

Harry J Gilbert

List of Publications by Year in descending order

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72
papers

9,680
citations

46918

47
h-index

74018

75
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78
all docs

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docs citations

78
times ranked

8575
citing authors

#	ARTICLE	IF	CITATIONS
1	Sulfation of Arabinogalactan Proteins Confers Privileged Nutrient Status to <i>Bacteroides plebeius</i> . <i>MBio</i> , 2021, 12, e0136821.	1.8	7
2	Structure–function analyses generate novel specificities to assemble the components of multienzyme bacterial cellulosome complexes. <i>Journal of Biological Chemistry</i> , 2018, 293, 4201-4212.	1.6	12
3	PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , 2018, 46, D677-D683.	6.5	191
4	Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic <i>Bacteroides</i> . <i>Nature Microbiology</i> , 2018, 3, 210-219.	5.9	263
5	Biochemistry of complex glycan depolymerisation by the human gut microbiota. <i>FEMS Microbiology Reviews</i> , 2018, 42, 146-164.	3.9	188
6	Target highlights from the first post-PSI CASP experiment (CASP12, May–August 2016). <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 27-50.	1.5	11
7	A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. <i>Nature Microbiology</i> , 2018, 3, 1314-1326.	5.9	103
8	Higher order scaffoldin assembly in <i>Ruminococcus flavefaciens</i> cellulosome is coordinated by a discrete cohesin-dockerin interaction. <i>Scientific Reports</i> , 2018, 8, 6987.	1.6	6
9	Complexity of the <i>Ruminococcus flavefaciens</i> FD-1 cellulosome reflects an expansion of family-related protein-protein interactions. <i>Scientific Reports</i> , 2017, 7, 42355.	1.6	31
10	Unusual active site location and catalytic apparatus in a glycoside hydrolase family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4936-4941.	3.3	38
11	A <i>Bacteroidetes</i> locus dedicated to fungal 1,6- β -glucan degradation: Unique substrate conformation drives specificity of the key endo-1,6- β -glucanase. <i>Journal of Biological Chemistry</i> , 2017, 292, 10639-10650.	1.6	65
12	An evolutionarily distinct family of polysaccharide lyases removes rhamnose capping of complex arabinogalactan proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 13271-13283.	1.6	26
13	Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , 2017, 544, 65-70.	13.7	447
14	Assembly of <i>Ruminococcus flavefaciens</i> cellulosome revealed by structures of two cohesin-dockerin complexes. <i>Scientific Reports</i> , 2017, 7, 759.	1.6	20
15	How members of the human gut microbiota overcome the sulfation problem posed by glycosaminoglycans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7037-7042.	3.3	99
16	Diverse specificity of cellulosome attachment to the bacterial cell surface. <i>Scientific Reports</i> , 2016, 6, 38292.	1.6	20
17	Editorial overview: Carbohydrate–protein interactions and glycosylation: integrating structural biology, informatics and systems modelling to understand glycan structure and glycan-protein interactions. <i>Current Opinion in Structural Biology</i> , 2016, 40, v-viii.	2.6	1
18	Single Binding Mode Integration of Hemicellulose-degrading Enzymes via Adaptor Scaffoldins in <i>Ruminococcus flavefaciens</i> Cellulosome. <i>Journal of Biological Chemistry</i> , 2016, 291, 26658-26669.	1.6	19

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19	A Novel Carbohydrate-binding Module from Sugar Cane Soil Metagenome Featuring Unique Structural and Carbohydrate Affinity Properties. <i>Journal of Biological Chemistry</i> , 2016, 291, 23734-23743.	1.6	18
20	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
21	Complexity of the <i>Ruminococcus flavefaciens</i> cellulosome reflects an expansion in glycan recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7136-7141.	3.3	58
22	The Contribution of Non-catalytic Carbohydrate Binding Modules to the Activity of Lytic Polysaccharide Monoxygenases. <i>Journal of Biological Chemistry</i> , 2016, 291, 7439-7449.	1.6	102
23	Carbohydrate-binding module assisting glycosynthase-catalysed polymerizations. <i>Biochemical Journal</i> , 2015, 470, 15-22.	1.7	11
24	Human gut Bacteroidetes can utilize yeast mannan through a selfish mechanism. <i>Nature</i> , 2015, 517, 165-169.	13.7	427
25	Recognition of xyloglucan by the crystalline cellulose-binding site of a family 3a carbohydrate-binding module. <i>FEBS Letters</i> , 2015, 589, 2297-2303.	1.3	46
26	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015, 6, 7481.	5.8	328
27	Cell-surface Attachment of Bacterial Multienzyme Complexes Involves Highly Dynamic Protein-Protein Anchors. <i>Journal of Biological Chemistry</i> , 2015, 290, 13578-13590.	1.6	22
28	Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of Xyloglucan and β -1,3- α -1,4-Glucans through Distinct Mechanisms. <i>Journal of Biological Chemistry</i> , 2015, 290, 10572-10586.	1.6	36
29	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
30	The GH130 Family of Mannoside Phosphorylases Contains Glycoside Hydrolases That Target β -1,2-Mannosidic Linkages in <i>Candida</i> Mannan. <i>Journal of Biological Chemistry</i> , 2015, 290, 25023-25033.	1.6	32
31	Coevolution of yeast mannan digestion: Convergence of the civilized human diet, distal gut microbiome, and host immunity. <i>Gut Microbes</i> , 2015, 6, 334-339.	4.3	36
32	Automatic prediction of polysaccharide utilization loci in Bacteroidetes species. <i>Bioinformatics</i> , 2015, 31, 647-655.	1.8	195
33	Evidence That GH115 β -Glucuronidase Activity, Which Is Required to Degrade Plant Biomass, Is Dependent on Conformational Flexibility. <i>Journal of Biological Chemistry</i> , 2014, 289, 53-64.	1.6	63
34	Cloning, purification, crystallization and preliminary X-ray studies of a carbohydrate-binding module (CBM_E1) derived from sugarcane soil metagenome. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1232-1235.	0.4	2
35	Systems biology defines the biological significance of redox-active proteins during cellulose degradation in an aerobic bacterium. <i>Molecular Microbiology</i> , 2014, 94, 1121-1133.	1.2	51
36	Editorial overview: Carbohydrate-protein interactions: The future is taking shape. <i>Current Opinion in Structural Biology</i> , 2014, 28, v-vii.	2.6	0

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37	Understanding How the Complex Molecular Architecture of Mannan-degrading Hydrolases Contributes to Plant Cell Wall Degradation. <i>Journal of Biological Chemistry</i> , 2014, 289, 2002-2012.	1.6	47
38	Advances in understanding the molecular basis of plant cell wall polysaccharide recognition by carbohydrate-binding modules. <i>Current Opinion in Structural Biology</i> , 2013, 23, 669-677.	2.6	268
39	The Structure of a <i>Streptomyces avermitilis</i> α -L-Rhamnosidase Reveals a Novel Carbohydrate-binding Module CBM67 within the Six-domain Arrangement. <i>Journal of Biological Chemistry</i> , 2013, 288, 12376-12385.	1.6	67
40	4-O-methylation of glucuronic acid in <i>Arabidopsis</i> glucuronoxylan is catalyzed by a domain of unknown function family 579 protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14253-14258.	3.3	164
41	Innenrücktitelbild: The Reaction Coordinate of a Bacterial GH47 α -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
42	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
43	Structure and Function of an Arabinoxylan-specific Xylanase. <i>Journal of Biological Chemistry</i> , 2011, 286, 22510-22520.	1.6	89
44	The Structure and Function of an Arabinan-specific α -1,2-Arabinofuranosidase Identified from Screening the Activities of Bacterial GH43 Glycoside Hydrolases. <i>Journal of Biological Chemistry</i> , 2011, 286, 15483-15495.	1.6	85
45	Recognition and Degradation of Plant Cell Wall Polysaccharides by Two Human Gut Symbionts. <i>PLoS Biology</i> , 2011, 9, e1001221.	2.6	644
46	Mechanistic insights into a Ca ²⁺ -dependent family of α -mannosidases in a human gut symbiont. <i>Nature Chemical Biology</i> , 2010, 6, 125-132.	3.9	115
47	Carbohydrate-binding modules promote the enzymatic deconstruction of intact plant cell walls by targeting and proximity effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15293-15298.	3.3	219
48	The Biochemistry and Structural Biology of Plant Cell Wall Deconstruction. <i>Plant Physiology</i> , 2010, 153, 444-455.	2.3	290
49	Cellulosomes: Highly Efficient Nanomachines Designed to Deconstruct Plant Cell Wall Complex Carbohydrates. <i>Annual Review of Biochemistry</i> , 2010, 79, 655-681.	5.0	498
50	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
51	The Active Site of a Carbohydrate Esterase Displays Divergent Catalytic and Noncatalytic Binding Functions. <i>PLoS Biology</i> , 2009, 7, e1000071.	2.6	56
52	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
53	How the walls come crumbling down: recent structural biochemistry of plant polysaccharide degradation. <i>Current Opinion in Plant Biology</i> , 2008, 11, 338-348.	3.5	178
54	Cellulosomes: microbial nanomachines that display plasticity in quaternary structure. <i>Molecular Microbiology</i> , 2007, 63, 1568-1576.	1.2	124

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55	Understanding the Biological Rationale for the Diversity of Cellulose-directed Carbohydrate-binding Modules in Prokaryotic Enzymes. <i>Journal of Biological Chemistry</i> , 2006, 281, 29321-29329.	1.6	221
56	Structural and Biochemical Analysis of <i>Cellvibrio japonicus</i> Xylanase 10C. <i>Journal of Biological Chemistry</i> , 2004, 279, 11777-11788.	1.6	86
57	Carbohydrate-binding modules: fine-tuning polysaccharide recognition. <i>Biochemical Journal</i> , 2004, 382, 769-781.	1.7	1,720
58	Importance of Hydrophobic and Polar Residues in Ligand Binding in the Family 15 Carbohydrate-Binding Module from <i>Cellvibrio japonicus</i> Xyn10C. <i>Biochemistry</i> , 2003, 42, 9316-9323.	1.2	55
59	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
60	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
61	Substrate Distortion by a -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
62	Influence of the Aglycone Region of the Substrate Binding Cleft of <i>Pseudomonas</i> Xylanase 10A on Catalysis. <i>Biochemistry</i> , 2001, 40, 7404-7409.	1.2	33
63	Role of Hydrogen Bonding in the Interaction between a Xylan Binding Module and Xylan. <i>Biochemistry</i> , 2001, 40, 5700-5707.	1.2	57
64	Crystal Structure of Mannanase 26A from <i>Pseudomonas cellulosa</i> and Analysis of Residues Involved in Substrate Binding. <i>Journal of Biological Chemistry</i> , 2001, 276, 31186-31192.	1.6	81
65	The Structural Basis for the Ligand Specificity of Family 2 Carbohydrate-binding Modules. <i>Journal of Biological Chemistry</i> , 2000, 275, 41137-41142.	1.6	120
66	The X6 ðœThermostabilizingðœ Domains of Xylanases Are Carbohydrate-Binding Modules: ðœ% Structure and Biochemistry of the <i>Clostridium thermocellum</i> X6b Domain., <i>Biochemistry</i> , 2000, 39, 5013-5021.	1.2	154
67	Solution Structure of the CBM10 Cellulose Binding Module from <i>Pseudomonas</i> Xylanase A ðœ, ðœj. <i>Biochemistry</i> , 2000, 39, 978-984.	1.2	73
68	All three surface tryptophans in Type IIa cellulose binding domains play a pivotal role in binding both soluble and insoluble ligands. <i>FEBS Letters</i> , 1998, 429, 312-316.	1.3	77
69	The Topology of the Substrate Binding Clefts of Glycosyl Hydrolase Family 10 Xylanases Are Not Conserved. <i>Journal of Biological Chemistry</i> , 1998, 273, 32187-32199.	1.6	100
70	<i>Pseudomonas</i> cellulose-binding domains mediate their effects by increasing enzyme substrate proximity. <i>Biochemical Journal</i> , 1998, 331, 775-781.	1.7	261
71	Key Residues in Subsite F Play a Critical Role in the Activity of <i>Pseudomonas fluorescens</i> Subspecies <i>cellulosa</i> Xylanase A Against Xylooligosaccharides but Not Against Highly Polymeric Substrates such as Xylan. <i>Journal of Biological Chemistry</i> , 1997, 272, 2942-2951.	1.6	72
72	Mannanase A from <i>Pseudomonas fluorescens</i> ssp. <i>cellulosals</i> a Retaining Glycosyl Hydrolase in Which E212 and E320 Are the Putative Catalytic Residues ðœ. <i>Biochemistry</i> , 1996, 35, 16195-16204.	1.2	70