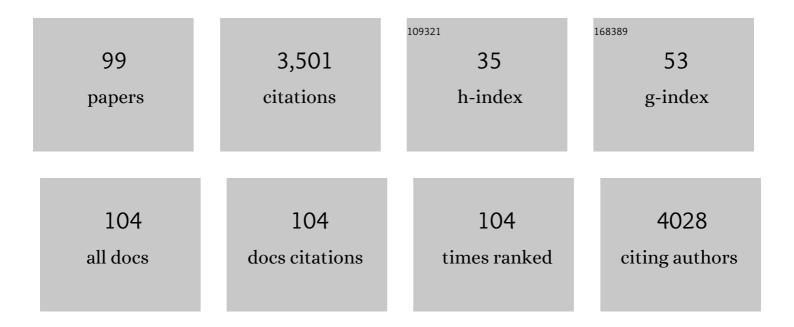
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Diversification of a Fucosyllactose Transporter within the Genus <i>Bifidobacterium</i> . Applied and Environmental Microbiology, 2022, 88, AEM0143721.	3.1	18
2	Activity-Based Protein Profiling of Retaining $\hat{I}\pm$ -Amylases in Complex Biological Samples. Journal of the American Chemical Society, 2021, 143, 2423-2432.	13.7	17
3	Structure and evolution of the bifidobacterial carbohydrate metabolism proteins and enzymes. Biochemical Society Transactions, 2021, 49, 563-578.	3.4	15
4	Discovery of fungal oligosaccharide-oxidising flavo-enzymes with previously unknown substrates, redox-activity profiles and interplay with LPMOs. Nature Communications, 2021, 12, 2132.	12.8	50
5	Molecular insight into a new lowâ€affinity xylan binding module from the xylanolytic gut symbiont RoseburiaÂintestinalis. FEBS Journal, 2020, 287, 2105-2117.	4.7	8
6	Loss of AA13 LPMOs impairs degradation of resistant starch and reduces the growth of Aspergillus nidulans. Biotechnology for Biofuels, 2020, 13, 135.	6.2	8
7	Butyrate producing colonic Clostridiales metabolise human milk oligosaccharides and cross feed on mucin via conserved pathways. Nature Communications, 2020, 11, 3285.	12.8	102
8	The Catalytic Acid–Base in GH109 Resides in a Conserved GGHGG Loop and Allows for Comparable α-Retaining and β-Inverting Activity in an <i>N</i> -Acetylgalactosaminidase from <i>Akkermansia muciniphila</i> . ACS Catalysis, 2020, 10, 3809-3819.	11.2	15
9	An 1,4-α-Glucosyltransferase Defines a New Maltodextrin Catabolism Scheme in Lactobacillus acidophilus. Applied and Environmental Microbiology, 2020, 86, .	3.1	8
10	Evolutionary adaptation in fucosyllactose uptake systems supports bifidobacteria-infant symbiosis. Science Advances, 2019, 5, eaaw7696.	10.3	120
11	A novel starch-binding laccase from the wheat pathogen Zymoseptoria tritici highlights the functional diversity of ascomycete laccases. BMC Biotechnology, 2019, 19, 61.	3.3	3
12	Substrate preference of an ABC importer corresponds to selective growth on β-(1,6)-galactosides in Bifidobacterium animalis subsp. lactis. Journal of Biological Chemistry, 2019, 294, 11701-11711.	3.4	21
13	Two binding proteins of the ABC transporter that confers growth of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> ATCC27673 on βâ€mannan possess distinct mannoâ€oligosaccharideâ€binding profiles. Molecular Microbiology, 2019, 112, 114-130.	2.5	24
14	The human gut Firmicute Roseburia intestinalis is a primary degrader of dietary β-mannans. Nature Communications, 2019, 10, 905.	12.8	202
15	1H, 13C and 15N backbone and side-chain assignment of a carbohydrate binding module from a xylanase from Roseburia intestinalis. Biomolecular NMR Assignments, 2019, 13, 55-58.	0.8	3
16	Differential bacterial capture and transport preferences facilitate co-growth on dietary xylan in the human gut. Nature Microbiology, 2018, 3, 570-580.	13.3	121
17	Effect of alginate size, mannuronic/guluronic acid content and pH on particle size, thermodynamics and composition of complexes with I²-lactoglobulin. Food Hydrocolloids, 2018, 75, 157-163.	10.7	24
18	An Extracellular Cell-Attached Pullulanase Confers Branched α-Glucan Utilization in Human Gut Lactobacillus acidophilus. Applied and Environmental Microbiology, 2017, 83, .	3.1	25

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19	Fungal secretomics to probe the biological functions of lytic polysaccharide monooxygenases. Carbohydrate Research, 2017, 448, 155-160.	2.3	48
20	Mucin- and carbohydrate-stimulated adhesion and subproteome changes of the probiotic bacterium Lactobacillus acidophilus NCFM. Journal of Proteomics, 2017, 163, 102-110.	2.4	66
21	Discovery of Î \pm -l-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. Journal of Biological Chemistry, 2017, 292, 21092-21101.	3.4	8
22	Effect of repeat unit structure and molecular mass of lactic acid bacteria hetero-exopolysaccharides on binding to milk proteins. Carbohydrate Polymers, 2017, 177, 406-414.	10.2	14
23	Data regarding the growth of Lactobacillus acidophilus NCFM on different carbohydrates and recombinant production of elongation factor G and pyruvate kinase. Data in Brief, 2017, 14, 118-122.	1.0	2
24	<i>Lactobacillus acidophilus</i> Metabolizes Dietary Plant Glucosides and Externalizes Their Bioactive Phytochemicals. MBio, 2017, 8, .	4.1	90
25	Lytic polysaccharide monooxygenases and other oxidative enzymes are abundantly secreted by Aspergillus nidulans grown on different starches. Biotechnology for Biofuels, 2016, 9, 187.	6.2	42
26	Using Carbohydrate Interaction Assays to Reveal Novel Binding Sites in Carbohydrate Active Enzymes. PLoS ONE, 2016, 11, e0160112.	2.5	22
27	Differential proteome and cellular adhesion analyses of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM grown on raffinose – an emerging prebiotic. Proteomics, 2016, 16, 1361-1375.	2.2	29
28	Plant αâ€glucan phosphatases SEX4 and LSF2 display different affinity for amylopectin and amylose. FEBS Letters, 2016, 590, 118-128.	2.8	18
29	<i>Fg</i> <scp>LPMO</scp> 9A from <i>Fusarium graminearum</i> cleaves xyloglucan independently of the backbone substitution pattern. FEBS Letters, 2016, 590, 3346-3356.	2.8	44
30	An ATP Binding Cassette Transporter Mediates the Uptake of α-(1,6)-Linked Dietary Oligosaccharides in Bifidobacterium and Correlates with Competitive Growth on These Substrates. Journal of Biological Chemistry, 2016, 291, 20220-20231.	3.4	54
31	Structural and Mechanical Properties of Thin Films of Bovine Submaxillary Mucin versus Porcine Gastric Mucin on a Hydrophobic Surface in Aqueous Solutions. Langmuir, 2016, 32, 9687-9696.	3.5	37
32	Fungal lytic polysaccharide monooxygenases bind starch and β yclodextrin similarly to amylolytic hydrolases. FEBS Letters, 2016, 590, 2737-2747.	2.8	16
33	An efficient arabinoxylan-debranching α-l-arabinofuranosidase of family GH62 from Aspergillus nidulans contains a secondary carbohydrate binding site. Applied Microbiology and Biotechnology, 2016, 100, 6265-6277.	3.6	23
34	Proteolytic Degradation of Bovine Submaxillary Mucin (BSM) and Its Impact on Adsorption and Lubrication at a Hydrophobic Surface. Langmuir, 2015, 31, 8303-8309.	3.5	20
35	The GH5 1,4-β-mannanase from Bifidobacterium animalis subsp. lactis Bl-04 possesses a low-affinity mannan-binding module and highlights the diversity of mannanolytic enzymes. BMC Biochemistry, 2015, 16, 26.	4.4	35
36	Analysis of Surface Binding Sites (SBS) within CH62, GH13, and CH77. Journal of Applied Glycoscience (1999), 2015, 62, 87-93.	0.7	8

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37	A Simplified Chromatographic Approach to Purify Commercially Available Bovine Submaxillary Mucins (BSM). Preparative Biochemistry and Biotechnology, 2015, 45, 84-99.	1.9	16
38	Oligosaccharide and Substrate Binding in the Starch Debranching Enzyme Barley Limit Dextrinase. Journal of Molecular Biology, 2015, 427, 1263-1277.	4.2	33
39	Lotus japonicus flowers are defended by a cyanogenic \hat{l}^2 -glucosidase with highly restricted expression to essential reproductive organs. Plant Molecular Biology, 2015, 89, 21-34.	3.9	25
40	Crystal Structure of Barley Limit Dextrinase-Limit Dextrinase Inhibitor (LD-LDI) Complex Reveals Insights into Mechanism and Diversity of Cereal Type Inhibitors. Journal of Biological Chemistry, 2015, 290, 12614-12629.	3.4	21
41	A β1â€6/β1â€ 3 galactosidase from B ifidobacterium animalis subsp. lactis †B lâ€04 gives insight into subâ€specificities of βâ€galactoside catabolism within B ifidobacterium. Molecular Microbiology, 2014, 94, 1024-1040.	2.5	35
42	Recent insight in α-glucan metabolism in probiotic bacteria. Biologia (Poland), 2014, 69, 713-721.	1.5	19
43	Analysis of surface binding sites (SBSs) in carbohydrate active enzymes with focus on glycoside hydrolase families 13 and 77 — a mini-review. Biologia (Poland), 2014, 69, 705-712.	1.5	55
44	Distinct substrate specificities of three glycoside hydrolase family 42 Â-galactosidases from Bifidobacterium longum subsp. infantis ATCC 15697. Glycobiology, 2014, 24, 208-216.	2.5	40
45	The evolutionary appearance of nonâ€cyanogenic hydroxynitrile glucosides in the <i><scp>L</scp>otus</i> genus is accompanied by the substrate specialization of paralogous β–glucosidases resulting from a crucial amino acid substitution. Plant Journal, 2014, 79, 299-311.	5.7	15
46	S2-5 Analysis of Surface Binding Sites (SBS) within GH62, GH13 and GH77(Recent Progress of) Tj ETQq0 0 0 rgE	3T /Overloc	ck 10 Tf 50 38
47	Transcriptional analysis of oligosaccharide utilization by Bifidobacterium lactisBl-04. BMC Genomics, 2013, 14, 312.	2.8	65
48	Recent insight into oligosaccharide uptake and metabolism in probiotic bacteria. Biocatalysis and Biotransformation, 2013, 31, 226-235.	2.0	23
49	Interaction of Nascent Chains with the Ribosomal Tunnel Proteins Rpl4, Rpl17, and Rpl39 of Saccharomyces cerevisiae. Journal of Biological Chemistry, 2013, 288, 33697-33707.	3.4	35
50	Structural basis for arabinoxyloâ€oligosaccharide capture by the probiotic <i><scp>B</scp>ifidobacterium animalis</i> subsp. <i>lactis</i> â€ <scp>Bl</scp> â€04. Molecular Microbiology, 2013, 90, 1100-1112.	2.5	58
51	Kinetic analysis of inhibition of glucoamylase and active site mutants via chemoselective oxime immobilization of acarbose on SPR chip surfaces. Carbohydrate Research, 2013, 375, 21-28.	2.3	11
52	Arabidopsis thaliana AMY3 Is a Unique Redox-regulated Chloroplastic α-Amylase. Journal of Biological Chemistry, 2013, 288, 33620-33633.	3.4	79
53	In vitro growth of four individual human gut bacteria on oligosaccharides produced by chemoenzymatic synthesis. Food and Function, 2013, 4, 784.	4.6	13
54	A Snapshot into the Metabolism of Isomalto-oligosaccharides in Probiotic Bacteria. Journal of Applied Glycoscience (1999), 2013, 60, 95-100.	0.7	5

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55	Surface Binding Sites (SBSs), Mechanism and Regulation of Enzymes Degrading Amylopectin and α-Limit Dextrins. Journal of Applied Glycoscience (1999), 2013, 60, 101-109.	0.7	1
56	Enzymology and Structure of the GH13_31 Glucan 1,6-α-Glucosidase That Confers Isomaltooligosaccharide Utilization in the Probiotic Lactobacillus acidophilus NCFM. Journal of Bacteriology, 2012, 194, 4249-4259.	2.2	69
57	Structure of the starch-debranching enzyme barley limit dextrinase reveals homology of the N-terminal domain to CBM21. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1008-1012.	0.7	22
58	Raffinose family oligosaccharide utilisation by probiotic bacteria: insight into substrate recognition, molecular architecture and diversity of GH36 α-galactosidases. Biocatalysis and Biotransformation, 2012, 30, 316-325.	2.0	15
59	Degradation of the starch components amylopectin and amylose by barley α-amylase 1: Role of surface binding site 2. Archives of Biochemistry and Biophysics, 2012, 528, 1-6.	3.0	21
60	Transcriptional Analysis of Prebiotic Uptake and Catabolism by Lactobacillus acidophilus NCFM. PLoS ONE, 2012, 7, e44409.	2.5	71
61	Isothermal titration calorimetry and surface plasmon resonance allow quantifying substrate binding to different binding sites of Bacillus subtilis xylanase. Analytical Biochemistry, 2012, 420, 90-92.	2.4	10
62	S3-2 Mechanism and regulation of enzymes degrading amylopectin and α-limit dextrins(Overseas Invited) Tj ET	Qq0,00 rg	gBT /Overlock
63	Recombinant production and characterisation of two related GH5 endo-β-1,4-mannanases from Aspergillus nidulans FGSC A4 showing distinctly different transglycosylation capacity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 1720-1729.	2.3	46
64	Crystal Structure of α-Galactosidase from Lactobacillus acidophilus NCFM: Insight into Tetramer Formation and Substrate Binding. Journal of Molecular Biology, 2011, 412, 466-480.	4.2	63
65	Efficient secretory expression of functional barley limit dextrinase inhibitor by high cell-density fermentation of Pichia pastoris. Protein Expression and Purification, 2011, 79, 217-222.	1.3	10
66	Starchâ€binding domains in the CBM45 family – lowâ€affinity domains from glucan, water dikinase and αâ€amylase involved in plastidial starch metabolism. FEBS Journal, 2011, 278, 1175-1185.	4.7	38
67	Enzymatic synthesis of β-xylosyl-oligosaccharides by transxylosylation using two β-xylosidases of glycoside hydrolase family 3 from Aspergillus nidulans FGSC A4. Carbohydrate Research, 2011, 346, 421-429.	2.3	19
68	Transcriptional and functional analysis of galactooligosaccharide uptake by <i>lacS</i> in <i>Lactobacillus acidophilus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17785-17790.	7.1	99
69	Expression of Enzymatically Inactive Wasp Venom Phospholipase A1 in Pichia pastoris. PLoS ONE, 2011, 6, e21267.	2.5	13
70	Efficient one-pot enzymatic synthesis of α-(1→4)-glucosidic disaccharides through a coupled reaction catalysed by Lactobacillus acidophilus NCFM maltose phosphorylase. Carbohydrate Research, 2010, 345, 1061-1064.	2.3	23
71	<i>Aspergillus nidulans</i> αâ€galactosidase of glycoside hydrolase family 36 catalyses the formation of αâ€galactoâ€oligosaccharides by transglycosylation. FEBS Journal, 2010, 277, 3538-3551.	4.7	38
72	Rational engineering of Lactobacillus acidophilus NCFM maltose phosphorylase into either trehalose or kojibiose dual specificity phosphorylase. Protein Engineering, Design and Selection, 2010, 23, 781-787.	2.1	24

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73	Genetic Screening Identifies Cyanogenesis-Deficient Mutants of <i>Lotus japonicus</i> and Reveals Enzymatic Specificity in Hydroxynitrile Glucoside Metabolism Â. Plant Cell, 2010, 22, 1605-1619.	6.6	57
74	Crystal Structure of an Essential Enzyme in Seed Starch Degradation: Barley Limit Dextrinase in Complex with Cyclodextrins. Journal of Molecular Biology, 2010, 403, 739-750.	4.2	55
75	Efficient chemoenzymatic oligosaccharide synthesis by reverse phosphorolysis using cellobiose phosphorylase and cellodextrin phosphorylase from Clostridium thermocellum. Biochimie, 2010, 92, 1818-1826.	2.6	53
76	Secretory expression of functional barley limit dextrinase by Pichia pastoris using high cell-density fermentation. Protein Expression and Purification, 2010, 69, 112-119.	1.3	26
77	New Insight into Structure/Function Relationships in Plant .ALPHAAmylase Family GH13 Members. Journal of Applied Glycoscience (1999), 2010, 57, 157-162.	0.7	4
78	A CBM20 lowâ€affinity starchâ€binding domain from glucan, water dikinase. FEBS Letters, 2009, 583, 1159-1163.	2.8	47
79	The carbohydrateâ€binding module family 20 – diversity, structure, and function. FEBS Journal, 2009, 276, 5006-5029.	4.7	168
80	The maltodextrin transport system and metabolism in <i>Lactobacillus acidophilus</i> NCFM and production of novel α â€glucosides through reverse phosphorolysis by maltose phosphorylase. FEBS Journal, 2009, 276, 7353-7365.	4.7	52
81	Two Secondary Carbohydrate Binding Sites on the Surface of Barley α-Amylase 1 Have Distinct Functions and Display Synergy in Hydrolysis of Starch Granules. Biochemistry, 2009, 48, 7686-7697.	2.5	72
82	An enzyme family reunion — similarities, differences and eccentricities in actions on α-glucans. Biologia (Poland), 2008, 63, 967-979.	1.5	8
83	Roles of multiple surface sites, long substrate binding clefts, and carbohydrate binding modules in the action of amylolytic enzymes on polysaccharide substrates. Biocatalysis and Biotransformation, 2008, 26, 59-67.	2.0	4
84	α-Amylases. Interaction with Polysaccharide Substrates, Proteinaceous Inhibitors and Regulatory Proteins. , 2008, , 20-36.		0
85	Mapping of barley α-amylases and outer subsite mutants reveals dynamic high-affinity subsites and barriers in the long substrate binding cleft. FEBS Letters, 2006, 580, 5049-5053.	2.8	22
86	Interactions of barley α-amylase isozymes with Ca2 + , substrates and proteinaceous inhibitors. Biocatalysis and Biotransformation, 2006, 24, 83-93.	2.0	1
87	Interactions between Barley .ALPHAAmylases, Substrates, Inhibitors and Regulatory Proteins. Journal of Applied Clycoscience (1999), 2006, 53, 163-169.	0.7	0
88	Mutational Analysis of Target Enzyme Recognition of the β-Trefoil Fold Barley α-Amylase/Subtilisin Inhibitor. Journal of Biological Chemistry, 2005, 280, 14855-14864.	3.4	22
89	The modular xylanase Xyn10A fromRhodothermus marinusis cell-attached, and its C-terminal domain has several putative homologues among cell-attached proteins within the phylum Bacteroidetes. FEMS Microbiology Letters, 2004, 241, 233-242.	1.8	27
90	Probing the stability of the modular family 10 xylanase from Rhodothermus marinus. Extremophiles, 2003, 7, 483-491.	2.3	38

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91	The Modular Organisation and Stability of a Thermostable Family 10 Xylanase. Biocatalysis and Biotransformation, 2003, 21, 253-260.	2.0	10
92	Calcium Binding and Thermostability of Carbohydrate Binding Module CBM4-2 of Xyn10A fromRhodothermus marinusâ€. Biochemistry, 2002, 41, 5720-5729.	2.5	41
93	The Solution Structure of the CBM4-2 Carbohydrate Binding Module from a ThermostableRhodothermus marinusXylanaseâ€. Biochemistry, 2002, 41, 5712-5719.	2.5	68
94	Rhodothermus marinus : a thermophilic bacterium producing dimeric and hexameric citrate synthase isoenzymes. Extremophiles, 2002, 6, 51-56.	2.3	11
95	Virtually complete 1H, 13C and 15N resonance assignments of the second family 4 xylan binding module of Rhodothermus marinus xylanase 10A. Journal of Biomolecular NMR, 2002, 22, 187-188.	2.8	4
96	Deletion of a cytotoxic, N-terminal putative signal peptide results in a significant increase in production yields in Escherichia coli and improved specific activity of Cel12A from Rhodothermus marinus. Applied Microbiology and Biotechnology, 2001, 55, 578-584.	3.6	27
97	Carbohydrate-binding modules from a thermostable Rhodothermus marinus xylanase: cloning, expression and binding studies. Biochemical Journal, 2000, 345, 53.	3.7	77
98	Carbohydrate-binding modules from a thermostable Rhodothermus marinus xylanase: cloning, expression and binding studies. Biochemical Journal, 2000, 345, 53-60.	3.7	89
99	Carbohydrate-binding modules from a thermostable Rhodothermus marinus xylanase: cloning, expression and binding studies. Biochemical Journal, 2000, 345 Pt 1, 53-60.	3.7	28