

David N Bolam

List of Publications by Year in Descending Order

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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	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
65	Insights into SusCD-mediated glycan import by a prominent gut symbiont. <i>Nature Communications</i> , 2021 , 12, 44	17.4	15
64	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
63	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
62	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
61	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
60	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
59	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
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	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
56	Glycan complexity dictates microbial resource allocation in the large intestine. <i>Nature Communications</i> , 2015 , 6, 7481	17.4	241
55	Evidence that GH115 Eglucuronidase 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
54	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
53	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
52	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
51	Glycan recognition by the Bacteroidetes Sus-like systems. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 563-9	8.1	45
50	A novel extracellular metallopeptidase domain shared by animal host-associated mutualistic and pathogenic microbes. <i>PLoS ONE</i> , 2012 , 7, e30287	3.7	71

49	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
48	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
47	Mechanistic insight into polysaccharide use within the intestinal microbiota. <i>Gut Microbes</i> , 2011 , 2, 86-908.8		31
46	Recognition and degradation of plant cell wall polysaccharides by two human gut symbionts. <i>PLoS Biology</i> , 2011 , 9, e1001221	9.7	480
45	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
44	Specificity of polysaccharide use in intestinal <i>bacteroides</i> species determines diet-induced microbiota alterations. <i>Cell</i> , 2010 , 141, 1241-52	56.2	450
43	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
42	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
41	The active site of a carbohydrate esterase displays divergent catalytic and noncatalytic binding functions. <i>PLoS Biology</i> , 2009 , 7, e71	9.7	49
40	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
39	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
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	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
36	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
35	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
34	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
33	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
32	Structural dissection and high-throughput screening of mannosylglycerate synthase. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 608-14	17.6	71

31	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
30	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
29	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
28	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
27	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
26	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
25	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
24	Carbohydrate-binding modules: fine-tuning polysaccharide recognition. <i>Biochemical Journal</i> , 2004 , 382, 769-81	3.8	1475
23	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
22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	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
14	<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

13	Role of hydrogen bonding in the interaction between a xylan binding module and xylan. <i>Biochemistry</i> , 2001 , 40, 5700-7	3.2	56
12	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
11	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
10	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
9	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
8	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
7	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
6	Synthesis of 2,4-dinitrophenyl glycosides of d-xylobiose and d-mannobiose. <i>Carbohydrate Research</i> , 1998 , 312, 85-89	2.9	2
5	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
4	<i>Pseudomonas</i> cellulose-binding domains mediate their effects by increasing enzyme substrate proximity. <i>Biochemical Journal</i> , 1998 , 331 (Pt 3), 775-81	3.8	246
3	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
2	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
1	Extensive transfer of genes for edible seaweed digestion from marine to human gut bacteria		11