

David N Bolam

List of Publications by Citations

Source: <https://exaly.com/author-pdf/7331059/david-n-bolam-publications-by-citations.pdf>
Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66 papers	6,542 citations	43 h-index	70 g-index
70 ext. papers	7,339 ext. citations	8.4 avg, IF	5.29 L-index

#	Paper	IF	Citations
66	Carbohydrate-binding modules: fine-tuning polysaccharide recognition. <i>Biochemical Journal</i> , 2004 , 382, 769-81	3.8	1475
65	Recognition and degradation of plant cell wall polysaccharides by two human gut symbionts. <i>PLoS Biology</i> , 2011 , 9, e1001221	9.7	480
64	Specificity of polysaccharide use in intestinal bacteroides species determines diet-induced microbiota alterations. <i>Cell</i> , 2010 , 141, 1241-52	56.2	450
63	Pseudomonas cellulose-binding domains mediate their effects by increasing enzyme substrate proximity. <i>Biochemical Journal</i> , 1998 , 331 (Pt 3), 775-81	3.8	246
62	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015 , 6, 7481	17.4	241
61	Understanding the biological rationale for the diversity of cellulose-directed carbohydrate-binding modules in prokaryotic enzymes. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29321-9	5.4	192
60	The pattern of xylan acetylation suggests xylan may interact with cellulose microfibrils as a twofold helical screw in the secondary plant cell wall of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2014 , 79, 492-506	6.9	181
59	The X6 "thermostabilizing" domains of xylanases are carbohydrate-binding modules: structure and biochemistry of the <i>Clostridium thermocellum</i> X6b domain. <i>Biochemistry</i> , 2000 , 39, 5013-21	3.2	149
58	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017 , 541, 407-411	50.4	119
57	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, 5336-41	11.5	114
56	Differential recognition of plant cell walls by microbial xylan-specific carbohydrate-binding modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4765-70	11.5	109
55	The structural basis for the ligand specificity of family 2 carbohydrate-binding modules. <i>Journal of Biological Chemistry</i> , 2000 , 275, 41137-42	5.4	102
54	Glycoside hydrolase carbohydrate-binding modules as molecular probes for the analysis of plant cell wall polymers. <i>Analytical Biochemistry</i> , 2004 , 326, 49-54	3.1	96
53	The location of the ligand-binding site of carbohydrate-binding modules that have evolved from a common sequence is not conserved. <i>Journal of Biological Chemistry</i> , 2001 , 276, 48580-7	5.4	93
52	Xyloglucan is recognized by carbohydrate-binding modules that interact with beta-glucan chains. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8815-28	5.4	87
51	The family 11 carbohydrate-binding module of <i>Clostridium thermocellum</i> Lic26A-Cel5E accommodates beta-1,4- and beta-1,3-1,4-mixed linked glucans at a single binding site. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34785-93	5.4	85
50	Structure of a family 15 carbohydrate-binding module in complex with xylopentaose. Evidence that xylan binds in an approximate 3-fold helical conformation. <i>Journal of Biological Chemistry</i> , 2001 , 276, 49061-5	5.4	84

49	The family 6 carbohydrate binding module CmCBM6-2 contains two ligand-binding sites with distinct specificities. <i>Journal of Biological Chemistry</i> , 2004 , 279, 21552-9	5.4	83
48	A family IIb xylan-binding domain has a similar secondary structure to a homologous family IIa cellulose-binding domain but different ligand specificity. <i>Structure</i> , 1999 , 7, 853-64	5.2	83
47	Probing the breadth of macrolide glycosyltransferases: in vitro remodeling of a polyketide antibiotic creates active bacterial uptake and enhances potency. <i>Journal of the American Chemical Society</i> , 2005 , 127, 9336-7	16.4	82
46	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, 14077-82	11.5	81
45	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, 1143-52		77
44	Evidence for synergy between family 2b carbohydrate binding modules in <i>Cellulomonas fimi</i> xylanase 11A. <i>Biochemistry</i> , 2001 , 40, 2468-77	3.2	77
43	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, 31186-92	5.4	76
42	<i>Clostridium thermocellum</i> Xyn10B carbohydrate-binding module 22-2: the role of conserved amino acids in ligand binding. <i>Biochemistry</i> , 2001 , 40, 9167-76	3.2	73
41	A novel extracellular metallopeptidase domain shared by animal host-associated mutualistic and pathogenic microbes. <i>PLoS ONE</i> , 2012 , 7, e30287	3.7	71
40	Structural dissection and high-throughput screening of mannosylglycerate synthase. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 608-14	17.6	71
39	The type II and X cellulose-binding domains of <i>Pseudomonas</i> xylanase A potentiate catalytic activity against complex substrates by a common mechanism. <i>Biochemical Journal</i> , 1999 , 342, 473-480	3.8	69
38	Family 6 carbohydrate binding modules in beta-agarases display exquisite selectivity for the non-reducing termini of agarose chains. <i>Journal of Biological Chemistry</i> , 2006 , 281, 17099-17107	5.4	68
37	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	11.5	67
36	Mannanase A from <i>Pseudomonas fluorescens</i> ssp. <i>cellulosa</i> is a retaining glycosyl hydrolase in which E212 and E320 are the putative catalytic residues. <i>Biochemistry</i> , 1996 , 35, 16195-204	3.2	66
35	A novel carbohydrate-binding protein is a component of the plant cell wall-degrading complex of <i>Piromyces equi</i> . <i>Journal of Biological Chemistry</i> , 2001 , 276, 43010-7	5.4	65
34	Complex N-glycan breakdown by gut <i>Bacteroides</i> involves an extensive enzymatic apparatus encoded by multiple co-regulated genetic loci. <i>Nature Microbiology</i> , 2019 , 4, 1571-1581	26.6	64
33	A scissor blade-like closing mechanism implicated in transmembrane signaling in a <i>Bacteroides</i> hybrid two-component system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 7298-303	11.5	64
32	X4 modules represent a new family of carbohydrate-binding modules that display novel properties. <i>Journal of Biological Chemistry</i> , 2004 , 279, 22953-63	5.4	62

31	The crystal structure of the family 6 carbohydrate binding module from <i>Cellvibrio mixtus</i> endoglucanase 5a in complex with oligosaccharides reveals two distinct binding sites with different ligand specificities. <i>Journal of Biological Chemistry</i> , 2004 , 279, 21560-8	5.4	58
30	Role of hydrogen bonding in the interaction between a xylan binding module and xylan. <i>Biochemistry</i> , 2001 , 40, 5700-7	3.2	56
29	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, 9316-23	3.2	55
28	Cellulose binding domains and linker sequences potentiate the activity of hemicellulases against complex substrates. <i>Journal of Biotechnology</i> , 1997 , 57, 59-69	3.7	50
27	The active site of a carbohydrate esterase displays divergent catalytic and noncatalytic binding functions. <i>PLoS Biology</i> , 2009 , 7, e71	9.7	49
26	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	5.4	46
25	Glycan recognition by the Bacteroidetes Sus-like systems. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 563-9	8.1	45
24	Structure of a mannan-specific family 35 carbohydrate-binding module: evidence for significant conformational changes upon ligand binding. <i>Journal of Molecular Biology</i> , 2005 , 347, 287-96	6.5	45
23	Reduction of starch granule size by expression of an engineered tandem starch-binding domain in potato plants. <i>Plant Biotechnology Journal</i> , 2004 , 2, 251-60	11.6	43
22	Calcium binding and thermostability of carbohydrate binding module CBM4-2 of Xyn10A from <i>Rhodothermus marinus</i> . <i>Biochemistry</i> , 2002 , 41, 5720-9	3.2	39
21	Secretion and assembly of functional mini-cellulosomes from synthetic chromosomal operons in <i>Clostridium acetobutylicum</i> ATCC 824. <i>Biotechnology for Biofuels</i> , 2013 , 6, 117	7.8	38
20	Ligand-mediated dimerization of a carbohydrate-binding molecule reveals a novel mechanism for protein-carbohydrate recognition. <i>Journal of Molecular Biology</i> , 2004 , 337, 417-26	6.5	35
19	Prominent members of the human gut microbiota express endo-acting O-glycanases to initiate mucin breakdown. <i>Nature Communications</i> , 2020 , 11, 4017	17.4	34
18	Tuning transcription of nutrient utilization genes to catabolic rate promotes growth in a gut bacterium. <i>Molecular Microbiology</i> , 2014 , 93, 1010-25	4.1	32
17	Circular permutation provides an evolutionary link between two families of calcium-dependent carbohydrate binding modules. <i>Journal of Biological Chemistry</i> , 2010 , 285, 31742-54	5.4	32
16	Probing the mechanism of ligand recognition in family 29 carbohydrate-binding modules. <i>Journal of Biological Chemistry</i> , 2005 , 280, 23718-26	5.4	32
15	Mechanistic insight into polysaccharide use within the intestinal microbiota. <i>Gut Microbes</i> , 2011 , 2, 86-90	8.8	31
14	Functional insights into the role of novel type I cohesin and dockerin domains from <i>Clostridium thermocellum</i> . <i>Biochemical Journal</i> , 2009 , 424, 375-84	3.8	31

13	TonB-dependent transport by the gut microbiota: novel aspects of an old problem. <i>Current Opinion in Structural Biology</i> , 2018 , 51, 35-43	8.1	28
12	The alpha-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, 20286-92	5.4	27
11	The type II and X cellulose-binding domains of <i>Pseudomonas</i> xylanase A potentiate catalytic activity against complex substrates by a common mechanism. <i>Biochemical Journal</i> , 1999 , 342, 473	3.8	26
10	Novel <i>Clostridium thermocellum</i> type I cohesin-dockerin complexes reveal a single binding mode. <i>Journal of Biological Chemistry</i> , 2012 , 287, 44394-405	5.4	25
9	Genetic Variation of the SusC/SusD Homologs from a Polysaccharide Utilization Locus Underlies Divergent Fructan Specificities and Functional Adaptation in Strains. <i>MSphere</i> , 2018 , 3,	5	20
8	Insights into SusCD-mediated glycan import by a prominent gut symbiont. <i>Nature Communications</i> , 2021 , 12, 44	17.4	15
7	Cloning, purification and biochemical characterisation of a GH35 beta-1,3/beta-1,6-galactosidase from the mucin-degrading gut bacterium <i>Akkermansia muciniphila</i> . <i>Glycoconjugate Journal</i> , 2018 , 35, 255-263	3	11
6	Extensive transfer of genes for edible seaweed digestion from marine to human gut bacteria		11
5	Family 6 carbohydrate-binding modules display multiple beta1,3-linked glucan-specific binding interfaces. <i>FEMS Microbiology Letters</i> , 2009 , 300, 48-57	2.9	8
4	Diverse events have transferred genes for edible seaweed digestion from marine to human gut bacteria.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	3
3	Synthesis of 2,4-dinitrophenyl glycosides of d-xylobiose and d-mannobiose. <i>Carbohydrate Research</i> , 1998 , 312, 85-89	2.9	2
2	Crystallization and preliminary X-ray diffraction studies of a family 26 endo-beta-1,4 mannanase (ManA) from <i>Pseudomonas fluorescens</i> subspecies <i>cellulosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 129-31		2
1	A novel glycosidase plate-based assay for the quantification of galactosylation and sialylation on human IgG. <i>Glycoconjugate Journal</i> , 2020 , 37, 691-702	3	1