

Gideon Davies

List of Publications by Year in descending order

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401
papers

37,597
citations

3668

92
h-index

4414

178
g-index

441
all docs

441
docs citations

441
times ranked

25948
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

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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: A Analysis of a Retaining Î ² -Glycoside Hydrolase. <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: A Substrate Distortion Gives Rise to the Preferred Axial Orientation for the Leaving Group. <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 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... Resolution. <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

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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

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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

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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> chitobiase is a retaining glycosidase utilizing substrate acetamido group participation. <i>Biochemical Journal</i> , 1997, 328, 945-949.	1.7	97

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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

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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

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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
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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