Birte Svensson

List of Publications by Year in descending order

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288 papers 12,621 citations

59 h-index 94 g-index

297 all docs

297 docs citations

times ranked

297

8416 citing authors

#	Article	IF	CITATIONS
1	Structure, function and enzymatic synthesis of glucosaccharides assembled mainly by α1Â→Â6 linkages – A review. Carbohydrate Polymers, 2022, 275, 118705.	5.1	9
2	Maltogenic \hat{l}_{\pm} -amylase hydrolysis of wheat starch granules: Mechanism and relation to starch retrogradation. Food Hydrocolloids, 2022, 124, 107256.	5.6	30
3	A healthy Bifidobacterium dentium caramel cocktail. Journal of Biological Chemistry, 2022, 298, 101452.	1.6	4
4	Characterization of five marine family 29 glycoside hydrolases reveals an \hat{l} ±-L-fucosidase targeting specifically Fuc($\langle i \rangle \hat{l}$ ± $\langle j \rangle 1$,4)GlcNAc. Glycobiology, 2022, 32, 529-539.	1.3	7
5	Improved production of gamma-cyclodextrin from high-concentrated starch using enzyme pretreatment under swelling condition. Carbohydrate Polymers, 2022, 284, 119124.	5.1	9
6	How many α-amylase GH families are there in the CAZy database?. Amylase, 2022, 6, 1-10.	0.7	18
7	Distinct effects of different α-amylases on cross-linked tapioca starch and gel-improving mechanism. Food Hydrocolloids, 2022, 128, 107580.	5.6	10
8	Mechanistic Basis for Understanding the Dual Activities of the Bifunctional Azotobacter vinelandii Mannuronan C-5-Epimerase and Alginate Lyase AlgE7. Applied and Environmental Microbiology, 2022, 88, AEM0183621.	1.4	6
9	Metabolic Profiling of Interspecies Interactions During Sessile Bacterial Cultivation Reveals Growth and Sporulation Induction in Paenibacillus amylolyticus in Response to Xanthomonas retroflexus. Frontiers in Cellular and Infection Microbiology, 2022, 12, 805473.	1.8	1
10	Structure, Function and Protein Engineering of Cereal-Type Inhibitors Acting on Amylolytic Enzymes. Frontiers in Molecular Biosciences, 2022, 9, 868568.	1.6	4
11	Enhancing gel strength of Thermoproteus uzoniensis 4-α-glucanotransferase modified starch by amylosucrase treatment. International Journal of Biological Macromolecules, 2022, 209, 1-8.	3.6	4
12	Effect of Starch Primers on the Fine Structure of Enzymatically Synthesized Glycogen-like Glucan. Journal of Agricultural and Food Chemistry, 2022, 70, 6202-6212.	2.4	4
13	Tunable mixed micellization of \hat{l}^2 -casein in the presence of \hat{l}^2 -casein. Food Hydrocolloids, 2021, 113, 106459.	5.6	7
14	Enzymes in grain processing. Current Opinion in Food Science, 2021, 37, 153-159.	4.1	4
15	<i>O</i> -/ <i>N</i> -/ <i>S</i> -Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. ACS Catalysis, 2021, 11, 1810-1815.	5.5	42
16	Impact of Alginate Mannuronic-Guluronic Acid Contents and pH on Protein Binding Capacity and Complex Size. Biomacromolecules, 2021, 22, 649-660.	2.6	19
17	Functional diversity of three tandem C-terminal carbohydrate-binding modules of a \hat{l}^2 -mannanase. Journal of Biological Chemistry, 2021, 296, 100638.	1.6	10
18	Binding Sites for Oligosaccharide Repeats from Lactic Acid Bacteria Exopolysaccharides on Bovine β-Lactoglobulin Identified by NMR Spectroscopy. ACS Omega, 2021, 6, 9039-9052.	1.6	7

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19	Quantitative Label-Free Comparison of the Metabolic Protein Fraction in Old and Modern Italian Wheat Genotypes by a Shotgun Approach. Molecules, 2021, 26, 2596.	1.7	9
20	A putative novel starch-binding domain revealed by in silico analysis of the N-terminal domain in bacterial amylomaltases from the family GH77. 3 Biotech, 2021, 11, 229.	1.1	7
21	Wheat ATIs: Characteristics and Role in Human Disease. Frontiers in Nutrition, 2021, 8, 667370.	1.6	42
22	Rational Enzyme Design without Structural Knowledge: A Sequenceâ€Based Approach for Efficient Generation of Transglycosylases. Chemistry - A European Journal, 2021, 27, 10323-10334.	1.7	29
23	Deamidation and glycation of a $\langle i \rangle$ Bacillus licheniformis $\langle i \rangle$ α-amylase during industrial fermentation can improve detergent wash performance. Amylase, 2021, 5, 38-49.	0.7	1
24	Exceptionally rich keratinolytic enzyme profile found in the rare actinomycetes Amycolatopsis keratiniphila D2T. Applied Microbiology and Biotechnology, 2021, 105, 8129-8138.	1.7	8
25	Controlling the Fine Structure of Glycogen-like Glucan by Rational Enzymatic Synthesis. Journal of Agricultural and Food Chemistry, 2021, 69, 14951-14960.	2.4	4
26	Roles of the N-terminal domain and remote substrate binding subsites in activity of the debranching barley limit dextrinase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2020, 1868, 140294.	1.1	6
27	Qualitative proteomic comparison of metabolic and CM-like protein fractions in old and modern wheat Italian genotypes by a shotgun approach. Journal of Proteomics, 2020, 211, 103530.	1.2	16
28	A Single Point Mutation Converts GH84 <i>O</i> -GlcNAc Hydrolases into Phosphorylases: Experimental and Theoretical Evidence. Journal of the American Chemical Society, 2020, 142, 2120-2124.	6.6	25
29	Azo dying of αâ€keratin material improves microbial keratinase screening and standardization. Microbial Biotechnology, 2020, 13, 984-996.	2.0	11
30	Two novel S1 peptidases from Amycolatopsis keratinophila subsp. keratinophila D2T degrading keratinous slaughterhouse by-products. Applied Microbiology and Biotechnology, 2020, 104, 2513-2522.	1.7	5
31	Identification and Characterization of a \hat{l}^2 -N-Acetylhexosaminidase with a Biosynthetic Activity from the Marine Bacterium Paraglaciecola hydrolytica S66T. International Journal of Molecular Sciences, 2020, 21, 417.	1.8	12
32	Thermophilic 4-α-Glucanotransferase from <i>Thermoproteus Uzoniensis</i> Retards the Long-Term Retrogradation but Maintains the Short-Term Gelation Strength of Tapioca Starch. Journal of Agricultural and Food Chemistry, 2020, 68, 5658-5667.	2.4	13
33	An $1,4-\hat{l}\pm$ -Glucosyltransferase Defines a New Maltodextrin Catabolism Scheme in Lactobacillus acidophilus. Applied and Environmental Microbiology, 2020, 86, .	1.4	8
34	Community-intrinsic properties enhance keratin degradation from bacterial consortia. PLoS ONE, 2020, 15, e0228108.	1.1	16
35	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		O
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37	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		O
38	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		0
39	Expanding the citrullinome of synovial fibrinogen from rheumatoid arthritis patients. Journal of Proteomics, 2019, 208, 103484.	1.2	16
40	Structural and functional aspects of mannuronic acid–specific PL6 alginate lyase from the human gut microbe Bacteroides cellulosilyticus. Journal of Biological Chemistry, 2019, 294, 17915-17930.	1.6	40
41	A carbohydrate-binding family 48 module enables feruloyl esterase action on polymeric arabinoxylan. Journal of Biological Chemistry, 2019, 294, 17339-17353.	1.6	21
42	Starch-binding domains as CBM families–history, occurrence, structure, function and evolution. Biotechnology Advances, 2019, 37, 107451.	6.0	83
43	Substrate preference of an ABC importer corresponds to selective growth on \hat{l}^2 -(1,6)-galactosides in Bifidobacterium animalis subsp. lactis. Journal of Biological Chemistry, 2019, 294, 11701-11711.	1.6	21
44	Quantitative Proteomics Analysis of Barley-Based Liquid Feed and the Effect of Protease Inhibitors and NADPH-Dependent Thioredoxin Reductase/Thioredoxin (NTR/Trx) System. Journal of Agricultural and Food Chemistry, 2019, 67, 6432-6444.	2.4	1
45	An integrated strategy for the effective production of bristle protein hydrolysate by the keratinolytic filamentous bacterium Amycolatopsis keratiniphila D2. Waste Management, 2019, 89, 94-102.	3.7	18
46	Alginate Trisaccharide Binding Sites on the Surface of $\hat{1}^2$ -Lactoglobulin Identified by NMR Spectroscopy: Implications for Molecular Network Formation. ACS Omega, 2019, 4, 6165-6174.	1.6	11
47	Dataset of the metabolic and CM-like protein fractions in old and modern wheat Italian genotypes. Data in Brief, 2019, 27, 104730.	0.5	2
48	The exopolysaccharide properties and structures database: EPS-DB. Application to bacterial exopolysaccharides. Carbohydrate Polymers, 2019, 205, 565-570.	5.1	34
49	Asp271 is critical for substrate interaction with the surface binding site in βâ€agarase a from <i>Zobellia galactanivorans</i> . Proteins: Structure, Function and Bioinformatics, 2019, 87, 34-40.	1.5	0
50	Mass-Spectrometry-Based Identification of Cross-Links in Proteins Exposed to Photo-Oxidation and Peroxyl Radicals Using 18O Labeling and Optimized Tandem Mass Spectrometry Fragmentation. Journal of Proteome Research, 2018, 17, 2017-2027.	1.8	30
51	Interaction between structurally different heteroexopolysaccharides and \hat{l}^2 -lactoglobulin studied by solution scattering and analytical ultracentrifugation. International Journal of Biological Macromolecules, 2018, 111, 746-754.	3.6	4
52	Isoenergic modification of whey protein structure by denaturation and crosslinking using transglutaminase. Food and Function, 2018, 9, 797-805.	2.1	24
53	Effect of alginate size, mannuronic/guluronic acid content and pH on particle size, thermodynamics and composition of complexes with l^2 -lactoglobulin. Food Hydrocolloids, 2018, 75, 157-163.	5.6	24
54	Plant Polyphenols Stimulate Adhesion to Intestinal Mucosa and Induce Proteome Changes in the Probiotic <i>Lactobacillus acidophilus</i> NCFM. Molecular Nutrition and Food Research, 2018, 62, 1700638.	1.5	31

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55	New Insights into the Potential of Endogenous Redox Systems in Wheat Bread Dough. Antioxidants, 2018, 7, 190.	2.2	5
56	Functional Roles of Starch Binding Domains and Surface Binding Sites in Enzymes Involved in Starch Biosynthesis. Frontiers in Plant Science, 2018, 9, 1652.	1.7	38
57	High-Throughput In Vitro Screening for Inhibitors of Cereal α-Glucosidase. Methods in Molecular Biology, 2018, 1795, 101-115.	0.4	1
58	Revealing the Dimeric Crystal and Solution Structure of β-Lactoglobulin at pH 4 and Its pH and Salt Dependent Monomer–Dimer Equilibrium. Biomacromolecules, 2018, 19, 2905-2912.	2.6	20
59	Barley Proteomics. Compendium of Plant Genomes, 2018, , 345-361.	0.3	3
60	Dietary Nutrients, Proteomes, and Adhesion of Probiotic Lactobacilli to Mucin and Host Epithelial Cells. Microorganisms, 2018, 6, 90.	1.6	35
61	An NAD ⁺ -Dependent Sirtuin Depropionylase and Deacetylase (Sir2La) from the Probiotic Bacterium <i>Lactobacillus acidophilus</i> NCFM. Biochemistry, 2018, 57, 3903-3915.	1.2	12
62	Exo―and surface proteomes of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM. Proteomics, 2017, 17, 1700019.	1.3	12
63	The starchâ€binding domain family CBM41â€"An <i>in silico</i> analysis of evolutionary relationships. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1480-1492.	1.5	18
64	Affinity Electrophoresis for Analysis of Catalytic Module-Carbohydrate Interactions. Methods in Molecular Biology, 2017, 1588, 119-127.	0.4	6
65	An Extracellular Cell-Attached Pullulanase Confers Branched α-Glucan Utilization in Human Gut Lactobacillus acidophilus. Applied and Environmental Microbiology, 2017, 83, .	1.4	25
66	The structure of Lactococcus lactis thioredoxin reductase reveals molecular features of photo-oxidative damage. Scientific Reports, 2017, 7, 46282.	1.6	10
67	Mucin- and carbohydrate-stimulated adhesion and subproteome changes of the probiotic bacterium Lactobacillus acidophilus NCFM. Journal of Proteomics, 2017, 163, 102-110.	1.2	66
68	Investigation of the indigenous fungal community populating barley grains: Secretomes and xylanolytic potential. Journal of Proteomics, 2017, 169, 153-164.	1.2	9
69	Revealing the Compact Structure of Lactic Acid Bacterial Heteroexopolysaccharides by SAXS and DLS. Biomacromolecules, 2017, 18, 747-756.	2.6	11
70	Comparative proteomics of oxidative stress response of <i>Lactobacillus acidophilus</i> NCFM reveals effects on DNA repair and cysteine <i>de novo</i> synthesis. Proteomics, 2017, 17, 1600178.	1.3	35
71	Discovery of \hat{l}_{\pm} -l-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. Journal of Biological Chemistry, 2017, 292, 21092-21101.	1.6	8
72	The Reducing Capacity of Thioredoxin on Oxidized Thiols in Boiled Wort. Journal of Agricultural and Food Chemistry, 2017, 65, 10101-10106.	2.4	2

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73	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.	5.1	14
74	Unrestricted Mass Spectrometric Data Analysis for Identification, Localization, and Quantification of Oxidative Protein Modifications. Journal of Proteome Research, 2017, 16, 3978-3988.	1.8	20
75	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.	0.5	2
76	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. Scientific Reports, 2017, 7, 16483.	1.6	51
77	GH62 arabinofuranosidases: Structure, function and applications. Biotechnology Advances, 2017, 35, 792-804.	6.0	64
78	Functional and structural characterization of plastidic starch phosphorylase during barley endosperm development. PLoS ONE, 2017, 12, e0175488.	1.1	33
79	Development of novel monoclonal antibodies against starch and ulvan - implications for antibody production against polysaccharides with limited immunogenicity. Scientific Reports, 2017, 7, 9326.	1.6	18
80	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
81	Using Carbohydrate Interaction Assays to Reveal Novel Binding Sites in Carbohydrate Active Enzymes. PLoS ONE, 2016, 11, e0160112.	1.1	22
82	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.	1.3	29
83	Plant αâ€glucan phosphatases SEX4 and LSF2 display different affinity for amylopectin and amylose. FEBS Letters, 2016, 590, 118-128.	1.3	18
84	Exploring the Plant–Microbe Interface by Profiling the Surface-Associated Proteins of Barley Grains. Journal of Proteome Research, 2016, 15, 1151-1167.	1.8	14
85	Barley germination: Spatio-temporal considerations for designing and interpreting â€~omics' experiments. Journal of Cereal Science, 2016, 70, 29-37.	1.8	21
86	Structure and function of α-glucan debranching enzymes. Cellular and Molecular Life Sciences, 2016, 73, 2619-2641.	2.4	68
87	Iminosugar inhibitors of carbohydrate-active enzymes that underpin cereal grain germination and endosperm metabolism. Biochemical Society Transactions, 2016, 44, 159-165.	1.6	8
88	Structural biology of starch-degrading enzymes and their regulation. Current Opinion in Structural Biology, 2016, 40, 33-42.	2.6	35
89	An ATP Binding Cassette Transporter Mediates the Uptake of \hat{i}_{\pm} -(1,6)-Linked Dietary Oligosaccharides in Bifidobacterium and Correlates with Competitive Growth on These Substrates. Journal of Biological Chemistry, 2016, 291, 20220-20231.	1.6	54
90	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.	1.6	37

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91	Amylolytic glycoside hydrolases. Cellular and Molecular Life Sciences, 2016, 73, 2601-2602.	2.4	6
92	An efficient arabinoxylan-debranching \hat{l}_{\pm} -l-arabinofuranosidase of family GH62 from Aspergillus nidulans contains a secondary carbohydrate binding site. Applied Microbiology and Biotechnology, 2016, 100, 6265-6277.	1.7	23
93	Seed thioredoxin h. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 974-982.	1.1	20
94	Proteolytic Degradation of Bovine Submaxillary Mucin (BSM) and Its Impact on Adsorption and Lubrication at a Hydrophobic Surface. Langmuir, 2015, 31, 8303-8309.	1.6	20
95	The GH5 $1,4-\hat{l}^2$ -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
96	The Differential Proteome of the Probiotic $\langle i \rangle$ Lactobacillus acidophilus $\langle i \rangle$ NCFM Grown on the Potential Prebiotic Cellobiose Shows Upregulation of Two $\langle i \rangle$ $\hat{l}^2 \langle i \rangle$ -Glycoside Hydrolases. BioMed Research International, 2015, 2015, 1-9.	0.9	11
97	Analysis of Surface Binding Sites (SBS) within GH62, GH13, and GH77. Journal of Applied Glycoscience (1999), 2015, 62, 87-93.	0.3	8
98	Serological assessment of neutrophil elastase activity on elastin during lung ECM remodeling. BMC Pulmonary Medicine, 2015, 15, 53.	0.8	40
99	A Simplified Chromatographic Approach to Purify Commercially Available Bovine Submaxillary Mucins (BSM). Preparative Biochemistry and Biotechnology, 2015, 45, 84-99.	1.0	16
100	Lactococcus lactisThioredoxin Reductase Is Sensitive to Light Inactivation. Biochemistry, 2015, 54, 1628-1637.	1.2	6
101	Surface binding sites in amylase have distinct roles in recognition of starch structure motifs and degradation. International Journal of Biological Macromolecules, 2015, 75, 338-345.	3.6	59
102	Oligosaccharide and Substrate Binding in the Starch Debranching Enzyme Barley Limit Dextrinase. Journal of Molecular Biology, 2015, 427, 1263-1277.	2.0	33
103	A redox-dependent dimerization switch regulates activity and tolerance for reactive oxygen species of barley seed glutathione peroxidase. Plant Physiology and Biochemistry, 2015, 90, 58-63.	2.8	3
104	Complementing DIGE proteomics and DNA subarray analyses to shed light on Oenococcus oeni adaptation to ethanol in wine-simulated conditions. Journal of Proteomics, 2015, 123, 114-127.	1.2	36
105	Two Lactococcus lactis thioredoxin paralogues play different roles in responses to arsenate and oxidative stress. Microbiology (United Kingdom), 2015, 161, 528-538.	0.7	6
106	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.	1.6	21
107	Barley Grain Proteins. , 2014, , 123-168.		4
108	The Role of Extracellular Matrix Quality in Pulmonary Fibrosis. Respiration, 2014, 88, 487-499.	1.2	36

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109	Selectivity of the surface binding site (SBS) on barley starch synthase I. Biologia (Poland), 2014, 69, 1118-1121.	0.8	10
110	\hat{l}_{\pm} -Amylase: an enzyme specificity found in various families of glycoside hydrolases. Cellular and Molecular Life Sciences, 2014, 71, 1149-1170.	2.4	272
111	A novel twist on molecular interactions between thioredoxin and nicotinamide adenine dinucleotide phosphateâ€dependent thioredoxin reductase. Proteins: Structure, Function and Bioinformatics, 2014, 82, 607-619.	1.5	8
112	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.	1.2	35
113	Lactococcus lactis TrxD represents a subgroup of thioredoxins prevalent in Gram-positive bacteria containing WCXDC active site motifs. Archives of Biochemistry and Biophysics, 2014, 564, 164-172.	1.4	7
114	Recent insight in α-glucan metabolism in probiotic bacteria. Biologia (Poland), 2014, 69, 713-721.	0.8	19
115	Analysis of surface binding sites (SBSs) in carbohydrate active enzymes with focus on glycoside hydrolase families 13 and 77 $\hat{a} \in \mathbb{Z}$ a mini-review. Biologia (Poland), 2014, 69, 705-712.	0.8	55
116	Distinct substrate specificities of three glycoside hydrolase family 42 Â-galactosidases from Bifidobacterium longum subsp. infantis ATCC 15697. Glycobiology, 2014, 24, 208-216.	1.3	40
117	Synbiotic <i>Lactobacillus acidophilus</i> NCFM and cellobiose does not affect human gut bacterial diversity but increases abundance of lactobacilli, bifidobacteria and branched-chain fatty acids: a randomized, double-blinded cross-over trial. FEMS Microbiology Ecology, 2014, 90, 225-236.	1.3	40
118	Transcriptional analysis of oligosaccharide utilization by Bifidobacterium lactisBl-04. BMC Genomics, 2013, 14, 312.	1.2	65
119	Recent insight into oligosaccharide uptake and metabolism in probiotic bacteria. Biocatalysis and Biotransformation, 2013, 31, 226-235.	1.1	23
120	Structural basis for arabinoxyloâ€oligosaccharide capture by the probiotic <i><scp>B</scp>ifidobacterium animalis</i> subsp. <i>lactis</i> â€ <scp>BI</scp> â€04. Molecular Microbiology, 2013, 90, 1100-1112.	1.2	58
121	Biochemical and kinetic characterisation of a novel xylooligosaccharide-upregulated GH43 \hat{l}^2 -d-xylosidase/ $\hat{l}\pm$ -l-arabinofuranosidase (BXA43) from the probiotic Bifidobacterium animalis subsp. lactis BB-12. AMB Express, 2013, 3, 56.	1.4	29
122	An exoproteome approach to monitor safety of a cheese-isolated Lactococcus lactis. Food Research International, 2013, 54, 1072-1079.	2.9	21
123	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.	1.1	11
124	Arabidopsis thaliana AMY3 Is a Unique Redox-regulated Chloroplastic α-Amylase. Journal of Biological Chemistry, 2013, 288, 33620-33633.	1.6	79
125	Recent development of phosphorylases possessing large potential for oligosaccharide synthesis. Current Opinion in Chemical Biology, 2013, 17, 301-309.	2.8	122
126	The barley grain thioredoxin system – an update. Frontiers in Plant Science, 2013, 4, 151.	1.7	7

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127	In vitro growth of four individual human gut bacteria on oligosaccharides produced by chemoenzymatic synthesis. Food and Function, 2013, 4, 784.	2.1	13
128	Application of proteomics for improving crop protection/artificial regulation. Frontiers in Plant Science, 2013, 4, 522.	1.7	24
129	A Bacterial Glucanotransferase Can Replace the Complex Maltose Metabolism Required for Starch to Sucrose Conversion in Leaves at Night. Journal of Biological Chemistry, 2013, 288, 28581-28598.	1.6	34
130	Comparative fermentation of insoluble carbohydrates in an in vitro human feces model spiked with <i>Lactobacillus acidophilus </i> NCFM. Starch/Staerke, 2013, 65, 346-353.	1.1	6
131	A Snapshot into the Metabolism of Isomalto-oligosaccharides in Probiotic Bacteria. Journal of Applied Glycoscience (1999), 2013, 60, 95-100.	0.3	5
132	Surface binding sites in carbohydrate active enzymes: an emerging picture of structural and functional diversity. Carbohydrate Chemistry, 2013, , 204-221.	0.3	29
133	Surface Binding Sites (SBSs), Mechanism and Regulation of Enzymes Degrading Amylopectin and \hat{l}_{\pm} -Limit Dextrins. Journal of Applied Glycoscience (1999), 2013, 60, 101-109.	0.3	1
134	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.	1.0	69
135	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
136	Raffinose family oligosaccharide utilisation by probiotic bacteria: insight into substrate recognition, molecular architecture and diversity of GH36 \hat{l}_{\pm} -galactosidases. Biocatalysis and Biotransformation, 2012, 30, 316-325.	1.1	15
137	Dissecting Molecular Interactions Involved in Recognition of Target Disulfides by the Barley Thioredoxin System. Biochemistry, 2012, 51, 9930-9939.	1.2	10
138	Inactivation of barley limit dextrinase inhibitor by thioredoxinâ€catalysed disulfide reduction. FEBS Letters, 2012, 586, 2479-2482.	1.3	15
139	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.	1.4	21
140	Binding Interactions Between α-glucans from Lactobacillus reuteri and Milk Proteins Characterised by Surface Plasmon Resonance. Food Biophysics, 2012, 7, 220-226.	1.4	15
141	Transcriptional Analysis of Prebiotic Uptake and Catabolism by Lactobacillus acidophilus NCFM. PLoS ONE, 2012, 7, e44409.	1.1	71
142	Twoâ€dimensional gelâ€based alkaline proteome of the probiotic bacterium <i><scp>L</scp>actobacillus acidophilus</i> <scp>NCFM</scp> . Proteomics, 2012, 12, 1006-1014.	1.3	7
143	Structural and physical effects of aroma compound binding to native starch granules. Starch/Staerke, 2012, 64, 461-469.	1.1	13
144	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.	1.1	10

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145	Insights into physiological traits of Bifidobacterium animalis subsp. lactis BB-12 through membrane proteome analysis. Journal of Proteomics, 2012, 75, 1190-1200.	1.2	12
146	The Effect of Selected Synbiotics on Microbial Composition and Short-Chain Fatty Acid Production in a Model System of the Human Colon. PLoS ONE, 2012, 7, e47212.	1.1	90
147	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.	1.1	46
148	Crystal Structure of α-Galactosidase from Lactobacillus acidophilus NCFM: Insight into Tetramer Formation and Substrate Binding. Journal of Molecular Biology, 2011, 412, 466-480.	2.0	63
149	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.	0.6	10
150	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.	2.2	38
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