

# Harry J Gilbert

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8903031/publications.pdf>

Version: 2024-02-01

72  
papers

9,680  
citations

47006

47  
h-index

74163

75  
g-index

78  
all docs

78  
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.   | 4.1  | 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.  | 3.4  | 12        |
| 3  | PULDB: the expanded database of Polysaccharide Utilization Loci. <i>Nucleic Acids Research</i> , 2018, 46, D677-D683.   | 14.5 | 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.   | 13.3 | 263       |
| 5  | Biochemistry of complex glycan depolymerisation by the human gut microbiota. <i>FEMS Microbiology Reviews</i> , 2018, 42, 146-164.  | 8.6  | 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.   | 2.6  | 11        |
| 7  | A surface endogalactanase in <i>Bacteroides thetaiotaomicron</i> confers keystone status for arabinogalactan degradation. <i>Nature Microbiology</i> , 2018, 3, 1314-1326.  | 13.3 | 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.  | 3.3  | 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.   | 3.3  | 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.  | 7.1  | 38        |
| 11 | A <i>Bacteroidetes</i> locus dedicated to fungal 1,6- $\beta$ -glucan degradation: Unique substrate conformation drives specificity of the key endo-1,6- $\beta$ -glucanase. <i>Journal of Biological Chemistry</i> , 2017, 292, 10639-10650.                               | 3.4  | 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.   | 3.4  | 26        |
| 13 | Complex pectin metabolism by gut bacteria reveals novel catalytic functions. <i>Nature</i> , 2017, 544, 65-70.  | 27.8 | 447       |
| 14 | Assembly of <i>Ruminococcus flavefaciens</i> cellulosome revealed by structures of two cohesin-dockerin complexes. <i>Scientific Reports</i> , 2017, 7, 759.  | 3.3  | 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.  | 7.1  | 99        |
| 16 | Diverse specificity of cellulosome attachment to the bacterial cell surface. <i>Scientific Reports</i> , 2016, 6, 38292.  | 3.3  | 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. | 5.7  | 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.  | 3.4  | 19        |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 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.   | 3.4  | 18        |
| 20 | A $\beta$ -Mannanase with a Lysozyme-like Fold and a Novel Molecular Catalytic Mechanism. <i>ACS Central Science</i> , 2016, 2, 896-903.   | 11.3 | 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.                               | 7.1  | 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.   | 3.4  | 102       |
| 23 | Carbohydrate-binding module assisting glycosynthase-catalysed polymerizations. <i>Biochemical Journal</i> , 2015, 470, 15-22.  | 3.7  | 11        |
| 24 | Human gut Bacteroidetes can utilize yeast mannan through a selfish mechanism. <i>Nature</i> , 2015, 517, 165-169.  | 27.8 | 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.  | 2.8  | 46        |
| 26 | Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015, 6, 7481.   | 12.8 | 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.   | 3.4  | 22        |
| 28 | Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of Xyloglucan and $\beta$ -1,3- $\alpha$ -1,4-Glucans through Distinct Mechanisms. <i>Journal of Biological Chemistry</i> , 2015, 290, 10572-10586.                        | 3.4  | 36        |
| 29 | Structure of the GH76 $\beta$ -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 $\beta$ -1,2-Mannosidic Linkages in <i>Candida Mannan</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 25023-25033.                                      | 3.4  | 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.  | 9.8  | 36        |
| 32 | Automatic prediction of polysaccharide utilization loci in Bacteroidetes species. <i>Bioinformatics</i> , 2015, 31, 647-655.   | 4.1  | 195       |
| 33 | Evidence That GH115 $\beta$ -Glucuronidase Activity, Which Is Required to Degrade Plant Biomass, Is Dependent on Conformational Flexibility. <i>Journal of Biological Chemistry</i> , 2014, 289, 53-64.  | 3.4  | 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. | 0.8  | 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.  | 2.5  | 51        |
| 36 | Editorial overview: Carbohydrate-protein interactions: The future is taking shape. <i>Current Opinion in Structural Biology</i> , 2014, 28, v-vii.   | 5.7  | 0         |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 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.  | 3.4  | 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.  | 5.7  | 268       |
| 39 | The Structure of a <i>Streptomyces avermitilis</i> $\alpha$ -L-Rhamnosidase Reveals a Novel Carbohydrate-binding Module CBM67 within the Six-domain Arrangement. <i>Journal of Biological Chemistry</i> , 2013, 288, 12376-12385.                         | 3.4  | 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. | 7.1  | 164       |
| 41 | Innenrücktitelbild: The Reaction Coordinate of a Bacterial GH47 $\alpha$ -Mannosidase: A Combined Quantum Mechanical and Structural Approach ( <i>Angew. Chem.</i> 44/2012). <i>Angewandte Chemie</i> , 2012, 124, 11333-11333.                           | 2.0  | 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.                           | 7.1  | 97        |
| 43 | Structure and Function of an Arabinoxylan-specific Xylanase. <i>Journal of Biological Chemistry</i> , 2011, 286, 22510-22520.   | 3.4  | 89        |
| 44 | The Structure and Function of an Arabinan-specific $\alpha$ -1,2-Arabinofuranosidase Identified from Screening the Activities of Bacterial GH43 Glycoside Hydrolases. <i>Journal of Biological Chemistry</i> , 2011, 286, 15483-15495.                    | 3.4  | 85        |
| 45 | Recognition and Degradation of Plant Cell Wall Polysaccharides by Two Human Gut Symbionts. <i>PLoS Biology</i> , 2011, 9, e1001221.   | 5.6  | 644       |
| 46 | Mechanistic insights into a Ca <sup>2+</sup> -dependent family of $\alpha$ -mannosidases in a human gut symbiont. <i>Nature Chemical Biology</i> , 2010, 6, 125-132.  | 8.0  | 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.         | 7.1  | 219       |
| 48 | The Biochemistry and Structural Biology of Plant Cell Wall Deconstruction. <i>Plant Physiology</i> , 2010, 153, 444-455.  | 4.8  | 290       |
| 49 | Cellulosomes: Highly Efficient Nanomachines Designed to Deconstruct Plant Cell Wall Complex Carbohydrates. <i>Annual Review of Biochemistry</i> , 2010, 79, 655-681.  | 11.1 | 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.                                 | 7.1  | 109       |
| 51 | The Active Site of a Carbohydrate Esterase Displays Divergent Catalytic and Noncatalytic Binding Functions. <i>PLoS Biology</i> , 2009, 7, e1000071.  | 5.6  | 56        |
| 52 | Structural and biochemical evidence for a boat-like transition state in $\beta$ -mannosidases. <i>Nature Chemical Biology</i> , 2008, 4, 306-312.   | 8.0  | 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.   | 7.1  | 178       |
| 54 | Cellulosomes: microbial nanomachines that display plasticity in quaternary structure. <i>Molecular Microbiology</i> , 2007, 63, 1568-1576.  | 2.5  | 124       |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 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.   | 3.4  | 221       |
| 56 | Structural and Biochemical Analysis of <i>Cellvibrio japonicus</i> Xylanase 10C. <i>Journal of Biological Chemistry</i> , 2004, 279, 11777-11788.  | 3.4  | 86        |
| 57 | Carbohydrate-binding modules: fine-tuning polysaccharide recognition. <i>Biochemical Journal</i> , 2004, 382, 769-781.   | 3.7  | 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.  | 2.5  | 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.            | 7.1  | 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.  | 3.3  | 74        |
| 61 | Substrate Distortion by a -Mannanase: Snapshots of the Michaelis and Covalent-Intermediate Complexes Suggest a B <sub>2,5</sub> Conformation for the Transition State. <i>Angewandte Chemie - International Edition</i> , 2002, 41, 2824-2827.   | 13.8 | 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.  | 2.5  | 33        |
| 63 | Role of Hydrogen Bonding in the Interaction between a Xylan Binding Module and Xylan. <i>Biochemistry</i> , 2001, 40, 5700-5707.   | 2.5  | 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.  | 3.4  | 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.   | 3.4  | 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.  | 2.5  | 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.  | 2.5  | 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.   | 2.8  | 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.   | 3.4  | 100       |
| 70 | <i>Pseudomonas</i> cellulose-binding domains mediate their effects by increasing enzyme substrate proximity. <i>Biochemical Journal</i> , 1998, 331, 775-781.  | 3.7  | 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. | 3.4  | 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.   | 2.5  | 70        |