

Maher Abou Hachem

List of Publications by Year in descending order

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docs citations

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4412
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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.	1.4	18
2	Activity-Based Protein Profiling of Retaining α -Amylases in Complex Biological Samples. Journal of the American Chemical Society, 2021, 143, 2423-2432.	6.6	17
3	Structure and evolution of the bifidobacterial carbohydrate metabolism proteins and enzymes. Biochemical Society Transactions, 2021, 49, 563-578.	1.6	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.	5.8	50
5	Molecular insight into a new low-affinity xylan binding module from the xylanolytic gut symbiont <i>Roseburia intestinalis</i> . FEBS Journal, 2020, 287, 2105-2117.	2.2	8
6	Loss of AA13 LPMOs impairs degradation of resistant starch and reduces the growth of <i>Aspergillus nidulans</i> . 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.	5.8	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.	5.5	15
9	An α -1,4-Glucosyltransferase Defines a New Maltodextrin Catabolism Scheme in <i>Lactobacillus acidophilus</i> . Applied and Environmental Microbiology, 2020, 86, .	1.4	8
10	Evolutionary adaptation in fucosyllactose uptake systems supports bifidobacteria-infant symbiosis. Science Advances, 2019, 5, eaaw7696.	4.7	120
11	A novel starch-binding laccase from the wheat pathogen <i>Zymoseptoria tritici</i> highlights the functional diversity of ascomycete laccases. BMC Biotechnology, 2019, 19, 61.	1.7	3
12	Substrate preference of an ABC importer corresponds to selective growth on β -(1,6)-galactosides in <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> . Journal of Biological Chemistry, 2019, 294, 11701-11711.	1.6	21
13	Two binding proteins of the ABC transporter that confers growth of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> ATCC27673 on α -mannan possess distinct manno-oligosaccharide-binding profiles. Molecular Microbiology, 2019, 112, 114-130.	1.2	24
14	The human gut Firmicute <i>Roseburia intestinalis</i> is a primary degrader of dietary β -mannans. Nature Communications, 2019, 10, 905.	5.8	202
15	^1H , ^{13}C and ^{15}N backbone and side-chain assignment of a carbohydrate binding module from a xylanase from <i>Roseburia intestinalis</i> . Biomolecular NMR Assignments, 2019, 13, 55-58.	0.4	3
16	Differential bacterial capture and transport preferences facilitate co-growth on dietary xylan in the human gut. Nature Microbiology, 2018, 3, 570-580.	5.9	121
17	Effect of alginate size, mannuronic/guluronic acid content and pH on particle size, thermodynamics and composition of complexes with β -lactoglobulin. Food Hydrocolloids, 2018, 75, 157-163.	5.6	24
18	An Extracellular Cell-Attached Pullulanase Confers Branched α -Glucan Utilization in Human Gut <i>Lactobacillus acidophilus</i> . Applied and Environmental Microbiology, 2017, 83, .	1.4	25

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19	Fungal secretomics to probe the biological functions of lytic polysaccharide monoxygenases. <i>Carbohydrate Research</i> , 2017, 448, 155-160.	1.1	48
20	Mucin- and carbohydrate-stimulated adhesion and subproteome changes of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Proteomics</i> , 2017, 163, 102-110.	1.2	66
21	Discovery of α -L-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. <i>Journal of Biological Chemistry</i> , 2017, 292, 21092-21101.	1.6	8
22	Effect of repeat unit structure and molecular mass of lactic acid bacteria hetero-exopolysaccharides on binding to milk proteins. <i>Carbohydrate Polymers</i> , 2017, 177, 406-414.	5.1	14
23	Data regarding the growth of <i>Lactobacillus acidophilus</i> NCFM on different carbohydrates and recombinant production of elongation factor G and pyruvate kinase. <i>Data in Brief</i> , 2017, 14, 118-122.	0.5	2
24	<i>Lactobacillus acidophilus</i> Metabolizes Dietary Plant Glucosides and Externalizes Their Bioactive Phytochemicals. <i>MBio</i> , 2017, 8, .	1.8	90
25	Lytic polysaccharide monoxygenases and other oxidative enzymes are abundantly secreted by <i>Aspergillus nidulans</i> grown on different starches. <i>Biotechnology for Biofuels</i> , 2016, 9, 187.	6.2	42
26	Using Carbohydrate Interaction Assays to Reveal Novel Binding Sites in Carbohydrate Active Enzymes. <i>PLoS ONE</i> , 2016, 11, e0160112.	1.1	22
27	Differential proteome and cellular adhesion analyses of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM grown on raffinose – an emerging prebiotic. <i>Proteomics</i> , 2016, 16, 1361-1375.	1.3	29
28	Plant α -glucan phosphatases SEX4 and LSF2 display different affinity for amylopectin and amylose. <i>FEBS Letters</i> , 2016, 590, 118-128.	1.3	18
29	<i>Fg</i> LPMO 9A from <i>Fusarium graminearum</i> cleaves xyloglucan independently of the backbone substitution pattern. <i>FEBS Letters</i> , 2016, 590, 3346-3356.	1.3	44
30	An ATP Binding Cassette Transporter Mediates the Uptake of α -(1,6)-Linked Dietary Oligosaccharides in <i>Bifidobacterium</i> and Correlates with Competitive Growth on These Substrates. <i>Journal of Biological Chemistry</i> , 2016, 291, 20220-20231.	1.6	54
31	Structural and Mechanical Properties of Thin Films of Bovine Submaxillary Mucin versus Porcine Gastric Mucin on a Hydrophobic Surface in Aqueous Solutions. <i>Langmuir</i> , 2016, 32, 9687-9696.	1.6	37
32	Fungal lytic polysaccharide monoxygenases bind starch and α -cyclodextrin similarly to amylolytic hydrolases. <i>FEBS Letters</i> , 2016, 590, 2737-2747.	1.3	16
33	An efficient arabinoxylan-debranching α -L-arabinofuranosidase of family GH62 from <i>Aspergillus nidulans</i> contains a secondary carbohydrate binding site. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6265-6277.	1.7	23
34	Proteolytic Degradation of Bovine Submaxillary Mucin (BSM) and Its Impact on Adsorption and Lubrication at a Hydrophobic Surface. <i>Langmuir</i> , 2015, 31, 8303-8309.	1.6	20
35	The GH5 1,4- β -mannanase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Bl-04 possesses a low-affinity mannan-binding module and highlights the diversity of mannanolytic enzymes. <i>BMC Biochemistry</i> , 2015, 16, 26.	4.4	35
36	Analysis of Surface Binding Sites (SBS) within GH62, GH13, and GH77. <i>Journal of Applied Glycoscience</i> (1999), 2015, 62, 87-93.	0.3	8

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37	A Simplified Chromatographic Approach to Purify Commercially Available Bovine Submaxillary Mucins (BSM). <i>Preparative Biochemistry and Biotechnology</i> , 2015, 45, 84-99.	1.0	16
38	Oligosaccharide and Substrate Binding in the Starch Debranching Enzyme Barley Limit Dextrinase. <i>Journal of Molecular Biology</i> , 2015, 427, 1263-1277.	2.0	33
39	Lotus japonicus flowers are defended by a cyanogenic Î²-glucosidase with highly restricted expression to essential reproductive organs. <i>Plant Molecular Biology</i> , 2015, 89, 21-34.	2.0	25
40	Crystal Structure of Barley Limit Dextrinase-Limit Dextrinase Inhibitor (LD-LDI) Complex Reveals Insights into Mechanism and Diversity of Cereal Type Inhibitors. <i>Journal of Biological Chemistry</i> , 2015, 290, 12614-12629.	1.6	21
41	A Î²1,6-Î²-galactosidase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> B-04 gives insight into substrate specificities of Î²-galactoside catabolism within <i>Bifidobacterium</i> . <i>Molecular Microbiology</i> , 2014, 94, 1024-1040.	1.2	35
42	Recent insight in Î±-glucan metabolism in probiotic bacteria. <i>Biologia (Poland)</i> , 2014, 69, 713-721.	0.8	19
43	Analysis of surface binding sites (SBSs) in carbohydrate active enzymes with focus on glycoside hydrolase families 13 and 77 a mini-review. <i>Biologia (Poland)</i> , 2014, 69, 705-712.	0.8	55
44	Distinct substrate specificities of three glycoside hydrolase family 42 Î²-galactosidases from <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697. <i>Glycobiology</i> , 2014, 24, 208-216.	1.3	40
45	The evolutionary appearance of non-cyanogenic hydroxynitrile glucosides in the <i>Lotus</i> genus is accompanied by the substrate specialization of paralogous Î²-galactosidases resulting from a crucial amino acid substitution. <i>Plant Journal</i> , 2014, 79, 299-311.	2.8	15
46	S2-5 Analysis of Surface Binding Sites (SBS) within GH62, GH13 and GH77 (Recent Progress of) <i>Trends in Glycoscience and Glycobiology</i> , 2014, 10, 50-58.	0.0	0
47	Transcriptional analysis of oligosaccharide utilization by <i>Bifidobacterium lactis</i> Bl-04. <i>BMC Genomics</i> , 2013, 14, 312.	1.2	65
48	Recent insight into oligosaccharide uptake and metabolism in probiotic bacteria. <i>Biocatalysis and Biotransformation</i> , 2013, 31, 226-235.	1.1	23
49	Interaction of Nascent Chains with the Ribosomal Tunnel Proteins Rpl4, Rpl17, and Rpl39 of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 33697-33707.	1.6	35
50	Structural basis for arabinoxylo-oligosaccharide capture by the probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> B-04. <i>Molecular Microbiology</i> , 2013, 90, 1100-1112.	1.2	58
51	Kinetic analysis of inhibition of glucoamylase and active site mutants via chemoselective oxime immobilization of acarbose on SPR chip surfaces. <i>Carbohydrate Research</i> , 2013, 375, 21-28.	1.1	11
52	<i>Arabidopsis thaliana</i> AMY3 Is a Unique Redox-regulated Chloroplastic Î±-Amylase. <i>Journal of Biological Chemistry</i> , 2013, 288, 33620-33633.	1.6	79
53	In vitro growth of four individual human gut bacteria on oligosaccharides produced by chemoenzymatic synthesis. <i>Food and Function</i> , 2013, 4, 784.	2.1	13
54	A Snapshot into the Metabolism of Isomalto-oligosaccharides in Probiotic Bacteria. <i>Journal of Applied Glycoscience</i> (1999), 2013, 60, 95-100.	0.3	5

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55	Surface Binding Sites (SBSs), Mechanism and Regulation of Enzymes Degrading Amylopectin and α -Limit Dextrins. <i>Journal of Applied Glycoscience</i> (1999), 2013, 60, 101-109.	0.3	1
56	Enzymology and Structure of the GH13_31 Glucan 1,6- α -Glucosidase That Confers Isomaltooligosaccharide Utilization in the Probiotic <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Bacteriology</i> , 2012, 194, 4249-4259.	1.0	69
57	Structure of the starch-debranching enzyme barley limit dextrinase reveals homology of the N-terminal domain to CBM21. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 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 β -galactosidases. <i>Biocatalysis and Biotransformation</i> , 2012, 30, 316-325.	1.1	15
59	Degradation of the starch components amylopectin and amylose by barley α -amylase 1: Role of surface binding site 2. <i>Archives of Biochemistry and Biophysics</i> , 2012, 528, 1-6.	1.4	21
60	Transcriptional Analysis of Prebiotic Uptake and Catabolism by <i>Lactobacillus acidophilus</i> NCFM. <i>PLoS ONE</i> , 2012, 7, e44409.	1.1	71
61	Isothermal titration calorimetry and surface plasmon resonance allow quantifying substrate binding to different binding sites of <i>Bacillus subtilis</i> xylanase. <i>Analytical Biochemistry</i> , 2012, 420, 90-92.	1.1	10
62	S3-2 Mechanism and regulation of enzymes degrading amylopectin and α -limit dextrins(Overseas Invited) Tj ETQq0.0.0 rgBT 0	0.0	0
63	Recombinant production and characterisation of two related GH5 endo- β -1,4-mannanases from <i>Aspergillus nidulans</i> FGSC A4 showing distinctly different transglycosylation capacity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1720-1729.	1.1	46
64	Crystal Structure of β -Galactosidase from <i>Lactobacillus acidophilus</i> NCFM: Insight into Tetramer Formation and Substrate Binding. <i>Journal of Molecular Biology</i> , 2011, 412, 466-480.	2.0	63
65	Efficient secretory expression of functional barley limit dextrinase inhibitor by high cell-density fermentation of <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 2011, 79, 217-222.	0.6	10
66	Starch-binding domains in the CBM45 family " low-affinity domains from glucan, water dikinase and α -amylase involved in plastidial starch metabolism. <i>FEBS Journal</i> , 2011, 278, 1175-1185.	2.2	38
67	Enzymatic synthesis of β -xylosyl-oligosaccharides by transxylosylation using two β -xylosidases of glycoside hydrolase family 3 from <i>Aspergillus nidulans</i> FGSC A4. <i>Carbohydrate Research</i> , 2011, 346, 421-429.	1.1	19
68	Transcriptional and functional analysis of galactooligosaccharide uptake by <i>Lactobacillus acidophilus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17785-17790.	3.3	99
69	Expression of Enzymatically Inactive Wasp Venom Phospholipase A1 in <i>Pichia pastoris</i> . <i>PLoS ONE</i> , 2011, 6, e21267.	1.1	13
70	Efficient one-pot enzymatic synthesis of α -(1 α '4)-glucosidic disaccharides through a coupled reaction catalysed by <i>Lactobacillus acidophilus</i> NCFM maltose phosphorylase. <i>Carbohydrate Research</i> , 2010, 345, 1061-1064.	1.1	23
71	<i>Aspergillus nidulans</i> β -galactosidase of glycoside hydrolase family 36 catalyses the formation of β -galactooligosaccharides by transglycosylation. <i>FEBS Journal</i> , 2010, 277, 3538-3551.	2.2	38
72	Rational engineering of <i>Lactobacillus acidophilus</i> NCFM maltose phosphorylase into either trehalose or kojibiose dual specificity phosphorylase. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 781-787.	1.0	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. <i>Plant Cell</i> , 2010, 22, 1605-1619.	3.1	57
74	Crystal Structure of an Essential Enzyme in Seed Starch Degradation: Barley Limit Dextrinase in Complex with Cyclodextrins. <i>Journal of Molecular Biology</i> , 2010, 403, 739-750.	2.0	55
75	Efficient chemoenzymatic oligosaccharide synthesis by reverse phosphorolysis using cellobiose phosphorylase and cellodextrin phosphorylase from <i>Clostridium thermocellum</i> . <i>Biochimie</i> , 2010, 92, 1818-1826.	1.3	53
76	Secretory expression of functional barley limit dextrinase by <i>Pichia pastoris</i> using high cell-density fermentation. <i>Protein Expression and Purification</i> , 2010, 69, 112-119.	0.6	26
77	New Insight into Structure/Function Relationships in Plant .ALPHA.-Amylase Family GH13 Members. <i>Journal of Applied Glycoscience</i> (1999), 2010, 57, 157-162.	0.3	4
78	A CBM20 low-affinity starch-binding domain from glucan, water dikinase. <i>FEBS Letters</i> , 2009, 583, 1159-1163.	1.3	47
79	The carbohydrate-binding module family 20 diversity, structure, and function. <i>FEBS Journal</i> , 2009, 276, 5006-5029.	2.2	168
80	The maltodextrin transport system and metabolism in <i>Lactobacillus acidophilus</i> NCFM and production of novel oligoglucosides through reverse phosphorolysis by maltose phosphorylase. <i>FEBS Journal</i> , 2009, 276, 7353-7365.	2.2	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. <i>Biochemistry</i> , 2009, 48, 7686-7697.	1.2	72
82	An enzyme family reunion similarities, differences and eccentricities in actions on α -glucans. <i>Biologia (Poland)</i> , 2008, 63, 967-979.	0.8	8
83	Roles of multiple surface sites, long substrate binding clefts, and carbohydrate binding modules in the action of amylolytic enzymes on polysaccharide substrates. <i>Biocatalysis and Biotransformation</i> , 2008, 26, 59-67.	1.1	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. <i>FEBS Letters</i> , 2006, 580, 5049-5053.	1.3	22
86	Interactions of barley α -amylase isozymes with Ca^{2+} , substrates and proteinaceous inhibitors. <i>Biocatalysis and Biotransformation</i> , 2006, 24, 83-93.	1.1	1
87	Interactions between Barley .ALPHA.-Amylases, Substrates, Inhibitors and Regulatory Proteins. <i>Journal of Applied Glycoscience</i> (1999), 2006, 53, 163-169.	0.3	0
88	Mutational Analysis of Target Enzyme Recognition of the β -Trefoil Fold Barley α -Amylase/Subtilisin Inhibitor. <i>Journal of Biological Chemistry</i> , 2005, 280, 14855-14864.	1.6	22
89	The modular xylanase Xyn10A from <i>Rhodothermus marinus</i> cell-attached, and its C-terminal domain has several putative homologues among cell-attached proteins within the phylum Bacteroidetes. <i>FEMS Microbiology Letters</i> , 2004, 241, 233-242.	0.7	27
90	Probing the stability of the modular family 10 xylanase from <i>Rhodothermus marinus</i> . <i>Extremophiles</i> , 2003, 7, 483-491.	0.9	38

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91	The Modular Organisation and Stability of a Thermostable Family 10 Xylanase. <i>Biocatalysis and Biotransformation</i> , 2003, 21, 253-260.	1.1	10
92	Calcium Binding and Thermostability of Carbohydrate Binding Module CBM4-2 of Xyn10A from <i>Rhodothermus marinus</i> . <i>Biochemistry</i> , 2002, 41, 5720-5729.	1.2	41
93	The Solution Structure of the CBM4-2 Carbohydrate Binding Module from a Thermostable <i>Rhodothermus marinus</i> Xylanase. <i>Biochemistry</i> , 2002, 41, 5712-5719.	1.2	68
94	<i>Rhodothermus marinus</i> : a thermophilic bacterium producing dimeric and hexameric citrate synthase isoenzymes. <i>Extremophiles</i> , 2002, 6, 51-56.	0.9	11
95	Virtually complete ¹ H, ¹³ C and ¹⁵ N resonance assignments of the second family 4 xylan binding module of <i>Rhodothermus marinus</i> xylanase 10A. <i>Journal of Biomolecular NMR</i> , 2002, 22, 187-188.	1.6	4
96	Deletion of a cytotoxic, N-terminal putative signal peptide results in a significant increase in production yields in <i>Escherichia coli</i> and improved specific activity of Cel12A from <i>Rhodothermus marinus</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 55, 578-584.	1.7	27
97	Carbohydrate-binding modules from a thermostable <i>Rhodothermus marinus</i> xylanase: cloning, expression and binding studies. <i>Biochemical Journal</i> , 2000, 345, 53.	1.7	77
98	Carbohydrate-binding modules from a thermostable <i>Rhodothermus marinus</i> xylanase: cloning, expression and binding studies. <i>Biochemical Journal</i> , 2000, 345, 53-60.	1.7	89
99	Carbohydrate-binding modules from a thermostable <i>Rhodothermus marinus</i> xylanase: cloning, expression and binding studies. <i>Biochemical Journal</i> , 2000, 345 Pt 1, 53-60.	1.7	28