

Birte Svensson

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/3829154/birte-svensson-publications-by-year.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.

287 papers	10,461 citations	54 h-index	87 g-index
296 ext. papers	11,410 ext. citations	5 avg, IF	6.2 L-index

#	Paper	IF	Citations
287	Improved production of gamma-cyclodextrin from high-concentrated starch using enzyme pretreatment under swelling condition.. <i>Carbohydrate Polymers</i> , 2022 , 284, 119124	10.3	1
286	How many α -amylase GH families are there in the CAZy database?. <i>Amylase</i> , 2022 , 6, 1-10	0.8	3
285	Distinct effects of different α -amylases on cross-linked tapioca starch and gel-improving mechanism. <i>Food Hydrocolloids</i> , 2022 , 128, 107580	10.6	2
284	Maltogenic α -amylase hydrolysis of wheat starch granules: Mechanism and relation to starch retrogradation. <i>Food Hydrocolloids</i> , 2022 , 124, 107256	10.6	5
283	Structure, function and enzymatic synthesis of glucosaccharides assembled mainly by α 1 \rightarrow 6 linkages - A review. <i>Carbohydrate Polymers</i> , 2022 , 275, 118705	10.3	2
282	Metabolic Profiling of Interspecies Interactions During Sessile Bacterial Cultivation Reveals Growth and Sporulation Induction in in Response to .. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022 , 12, 805473	5.9	
281	Structure, Function and Protein Engineering of Cereal-Type Inhibitors Acting on Amylolytic Enzymes.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 868568	5.6	
280	Mechanistic basis for understanding the dual activities of the bifunctional mannuronan C-5 epimerase and alginate lyase AlgE7. <i>Applied and Environmental Microbiology</i> , 2021 , AEM0183621	4.8	2
279	A healthy B. dentium caramel cocktail. <i>Journal of Biological Chemistry</i> , 2021 , 101452	5.4	3
278	Exceptionally rich keratinolytic enzyme profile found in the rare actinomycetes Amycolatopsis keratiniphila D2. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 8129-8138	5.7	1
277	Binding Sites for Oligosaccharide Repeats from Lactic Acid Bacteria Exopolysaccharides on Bovine β -Lactoglobulin Identified by NMR Spectroscopy. <i>ACS Omega</i> , 2021 , 6, 9039-9052	3.9	2
276	Quantitative Label-Free Comparison of the Metabolic Protein Fraction in Old and Modern Italian Wheat Genotypes by a Shotgun Approach. <i>Molecules</i> , 2021 , 26,	4.8	5
275	A putative novel starch-binding domain revealed by in silico analysis of the N-terminal domain in bacterial amylomaltases from the family GH77. <i>3 Biotech</i> , 2021 , 11, 229	2.8	2
274	Wheat ATIs: Characteristics and Role in Human Disease. <i>Frontiers in Nutrition</i> , 2021 , 8, 667370	6.2	12
273	Rational Enzyme Design without Structural Knowledge: A Sequence-Based Approach for Efficient Generation of Transglycosylases. <i>Chemistry - A European Journal</i> , 2021 , 27, 10323-10334	4.8	8
272	Tunable mixed micellization of β -casein in the presence of β -casein. <i>Food Hydrocolloids</i> , 2021 , 113, 106459	10.6	2
271	Enzymes in grain processing. <i>Current Opinion in Food Science</i> , 2021 , 37, 153-159	9.8	1

270	O-/N-/S-Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. <i>ACS Catalysis</i> , 2021 , 11, 1810-1815	13.1	10
269	Impact of Alginate Mannuronic-Guluronic Acid Contents and pH on Protein Binding Capacity and Complex Size. <i>Biomacromolecules</i> , 2021 , 22, 649-660	6.9	2
268	Functional diversity of three tandem C-terminal carbohydrate-binding modules of a β mannanase. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100638	5.4	3
267	Deamidation and glycation of a <i>Bacillus licheniformis</i> β amylase during industrial fermentation can improve detergent wash performance. <i>Amylase</i> , 2021 , 5, 38-49	0.8	
266	Azo dyeing of β keratin material improves microbial keratinase screening and standardization. <i>Microbial Biotechnology</i> , 2020 , 13, 984-996	6.3	5
265	Two novel S1 peptidases from <i>Amycolatopsis keratinophila</i> subsp. <i>keratinophila</i> D2 degrading keratinous slaughterhouse by-products. <i>Applied Microbiology and Biotechnology</i> , 2020 , 104, 2513-2522	5.7	4
264	Identification and Characterization of a β Acetylhexosaminidase with a Biosynthetic Activity from the Marine Bacterium S66. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	6
263	Thermophilic 4- β Glucanotransferase from Retards the Long-Term Retrogradation but Maintains the Short-Term Gelation Strength of Tapioca Starch. <i>Journal of Agricultural and Food Chemistry</i> , 2020 , 68, 5658-5667	5.7	6
262	An 1,4- β Glucosyltransferase Defines a New Maltodextrin Catabolism Scheme in <i>Lactobacillus acidophilus</i> . <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	5
261	Community-intrinsic properties enhance keratin degradation from bacterial consortia. <i>PLoS ONE</i> , 2020 , 15, e0228108	3.7	11
260	Roles of the N-terminal domain and remote substrate binding subsites in activity of the debranching barley limit dextrinase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020 , 1868, 140294	4	3
259	Qualitative proteomic comparison of metabolic and CM-like protein fractions in old and modern wheat Italian genotypes by a shotgun approach. <i>Journal of Proteomics</i> , 2020 , 211, 103530	3.9	8
258	A Single Point Mutation Converts GH84 -GlcNAc Hydrolases into Phosphorylases: Experimental and Theoretical Evidence. <i>Journal of the American Chemical Society</i> , 2020 , 142, 2120-2124	16.4	16
257	Community-intrinsic properties enhance keratin degradation from bacterial consortia 2020 , 15, e0228108		
256	Community-intrinsic properties enhance keratin degradation from bacterial consortia 2020 , 15, e0228108		
255	Community-intrinsic properties enhance keratin degradation from bacterial consortia 2020 , 15, e0228108		
254	Community-intrinsic properties enhance keratin degradation from bacterial consortia 2020 , 15, e0228108		
253	A carbohydrate-binding family 48 module enables feruloyl esterase action on polymeric arabinoxylan. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17339-17353	5.4	12

252	Starch-binding domains as CBM families-history, occurrence, structure, function and evolution. <i>Biotechnology Advances</i> , 2019 , 37, 107451	17.8	51
251	Substrate preference of an ABC importer corresponds to selective growth on β (1,6)-galactosides in subsp.. <i>Journal of Biological Chemistry</i> , 2019 , 294, 11701-11711	5.4	13
250	Quantitative Proteomics Analysis of Barley-Based Liquid Feed and the Effect of Protease Inhibitors and NADPH-Dependent Thioredoxin Reductase/Thioredoxin (NTR/Trx) System. <i>Journal of Agricultural and Food Chemistry</i> , 2019 , 67, 6432-6444	5.7	1
249	An integrated strategy for the effective production of bristle protein hydrolysate by the keratinolytic filamentous bacterium <i>Amycolatopsis keratiniphila</i> D2. <i>Waste Management</i> , 2019 , 89, 94-102	8.6	15
248	Alginate Trisaccharide Binding Sites on the Surface of β Lactoglobulin Identified by NMR Spectroscopy: Implications for Molecular Network Formation. <i>ACS Omega</i> , 2019 , 4, 6165-6174	3.9	5
247	Expanding the citrullinome of synovial fibrinogen from rheumatoid arthritis patients. <i>Journal of Proteomics</i> , 2019 , 208, 103484	3.9	11
246	Structural and functional aspects of mannuronic acid-specific PL6 alginate lyase from the human gut microbe. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17915-17930	5.4	21
245	Dataset of the metabolic and CM-like protein fractions in old and modern wheat Italian genotypes. <i>Data in Brief</i> , 2019 , 27, 104730	1.2	1
244	The exopolysaccharide properties and structures database: EPS-DB. Application to bacterial exopolysaccharides. <i>Carbohydrate Polymers</i> , 2019 , 205, 565-570	10.3	24
243	Asp271 is critical for substrate interaction with the surface binding site in β agarase a from <i>Zobellia galactanivorans</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 34-40	4.2	
242	Mass-Spectrometry-Based Identification of Cross-Links in Proteins Exposed to Photo-Oxidation and Peroxyl Radicals Using O Labeling and Optimized Tandem Mass Spectrometry Fragmentation. <i>Journal of Proteome Research</i> , 2018 , 17, 2017-2027	5.6	24
241	Interaction between structurally different heteroexopolysaccharides and β Lactoglobulin studied by solution scattering and analytical ultracentrifugation. <i>International Journal of Biological Macromolecules</i> , 2018 , 111, 746-754	7.9	4
240	Isoenergetic modification of whey protein structure by denaturation and crosslinking using transglutaminase. <i>Food and Function</i> , 2018 , 9, 797-805	6.1	15
239	Effect of alginate size, mannuronic/guluronic acid content and pH on particle size, thermodynamics and composition of complexes with β Lactoglobulin. <i>Food Hydrocolloids</i> , 2018 , 75, 157-163	10.6	11
238	Barley Proteomics. <i>Compendium of Plant Genomes</i> , 2018 , 345-361	0.8	3
237	Dietary Nutrients, Proteomes, and Adhesion of Probiotic Lactobacilli to Mucin and Host Epithelial Cells. <i>Microorganisms</i> , 2018 , 6,	4.9	20
236	An NAD-Dependent Sirtuin Depropionylase and Deacetylase (Sir2La) from the Probiotic Bacterium <i>Lactobacillus acidophilus</i> NCFM. <i>Biochemistry</i> , 2018 , 57, 3903-3915	3.2	8
235	Plant Polyphenols Stimulate Adhesion to Intestinal Mucosa and Induce Proteome Changes in the Probiotic <i>Lactobacillus acidophilus</i> NCFM. <i>Molecular Nutrition and Food Research</i> , 2018 , 62, 1700638	5.9	18

234 Proteomics of Disulphide and Cysteine Oxidoreduction **2018**, 71-97

233 New Insights into the Potential of Endogenous Redox Systems in Wheat Bread Dough. *Antioxidants*, **2018**, 7, 7.1 2

232 Functional Roles of Starch Binding Domains and Surface Binding Sites in Enzymes Involved in Starch Biosynthesis. *Frontiers in Plant Science*, **2018**, 9, 1652 6.2 14

231 High-Throughput In Vitro Screening for Inhibitors of Cereal α -Glucosidase. *Methods in Molecular Biology*, **2018**, 1795, 101-115 1.4 1

230 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 6.9 10

229 Exo- and surface proteomes of the probiotic bacterium *Lactobacillus acidophilus* NCFM. *Proteomics*, **2017**, 17, 1700019 4.8 8

228 The starch-binding domain family CBM41-An in silico analysis of evolutionary relationships. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 1480-1492 4.2 13

227 Affinity Electrophoresis for Analysis of Catalytic Module-Carbohydrate Interactions. *Methods in Molecular Biology*, **2017**, 1588, 119-127 1.4 4

226 An Extracellular Cell-Attached Pullulanase Confers Branched α -Glucan Utilization in Human Gut *Lactobacillus acidophilus*. *Applied and Environmental Microbiology*, **2017**, 83, 4.8 19

225 The structure of *Lactococcus lactis* thioredoxin reductase reveals molecular features of photo-oxidative damage. *Scientific Reports*, **2017**, 7, 46282 4.9 7

224 Mucin- and carbohydrate-stimulated adhesion and subproteome changes of the probiotic bacterium *Lactobacillus acidophilus* NCFM. *Journal of Proteomics*, **2017**, 163, 102-110 3.9 44

223 Investigation of the indigenous fungal community populating barley grains: Secretomes and xylanolytic potential. *Journal of Proteomics*, **2017**, 169, 153-164 3.9 8

222 Revealing the Compact Structure of Lactic Acid Bacterial Heteroexopolysaccharides by SAXS and DLS. *Biomacromolecules*, **2017**, 18, 747-756 6.9 9

221 Comparative proteomics of oxidative stress response of *Lactobacillus acidophilus* NCFM reveals effects on DNA repair and cysteine de novo synthesis. *Proteomics*, **2017**, 17, 1600178 4.8 19

220 Discovery of β -arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42. *Journal of Biological Chemistry*, **2017**, 292, 21092-21101 5.4 6

219 The Reducing Capacity of Thioredoxin on Oxidized Thiols in Boiled Wort. *Journal of Agricultural and Food Chemistry*, **2017**, 65, 10101-10106 5.7 0

218 Functional and structural characterization of plastidic starch phosphorylase during barley endosperm development. *PLoS ONE*, **2017**, 12, e0175488 3.7 26

217 Development of novel monoclonal antibodies against starch and ulvan - implications for antibody production against polysaccharides with limited immunogenicity. *Scientific Reports*, **2017**, 7, 9326 4.9 15

216	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	10.3	12
215	Unrestricted Mass Spectrometric Data Analysis for Identification, Localization, and Quantification of Oxidative Protein Modifications. <i>Journal of Proteome Research</i> , 2017 , 16, 3978-3988	5.6	15
214	Data regarding the growth of NCFM on different carbohydrates and recombinant production of elongation factor G and pyruvate kinase. <i>Data in Brief</i> , 2017 , 14, 118-122	1.2	2
213	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. <i>Scientific Reports</i> , 2017 , 7, 16483	4.9	35
212	GH62 arabinofuranosidases: Structure, function and applications. <i>Biotechnology Advances</i> , 2017 , 35, 792-804	4.4	36
211	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. <i>Journal of Biological Chemistry</i> , 2016 , 291, 20220-31	5.4	32
210	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, 9687-96	4	25
209	An efficient arabinoxylan-debranching β -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	5.7	18
208	Seed thioredoxin h. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016 , 1864, 974-82	4	13
207	Lytic polysaccharide monooxygenases and other oxidative enzymes are abundantly secreted by <i>Aspergillus nidulans</i> grown on different starches. <i>Biotechnology for Biofuels</i> , 2016 , 9, 187	7.8	33
206	Using Carbohydrate Interaction Assays to Reveal Novel Binding Sites in Carbohydrate Active Enzymes. <i>PLoS ONE</i> , 2016 , 11, e0160112	3.7	15
205	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, 1361-75	4.8	22
204	Plant α -glucan phosphatases SEX4 and LSF2 display different affinity for amylopectin and amylose. <i>FEBS Letters</i> , 2016 , 590, 118-28	3.8	17
203	Exploring the Plant-Microbe Interface by Profiling the Surface-Associated Proteins of Barley Grains. <i>Journal of Proteome Research</i> , 2016 , 15, 1151-67	5.6	11
202	Barley germination: Spatio-temporal considerations for designing and interpreting δ omics experiments. <i>Journal of Cereal Science</i> , 2016 , 70, 29-37	3.8	17
201	Structure and function of α -glucan debranching enzymes. <i>Cellular and Molecular Life Sciences</i> , 2016 , 73, 2619-41	10.3	51
200	Iminosugar inhibitors of carbohydrate-active enzymes that underpin cereal grain germination and endosperm metabolism. <i>Biochemical Society Transactions</i> , 2016 , 44, 159-65	5.1	6
199	Structural biology of starch-degrading enzymes and their regulation. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 33-42	8.1	25

198	Oligosaccharide and substrate binding in the starch debranching enzyme barley limit dextrinase. <i>Journal of Molecular Biology</i> , 2015 , 427, 1263-1277	6.5	25
197	A redox-dependent dimerization switch regulates activity and tolerance for reactive oxygen species of barley seed glutathione peroxidase. <i>Plant Physiology and Biochemistry</i> , 2015 , 90, 58-63	5.4	3
196	Complementing DIGE proteomics and DNA subarray analyses to shed light on <i>Oenococcus oeni</i> adaptation to ethanol in wine-simulated conditions. <i>Journal of Proteomics</i> , 2015 , 123, 114-27	3.9	25
195	Two <i>Lactococcus lactis</i> thioredoxin paralogues play different roles in responses to arsenate and oxidative stress. <i>Microbiology (United Kingdom)</i> , 2015 , 161, 528-38	2.9	6
194	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, 12614-29	5.4	16
193	Proteolytic Degradation of Bovine Submaxillary Mucin (BSM) and Its Impact on Adsorption and Lubrication at a Hydrophobic Surface. <i>Langmuir</i> , 2015 , 31, 8303-9	4	17
192	The GH5 1,4- β -mannanase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BI-04 possesses a low-affinity mannan-binding module and highlights the diversity of mannanolytic enzymes. <i>BMC Biochemistry</i> , 2015 , 16, 26	4.8	29
191	The Differential Proteome of the Probiotic <i>Lactobacillus acidophilus</i> NCFM Grown on the Potential Prebiotic Cellobiose Shows Upregulation of Two β -Glycoside Hydrolases. <i>BioMed Research International</i> , 2015 , 2015, 347216	3	8
190	Analysis of Surface Binding Sites (SBS) within GH62, GH13, and GH77. <i>Journal of Applied Glycoscience (1999)</i> , 2015 , 62, 87-93	1	5
189	Serological assessment of neutrophil elastase activity on elastin during lung ECM remodeling. <i>BMC Pulmonary Medicine</i> , 2015 , 15, 53	3.5	31
188	A simplified chromatographic approach to purify commercially available bovine submaxillary mucins (BSM). <i>Preparative Biochemistry and Biotechnology</i> , 2015 , 45, 84-99	2.4	14
187	<i>Lactococcus lactis</i> thioredoxin reductase is sensitive to light inactivation. <i>Biochemistry</i> , 2015 , 54, 1628-33	3.2	4
186	Surface binding sites in amylase have distinct roles in recognition of starch structure motifs and degradation. <i>International Journal of Biological Macromolecules</i> , 2015 , 75, 338-45	7.9	45
185	A novel twist on molecular interactions between thioredoxin and nicotinamide adenine dinucleotide phosphate-dependent thioredoxin reductase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 607-19	4.2	7
184	A β -6/ β -3 galactosidase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BI-04 gives insight into sub-specificities of β -galactoside catabolism within <i>Bifidobacterium</i> . <i>Molecular Microbiology</i> , 2014 , 94, 1024	4.1	26
183	<i>Lactococcus lactis</i> TrxD represents a subgroup of thioredoxins prevalent in Gram-positive bacteria containing WCXDC active site motifs. <i>Archives of Biochemistry and Biophysics</i> , 2014 , 564, 164-72	4.1	7
182	Recent insight in β -glucan metabolism in probiotic bacteria. <i>Biologia (Poland)</i> , 2014 , 69, 713-721	1.5	9
181	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	1.5	43

180	Distinct substrate specificities of three glycoside hydrolase family 42 β -galactosidases from <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697. <i>Glycobiology</i> , 2014 , 24, 208-16	5.8	31
179	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. <i>FEMS Microbiology Ecology</i> , 2014 , 90, 225-36	4.3	26
178	Barley Grain Proteins 2014 , 123-168		1
177	The role of extracellular matrix quality in pulmonary fibrosis. <i>Respiration</i> , 2014 , 88, 487-99	3.7	28
176	Selectivity of the surface binding site (SBS) on barley starch synthase I. <i>Biologia (Poland)</i> , 2014 , 69, 1118-1121	1.5	10
175	β -Amylase: an enzyme specificity found in various families of glycoside hydrolases. <i>Cellular and Molecular Life Sciences</i> , 2014 , 71, 1149-70	10.3	206
174	Transcriptional analysis of oligosaccharide utilization by <i>Bifidobacterium lactis</i> BL-04. <i>BMC Genomics</i> , 2013 , 14, 312	4.5	54
173	Recent insight into oligosaccharide uptake and metabolism in probiotic bacteria. <i>Biocatalysis and Biotransformation</i> , 2013 , 31, 226-235	2.5	19
172	Structural basis for arabinoxylo-oligosaccharide capture by the probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BL-04. <i>Molecular Microbiology</i> , 2013 , 90, 1100-12	4.1	48
171	Biochemical and kinetic characterisation of a novel xylooligosaccharide-upregulated GH43 β -xylosidase/ β -arabinofuranosidase (BXA43) from the probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12. <i>AMB Express</i> , 2013 , 3, 56	4.1	23
170	An exoproteome approach to monitor safety of a cheese-isolated <i>Lactococcus lactis</i> . <i>Food Research International</i> , 2013 , 54, 1072-1079	7	17
169	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, 21-8	2.9	11
168	<i>Arabidopsis thaliana</i> AMY3 is a unique redox-regulated chloroplastic β -amylase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 33620-33633	5.4	67
167	Recent development of phosphorylases possessing large potential for oligosaccharide synthesis. <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 301-9	9.7	102
166	The barley grain thioredoxin system - an update. <i>Frontiers in Plant Science</i> , 2013 , 4, 151	6.2	7
165	In vitro growth of four individual human gut bacteria on oligosaccharides produced by chemoenzymatic synthesis. <i>Food and Function</i> , 2013 , 4, 784-93	6.1	13
164	Application of proteomics for improving crop protection/artificial regulation. <i>Frontiers in Plant Science</i> , 2013 , 4, 522	6.2	18
163	A bacterial glucanotransferase can replace the complex maltose metabolism required for starch to sucrose conversion in leaves at night. <i>Journal of Biological Chemistry</i> , 2013 , 288, 28581-98	5.4	28

162	Comparative fermentation of insoluble carbohydrates in an in vitro human feces model spiked with <i>Lactobacillus acidophilus</i> NCFM. <i>Starch/Staerke</i> , 2013 , 65, 346-353	2.3	5
161	A Snapshot into the Metabolism of Isomalto-oligosaccharides in Probiotic Bacteria. <i>Journal of Applied Glycoscience</i> (1999), 2013 , 60, 95-100	1	4
160	Surface Binding Sites (SBSs), Mechanism and Regulation of Enzymes Degrading Amylopectin and Limit Dextrins. <i>Journal of Applied Glycoscience</i> (1999), 2013 , 60, 101-109	1	1
159	Surface binding sites in carbohydrate active enzymes: an emerging picture of structural and functional diversity. <i>Carbohydrate Chemistry</i> , 2013 , 204-221	3	20
158	Insights into physiological traits of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 through membrane proteome analysis. <i>Journal of Proteomics</i> , 2012 , 75, 1190-200	3.9	12
157	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, 1008-12		14
156	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	2.5	11
155	Dissecting molecular interactions involved in recognition of target disulfides by the barley thioredoxin system. <i>Biochemistry</i> , 2012 , 51, 9930-9	3.2	9
154	Inactivation of barley limit dextrinase inhibitor by thioredoxin-catalysed disulfide reduction. <i>FEBS Letters</i> , 2012 , 586, 2479-82	3.8	12
153	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	4.1	19
152	Binding Interactions Between β -glucans from <i>Lactobacillus reuteri</i> and Milk Proteins Characterised by Surface Plasmon Resonance. <i>Food Biophysics</i> , 2012 , 7, 220-226	3.2	10
151	Transcriptional analysis of prebiotic uptake and catabolism by <i>Lactobacillus acidophilus</i> NCFM. <i>PLoS ONE</i> , 2012 , 7, e44409	3.7	50
150	Two-dimensional gel-based alkaline proteome of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM. <i>Proteomics</i> , 2012 , 12, 1006-14	4.8	4
149	Structural and physical effects of aroma compound binding to native starch granules. <i>Starch/Staerke</i> , 2012 , 64, 461-469	2.3	8
148	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, 90-2	3.1	8
147	Enzymology and structure of the GH13_31 glucan 1,6- β -glucosidase that confers isomaltooligosaccharide utilization in the probiotic <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Bacteriology</i> , 2012 , 194, 4249-59	3.5	47
146	The effect of selected synbiotics on microbial composition and short-chain fatty acid production in a model system of the human colon. <i>PLoS ONE</i> , 2012 , 7, e47212	3.7	67
145	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, 1720-9	4	39

144	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, 466-80	6.5	51
143	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, 217-22	2	9
142	Starch-binding domains in the CBM45 family--low-affinity domains from glucan, water dikinase and β -amylase involved in plastidial starch metabolism. <i>FEBS Journal</i> , 2011 , 278, 1175-85	5.7	37
141	Transglycosylation by barley β -amylase 1. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2011 , 72, 229-237		7
140	Structural and evolutionary aspects of two families of non-catalytic domains present in starch and glycogen binding proteins from microbes, plants and animals. <i>Enzyme and Microbial Technology</i> , 2011 , 49, 429-40	3.8	101
139	Using Surface Plasmon Resonance Technology to Screen Interactions Between Exopolysaccharides and Milk Proteins. <i>Food Biophysics</i> , 2011 , 6, 468-473	3.2	9
138	Proteomes of the barley aleurone layer: A model system for plant signalling and protein secretion. <i>Proteomics</i> , 2011 , 11, 1595-605	4.8	39
137	The extracellular proteome of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 reveals proteins with putative roles in probiotic effects. <i>Proteomics</i> , 2011 , 11, 2503-14	4.8	56
136	Proteome reference map of <i>Lactobacillus acidophilus</i> NCFM and quantitative proteomics towards understanding the prebiotic action of lactitol. <i>Proteomics</i> , 2011 , 11, 3470-81	4.8	40
135	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, 421-9	3.9	17
134	Plant redox proteomics. <i>Journal of Proteomics</i> , 2011 , 74, 1450-62	3.9	38
133	Transcriptional and functional analysis of galactooligosaccharide uptake by <i>lacS</i> in <i>Lactobacillus acidophilus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 17785-90	11.5	82
132	<i>Aspergillus nidulans</i> α -galactosidase of glycoside hydrolase family 36 catalyses the formation of α -galacto-oligosaccharides by transglycosylation. <i>FEBS Journal</i> , 2010 , 277, 3538-51	5.7	37
131	Combined transcriptome and proteome analysis of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12 grown on xylo-oligosaccharides and a model of their utilization. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 7285-91	4.8	54
130	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, 781-7	1.9	21
129	Dynamics of starch granule biogenesis [The role of redox-regulated enzymes and low-affinity carbohydrate-binding modules. <i>Biocatalysis and Biotransformation</i> , 2010 , 28, 3-9	2.5	11
128	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, 739-50	6.5	46
127	Efficient chemoenzymatic oligosaccharide synthesis by reverse phosphorolysis using cellobiose phosphorylase and cellodextrin phosphorylase from <i>Clostridium thermocellum</i> . <i>Biochimie</i> , 2010 , 92, 1818-26	4.6	47

126	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, 112-9	2	21
125	Kinetic and thermodynamic properties of two barley thioredoxin h isozymes, HvTrxh1 and HvTrxh2. <i>FEBS Letters</i> , 2010 , 584, 3376-80	3.8	15
124	Identification of thioredoxin target disulfides in proteins released from barley aleurone layers. <i>Journal of Proteomics</i> , 2010 , 73, 1133-6	3.9	20
123	Proteomic and activity profiles of ascorbate-glutathione cycle enzymes in germinating barley embryo. <i>Phytochemistry</i> , 2010 , 71, 1650-6	4	19
122	Efficient one-pot enzymatic synthesis of alpha-(1-->4)-glucosidic disaccharides through a coupled reaction catalysed by <i>Lactobacillus acidophilus</i> NCFM maltose phosphorylase. <i>Carbohydrate Research</i> , 2010 , 345, 1061-4	2.9	18
121	New Insight into Structure/Function Relationships in Plant .ALPHA.-Amylase Family GH13 Members. <i>Journal of Applied Glycoscience (1999)</i> , 2010 , 57, 157-162	1	3
120	Chapter 15 Molecular Recognition in NADPH-Dependent Plant Thioredoxin SystemsCatalytic Mechanisms, Structural Snapshots and Target Identifications. <i>Advances in Botanical Research</i> , 2009 , 52, 461-495	2.2	4
119	From proteomics to structural studies of cytosolic/mitochondrial-type thioredoxin systems in barley seeds. <i>Molecular Plant</i> , 2009 , 2, 378-89	14.4	23
118	A CBM20 low-affinity starch-binding domain from glucan, water dikinase. <i>FEBS Letters</i> , 2009 , 583, 1159-63	3.8	37
117	Integration of the barley genetic and seed proteome maps for chromosome 1H, 2H, 3H, 5H and 7H. <i>Functional and Integrative Genomics</i> , 2009 , 9, 135-43	3.8	16
116	Structure of <i>Hordeum vulgare</i> NADPH-dependent thioredoxin reductase 2. Unwinding the reaction mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009 , 65, 932-41		16
115	The carbohydrate-binding module family 20--diversity, structure, and function. <i>FEBS Journal</i> , 2009 , 276, 5006-29	5.7	144
114	The maltodextrin transport system and metabolism in <i>Lactobacillus acidophilus</i> NCFM and production of novel alpha-glucosides through reverse phosphorolysis by maltose phosphorylase. <i>FEBS Journal</i> , 2009 , 276, 7353-65	5.7	41
113	Barley seed proteomics from spots to structures. <i>Journal of Proteomics</i> , 2009 , 72, 315-24	3.9	85
112	Two secondary carbohydrate binding sites on the surface of barley alpha-amylase 1 have distinct functions and display synergy in hydrolysis of starch granules. <i>Biochemistry</i> , 2009 , 48, 7686-97	3.2	65
111	Multi-site substrate binding and interplay in barley alpha-amylase 1. <i>FEBS Letters</i> , 2008 , 582, 2567-71	3.8	16
110	Identification of thioredoxin disulfide targets using a quantitative proteomics approach based on isotope-coded affinity tags. <i>Journal of Proteome Research</i> , 2008 , 7, 5270-6	5.6	97
109	The NADPH-dependent thioredoxin reductase/thioredoxin system in germinating barley seeds: gene expression, protein profiles, and interactions between isoforms of thioredoxin h and thioredoxin reductase. <i>Plant Physiology</i> , 2008 , 146, 789-99	6.6	60

108	Small angle X-ray studies reveal that <i>Aspergillus niger</i> glucoamylase has a defined extended conformation and can form dimers in solution. <i>Journal of Biological Chemistry</i> , 2008 , 283, 14772-80	5.4	16
107	Crystal structures of barley thioredoxin h isoforms HvTrxh1 and HvTrxh2 reveal features involved in protein recognition and possibly in discriminating the isoform specificity. <i>Protein Science</i> , 2008 , 17, 1015-24	6.3	26
106	An enzyme family reunion: similarities, differences and eccentricities in actions on β -glucans. <i>Biologia (Poland)</i> , 2008 , 63, 967-979	1.5	6
105	Spatio-temporal changes in germination and radical elongation of barley seeds tracked by proteome analysis of dissected embryo, aleurone layer, and endosperm tissues. <i>Proteomics</i> , 2007 , 7, 4528-40	4.8	65
104	Spatio-temporal profiling and degradation of alpha-amylase isozymes during barley seed germination. <i>FEBS Journal</i> , 2007 , 274, 2552-65	5.7	38
103	The 'pair of sugar tongs' site on the non-catalytic domain C of barley alpha-amylase participates in substrate binding and activity. <i>FEBS Journal</i> , 2007 , 274, 5055-67	5.7	56
102	Barley peroxidase isozymes. <i>International Journal of Mass Spectrometry</i> , 2007 , 268, 244-253	1.9	33
101	A remote but significant sequence homology between glycoside hydrolase clan GH-H and family GH31. <i>FEBS Letters</i> , 2007 , 581, 1261-8	3.8	38
100	Structural basis for target protein recognition by the protein disulfide reductase thioredoxin. <i>Structure</i> , 2006 , 14, 1701-10	5.2	87
99	Proteinaceous inhibitors of carbohydrate-active enzymes in cereals: implication in agriculture, cereal processing and nutrition. <i>Journal of the Science of Food and Agriculture</i> , 2006 , 86, 1573-1586	4.3	33
98	Production of enzymatically active recombinant full-length barley high pI alpha-glucosidase of glycoside family 31 by high cell-density fermentation of <i>Pichia pastoris</i> and affinity purification. <i>Protein Expression and Purification</i> , 2006 , 46, 56-63	2	20
97	Mapping of barley alpha-amylases and outer subsite mutants reveals dynamic high-affinity subsites and barriers in the long substrate binding cleft. <i>FEBS Letters</i> , 2006 , 580, 5049-53	3.8	22
96	Differential appearance of isoforms and cultivar variation in protein temporal profiles revealed in the maturing barley grain proteome. <i>Plant Science</i> , 2006 , 170, 808-821	5.3	53
95	The activity of barley alpha-amylase on starch granules is enhanced by fusion of a starch binding domain from <i>Aspergillus niger</i> glucoamylase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006 , 1764, 275-84	4	37
94	Interactions between Barley .ALPHA.-Amylases, Substrates, Inhibitors and Regulatory Proteins. <i>Journal of Applied Glycoscience (1999)</i> , 2006 , 53, 163-169	1	
93	Involvement of individual subsites and secondary substrate binding sites in multiple attack on amylose by barley alpha-amylase. <i>Biochemistry</i> , 2005 , 44, 1824-32	3.2	37
92	A new clan of CBM families based on bioinformatics of starch-binding domains from families CBM20 and CBM21. <i>FEBS Journal</i> , 2005 , 272, 5497-513	5.7	59
91	AFM Images of Complexes between Amylose and <i>Aspergillus niger</i> Glucoamylase Mutants, Native and Mutant Starch Binding Domains: A Model for the Action of Glucoamylase. <i>Starch/Staerke</i> , 2005 , 57, 1-7	2.3	43

90	Identification of thioredoxin h-reducible disulphides in proteomes by differential labelling of cysteines: insight into recognition and regulation of proteins in barley seeds by thioredoxin h. <i>Proteomics</i> , 2005 , 5, 1634-44	4.8	56
89	Biased mutagenesis in the N-terminal region by degenerate oligonucleotide gene shuffling enhances secretory expression of barley alpha-amylase 2 in yeast. <i>Protein Engineering, Design and Selection</i> , 2005 , 18, 515-26	1.9	11
88	Mutational analysis of target enzyme recognition of the beta-trefoil fold barley alpha-amylase/subtilisin inhibitor. <i>Journal of Biological Chemistry</i> , 2005 , 280, 14855-64	5.4	19
87	Oligosaccharide binding to barley alpha-amylase 1. <i>Journal of Biological Chemistry</i> , 2005 , 280, 32968-78	5.4	63
86	Tyrosine 105 and threonine 212 at outermost substrate binding subsites -6 and +4 control substrate specificity, oligosaccharide cleavage patterns, and multiple binding modes of barley alpha-amylase 1. <i>Journal of Biological Chemistry</i> , 2004 , 279, 10093-102	5.4	32
85	Two-dimensional gel electrophoresis pattern (pH 6-11) and identification of water-soluble barley seed and malt proteins by mass spectrometry. <i>Proteomics</i> , 2004 , 4, 728-42	4.8	71
84	Environmental and transgene expression effects on the barley seed proteome. <i>Phytochemistry</i> , 2004 , 65, 1619-27	4	31
83	Proteinaceous alpha-amylase inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004 , 1696, 145-56	4	116
82	Barley alpha-amylase/subtilisin inhibitor: structure, biophysics and protein engineering. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004 , 1696, 157-64	4	44
81	Cy5 maleimide labelling for sensitive detection of free thiols in native protein extracts: identification of seed proteins targeted by barley thioredoxin h isoforms. <i>Biochemical Journal</i> , 2004 , 378, 497-507	3.8	107
80	The structure of barley alpha-amylase isozyme 1 reveals a novel role of domain C in substrate recognition and binding: a pair of sugar tongs. <i>Structure</i> , 2003 , 11, 973-84	5.2	127
79	Feasibility study of a tissue-specific approach to barley proteome analysis: aleurone layer, endosperm, embryo and single seeds. <i>Journal of Cereal Science</i> , 2003 , 38, 217-227	3.8	58
78	Chemoenzymatic synthesis of branched oligo- and polysaccharides as potential substrates for starch active enzymes. <i>ChemBioChem</i> , 2003 , 4, 1307-11	3.8	12
77	Relation between domain evolution, specificity, and taxonomy of the alpha-amylase family members containing a C-terminal starch-binding domain. <i>FEBS Journal</i> , 2003 , 270, 635-45		88
76	Identification, cloning and characterization of two thioredoxin h isoforms, HvTrxh1 and HvTrxh2, from the barley seed proteome. <i>FEBS Journal</i> , 2003 , 270, 2633-43		46
75	On the mechanism of alpha-amylase. <i>FEBS Journal</i> , 2003 , 270, 3871-9		52
74	Kinetics and energetics of the binding between barley alpha-amylase/subtilisin inhibitor and barley alpha-amylase 2 analyzed by surface plasmon resonance and isothermal titration calorimetry. <i>Biochemistry</i> , 2003 , 42, 1478-87	3.2	43
73	Purification and characterization of the beta-trefoil fold protein barley alpha-amylase/subtilisin inhibitor overexpressed in Escherichia coli. <i>Protein Expression and Purification</i> , 2003 , 30, 185-93	2	17

72	Impact on Substrate Specificity of Mutational Subsite Isozyme Mimicry in Barley .ALPHA.-Amylase. <i>Journal of Applied Glycoscience</i> (1999), 2003 , 50, 143-145	1	
71	Chemoenzymatic syntheses of linear and branched hemithiomaltodextrins as potential inhibitors for starch-debranching enzymes. <i>Chemistry - A European Journal</i> , 2002 , 8, 5447-55	4.8	21
70	Expression, purification and preliminary crystallographic studies of alpha-amylase isozyme 1 from barley seeds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 683-6		7
69	Barley alpha-amylase Met53 situated at the high-affinity subsite -2 belongs to a substrate binding motif in the beta-->alpha loop 2 of the catalytic (beta/alpha)8-barrel and is critical for activity and substrate specificity. <i>FEBS Journal</i> , 2002 , 269, 5377-90		25
68	Initial proteome analysis of mature barley seeds and malt. <i>Proteomics</i> , 2002 , 2, 733-9	4.8	95
67	Proteome analysis of grain filling and seed maturation in barley. <i>Plant Physiology</i> , 2002 , 129, 1308-19	6.6	210
66	Modulation of activity and substrate binding modes by mutation of single and double subsites +1/+2 and -5/-6 of barley alpha-amylase 1. <i>FEBS Journal</i> , 2001 , 268, 6545-58		31
65	Relationship of sequence and structure to specificity in the alpha-amylase family of enzymes. <i>BBA - Proteins and Proteomics</i> , 2001 , 1546, 1-20		470
64	Modulation of the multisubstrate specificity of Thermus maltogenic amylase by truncation of the N-terminal domain and by a salt-induced shift of the monomer/dimer equilibrium. <i>Biochemistry</i> , 2001 , 40, 14182-90	3.2	39
63	Both binding sites of the starch-binding domain of Aspergillus niger glucoamylase are essential for inducing a conformational change in amylose. <i>Journal of Molecular Biology</i> , 2001 , 313, 1149-59	6.5	72
62	Specificity modulation of barley alpha-amylase through biased random mutagenesis involving a conserved tripeptide in beta --> alpha loop 7 of the catalytic (beta/alpha)(8)-barrel domain. <i>Biochemistry</i> , 2001 , 40, 12844-54	3.2	16
61	Specific inhibition of barley alpha-amylase 2 by barley alpha-amylase/subtilisin inhibitor depends on charge interactions and can be conferred to isozyme 1 by mutation. <i>FEBS Journal</i> , 2000 , 267, 1019-29		33
60	Involvement of Gln937 of Streptococcus downei GTF-I glucansucrase in transition-state stabilization. <i>FEBS Journal</i> , 2000 , 267, 4127-36		30
59	Location of repeat elements in glucansucrases of Leuconostoc and Streptococcus species. <i>FEMS Microbiology Letters</i> , 2000 , 192, 53-7	2.9	38
58	Structure, specificity and function of cyclomaltodextrinase, a multispecific enzyme of the alpha-amylase family. <i>BBA - Proteins and Proteomics</i> , 2000 , 1478, 165-85		142
57	Glucoamylase: structure/function relationships, and protein engineering. <i>BBA - Proteins and Proteomics</i> , 2000 , 1543, 275-293		147
56	Purification, enzymatic characterization, and nucleotide sequence of a high-isoelectric-point alpha-glucosidase from barley malt. <i>Plant Physiology</i> , 2000 , 123, 275-86	6.6	37
55	Identification of key amino acid residues in Neisseria polysaccharea amylosucrase. <i>FEBS Letters</i> , 2000 , 474, 33-7	3.8	42

54	Energetic and mechanistic studies of glucoamylase using molecular recognition of maltose OH groups coupled with site-directed mutagenesis. <i>Biochemistry</i> , 2000 , 39, 8585-92	3.2	15
53	Structure-function relationships in glucoamylases encoded by variant <i>Saccharomycopsis fibuligera</i> genes. <i>FEBS Journal</i> , 1999 , 264, 756-64		13
52	Isolation and characterization of the gene encoding the starch debranching enzyme limit dextrinase from germinating barley. <i>BBA - Proteins and Proteomics</i> , 1999 , 1431, 538-46		44
51	Mass spectrometric identification of a stable catalytic cysteinesulfinic acid residue in an enzymatically active chemically modified glucoamylase mutant. <i>Journal of Mass Spectrometry</i> , 1999 , 34, 952-7	2.2	3
50	Nachweis der Liganden-induzierten Bewegung der beiden Domänen von Glucoamylase G1 aus <i>Aspergillus niger</i> durch dynamische Lichtstreuung unter Verwendung heterobifunktioneller Substratanaloga. <i>Angewandte Chemie</i> , 1999 , 111, 1027-1030	3.6	1
49	Dynamic Light Scattering Evidence for a Ligand-Induced Motion between the Two Domains of Glucoamylase G1 of <i>Aspergillus niger</i> with Heterobivalent Substrate Analogues. <i>Angewandte Chemie - International Edition</i> , 1999 , 38, 974-977	16.4	13
48	Thermodynamics of reversible and irreversible unfolding and domain interactions of glucoamylase from <i>Aspergillus niger</i> studied by differential scanning and isothermal titration calorimetry. <i>Biochemistry</i> , 1999 , 38, 6300-10	3.2	28
47	Studies on Structure, Function, and Protein Engineering of Starch-Degrading Enzymes.. <i>Journal of Applied Glycoscience (1999)</i> , 1999 , 46, 49-63	1	10
46	Plant alpha-glucosidases of the glycoside hydrolase family 31. Molecular properties, substrate specificity, reaction mechanism, and comparison with family members of different origin. <i>Plant Molecular Biology</i> , 1998 , 37, 1-13	4.6	97
45	Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9 Å resolution. <i>Structure</i> , 1998 , 6, 649-59	5.2	114
44	Molecular structure of a barley alpha-amylase-inhibitor complex: implications for starch binding and catalysis. <i>Journal of Molecular Biology</i> , 1998 , 278, 205-17	6.5	160
43	Large-Scale Purification and Characterization of Barley Limit Dextrinase, a Member of the Amylase Structural Family. <i>Cereal Chemistry</i> , 1998 , 75, 473-479	2.4	23
42	Overexpression and characterization of <i>Aspergillus awamori</i> wild-type and mutant glucoamylase secreted by the methylotrophic yeast <i>Pichia pastoris</i> : comparison with wild-type recombinant glucoamylase produced using <i>Saccharomyces cerevisiae</i> and <i>Aspergillus niger</i> as hosts. <i>Protein Expression and Purification</i> , 1997 , 9, 159-70	2	40
41	Some details of the reaction mechanism of glucoamylase from <i>Aspergillus niger</i> --kinetic and structural studies on Trp52-->Phe and Trp317-->Phe mutants. <i>FEBS Journal</i> , 1997 , 250, 638-45		19
40	Domain evolution in the alpha-amylase family. <i>Journal of Molecular Evolution</i> , 1997 , 45, 322-31	3.1	131
39	Substrate binding mechanism of Glu180-->Gln, Asp176-->Asn, and wild-type glucoamylases from <i>Aspergillus niger</i> . <i>Biochemistry</i> , 1996 , 35, 15009-18	3.2	32
38	Crystallographic complexes of glucoamylase with maltooligosaccharide analogs: relationship of stereochemical distortions at the nonreducing end to the catalytic mechanism. <i>Biochemistry</i> , 1996 , 35, 8319-28	3.2	94
37	A circularly permuted alpha-amylase-type alpha/beta-barrel structure in glucan-synthesizing glucosyltransferases. <i>FEBS Letters</i> , 1996 , 378, 263-6	3.8	127

36	Overexpression, purification, and characterization of recombinant barley alpha-amylases 1 and 2 secreted by the methylotrophic yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 1996 , 8, 204-14 ²	64
35	Electrospray ionization and matrix assisted laser desorption/ionization mass spectrometry: powerful analytical tools in recombinant protein chemistry. <i>Nature Biotechnology</i> , 1996 , 14, 449-57	44.5 99
34	Thermodynamics of inhibitor binding to mutant forms of glucoamylase from <i>Aspergillus niger</i> determined by isothermal titration calorimetry. <i>Biochemistry</i> , 1995 , 34, 10153-61	3.2 48
33	Mutational analysis of the roles in catalysis and substrate recognition of arginines 54 and 305, aspartic acid 309, and tryptophan 317 located at subsites 1 and 2 in glucoamylase from <i>Aspergillus niger</i> . <i>Biochemistry</i> , 1995 , 34, 10162-9	3.2 48
32	Refined structure for the complex of D-glucosylated acarbose with glucoamylase from <i>Aspergillus awamori</i> var. X100 to 2.2 Å resolution: dual conformations for extended inhibitors bound to the active site of glucoamylase. <i>FEBS Letters</i> , 1995 , 358, 57-61	3.8 52
31	Stopped-flow kinetic studies of the reaction of barley alpha-amylase/subtilisin inhibitor and the high pI barley alpha-amylase. <i>FEBS Letters</i> , 1995 , 361, 250-4	3.8 20
30	Isozyme hybrids within the protruding third loop domain of the barley alpha-amylase (beta/alpha)8-barrel. Implication for BASI sensitivity and substrate affinity. <i>FEBS Letters</i> , 1995 , 363, 299-303	3.8 32
29	Protein engineering in the alpha-amylase family: catalytic mechanism, substrate specificity, and stability. <i>Plant Molecular Biology</i> , 1994 , 25, 141-57	4.6 344
28	Localization of an O-glycosylated site in the recombinant barley alpha-amylase 1 produced in yeast and correction of the amino acid sequence using matrix-assisted laser desorption/ionization mass spectrometry of peptide mixtures. <i>Biological Mass Spectrometry</i> , 1994 , 23, 547-54	16
27	Thermodynamics of ligand binding to the starch-binding domain of glucoamylase from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 1994 , 225, 133-41	43
26	Domain B protruding at the third beta strand of the alpha/beta barrel in barley alpha-amylase confers distinct isozyme-specific properties. <i>FEBS Journal</i> , 1994 , 221, 277-84	40
25	NMR spectroscopy of exchangeable protons of glucoamylase and of complexes with inhibitors in the 9-15-ppm range. <i>FEBS Journal</i> , 1994 , 223, 293-302	11
24	Production of active, insect-specific scorpion neurotoxin in yeast. <i>FEBS Journal</i> , 1994 , 223, 637-45	29
23	Thermodynamics of inhibitor binding to the catalytic site of glucoamylase from <i>Aspergillus niger</i> determined by displacement titration calorimetry. <i>Biochemistry</i> , 1994 , 33, 10191-9	3.2 73
22	Crystal and molecular structure of barley alpha-amylase. <i>Journal of Molecular Biology</i> , 1994 , 239, 104-216.5	210
21	Site-directed mutagenesis of the catalytic base glutamic acid 400 in glucoamylase from <i>Aspergillus niger</i> and of tyrosine 48 and glutamine 401, both hydrogen-bonded to the gamma-carboxylate group of glutamic acid 400. <i>Biochemistry</i> , 1994 , 33, 13808-16	3.2 84
20	Reaction mechanisms of Trp120-->Phe and wild-type glucoamylases from <i>Aspergillus niger</i> . Interactions with maltooligosaccharides and acarbose. <i>Biochemistry</i> , 1993 , 32, 9686-93	3.2 54
19	Amylases: structure and function. <i>Carbohydrate Polymers</i> , 1993 , 21, 137-146	10.3 26

18	Starch- and glycogen-debranching and branching enzymes: prediction of structural features of the catalytic (beta/alpha)8-barrel domain and evolutionary relationship to other amylolytic enzymes. <i>The Protein Journal</i> , 1993 , 12, 791-805		233
17	Electrospray mass spectrometry characterization of post-translational modifications of barley alpha-amylase 1 produced in yeast. <i>Nature Biotechnology</i> , 1993 , 11, 1162-5	44.5	18
16	Barley malt-alpha-amylase. Purification, action pattern, and subsite mapping of isozyme 1 and two members of the isozyme 2 subfamily using p-nitrophenylated maltooligosaccharide substrates. <i>BBA - Proteins and Proteomics</i> , 1992 , 1159, 193-202		73
15	Stopped-flow fluorescence and steady-state kinetic studies of ligand-binding reactions of glucoamylase from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 1992 , 209, 777-84		40
14	Structure/Function Relationships in Starch-Hydrolases and Related Enzymes.. <i>Journal of the Japanese Society of Starch Science</i> , 1991 , 38, 125-135		12
13	Identification of carboxylic acid residues in glucoamylase G2 from <i>Aspergillus niger</i> that participate in catalysis and substrate binding. <i>FEBS Journal</i> , 1990 , 188, 29-38		47
12	Expression of cDNAs encoding barley alpha-amylase 1 and 2 in yeast and characterization of the secreted proteins. <i>Gene</i> , 1990 , 94, 173-9	3.8	73
11	Catalytic mechanism of fungal glucoamylase as defined by mutagenesis of Asp176, Glu179 and Glu180 in the enzyme from <i>Aspergillus awamori</i> . <i>Protein Engineering, Design and Selection</i> , 1990 , 3, 193-8	1.9	95
10	Regional distant sequence homology between amylases, alpha-glucosidases and transglucanosylases. <i>FEBS Letters</i> , 1988 , 230, 72-6	3.8	128
9	Identification of tryptophanyl residues involved in binding of carbohydrate ligands to barley amylase 2. <i>Carlsberg Research Communications</i> , 1987 , 52, 373-379		45
8	Characterization of a glucoamylase G2 from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 1986 , 154, 497-502		110
7	Partial amino acid sequences of amylase isozymes from barley malt. <i>Carlsberg Research Communications</i> , 1985 , 50, 15-22		55
6	The role of tryptophanyl residues in the function of <i>Aspergillus niger</i> glucoamylase G1 and G2. <i>Carlsberg Research Communications</i> , 1984 , 49, 111-122		70
5	The complete amino acid sequence of the glycoprotein, glucoamylase G1, from <i>Aspergillus niger</i> . <i>Carlsberg Research Communications</i> , 1983 , 48, 529-544		176
4	Characterization of two forms of glucoamylase from <i>aspergillus niger</i> . <i>Carlsberg Research Communications</i> , 1982 , 47, 55-69		145
3	Inhibition of collagenase from <i>Achromobacter iophagus</i> by synthetic peptides. <i>FEBS Journal</i> , 1975 , 60, 423-5		7
2	Rational Enzyme Design Without Structural Knowledge: A Sequence-Based Approach for Efficient Generation of Glycosylation Catalysts		4
1	Intracellular Hydrolysis of Peptides. <i>Novartis Foundation Symposium</i> , 177-198		

