i> , 2015, 33, 747-761.	4.9	233
33	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, 13809-13814.	3.3	230
34	Glycosidase inhibition: assessing mimicry of the transition state. <i>Organic and Biomolecular Chemistry</i> , 2010, 8, 305-320.	1.5	217
35	Structure of the <i>Aspergillus oryzae</i> Î±-Amylase Complexed with the Inhibitor Acarbose at 2.0 Å... Resolutionâ€â€. <i>Biochemistry</i> , 1997, 36, 10837-10845.	1.2	216
36	Conformational Analyses of the Reaction Coordinate of Glycosidases. <i>Accounts of Chemical Research</i> , 2012, 45, 308-316.	7.6	212

#	ARTICLE	IF	CITATIONS
37	On the catalytic mechanisms of lytic polysaccharide monoxygenases. <i>Current Opinion in Chemical Biology</i> , 2016, 31, 195-207.	2.8	195
38	An ancient family of lytic polysaccharide monoxygenases with roles in arthropod development and biomass digestion. <i>Nature Communications</i> , 2018, 9, 756.	5.8	192
39	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
40	Spectroscopic and computational insight into the activation of O ₂ by the mononuclear Cu center in polysaccharide monoxygenases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8797-8802.	3.3	190
41	Structure and mechanism of a bacterial β -glucosaminidase having O-GlcNAcase activity. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 365-371.	3.6	182
42	Genome analyses highlight the different biological roles of cellulases. <i>Nature Reviews Microbiology</i> , 2012, 10, 227-234.	13.6	180
43	Recent insights into copper-containing lytic polysaccharide mono-oxygenases. <i>Current Opinion in Structural Biology</i> , 2013, 23, 660-668.	2.6	175
44	The Copper Active Site of CBM33 Polysaccharide Oxygenases. <i>Journal of the American Chemical Society</i> , 2013, 135, 6069-6077.	6.6	170
45	Insights into Trehalose Synthesis Provided by the Structure of the Retaining Glucosyltransferase OtsA. <i>Chemistry and Biology</i> , 2002, 9, 1337-1346.	6.2	164
46	Crystal structure of the catalytic domain of a bacterial cellulase belonging to family 5. <i>Structure</i> , 1995, 3, 939-949.	1.6	159
47	<i>Cellvibrio japonicus</i> β -L-arabinanase 43A has a novel five-blade β -propeller fold. <i>Nature Structural Biology</i> , 2002, 9, 665-668.	9.7	157
48	Mapping the conformational itinerary of β -glycosidases by X-ray crystallography. <i>Biochemical Society Transactions</i> , 2003, 31, 523-527.	1.6	155
49	Analysis of PUGNAc and NAG-thiazoline as Transition State Analogues for Human O-GlcNAcase: Mechanistic and Structural Insights into Inhibitor Selectivity and Transition State Poise. <i>Journal of the American Chemical Society</i> , 2007, 129, 635-644.	6.6	155
50	Structures of Oligosaccharide-Bound Forms of the Endoglucanase V from <i>Humicola insolens</i> at 1.9 Å Resolution. <i>Biochemistry</i> , 1995, 34, 16210-16220.	1.2	154
51	The X6 β -Thermostabilizing Domains of Xylanases Are Carbohydrate-Binding Modules: Structure and Biochemistry of the <i>Clostridium thermocellum</i> X6b Domain. <i>Biochemistry</i> , 2000, 39, 5013-5021.	1.2	154
52	Iminosugar Glycosidase Inhibitors: Structural and Thermodynamic Dissection of the Binding of Isofagomine and 1-Deoxynojirimycin to β -Glucosidases. <i>Journal of the American Chemical Society</i> , 2003, 125, 14313-14323.	6.6	154
53	Structure and function of endoglucanase V. <i>Nature</i> , 1993, 365, 362-364.	13.7	151
54	The Mechanisms by Which Family 10 Glycoside Hydrolases Bind Decorated Substrates. <i>Journal of Biological Chemistry</i> , 2004, 279, 9597-9605.	1.6	151

#	ARTICLE	IF	CITATIONS
55	Highly Efficient Synthesis of β (1 \rightarrow 4)-Oligo- and -Polysaccharides Using a Mutant Cellulase. <i>Journal of the American Chemical Society</i> , 2000, 122, 5429-5437.	6.6	149
56	Enzymatic Ketonization of 2-Hydroxymuconate: A Specificity and Mechanism Investigated by the Crystal Structures of Two Isomerases. <i>Biochemistry</i> , 1996, 35, 792-802.	1.2	148
57	Structural characterization of human heparanase reveals insights into substrate recognition. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 1016-1022.	3.6	137
58	Differential Oligosaccharide Recognition by Evolutionarily-related β -1,4 and β -1,3 Glucan-binding Modules. <i>Journal of Molecular Biology</i> , 2002, 319, 1143-1156.	2.0	135
59	Crystal structure of levansucrase from the Gram-negative bacterium <i>Gluconacetobacter diazotrophicus</i> . <i>Biochemical Journal</i> , 2005, 390, 19-27.	1.7	135
60	Mechanistic evidence for a front-side, S _N i-type reaction in a retaining glycosyltransferase. <i>Nature Chemical Biology</i> , 2011, 7, 631-638.	3.9	135
61	X-ray Structure of Novamyl, the Five-Domain α -Maltogenic Amylase from <i>Bacillus stearothermophilus</i> : Maltose and Acarbose Complexes at 1.7 Å... Resolution. <i>Biochemistry</i> , 1999, 38, 8385-8392.	1.2	133
62	The crystal structure of two macrolide glycosyltransferases provides a blueprint for host cell antibiotic immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5336-5341.	3.3	132
63	Bracing copper for the catalytic oxidation of C-H bonds. <i>Nature Catalysis</i> , 2018, 1, 571-577.	16.1	131
64	Substrate Distortion by a β -Mannanase: Snapshots of the Michaelis and Covalent-Intermediate Complexes Suggest a B _{2,5} Conformation for the Transition State. <i>Angewandte Chemie - International Edition</i> , 2002, 41, 2824-2827.	7.2	127
65	Structural Analysis of a Chimeric Bacterial α -Amylase. High-Resolution Analysis of Native and Ligand Complexes. <i>Biochemistry</i> , 2000, 39, 9099-9107.	1.2	126
66	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, 3089-3094.	3.3	124
67	Glycosidase Inhibition: An Assessment of the Binding of 18 Putative Transition-State Mimics. <i>Journal of the American Chemical Society</i> , 2007, 129, 2345-2354.	6.6	124
68	An Unusual Mechanism of Glycoside Hydrolysis Involving Redox and Elimination Steps by a Family 4 β -Glycosidase from <i>Thermotoga maritima</i> . <i>Journal of the American Chemical Society</i> , 2004, 126, 8354-8355.	6.6	119
69	Molecular Mechanism by which Prominent Human Gut Bacteroidetes Utilize Mixed-Linkage Beta-Glucans, Major Health-Promoting Cereal Polysaccharides. <i>Cell Reports</i> , 2017, 21, 417-430.	2.9	119
70	Three-dimensional structures of the Mn and Mg dTDP complexes of the family GT-2 glycosyltransferase SpsA: a comparison with related NDP-sugar glycosyltransferases 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 314, 655-661.	2.0	118
71	QM/MM Studies into the H ₂ O ₂ -Dependent Activity of Lytic Polysaccharide Monooxygenases: Evidence for the Formation of a Caged Hydroxyl Radical Intermediate. <i>ACS Catalysis</i> , 2018, 8, 1346-1351.	5.5	117
72	Structural Basis for Ligand Binding and Processivity in Cellobiohydrolase Cel6A from <i>Humicola insolens</i> . <i>Structure</i> , 2003, 11, 855-864.	1.6	116

#	ARTICLE	IF	CITATIONS
73	Mechanistic insights into a Ca ²⁺ -dependent family of β -mannosidases in a human gut symbiont. <i>Nature Chemical Biology</i> , 2010, 6, 125-132.	3.9	115
74	Dissecting conformational contributions to glycosidase catalysis and inhibition. <i>Current Opinion in Structural Biology</i> , 2014, 28, 1-13.	2.6	115
75	Catalysis and specificity in enzymatic glycoside hydrolysis: a 2,5B conformation for the glycosyl-enzyme intermediate revealed by the structure of the <i>Bacillus agaradhaerens</i> family 11 xylanase. <i>Chemistry and Biology</i> , 1999, 6, 483-492.	6.2	114
76	The Structure of the Feruloyl Esterase Module of Xylanase 10B from <i>Clostridium thermocellum</i> Provides Insights into Substrate Recognition. <i>Structure</i> , 2001, 9, 1183-1190.	1.6	112
77	Activity and specificity of human aldolases. <i>Journal of Molecular Biology</i> , 1991, 219, 573-576.	2.0	111
78	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, 3065-3070.	3.3	109
79	The X-ray crystal structure of phosphomannose isomerase from <i>Candida albicans</i> at 1.7 Å... resolution. <i>Nature Structural Biology</i> , 1996, 3, 470-479.	9.7	106
80	Elevation of Global O-GlcNAc Levels in 3T3-L1 Adipocytes by Selective Inhibition of O-GlcNAcase Does Not Induce Insulin Resistance. <i>Journal of Biological Chemistry</i> , 2008, 283, 34687-34695.	1.6	106
81	Secreted pectin monooxygenases drive plant infection by pathogenic oomycetes. <i>Science</i> , 2021, 373, 774-779.	6.0	106
82	Insights into the Synthesis of Lipopolysaccharide and Antibiotics through the Structures of Two Retaining Glycosyltransferases from Family GT4. <i>Chemistry and Biology</i> , 2006, 13, 1143-1152.	6.2	105
83	The Donor Subsite of Trehalose-6-phosphate Synthase. <i>Journal of Biological Chemistry</i> , 2004, 279, 1950-1955.	1.6	104
84	Structural and biochemical evidence for a boat-like transition state in β -mannosidases. <i>Nature Chemical Biology</i> , 2008, 4, 306-312.	3.9	104
85	Characterization and Three-dimensional Structures of Two Distinct Bacterial Xyloglucanases from Families GH5 and GH12. <i>Journal of Biological Chemistry</i> , 2007, 282, 19177-19189.	1.6	103
86	The Contribution of Non-catalytic Carbohydrate Binding Modules to the Activity of Lytic Polysaccharide Monooxygenases. <i>Journal of Biological Chemistry</i> , 2016, 291, 7439-7449.	1.6	102
87	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, 10968-10975.	1.6	99
88	The structure of the exo- β -(1,3)-glucanase from <i>Candida albicans</i> in native and bound forms: relationship between a pocket and groove in family 5 glycosyl hydrolases 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1999, 294, 771-783.	2.0	98
89	Structure of an O-GlcNAc transferase homolog provides insight into intracellular glycosylation. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 764-765.	3.6	98
90	<i>Serratia marcescens</i> chitinase is a retaining glycosidase utilizing substrate acetamido group participation. <i>Biochemical Journal</i> , 1997, 328, 945-949.	1.7	97

#	ARTICLE	IF	CITATIONS
91	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
92	Molecular Basis for Trehalase Inhibition Revealed by the Structure of Trehalase in Complex with Potent Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 4115-4119.	7.2	95
93	Understanding How Diverse β -Mannanases Recognize Heterogeneous Substrates. <i>Biochemistry</i> , 2009, 48, 7009-7018.	1.2	94
94	Structure of the <i>Bacillus agaradherans</i> Family 5 Endoglucanase at 1.6 Å... and Its Cellobiose Complex at 2.0 Å... Resolution. <i>Biochemistry</i> , 1998, 37, 1926-1932.	1.2	93
95	Total Syntheses of Casuarine and Its β -D-Glucoside: Complementary Inhibition towards Glycoside Hydrolases of the GH31 and GH37 Families. <i>Chemistry - A European Journal</i> , 2009, 15, 1627-1636.	1.7	92
96	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, 25517-25526.	1.6	91
97	Structure of the Endoglucanase I from <i>Fusarium oxysporum</i> : Native, Cellobiose, and 3,4-Epoxybutyl β -D-Cellobioside-Inhibited Forms, at 2.3 Å... Resolution. <i>Biochemistry</i> , 1997, 36, 5902-5911.	1.2	90
98	Structure of a Family 15 Carbohydrate-binding Module in Complex with Xylopentaose. <i>Journal of Biological Chemistry</i> , 2001, 276, 49061-49065.	1.6	90
99	Structure of a pullulanase from <i>Bacillus acidopullulyticus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 516-519.	1.5	90
100	Promiscuity in ligand-binding: The three-dimensional structure of a <i>Piromyces</i> carbohydrate-binding module, CBM29-2, in complex with cello- and mannohexaose. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14077-14082.	3.3	89
101	Convergent evolution sheds light on the anti- β -elimination mechanism common to family 1 and 10 polysaccharide lyases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12067-12072.	3.3	89
102	Novel Catalytic Mechanism of Glycoside Hydrolysis Based on the Structure of an NAD ⁺ /Mn ²⁺ -Dependent Phospho- β -Glucosidase from <i>Bacillus subtilis</i> . <i>Structure</i> , 2004, 12, 1619-1629.	1.6	88
103	Structural and functional insight into human O-GlcNAcase. <i>Nature Chemical Biology</i> , 2017, 13, 610-612.	3.9	88
104	Structural and Biochemical Analysis of <i>Cellvibrio japonicus</i> Xylanase 10C. <i>Journal of Biological Chemistry</i> , 2004, 279, 11777-11788.	1.6	86
105	Structural insight into the ligand specificity of a thermostable family 51 arabinofuranosidase, Araf51, from <i>Clostridium thermocellum</i> . <i>Biochemical Journal</i> , 2006, 395, 31-37.	1.7	85
106	Mechanistic Insight into Enzymatic Glycosyl Transfer with Retention of Configuration through Analysis of Glycomimetic Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 1234-1237.	7.2	85
107	Direct Observation of the Protonation State of an Imino Sugar Glycosidase Inhibitor upon Binding. <i>Journal of the American Chemical Society</i> , 2003, 125, 7496-7497.	6.6	84
108	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	84

#	ARTICLE	IF	CITATIONS
109	Structural Changes of the Active Site Tunnel of <i>Humicola insolens</i> Cellobiohydrolase, Cel6A, upon Oligosaccharide Binding. <i>Biochemistry</i> , 1999, 38, 8884-8891.	1.2	83
110	Protein-carbohydrate interactions: learning lessons from nature. <i>Trends in Biotechnology</i> , 2001, 19, 356-362.	4.9	82
111	Structural dissection and high-throughput screening of mannosylglycerate synthase. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 608-614.	3.6	81
112	Divergence of Catalytic Mechanism within a Glycosidase Family Provides Insight into Evolution of Carbohydrate Metabolism by Human Gut Flora. <i>Chemistry and Biology</i> , 2008, 15, 1058-1067.	6.2	81
113	Functional and informatics analysis enables glycosyltransferase activity prediction. <i>Nature Chemical Biology</i> , 2018, 14, 1109-1117.	3.9	81
114	<i>Clostridium thermocellum</i> Xyn10B Carbohydrate-Binding Module 22-2: The Role of Conserved Amino Acids in Ligand Binding. <i>Biochemistry</i> , 2001, 40, 9167-9176.	1.2	80
115	Tailored catalysts for plant cell-wall degradation: Redesigning the exo/endo preference of <i>Cellvibrio japonicus</i> arabinanase 43A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2697-2702.	3.3	80
116	A census of carbohydrate-active enzymes in the genome of <i>Arabidopsis thaliana</i> . , 2001, , 55-72.		80
117	Crystal Structures of <i>Clostridium thermocellum</i> Xyloglucanase, XGH74A, Reveal the Structural Basis for Xyloglucan Recognition and Degradation. <i>Journal of Biological Chemistry</i> , 2006, 281, 24922-24933.	1.6	79
118	Biosynthesis of the tunicamycin antibiotics proceeds via unique exo-glycal intermediates. <i>Nature Chemistry</i> , 2012, 4, 539-546.	6.6	79
119	Structure-function characterization reveals new catalytic diversity in the galactose oxidase and glyoxal oxidase family. <i>Nature Communications</i> , 2015, 6, 10197.	5.8	79
120	Crystal structure of the family 7 endoglucanase I (Cel7B) from <i>Humicola insolens</i> at 2.2 Å resolution and identification of the catalytic nucleophile by trapping of the covalent glycosyl-enzyme intermediate. <i>Biochemical Journal</i> , 1998, 335, 409-416.	1.7	77
121	Learning from microbial strategies for polysaccharide degradation. <i>Biochemical Society Transactions</i> , 2016, 44, 94-108.	1.6	77
122	Ab Initio Structure Determination and Functional Characterization Of CBM36. <i>Structure</i> , 2004, 12, 1177-1187.	1.6	76
123	An overview of activity-based probes for glycosidases. <i>Current Opinion in Chemical Biology</i> , 2019, 53, 25-36.	2.8	76
124	Activity-based probes for functional interrogation of retaining Î²-glucuronidases. <i>Nature Chemical Biology</i> , 2017, 13, 867-873.	3.9	76
125	Crystal structure of the catalytic core domain of the family 6 cellobiohydrolase II, Cel6A, from <i>Humicola insolens</i> , at 1.92 Å resolution. <i>Biochemical Journal</i> , 1999, 337, 297-304.	1.7	74
126	The Structural Basis for Catalysis and Specificity of the <i>Pseudomonas cellulosa</i> Î±-Glucuronidase, GlcA67A. <i>Structure</i> , 2002, 10, 547-556.	1.6	74

#	ARTICLE	IF	CITATIONS
127	The <i>Cellvibrio japonicus</i> Mannanase CjMan26C Displays a Unique exo-Mode of Action That Is Conferred by Subtle Changes to the Distal Region of the Active Site. <i>Journal of Biological Chemistry</i> , 2008, 283, 34403-34413.	1.6	74
128	Structural and mechanistic insight into N-glycan processing by endo- α -mannosidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 781-786.	3.3	74
129	Carbohydrate anomalies in the PDB. <i>Nature Chemical Biology</i> , 2015, 11, 303-303.	3.9	74
130	The structure of a thermally stable 3-phosphoglycerate kinase and a comparison with its mesophilic equivalent. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 283-289.	1.5	73
131	Three-Dimensional Structures of UDP-Sugar Glycosyltransferases Illuminate the Biosynthesis of Plant Polysaccharides. <i>Plant Physiology</i> , 2001, 125, 527-531.	2.3	72
132	Family 6 Carbohydrate Binding Modules in β -Agarases Display Exquisite Selectivity for the Non-reducing Termini of Agarose Chains*. <i>Journal of Biological Chemistry</i> , 2006, 281, 17099-17107.	1.6	71
133	A Glycosynthase Catalyst for the Synthesis of Flavonoid Glycosides. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 3885-3888.	7.2	71
134	The <i>Clostridium cellulolyticum</i> Dockerin Displays a Dual Binding Mode for Its Cohesin Partner. <i>Journal of Biological Chemistry</i> , 2008, 283, 18422-18430.	1.6	71
135	Substrate Specificity in Glycoside Hydrolase Family 10. <i>Journal of Biological Chemistry</i> , 2000, 275, 23020-23026.	1.6	70
136	Visualizing the Reaction Coordinate of an O-GlcNAc Hydrolase. <i>Journal of the American Chemical Society</i> , 2010, 132, 1807-1809.	6.6	70
137	Structural and enzymatic characterization of a glycoside hydrolase family 31 α -xylosidase from <i>Cellvibrio japonicus</i> involved in xyloglucan saccharification. <i>Biochemical Journal</i> , 2011, 436, 567-580.	1.7	69
138	Structure of the laccase from <i>Coprinus cinereus</i> at 1.68 Å resolution: evidence for different 'type 2 Cu-depleted' isoforms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 333-336.	2.5	67
139	Anatomy of Glycosynthesis. <i>Chemistry and Biology</i> , 2003, 10, 619-628.	6.2	67
140	Multifunctional Xylooligosaccharide/Cephalosporin C Deacetylase Revealed by the Hexameric Structure of the <i>Bacillus subtilis</i> Enzyme at 1.9 Å Resolution. <i>Journal of Molecular Biology</i> , 2003, 330, 593-606.	2.0	67
141	Structure of a group A streptococcal phage-encoded virulence factor reveals a catalytically active triple-stranded α -helix. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17652-17657.	3.3	67
142	Mannose Foraging by <i>Bacteroides thetaiotaomicron</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 11291-11299.	1.6	67
143	Inhibition of O-GlcNAcase Using a Potent and Cell-Permeable Inhibitor Does Not Induce Insulin Resistance in 3T3-L1 Adipocytes. <i>Chemistry and Biology</i> , 2010, 17, 937-948.	6.2	67
144	Expansion of the glycosynthase repertoire to produce defined manno-oligosaccharides. <i>Chemical Communications</i> , 2003, , 1327-1329.	2.2	66

#	ARTICLE	IF	CITATIONS
145	Formation of a Copper(II)â€“Tyrosyl Complex at the Active Site of Lytic Polysaccharide Monooxygenases Following Oxidation by H ₂ O ₂ . <i>Journal of the American Chemical Society</i> , 2019, 141, 18585-18599.	6.6	66
146	Structure and Ligand Binding of Carbohydrate-binding Module CsCBM6-3 Reveals Similarities with Fucose-specific Lectins and â€œGalactose-bindingâ€•Domains. <i>Journal of Molecular Biology</i> , 2003, 327, 659-669.	2.0	65
147	DNA-Nogalamycin Interactions: The Crystal Structure of d(TGATCA) Complexed with Nogalamycin. <i>Biochemistry</i> , 1995, 34, 415-425.	1.2	63
148	Analysis of the Reaction Coordinate of Î±-Fucosidases: A Combined Structural and Quantum Mechanical Approach. <i>Journal of the American Chemical Society</i> , 2010, 132, 1804-1806.	6.6	63
149	A complex gene locus enables xyloglucan utilization in the model saprophyte <i>Cellvibrio japonicus</i> . <i>Molecular Microbiology</i> , 2014, 94, 418-433.	1.2	63
150	Structural and Thermodynamic Dissection of Specific Mannan Recognition by a Carbohydrate Binding Module, TmCBM27. <i>Structure</i> , 2003, 11, 665-675.	1.6	62
151	Structural Studies of the Î²-Glycosidase from <i>Sulfolobus solfataricus</i> in Complex with Covalently and Noncovalently Bound Inhibitorsâ€•. <i>Biochemistry</i> , 2004, 43, 6101-6109.	1.2	62
152	<i>Mycobacterium tuberculosis</i> Strains Possess Functional Cellulases. <i>Journal of Biological Chemistry</i> , 2005, 280, 20181-20184.	1.6	62
153	Molecular Basis for Inhibition of GH84 Glycoside Hydrolases by Substituted Azepanes: Conformational Flexibility Enables Probing of Substrate Distortion. <i>Journal of the American Chemical Society</i> , 2009, 131, 5390-5392.	6.6	62
154	A classification of nucleotide-diphospho-sugar glycosyltransferases based on amino acid sequence similarities. <i>Biochemical Journal</i> , 1998, 329, 719-719.	1.7	61
155	Structure and function of <i>Humicola insolens</i> family 6 cellulases: structure of the endoglucanase, Cel6B, at 1.6Å... resolution. <i>Biochemical Journal</i> , 2000, 348, 201-207.	1.7	61
156	The crystal structure of human muscle aldolase at 3.0 Å... resolution. <i>FEBS Letters</i> , 1990, 262, 282-286.	1.3	60
157	The <i>Streptomyces lividans</i> Family 12 Endoglucanase:â€• Construction of the Catalytic Core, Expression, and X-ray Structure at 1.75 Å... Resolution,. <i>Biochemistry</i> , 1997, 36, 16032-16039.	1.2	60
158	Structural enzymology of carbohydrate-active enzymes: implications for the post-genomic era. <i>Biochemical Society Transactions</i> , 2002, 30, 291-297.	1.6	60
159	The Three-dimensional Structure of the N-Acetylglucosamine-6-phosphate Deacetylase, NagA, from <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 2809-2816.	1.6	60
160	How Family 26 Glycoside Hydrolases Orchestrate Catalysis on Different Polysaccharides. <i>Journal of Biological Chemistry</i> , 2005, 280, 32761-32767.	1.6	60
161	Inhibition of O-GlcNAcase by a gluco-configured nagstatin and a PUGNAcâ€•imidazole hybrid inhibitor. <i>Chemical Communications</i> , 2006, , 4372-4374.	2.2	60
162	YihQ is a sulfoquinovosidase that cleaves sulfoquinovosyl diacylglyceride sulfolipids. <i>Nature Chemical Biology</i> , 2016, 12, 215-217.	3.9	60

#	ARTICLE	IF	CITATIONS
163	The Reaction Coordinate of a Bacterial GH47 β -Mannosidase: A Combined Quantum Mechanical and Structural Approach. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 10997-11001.	7.2	57
164	The Crystal Structure of a 2-Fluorocellotriosyl Complex of the <i>Streptomyces lividans</i> Endoglucanase CelB2 at 1.2 Å... Resolution. <i>Biochemistry</i> , 1999, 38, 4826-4833.	1.2	56
165	The Active Site of a Carbohydrate Esterase Displays Divergent Catalytic and Noncatalytic Binding Functions. <i>PLoS Biology</i> , 2009, 7, e1000071.	2.6	56
166	Structure of the ADP complex of the 3-phosphoglycerate kinase from <i>Bacillus stearothermophilus</i> at 1.65 Å... <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1994, 50, 202-209.	2.5	55
167	Lateral Protonation of a Glycosidase Inhibitor. Structure of the <i>Bacillus agaradhaerens</i> Cel5A in Complex with a Cellobiose-Derived Imidazole at 0.97 Å... Resolution. <i>Journal of the American Chemical Society</i> , 1999, 121, 2621-2622.	6.6	55
168	NAD ⁺ and Metal-ion Dependent Hydrolysis by Family 4 Glycosidases: Structural Insight into Specificity for Phospho- β -d-glucosides. <i>Journal of Molecular Biology</i> , 2005, 346, 423-435.	2.0	52
169	Substrate Specificity in Glycoside Hydrolase Family 10. <i>Journal of Biological Chemistry</i> , 2000, 275, 23027-23033.	1.6	51
170	Activity, stability and 3-D structure of the Cu(<i>II</i>) form of a chitin-active lytic polysaccharide monooxygenase from <i>Bacillus amyloliquefaciens</i> . <i>Dalton Transactions</i> , 2016, 45, 16904-16912.	1.6	50
171	A Fluorescence Polarization Activity-Based Protein Profiling Assay in the Discovery of Potent, Selective Inhibitors for Human Nonlysosomal Glucosylceramidase. <i>Journal of the American Chemical Society</i> , 2017, 139, 14192-14197.	6.6	50
172	Structural, Kinetic, and Thermodynamic Analysis of Glucoimidazole-Derived Glycosidase Inhibitors. <i>Biochemistry</i> , 2006, 45, 11879-11884.	1.2	47
173	Carbohydrate-active enzymes: sequences, shapes, contortions and cells. <i>Biochemical Society Transactions</i> , 2016, 44, 79-87.	1.6	47
174	Insights into ligand-induced conformational change in Cel5A from <i>Bacillus agaradhaerens</i> revealed by a catalytically active crystal form. <i>Journal of Molecular Biology</i> , 2000, 297, 819-828.	2.0	46
175	The Use of Forced Protein Evolution to Investigate and Improve Stability of Family 10 Xylanases. <i>Journal of Biological Chemistry</i> , 2004, 279, 54369-54379.	1.6	46
176	Glycosidase inhibition by ring-modified castanospermine analogues: tackling enzyme selectivity by inhibitor tailoring. <i>Organic and Biomolecular Chemistry</i> , 2009, 7, 2738.	1.5	46
177	Molecular mechanisms regulating O-linked N-acetylglucosamine (O-GlcNAc) "processing enzymes. <i>Current Opinion in Chemical Biology</i> , 2019, 53, 131-144.	2.8	46
178	Discovering the Microbial Enzymes Driving Drug Toxicity with Activity-Based Protein Profiling. <i>ACS Chemical Biology</i> , 2020, 15, 217-225.	1.6	46
179	Discovery of a Fungal Copper Radical Oxidase with High Catalytic Efficiency toward 5-Hydroxymethylfurfural and Benzyl Alcohols for Bioprocessing. <i>ACS Catalysis</i> , 2020, 10, 3042-3058.	5.5	46
180	Structural basis for cyclophellitol inhibition of a β -glucosidase. <i>Organic and Biomolecular Chemistry</i> , 2007, 5, 444-446.	1.5	45

#	ARTICLE	IF	CITATIONS
181	Detection of Active Mammalian GH31 β -Glucosidases in Health and Disease Using In-Class, Broad-Spectrum Activity-Based Probes. <i>ACS Central Science</i> , 2016, 2, 351-358.	5.3	45
182	Structural dissection of a complex <i>Bacteroides ovatus</i> gene locus conferring xyloglucan metabolism in the human gut. <i>Open Biology</i> , 2016, 6, 160142.	1.5	45
183	In vitro and in vivo comparative and competitive activity-based protein profiling of GH29 β -fucosidases. <i>Chemical Science</i> , 2015, 6, 2782-2789.	3.7	44
184	Activation of O ₂ and H ₂ O ₂ by Lytic Polysaccharide Monooxygenases. <i>ACS Catalysis</i> , 2020, 10, 12760-12769.	5.5	44
185	A new variant of the Ntn hydrolase fold revealed by the crystal structure of l-aminopeptidase d-Ala-esterase/amidase from <i>Ochrobactrum anthropi</i> . <i>Structure</i> , 2000, 8, 153-162.	1.6	43
186	Insight into a strategy for attenuating AmpC-mediated β -lactam resistance: Structural basis for selective inhibition of the glycoside hydrolase NagZ. <i>Protein Science</i> , 2009, 18, 1541-1551.	3.1	43
187	Identifying the Catalytic Acid/Base in GH29 β -Fucosidase Subfamilies. <i>Biochemistry</i> , 2013, 52, 5857-5864.	1.2	43
188	1,6-Cyclophellitol Cyclosulfates: A New Class of Irreversible Glycosidase Inhibitor. <i>ACS Central Science</i> , 2017, 3, 784-793.	5.3	43
189	Mechanistic basis of substrate-O ₂ coupling within a chitin-active lytic polysaccharide monooxygenase: An integrated NMR/EPR study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19178-19189.	3.3	42
190	Identification of the Catalytic Nucleophile of Endoglucanase I from <i>Fusarium oxysporum</i> by Mass Spectrometry. <i>Biochemistry</i> , 1997, 36, 5893-5901.	1.2	41
191	Structural studies on cellulases. <i>Biochemical Society Transactions</i> , 1998, 26, 167-172.	1.6	41
192	Pectate lyase 10A from <i>Pseudomonas cellulosa</i> is a modular enzyme containing a family 2a carbohydrate-binding module. <i>Biochemical Journal</i> , 2001, 355, 155-165.	1.7	41
193	Substrate Distortion by a Lichenase Highlights the Different Conformational Itineraries Harnessed by Related Glycoside Hydrolases. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 5136-5140.	7.2	41
194	Structure and Kinetic Investigation of <i>Streptococcus pyogenes</i> Family GH38 β -Mannosidase. <i>PLoS ONE</i> , 2010, 5, e9006.	1.1	41
195	A Convenient Approach to Stereoisomeric Iminocyclitols: Generation of Potent Brain-Permeable OGA Inhibitors. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 15429-15433.	7.2	41
196	Interactions among residues CD3, E7, E10, and E11 in myoglobins: Attempts to simulate the ligand-binding properties of <i>Aplysia</i> myoglobin. <i>Biochemistry</i> , 1995, 34, 8715-8725.	1.2	40
197	Casuarine-6-O- β -d-glucoside and its analogues are tight binding inhibitors of insect and bacterial trehalases. <i>Chemical Communications</i> , 2010, 46, 2629.	2.2	40
198	Evidence for a Boat Conformation at the Transition State of GH76 β -Mannanases: Key Enzymes in Bacterial and Fungal Mannoprotein Metabolism. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 5378-5382.	7.2	40

#	ARTICLE	IF	CITATIONS
199	Combined Inhibitor Free-Energy Landscape and Structural Analysis Reports on the Mannosidase Conformational Coordinate. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1087-1091.	7.2	39
200	Bacterial β -Glucosidase Reveals the Structural and Functional Basis of Genetic Defects in Human Glucocerebrosidase 2 (GBA2). <i>ACS Chemical Biology</i> , 2016, 11, 1891-1900.	1.6	39
201	A β -Mannanase with a Lysozyme-like Fold and a Novel Molecular Catalytic Mechanism. <i>ACS Central Science</i> , 2016, 2, 896-903.	5.3	39
202	Distortion of a cellobio-derived isofagomine highlights the potential conformational itinerary of inverting β -glucosidases. Electronic supplementary information (ESI) available: details of data and structure quality for complex of cel6A with 1. See http://www.rsc.org/suppdata/cc/b3/b301592k/ . <i>Chemical Communications</i> , 2003, , 946-947.	2.2	38
203	Common Inhibition of Both β -Glucosidases and β -Mannosidases by Isofagomine Lactam Reflects Different Conformational Itineraries for Pyranoside Hydrolysis. <i>ChemBioChem</i> , 2004, 5, 1596-1599.	1.3	38
204	Structural analyses of enzymes involved in the O-GlcNAc modification. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2010, 1800, 122-133.	1.1	38
205	Three-dimensional structures of two heavily N-glycosylated <i>Aspergillus</i> sp. family GH3 β -D-glucosidases. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 254-265.	1.1	38
206	Structural, Thermodynamic, and Kinetic Analyses of Tetrahydrooxazine-derived Inhibitors Bound to β -Glucosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 49236-49242.	1.6	37
207	Ligand-mediated Dimerization of a Carbohydrate-binding Module Reveals a Novel Mechanism for Protein-Carbohydrate Recognition. <i>Journal of Molecular Biology</i> , 2004, 337, 417-426.	2.0	37
208	Structure and Kinetics of a Monomeric Glucosamine 6-Phosphate Deaminase. <i>Journal of Biological Chemistry</i> , 2005, 280, 19649-19655.	1.6	37
209	A 1-acetamido derivative of 6-epi-valienamine: an inhibitor of a diverse group of β -N-acetylglucosaminidases. <i>Organic and Biomolecular Chemistry</i> , 2007, 5, 3013.	1.5	37
210	Building Custom Polysaccharides in Vitro with an Efficient, Broad-Specificity Xyloglucan Glycosynthase and a Fucosyltransferase. <i>Journal of the American Chemical Society</i> , 2011, 133, 10892-10900.	6.6	37
211	Oligosaccharide binding to family 11 xylanases: both covalent intermediate and mutant product complexes display 2,5B conformations at the active centre. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1344-1347.	2.5	36
212	The X-ray Crystal Structure of an <i>Arthrobacter protophormiae</i> Endo- β -N-Acetylglucosaminidase Reveals a (β / α) β Catalytic Domain, Two Ancillary Domains and Active Site Residues Key for Transglycosylation Activity. <i>Journal of Molecular Biology</i> , 2009, 389, 1-9.	2.0	36
213	Circular Permutation Provides an Evolutionary Link between Two Families of Calcium-dependent Carbohydrate Binding Modules. <i>Journal of Biological Chemistry</i> , 2010, 285, 31742-31754.	1.6	36
214	Structural Enzymology of Cellvibrio japonicus Agd31B Protein Reveals β -Transglucosylase Activity in Glycoside Hydrolase Family 31. <i>Journal of Biological Chemistry</i> , 2012, 287, 43288-43299.	1.6	36
215	Increase of enzyme activity through specific covalent modification with fragments. <i>Chemical Science</i> , 2017, 8, 7772-7779.	3.7	36
216	Functional analysis of a group A streptococcal glycoside hydrolase Spy1600 from family 84 reveals it is a β -N-acetylglucosaminidase and not a hyaluronidase. <i>Biochemical Journal</i> , 2006, 399, 241-247.	1.7	35

#	ARTICLE	IF	CITATIONS
217	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
218	Discovery of Selective Small-Molecule Activators of a Bacterial Glycoside Hydrolase. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13419-13423.	7.2	35
219	β -1,3-Glucan Binding by a Thermostable Carbohydrate-Binding Module from <i>Thermotoga maritima</i> . <i>Biochemistry</i> , 2001, 40, 14679-14685.	1.2	34
220	Sweet secrets of synthesis. , 2001, 8, 98-100.		34
221	Insights into the Structural Determinants of Cohesin-Dockerin Specificity Revealed by the Crystal Structure of the Type II Cohesin from <i>Clostridium thermocellum</i> SdbA. <i>Journal of Molecular Biology</i> , 2005, 349, 909-915.	2.0	34
222	Dissection of Conformationally Restricted Inhibitors Binding to a β -Glucosidase. <i>ChemBioChem</i> , 2006, 7, 738-742.	1.3	34
223	Dynamic and Functional Profiling of Xylan-Degrading Enzymes in <i>Aspergillus</i> Secretomes Using Activity-Based Probes. <i>ACS Central Science</i> , 2019, 5, 1067-1078.	5.3	34
224	An Epoxide Intermediate in Glycosidase Catalysis. <i>ACS Central Science</i> , 2020, 6, 760-770.	5.3	34
225	Purification, crystallisation and preliminary X-ray analysis of the vanadium-dependent haloperoxidase from <i>Corallina officinalis</i> . <i>FEBS Letters</i> , 1995, 359, 244-246.	1.3	33
226	Probing the Mechanism of Ligand Recognition in Family 29 Carbohydrate-binding Modules. <i>Journal of Biological Chemistry</i> , 2005, 280, 23718-23726.	1.6	33
227	Molecular Basis for β -Glucosidase Inhibition by Ring-Modified Calystegine Analogues. <i>ChemBioChem</i> , 2008, 9, 2612-2618.	1.3	33
228	Substrate and Metal Ion Promiscuity in Mannosylglycerate Synthase. <i>Journal of Biological Chemistry</i> , 2011, 286, 15155-15164.	1.6	33
229	Analysis of transition state mimicry by tight binding aminothiazoline inhibitors provides insight into catalysis by human O-GlcNAcase. <i>Chemical Science</i> , 2016, 7, 3742-3750.	3.7	33
230	A Family of Dual-Activity Glycosyltransferase-Phosphorylases Mediates Mannogen Turnover and Virulence in <i>Leishmania</i> Parasites. <i>Cell Host and Microbe</i> , 2019, 26, 385-399.e9.	5.1	33
231	Rational Design of Mechanism-Based Inhibitors and Activity-Based Probes for the Identification of Retaining β -Arabinofuranosidases. <i>Journal of the American Chemical Society</i> , 2020, 142, 4648-4662.	6.6	33
232	The β -Glucuronidase, GlcA67A, of <i>Cellvibrio japonicus</i> Utilizes the Carboxylate and Methyl Groups of Aldobiouronic Acid as Important Substrate Recognition Determinants. <i>Journal of Biological Chemistry</i> , 2003, 278, 20286-20292.	1.6	32
233	X-ray Crystal Structure of a Non-crystalline Cellulose-specific Carbohydrate-binding Module: CBM28. <i>Journal of Molecular Biology</i> , 2004, 339, 253-258.	2.0	32
234	Structure and Activity of <i>Paenibacillus polymyxa</i> Xyloglucanase from Glycoside Hydrolase Family 44. <i>Journal of Biological Chemistry</i> , 2011, 286, 33890-33900.	1.6	32

#	ARTICLE	IF	CITATIONS
235	The GH130 Family of Mannoside Phosphorylases Contains Glycoside Hydrolases That Target β -1,2-Mannosidic Linkages in <i>Candida Mannan</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 25023-25033.	1.6	32
236	Crystal structure of the catalytic core domain of the family 6 cellobiohydrolase II, Cel6A, from <i>Humicola insolens</i> , at 1.92Å... resolution. <i>Biochemical Journal</i> , 1999, 337, 297.	1.7	31
237	The Enzymatic Synthesis of Glycosidic Bonds: "Glycosynthases" and Glycosyltransferases.. <i>Trends in Glycoscience and Glycotechnology</i> , 2001, 13, 105-120.	0.0	31
238	Carbohydrate structure: the rocky road to automation. <i>Current Opinion in Structural Biology</i> , 2017, 44, 39-47.	2.6	31
239	Structural and Biochemical Insights into the Function and Evolution of Sulfoquinovosidases. <i>ACS Central Science</i> , 2018, 4, 1266-1273.	5.3	31
240	Oligosaccharide specificity of a family 7 endoglucanase: insertion of potential sugar-binding subsites. <i>Journal of Biotechnology</i> , 1997, 57, 91-100.	1.9	30
241	Pectate lyase 10A from <i>Pseudomonas cellulosa</i> is a modular enzyme containing a family 2a carbohydrate-binding module. <i>Biochemical Journal</i> , 2001, 355, 155.	1.7	30
242	Direct experimental observation of the hydrogen-bonding network of a glycosidase along its reaction coordinate revealed by atomic resolution analyses of endoglucanase Cel5A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 447-452.	2.5	29
243	The crystal structure of a family GH25 lysozyme from <i>Bacillus anthracis</i> implies a neighboring-group catalytic mechanism with retention of anomeric configuration. <i>Carbohydrate Research</i> , 2009, 344, 1753-1757.	1.1	29
244	Three-dimensional structure of a <i>Streptomyces sviveus</i> GNAT acetyltransferase with similarity to the C-terminal domain of the human GH84 α -GlcNAcase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 186-195.	2.5	29
245	Functional and structural characterization of a potent α -xyloglucanase from the soil saprophyte <i>Cellvibrio japonicus</i> unravels the first step of xyloglucan degradation. <i>FEBS Journal</i> , 2016, 283, 1701-1719.	2.2	29
246	Structure of a <i>Bacillus halmapalus</i> family 13 β -amylase, BHA, in complex with an acarbose-derived nonasaccharide at 2.1Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 190-193.	2.5	28
247	Chitinase Inhibition by Chitobiose and Chitotriose Thiazolines. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 2599-2602.	7.2	28
248	β -Fucosidase Inhibition by Pyrrolidine-Ferrocene Hybrids: Rationalization of Ligand Binding Properties by Structural Studies. <i>Chemistry - A European Journal</i> , 2013, 19, 9526-9533.	1.7	28
249	Functionalized Cyclophellitols Are Selective Glucocerebrosidase Inhibitors and Induce a Bona Fide Neuropathic Gaucher Model in Zebrafish. <i>Journal of the American Chemical Society</i> , 2019, 141, 4214-4218.	6.6	28
250	Sequence and expression of the gene encoding 3-phosphoglycerate kinase from <i>Bacillus stearothermophilus</i> . <i>Gene</i> , 1991, 109, 39-45.	1.0	27
251	Towards broad spectrum activity-based glycosidase probes: synthesis and evaluation of deoxygenated cyclophellitol aziridines. <i>Chemical Communications</i> , 2017, 53, 12528-12531.	2.2	27
252	Discovery, activity and characterisation of an AA10 lytic polysaccharide oxygenase from the shipworm symbiont <i>Teredinibacter turnerae</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 232.	6.2	27

#	ARTICLE	IF	CITATIONS
253	Atomic resolution analyses of the binding of xylobiose-derived deoxynojirimycin and isofagomine to xylanase Xyn10A Electronic supplementary information (ESI) available: kinetics and structural methods. See http://www.rsc.org/suppdata/cc/b4/b405152a/ . <i>Chemical Communications</i> , 2004, , 1794.	2.2	26
254	Recent structural and mechanistic insights into post-translational enzymatic glycosylation. <i>Current Opinion in Chemical Biology</i> , 2012, 16, 479-487.	2.8	26
255	Exploring a Multivalent Approach to Fucosidase Inhibition. <i>European Journal of Organic Chemistry</i> , 2013, 2013, 7328-7336.	1.2	26
256	Structure determination and refinement of the <i>Humicola insolens</i> endoglucanase V at 1.5 Å Resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1996, 52, 7-17.	2.5	25
257	Structure of the <i>Humicola insolens</i> cellobiohydrolase Cel6A D416A mutant in complex with a non-hydrolysable substrate analogue, methyl cellobiosyl-4-thio-β-cellobioside, at 1.9 Å. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2201-2204.	2.5	25
258	Crystal structure of a family GT4 glycosyltransferase from <i>Bacillus anthracis</i> ORF BA1558. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 784-787.	1.5	25
259	Structure and function of <i>Humicola insolens</i> family 6 cellulases: structure of the endoglucanase, Cel6B, at 1.6 Å resolution. <i>Biochemical Journal</i> , 2000, 348, 201.	1.7	24
260	Atomic resolution structure of endoglucanase Cel5A in complex with methyl 4,4II,4III,4IV-tetrathio-β-cellopentoside highlights the alternative binding modes targeted by substrate mimics. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1739-1742.	2.5	24
261	Carba-cyclophellitols Are Neutral Retaining-Glucosidase Inhibitors. <i>Journal of the American Chemical Society</i> , 2017, 139, 6534-6537.	6.6	24
262	In vitro and in vivo characterization of three <i>Cellvibrio japonicus</i> glycoside hydrolase family 5 members reveals potent xyloglucan backbone-cleaving functions. <i>Biotechnology for Biofuels</i> , 2018, 11, 45.	6.2	24
263	Mannosidase mechanism: at the intersection of conformation and catalysis. <i>Current Opinion in Structural Biology</i> , 2020, 62, 79-92.	2.6	24
264	Manno-cyclophellitols Enable Activity-Based Protein Profiling of Human Mannosidases and Discovery of New Golgi Mannosidase II Inhibitors. <i>Journal of the American Chemical Society</i> , 2020, 142, 13021-13029.	6.6	24
265	Cryo-EM structure provides insights into the dimer arrangement of the O-linked N-acetylglucosamine transferase OGT. <i>Nature Communications</i> , 2021, 12, 6508.	5.8	24
266	Functional Characterization of Xyloglucan Glycosynthases from GH7, GH12, and GH16 Scaffolds. <i>Biomacromolecules</i> , 2009, 10, 1782-1788.	2.6	23
267	Metabolism of Vertebrate Amino Sugars with N-Glycolyl Groups. <i>Journal of Biological Chemistry</i> , 2012, 287, 28882-28897.	1.6	23
268	Structure and Activity of the <i>Streptomyces coelicolor</i> A3(2) N-Acetylhexosaminidase Provides Further Insight into GH20 Family Catalysis and Inhibition. <i>Biochemistry</i> , 2014, 53, 1789-1800.	1.2	23
269	Structure of <i>Papaver somniferum</i> O-Methyltransferase 1 Reveals Initiation of Noscapine Biosynthesis with Implications for Plant Natural Product Methylation. <i>ACS Catalysis</i> , 2019, 9, 3840-3848.	5.5	23
270	Validation tools: can they indicate the information content of macromolecular crystal structures?. <i>Structure</i> , 1998, 6, 685-690.	1.6	22

#	ARTICLE	IF	CITATIONS
271	Molecular determinants of substrate specificity in the feruloyl esterase module of xylanase 10B from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 194-197.	2.5	22
272	Structure of a carbohydrate esterase from <i>Bacillus anthracis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 250-252.	1.5	22
273	A Cell-Surface GH9 Endo-Glucanase Coordinates with Surface Glycan-Binding Proteins to Mediate Xyloglucan Uptake in the Gut Symbiont <i>Bacteroides ovatus</i> . <i>Journal of Molecular Biology</i> , 2019, 431, 981-995.	2.0	22
274	Sulfoglycolysis: catabolic pathways for metabolism of sulfoquinovose. <i>Chemical Society Reviews</i> , 2021, 50, 13628-13645.	18.7	22
275	Sorting the diverse: the sequence-based classifications of carbohydrate-active enzymes. <i>Biochemical Journal</i> , 2008, , 382.	1.7	21
276	Structural insight into the mechanism of streptozotocin inhibition of O-GlcNAcase. <i>Carbohydrate Research</i> , 2009, 344, 627-631.	1.1	21
277	Mixed-Linkage Cellooligosaccharides: A New Class of Glycoside Hydrolase Inhibitors. <i>ChemBioChem</i> , 2001, 2, 319-325.	1.3	20
278	Characterization of <i>Escherichia coli</i> OtsA, a trehalose-6-phosphate synthase from glycosyltransferase family 20. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 349-351.	2.5	20
279	Structure of the Michaelis complex of β -mannosidase, Man2A, provides insight into the conformational itinerary of mannoside hydrolysis. <i>Chemical Communications</i> , 2009, , 2484.	2.2	20
280	Dynamic Structural Changes Accompany the Production of Dihydroxypropanesulfonate by Sulfolactaldehyde Reductase. <i>ACS Catalysis</i> , 2020, 10, 2826-2836.	5.5	20
281	Crystal structure of the catalytic core domain of the family 6 cellobiohydrolase II, Cel6A, from <i>Humicola insolens</i> , at 1.92 Å resolution. <i>Biochemical Journal</i> , 1999, 337 (Pt 2), 297-304.	1.7	20
282	Three-dimensional structure of a variant 'Termamyl-like' <i>Geobacillus stearothermophilus</i> α -amylase at 1.9 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 66-70.	0.4	19
283	The three-dimensional structure of the cellobiohydrolase Cel7A from <i>Aspergillus fumigatus</i> at 1.5 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 114-120.	0.4	19
284	Exploiting the Hydrophobic Terrain in Fucosidases with Aryl-Substituted Pyrrolidine Iminosugars. <i>ChemBioChem</i> , 2015, 16, 277-283.	1.3	19
285	A Direct Fluorescent Activity Assay for Glycosyltransferases Enables Convenient High-Throughput Screening: Application to <i>O</i> -GlcNAc Transferase. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 9601-9609.	7.2	19
286	Sorting the diverse: The sequence-based classifications of carbohydrate-active enzymes. <i>Biochemist</i> , 2008, 30, 26-32.	0.2	19
287	Structure and function of <i>Humicola insolens</i> family 6 cellulases: structure of the endoglucanase, Cel6B, at 1.6 Å resolution. <i>Biochemical Journal</i> , 2000, 348 Pt 1, 201-7.	1.7	19
288	Structure of the catalytic core module of the <i>Chaetomium thermophilum</i> family GH6 cellobiohydrolase Cel6A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 875-882.	2.5	18

#	ARTICLE	IF	CITATIONS
289	Three dimensional structure of a bacterial α -L-fucosidase with a 5-membered iminocyclitol inhibitor. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 4751-4754.	1.4	18
290	Structural and Functional Characterization of a Novel Family GH115 4-O-Methyl- α -Glucuronidase with Specificity for Decorated Arabinogalactans. <i>Journal of Molecular Biology</i> , 2015, 427, 3935-3946.	2.0	18
291	Structural and mechanistic insights into a <i>Bacteroides vulgatus</i> retaining N-acetyl- β -galactosaminidase that uses neighbouring group participation. <i>Chemical Communications</i> , 2016, 52, 11096-11099.	2.2	18
292	A second-generation ferrocene- α -minosugar hybrid with improved fucosidase binding properties. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2016, 26, 1546-1549.	1.0	18
293	Discovery and characterization of a sulfoquinovose mutarotase using kinetic analysis at equilibrium by exchange spectroscopy. <i>Biochemical Journal</i> , 2018, 475, 1371-1383.	1.7	18
294	Substrate Engagement and Catalytic Mechanisms of N-Acetylglucosaminyltransferase V. <i>ACS Catalysis</i> , 2020, 10, 8590-8596.	5.5	18
295	Oxidative desulfurization pathway for complete catabolism of sulfoquinovose by bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	18
296	Structural and Thermodynamic Analyses of α -Fucosidase Inhibitors. <i>ChemBioChem</i> , 2010, 11, 1971-1974.	1.3	17
297	Structural and Kinetic Dissection of the <i>endo</i> - α -1,2-Mannanase Activity of Bacterial GH99 Glycoside Hydrolases from <i>Bacteroides</i> spp.. <i>Chemistry - A European Journal</i> , 2015, 21, 1966-1977.	1.7	17
298	Computational Design of Experiment Unveils the Conformational Reaction Coordinate of GH125 α -Mannosidases. <i>Journal of the American Chemical Society</i> , 2017, 139, 1085-1088.	6.6	17
299	Contribution of Shape and Charge to the Inhibition of a Family GH99 <i>endo</i> - α -1,2-Mannanase. <i>Journal of the American Chemical Society</i> , 2017, 139, 1089-1097.	6.6	17
300	Glucosyl-1H-imidazole: A New Class of Azole-Type β -Glucosidase Inhibitor. <i>Journal of the American Chemical Society</i> , 2018, 140, 5045-5048.	6.6	17
301	Crystal structure and substrate interactions of an unusual fungal non-CBM carrying GH26 <i>endo</i> - β -mannanase from <i>Yunnania penicillata</i> . <i>Scientific Reports</i> , 2019, 9, 2266.	1.6	17
302	Activity-Based Protein Profiling of Retaining α -Amylases in Complex Biological Samples. <i>Journal of the American Chemical Society</i> , 2021, 143, 2423-2432.	6.6	17
303	Phosphoglycerate kinase from the extreme thermophile <i>Thermus thermophilus</i> Crystallization and preliminary X-ray data. <i>FEBS Letters</i> , 1987, 225, 123-126.	1.3	16
304	Cysteine Nucleophiles in Glycosidase Catalysis: Application of a Covalent β -Arabinofuranosidase Inhibitor. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 5754-5758.	7.2	16
305	Molecular Basis of Sulfosugar Selectivity in Sulfoglycolysis. <i>ACS Central Science</i> , 2021, 7, 476-487.	5.3	16
306	Crystallization and preliminary X-ray analysis of the laccase from <i>Coprinus cinereus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 605-607.	2.5	15

#	ARTICLE	IF	CITATIONS
307	Inhibition of a bacterial O-GlcNAcase homologue by lactone and lactam derivatives: structural, kinetic and thermodynamic analyses. <i>Amino Acids</i> , 2011, 40, 829-839.	1.2	15
308	The Crystallization and Structural Analysis of Cellulases (and Other Glycoside Hydrolases). <i>Methods in Enzymology</i> , 2012, 510, 141-168.	0.4	15
309	Structural and Functional Characterization of Three Novel Fungal Amylases with Enhanced Stability and pH Tolerance. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4902.	1.8	15
310	Using automated glycan assembly (AGA) for the practical synthesis of heparan sulfate oligosaccharide precursors. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 1817-1821.	1.5	15
311	Profiling Substrate Promiscuity of Wild-Type Sugar Kinases for Multi-fluorinated Monosaccharides. <i>Cell Chemical Biology</i> , 2020, 27, 1199-1206.e5.	2.5	15
312	The structure of the Alic GH13 α -amylase from <i>Alicyclobacillus</i> sp. reveals the accommodation of starch branching points in the α -amylase family. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 1-7.	1.1	15
313	Bicyclic Picomolar OGA Inhibitors Enable Chemoproteomic Mapping of Its Endogenous Post-translational Modifications. <i>Journal of the American Chemical Society</i> , 2022, 144, 832-844.	6.6	15
314	Production and spectroscopic characterization of lytic polysaccharide monooxygenases. <i>Methods in Enzymology</i> , 2018, 613, 63-90.	0.4	14
315	Structure of human endo- α -1,2-mannosidase (MANEA), an antiviral host-glycosylation target. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29595-29601.	3.3	14
316	A Sulfoglycolytic Entner-Doudoroff Pathway in <i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> SRD1565. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	14
317	Crystallization and preliminary X-ray analysis of a fungal endoglucanase I. <i>Journal of Molecular Biology</i> , 1992, 228, 970-972.	2.0	13
318	A xylobiose-derived isofagomine lactam glycosidase inhibitor binds as its amide tautomer Electronic supplementary information (ESI) available: details of data and structure quality for complex of 1 with Xyn10A. See http://www.rsc.org/suppdata/cc/b3/b301829f/ . <i>Chemical Communications</i> , 2003, , 944-945.	2.2	13
319	Three-dimensional structure of a thermophilic family GH11 xylanase from <i>Thermobifida fusca</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 141-144.	0.7	13
320	Inverting family GH156 sialidases define an unusual catalytic motif for glycosidase action. <i>Nature Communications</i> , 2019, 10, 4816.	5.8	13
321	Glycosylated cyclophellitol-derived activity-based probes and inhibitors for cellulases. <i>RSC Chemical Biology</i> , 2020, 1, 148-155.	2.0	13
322	Structural enzymology of <i>Helicobacter pylori</i> methylthioadenosine nucleosidase in the futasoline pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 177-185.	2.5	13
323	The case of the missing base. <i>Nature Chemical Biology</i> , 2012, 8, 952-953.	3.9	12
324	Exploring the divalent effect in fucosidase inhibition with stereoisomeric pyrrolidine dimers. <i>Organic and Biomolecular Chemistry</i> , 2016, 14, 4718-4727.	1.5	12

#	ARTICLE	IF	CITATIONS
325	Conformational Analysis of the Mannosidase Inhibitor Kifunensine: A Quantum Mechanical and Structural Approach. <i>ChemBioChem</i> , 2017, 18, 1496-1501.	1.3	12
326	Structural insight into industrially relevant glucoamylases: flexible positions of starch-binding domains. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 463-470.	1.1	12
327	Structural Dynamics and Catalytic Properties of a Multimodular Xanthanase. <i>ACS Catalysis</i> , 2018, 8, 6021-6034.	5.5	12
328	Trapped in the act of catalysis. , 1999, 6, 406-408.		11
329	The structure of a family GH25 lysozyme from <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 973-977.	0.7	11
330	From 1,4-Disaccharide to 1,3-Glycosyl Carbasugar: Synthesis of a Bespoke Inhibitor of Family GH99 Endo- α -mannosidase. <i>Organic Letters</i> , 2018, 20, 7488-7492.	2.4	11
331	α -Gal-cyclophellitol cyclosulfamidate is a Michaelis complex analog that stabilizes therapeutic lysosomal α -galactosidase A in Fabry disease. <i>Chemical Science</i> , 2019, 10, 9233-9243.	3.7	11
332	Structural Insights into Pixatimod (PG545) Inhibition of Heparanase, a Key Enzyme in Cancer and Viral Infections. <i>Chemistry - A European Journal</i> , 2022, 28, .	1.7	11
333	Crystallization and preliminary X-ray analysis of nonglycosylated tissue inhibitor of metalloproteinases-1, N30QN78Q TIMP-1. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 435-437.	1.5	10
334	Crystallization and preliminary X-ray analysis of the 6-phospho- α -glucosidase from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1212-1214.	2.5	10
335	Synthesis and application of a highly branched, mechanism-based 2-deoxy-2-fluoro-oligosaccharide inhibitor of <i>endo</i> -xyloglucanases. <i>Organic and Biomolecular Chemistry</i> , 2018, 16, 8732-8741.	1.5	10
336	Structure and function of a glycoside hydrolase family 8 endoxylanase from <i>Teredinibacter turnerae</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 946-955.	1.1	10
337	Insights from semi-oriented EPR spectroscopy studies into the interaction of lytic polysaccharide monooxygenases with cellulose. <i>Dalton Transactions</i> , 2020, 49, 3413-3422.	1.6	10
338	An Overview of the Structure, Mechanism and Specificity of Human Heparanase. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1221, 139-167.	0.8	10
339	Crystallization and Preliminary X-ray Analysis of <i>Candida albicans</i> Phosphomannose Isomerase. <i>Journal of Molecular Biology</i> , 1994, 237, 349-350.	2.0	9
340	D-Glucosylated Derivatives of Isofagomine and Noeuromycin and Their Potential as Inhibitors of β -Glycoside Hydrolases. <i>Australian Journal of Chemistry</i> , 2007, 60, 549.	0.5	9
341	Cracking the code, slowly: the state of carbohydrate-active enzymes in 2013. <i>Current Opinion in Structural Biology</i> , 2013, 23, 649-651.	2.6	9
342	Spiro-epoxyglycosides as Activity-Based Probes for Glycoside Hydrolase Family 99 Endomannosidase/Endomannanase. <i>Chemistry - A European Journal</i> , 2018, 24, 9983-9992.	1.7	9

#	ARTICLE	IF	CITATIONS
343	Distortion of mannoimidazole supports a B _{2,5} boat transition state for the family GH125 β -1,6-mannosidase from <i>Clostridium perfringens</i> . <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 7863-7869.	1.5	9
344	Structural insights into heparanase activity using a fluorogenic heparan sulfate disaccharide. <i>Chemical Communications</i> , 2020, 56, 13780-13783.	2.2	9
345	Structure of the GH76 β -mannanase homolog, BT2949, from the gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 408-415.	2.5	8
346	Chemoenzymatic synthesis of 6-phospho- α -D-glucopyranosyl- β -D-glucopyranoside as a novel probe of α -D-glucosidases. <i>FEBS Letters</i> , 2016, 590, 461-468.	1.3	8
347	<i>Bacteroides thetaiotaomicron</i> generates diverse β -mannosidase activities through subtle evolution of a distal substrate-binding motif. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 394-404.	1.1	8
348	A Direct Fluorescent Activity Assay for Glycosyltransferases Enables Convenient High-Throughput Screening: Application to O-GlcNAc Transferase. <i>Angewandte Chemie</i> , 2020, 132, 9688-9696.	1.6	8
349	Structure of a GH51 β -arabinofuranosidase from <i>Meripilus giganteus</i> : conserved substrate recognition from bacteria to fungi. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1124-1133.	1.1	8
350	The O-GlcNAc modification: three-dimensional structure, enzymology and the development of selective inhibitors to probe disease. <i>Biochemical Society Transactions</i> , 2010, 38, 1179-1188.	1.6	7
351	Structure and activity of the <i>Streptococcus pyogenes</i> family GH1 6-phospho- β -glucosidase SPy1599. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 16-23.	2.5	7
352	Conformational Behaviour of Azasugars Based on Mannuronic Acid. <i>ChemBioChem</i> , 2017, 18, 1297-1304.	1.3	7
353	Exploration of Strategies for Mechanism-Based Inhibitor Design for Family GH99 α -1,2-Mannanases. <i>Chemistry - A European Journal</i> , 2018, 24, 7464-7473.	1.7	7
354	Design, Synthesis and Structural Analysis of Glucocerebrosidase Imaging Agents. <i>Chemistry - A European Journal</i> , 2021, 27, 16377-16388.	1.7	7
355	Oxidative cleavage of polysaccharides by a termite-derived superoxide dismutase boosts the degradation of biomass by glycoside hydrolases. <i>Green Chemistry</i> , 2022, 24, 4845-4858.	4.6	7
356	Purification, crystallization and preliminary X-ray analysis of the 3-phosphoglycerate kinase from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1992, 227, 1263-1264.	2.0	6
357	Crystallization and Preliminary X-ray Analysis of a Truncated Tissue Metalloproteinase Inhibitor β -128-194 TIMP-2. <i>Journal of Molecular Biology</i> , 1993, 229, 1163-1164.	2.0	6
358	Crystallization of a DNA and N-acetylserine Binding Fragment (Residues 1 to 233) of <i>Klebsiella aerogenes</i> CysB Protein, a Member of the LysR Family. <i>Journal of Molecular Biology</i> , 1994, 235, 1159-1161.	2.0	6
359	Characterization of a novel pectate lyase, Pel10A, from <i>Pseudomonas cellulosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1141-1143.	2.5	6
360	Regulators as agents: Modelling personality and power as evidence is brokered to support decisions on environmental risk. <i>Science of the Total Environment</i> , 2014, 466-467, 74-83.	3.9	6

#	ARTICLE	IF	CITATIONS
361	An atypical interaction explains the high-affinity of a non-hydrolyzable S-linked 1,6- β -mannanase inhibitor. <i>Chemical Communications</i> , 2017, 53, 9238-9241.	2.2	6
362	Structure and function of Bs164 β -mannosidase from <i>Bacteroides salyersiae</i> the founding member of glycoside hydrolase family GH164. <i>Journal of Biological Chemistry</i> , 2020, 295, 4316-4326.	1.6	6
363	Selective Fluorogenic β -Glucocerebrosidase Substrates for Convenient Analysis of Enzyme Activity in Cell and Tissue Homogenates. <i>ACS Chemical Biology</i> , 2020, 15, 824-829.	1.6	6
364	Crystallization and preliminary X-ray analysis of the complex between a mouse Fab fragment and a single IgG-binding domain from streptococcal protein G. <i>Journal of Molecular Biology</i> , 1992, 227, 1253-1254.	2.0	5
365	Structure and FTIR spectra of 3 : 2 complexes of trimethylamine N-oxide and 4-dimethylamine-2,6-dimethylpyridine N-oxide with perchloric acid. <i>Journal of Molecular Structure</i> , 1996, 375, 197-206.	1.8	5
366	Probing the β -1,3:1,4 glucanase, CtLic26A, with a thio-oligosaccharide and enzyme variants. <i>Organic and Biomolecular Chemistry</i> , 2008, 6, 851.	1.5	5
367	Fleetamine (3-O- β -d-glucopyranosyl-swainsonine): the synthesis of a hypothetical inhibitor of endo- β -mannosidase. <i>Tetrahedron: Asymmetry</i> , 2012, 23, 992-997.	1.8	5
368	The C-Type Lysozyme from the upper Gastrointestinal Tract of <i>Opisthocomus hoatzin</i> , the Stinkbird. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5531.	1.8	5
369	Structural studies of a surface-entropy reduction mutant of O-GlcNAcase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 70-78.	1.1	5
370	Mapping the protonation states of the histidine brace in an AA10 lytic polysaccharide monooxygenase using CW-EPR spectroscopy and DFT calculations. <i>Faraday Discussions</i> , 2022, 234, 336-348.	1.6	5
371	Activity-based protein profiling reveals dynamic substrate-specific cellulase secretion by saprotrophic basidiomycetes. , 2022, 15, 6.		5
372	Crystallization and preliminary X-ray diffraction analysis of levansucrase (LsdA) from <i>Gluconacetobacter diazotrophicus</i> SRT4. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 181-183.	2.5	4
373	Structure of a <i>Talaromyces pinophilus</i> GH62 arabinofuranosidase in complex with AraDNJ at 1.25 \AA resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 490-495.	0.4	4
374	Structure of the GH9 glucosidase/glicosaminidase from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 512-523.	0.4	4
375	Mechanistic Insights into the Chaperoning of Human Lysosomal-Galactosidase Activity: Highly Functionalized Aminocyclopentanes and C-5a-Substituted Derivatives of 4-epi-Isogagomine. <i>Molecules</i> , 2020, 25, 4025.	1.7	4
376	A baculoviral system for the production of human β -glucocerebrosidase enables atomic resolution analysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 565-580.	1.1	4
377	Synthesis of broad-specificity activity-based probes for <i>exo</i> - β -mannosidases. <i>Organic and Biomolecular Chemistry</i> , 2022, 20, 877-886.	1.5	4
378	Cloning, crystallization and preliminary X-ray analysis of a nucleotide-diphospho-sugar transferase <i>spsA</i> from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 677-678.	2.5	3

#	ARTICLE	IF	CITATIONS
379	Cloning, purification and characterization of the 6-phospho-3-hexulose isomerase YckF from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1138-1140.	2.5	3
380	The Chitopentaose Complex of a Mutant Hen Egg-White Lysozyme Displays No Distortion of the "1 Sugar Away from a 4C1 Chair Conformation. <i>Australian Journal of Chemistry</i> , 2009, 62, 528.	0.5	3
381	Structural studies of the unusual metal-ion site of the GH124 endoglucanase from <i>Ruminiclostridium thermocellum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 496-505.	0.4	3
382	Synthetic and Crystallographic Insight into Exploiting sp ² Hybridization in the Development of Fucosidase Inhibitors. <i>ChemBioChem</i> , 2019, 20, 1365-1368.	1.3	3
383	Cysteine Nucleophiles in Glycosidase Catalysis: Application of a Covalent Arabinofuranosidase Inhibitor. <i>Angewandte Chemie</i> , 2021, 133, 5818-5822.	1.6	3
384	Fungal GH25 muramidases: New family members with applications in animal nutrition and a crystal structure at 0.78Å resolution. <i>PLoS ONE</i> , 2021, 16, e0248190.	1.1	3
385	Development of Non-Hydrolysable Oligosaccharide Activity-Based Inactivators for Endoglycanases: A Case Study on 1,6 Mannanases. <i>Chemistry - A European Journal</i> , 2021, 27, 9519-9523.	1.7	2
386	Copper Oxygenases. , 2021, , 500-523.		2
387	The structure of <i>Phocaeicola vulgatus</i> sialic acid acetyltransferase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 647-657.	1.1	2
388	Deletion of AA9 Lytic Polysaccharide Monooxygenases Impacts <i>A. nidulans</i> Secretome and Growth on Lignocellulose. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
389	Structural studies on fungal endoglucanases from <i>Humicola insolens</i> . <i>Progress in Biotechnology</i> , 1995, , 225-237.	0.2	1
390	Crystallization and preliminary X-ray crystallographic analysis of a <i>Trichoderma reesei</i> 2-mannanase from glycoside hydrolase family 5. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1058-1060.	2.5	1
391	Sequence Families and Modular Organization of Carbohydrate-Active Enzymes. , 2003, , .		1
392	Detecting and identifying glycoside hydrolases using cyclophellitol-derived activity-based probes. <i>Methods in Enzymology</i> , 2022, 664, 103-134.	0.4	1
393	The sulfoquinovosyl glycerol binding protein SmoF binds and accommodates plant sulfolipids. <i>Current Research in Structural Biology</i> , 2022, 4, 51-58.	1.1	1
394	Structure and FTIR spectra of 3:2 complexes of trimethylamine N-oxide and 4-dimethylamine-2,6-dimethylpyridine N-oxide with perchloric acid. <i>Computational and Theoretical Chemistry</i> , 1996, 375, 197-206.	1.5	0
395	Structural genomics of carbohydrate-active enzymes: implications for the synthesis of plant polysaccharides. <i>Biochemical Society Transactions</i> , 2002, 30, A24-A24.	1.6	0
396	A master of its sulfate. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 686-687.	3.6	0

#	ARTICLE	IF	CITATIONS
397	Chemistry's prodigal child: enzyme mechanism. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 529-531.	2.8	0
398	InnenrÄ¼cktitelbild: The Reaction Coordinate of a Bacterial GH47 Î±-Mannosidase: A Combined Quantum Mechanical and Structural Approach (<i>Angew. Chem.</i> 44/2012). <i>Angewandte Chemie</i> , 2012, 124, 11333-11333.	1.6	0
399	Q&A: repeat-containing proteins. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 943-945.	3.6	0
400	Evolution of a New Pathway of Reserve Carbohydrate Biosynthesis in <i>Leishmania</i> Parasites. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
401	Multitasking in the gut: the X-ray structure of the multidomain BbgIII from <i>Bifidobacterium bifidum</i> offers possible explanations for its alternative functions. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1564-1578.	1.1	0