

# Birte Svensson

## List of Publications by Citations

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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	Relationship of sequence and structure to specificity in the alpha-amylase family of enzymes. <i>BBA - Proteins and Proteomics</i> , <b>2001</b> , 1546, 1-20		470
286	Protein engineering in the alpha-amylase family: catalytic mechanism, substrate specificity, and stability. <i>Plant Molecular Biology</i> , <b>1994</b> , 25, 141-57	4.6	344
285	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> , <b>1993</b> , 12, 791-805		233
284	Proteome analysis of grain filling and seed maturation in barley. <i>Plant Physiology</i> , <b>2002</b> , 129, 1308-19	6.6	210
283	Crystal and molecular structure of barley alpha-amylase. <i>Journal of Molecular Biology</i> , <b>1994</b> , 239, 104-21	6.5	210
282	Alpha-amylase: an enzyme specificity found in various families of glycoside hydrolases. <i>Cellular and Molecular Life Sciences</i> , <b>2014</b> , 71, 1149-70	10.3	206
281	The complete amino acid sequence of the glycoprotein, glucoamylase G1, from <i>Aspergillus niger</i> . <i>Carlsberg Research Communications</i> , <b>1983</b> , 48, 529-544		176
280	Molecular structure of a barley alpha-amylase-inhibitor complex: implications for starch binding and catalysis. <i>Journal of Molecular Biology</i> , <b>1998</b> , 278, 205-17	6.5	160
279	Glucoamylase: structure/function relationships, and protein engineering. <i>BBA - Proteins and Proteomics</i> , <b>2000</b> , 1543, 275-293		147
278	Characterization of two forms of glucoamylase from <i>aspergillus niger</i> . <i>Carlsberg Research Communications</i> , <b>1982</b> , 47, 55-69		145
277	The carbohydrate-binding module family 20--diversity, structure, and function. <i>FEBS Journal</i> , <b>2009</b> , 276, 5006-29	5.7	144
276	Structure, specificity and function of cyclomaltodextrinase, a multispecific enzyme of the alpha-amylase family. <i>BBA - Proteins and Proteomics</i> , <b>2000</b> , 1478, 165-85		142
275	Domain evolution in the alpha-amylase family. <i>Journal of Molecular Evolution</i> , <b>1997</b> , 45, 322-31	3.1	131
274	Regional distant sequence homology between amylases, alpha-glucosidases and transglucanases. <i>FEBS Letters</i> , <b>1988</b> , 230, 72-6	3.8	128
273	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> , <b>2003</b> , 11, 973-84	5.2	127
272	A circularly permuted alpha-amylase-type alpha/beta-barrel structure in glucan-synthesizing glucosyltransferases. <i>FEBS Letters</i> , <b>1996</b> , 378, 263-6	3.8	127
271	Proteinaceous alpha-amylase inhibitors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2004</b> , 1696, 145-56	4	116

270	Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9 Å resolution. <i>Structure</i> , <b>1998</b> , 6, 649-59	5.2	114
269	Characterization of a glucoamylase G2 from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , <b>1986</b> , 154, 497-502		110
268	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> , <b>2004</b> , 378, 497-507	3.8	107
267	Recent development of phosphorylases possessing large potential for oligosaccharide synthesis. <i>Current Opinion in Chemical Biology</i> , <b>2013</b> , 17, 301-9	9.7	102
266	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> , <b>2011</b> , 49, 429-40	3.8	101
265	Electrospray ionization and matrix assisted laser desorption/ionization mass spectrometry: powerful analytical tools in recombinant protein chemistry. <i>Nature Biotechnology</i> , <b>1996</b> , 14, 449-57	44.5	99
264	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> , <b>1998</b> , 37, 1-13	4.6	97
263	Identification of thioredoxin disulfide targets using a quantitative proteomics approach based on isotope-coded affinity tags. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 5270-6	5.6	97
262	Initial proteome analysis of mature barley seeds and malt. <i>Proteomics</i> , <b>2002</b> , 2, 733-9	4.8	95
261	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> , <b>1990</b> , 3, 193-8 <sup>1.9</sup>		95
260	Crystallographic complexes of glucoamylase with maltooligosaccharide analogs: relationship of stereochemical distortions at the nonreducing end to the catalytic mechanism. <i>Biochemistry</i> , <b>1996</b> , 35, 8319-28	3.2	94
259	Relation between domain evolution, specificity, and taxonomy of the alpha-amylase family members containing a C-terminal starch-binding domain. <i>FEBS Journal</i> , <b>2003</b> , 270, 635-45		88
258	Structural basis for target protein recognition by the protein disulfide reductase thioredoxin. <i>Structure</i> , <b>2006</b> , 14, 1701-10	5.2	87
257	Barley seed proteomics from spots to structures. <i>Journal of Proteomics</i> , <b>2009</b> , 72, 315-24	3.9	85
256	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> , <b>1994</b> , 33, 13808-16	3.2	84
255	Transcriptional and functional analysis of galactooligosaccharide uptake by lacS in <i>Lactobacillus acidophilus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 17785-90	11.5	82
254	Thermodynamics of inhibitor binding to the catalytic site of glucoamylase from <i>Aspergillus niger</i> determined by displacement titration calorimetry. <i>Biochemistry</i> , <b>1994</b> , 33, 10191-9	3.2	73
253	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> , <b>1992</b> , 1159, 193-202		73

252	Expression of cDNAs encoding barley alpha-amylase 1 and 2 in yeast and characterization of the secreted proteins. <i>Gene</i> , <b>1990</b> , 94, 173-9	3.8	73
251	Both binding sites of the starch-binding domain of <i>Aspergillus niger</i> glucoamylase are essential for inducing a conformational change in amylose. <i>Journal of Molecular Biology</i> , <b>2001</b> , 313, 1149-59	6.5	72
250	Two-dimensional gel electrophoresis pattern (pH 6-11) and identification of water-soluble barley seed and malt proteins by mass spectrometry. <i>Proteomics</i> , <b>2004</b> , 4, 728-42	4.8	71
249	The role of tryptophanyl residues in the function of <i>Aspergillus niger</i> glucoamylase G1 and G2. <i>Carlsberg Research Communications</i> , <b>1984</b> , 49, 111-122		70
248	<i>Arabidopsis thaliana</i> AMY3 is a unique redox-regulated chloroplastic $\alpha$ -amylase. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 33620-33633	5.4	67
247	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> , <b>2012</b> , 7, e47212	3.7	67
246	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> , <b>2009</b> , 48, 7686-97	3.2	65
245	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> , <b>2007</b> , 7, 4528-40	4.8	65
244	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> , <b>1996</b> , 8, 204-14 <sup>2</sup>		64
243	Oligosaccharide binding to barley alpha-amylase 1. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 32968-78	5.4	63
242	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> , <b>2008</b> , 146, 789-99	6.6	60
241	A new clan of CBM families based on bioinformatics of starch-binding domains from families CBM20 and CBM21. <i>FEBS Journal</i> , <b>2005</b> , 272, 5497-513	5.7	59
240	Feasibility study of a tissue-specific approach to barley proteome analysis: aleurone layer, endosperm, embryo and single seeds. <i>Journal of Cereal Science</i> , <b>2003</b> , 38, 217-227	3.8	58
239	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> , <b>2011</b> , 11, 2503-14	4.8	56
238	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> , <b>2007</b> , 274, 5055-67	5.7	56
237	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> , <b>2005</b> , 5, 1634-44	4.8	56
236	Partial amino acid sequences of $\alpha$ -amylase isozymes from barley malt. <i>Carlsberg Research Communications</i> , <b>1985</b> , 50, 15-22		55
235	Transcriptional analysis of oligosaccharide utilization by <i>Bifidobacterium lactis</i> BI-04. <i>BMC Genomics</i> , <b>2013</b> , 14, 312	4.5	54

234	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> , <b>2010</b> , 76, 7285-91	4.8	54
233	Reaction mechanisms of Trp120-->Phe and wild-type glucoamylases from <i>Aspergillus niger</i> . Interactions with maltooligodextrins and acarbose. <i>Biochemistry</i> , <b>1993</b> , 32, 9686-93	3.2	54
232	Differential appearance of isoforms and cultivar variation in protein temporal profiles revealed in the maturing barley grain proteome. <i>Plant Science</i> , <b>2006</b> , 170, 808-821	5.3	53
231	On the mechanism of alpha-amylase. <i>FEBS Journal</i> , <b>2003</b> , 270, 3871-9		52
230	Refined structure for the complex of D-glucosyl-di-hydroacarbose 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> , <b>1995</b> , 358, 57-61	3.8	52
229	Starch-binding domains as CBM families-history, occurrence, structure, function and evolution. <i>Biotechnology Advances</i> , <b>2019</b> , 37, 107451	17.8	51
228	Crystal structure of $\alpha$ -galactosidase from <i>Lactobacillus acidophilus</i> NCFM: insight into tetramer formation and substrate binding. <i>Journal of Molecular Biology</i> , <b>2011</b> , 412, 466-80	6.5	51
227	Structure and function of $\alpha$ -glucan debranching enzymes. <i>Cellular and Molecular Life Sciences</i> , <b>2016</b> , 73, 2619-41	10.3	51
226	Transcriptional analysis of prebiotic uptake and catabolism by <i>Lactobacillus acidophilus</i> NCFM. <i>PLoS ONE</i> , <b>2012</b> , 7, e44409	3.7	50
225	Structural basis for arabinoxyloligosaccharide capture by the probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BI-04. <i>Molecular Microbiology</i> , <b>2013</b> , 90, 1100-12	4.1	48
224	Thermodynamics of inhibitor binding to mutant forms of glucoamylase from <i>Aspergillus niger</i> determined by isothermal titration calorimetry. <i>Biochemistry</i> , <b>1995</b> , 34, 10153-61	3.2	48
223	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> , <b>1995</b> , 34, 10162-9	3.2	48
222	Efficient chemoenzymatic oligosaccharide synthesis by reverse phosphorylation using cellobiose phosphorylase and cellodextrin phosphorylase from <i>Clostridium thermocellum</i> . <i>Biochimie</i> , <b>2010</b> , 92, 1818-26	4.6	47
221	Enzymology and structure of the GH13_31 glucan 1,6- $\alpha$ -glucosidase that confers isomaltooligosaccharide utilization in the probiotic <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 4249-59	3.5	47
220	Identification of carboxylic acid residues in glucoamylase G2 from <i>Aspergillus niger</i> that participate in catalysis and substrate binding. <i>FEBS Journal</i> , <b>1990</b> , 188, 29-38		47
219	Crystal structure of an essential enzyme in seed starch degradation: barley limit dextrinase in complex with cyclodextrins. <i>Journal of Molecular Biology</i> , <b>2010</b> , 403, 739-50	6.5	46
218	Identification, cloning and characterization of two thioredoxin h isoforms, HvTrxh1 and HvTrxh2, from the barley seed proteome. <i>FEBS Journal</i> , <b>2003</b> , 270, 2633-43		46
217	Surface binding sites in amylase have distinct roles in recognition of starch structure motifs and degradation. <i>International Journal of Biological Macromolecules</i> , <b>2015</b> , 75, 338-45	7.9	45

216	Identification of tryptophanyl residues involved in binding of carbohydrate ligands to barley $\alpha$ -amylase 2. <i>Carlsberg Research Communications</i> , <b>1987</b> , 52, 373-379		45
215	Mucin- and carbohydrate-stimulated adhesion and subproteome changes of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Proteomics</i> , <b>2017</b> , 163, 102-110	3.9	44
214	Barley alpha-amylase/subtilisin inhibitor: structure, biophysics and protein engineering. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2004</b> , 1696, 157-64	4	44
213	Isolation and characterization of the gene encoding the starch debranching enzyme limit dextrinase from germinating barley. <i>BBA - Proteins and Proteomics</i> , <b>1999</b> , 1431, 538-46		44
212	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> , <b>2014</b> , 69, 705-712	1.5	43
211	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> , <b>2003</b> , 42, 1478-87	3.2	43
210	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> , <b>2005</b> , 57, 1-7	2.3	43
209	Thermodynamics of ligand binding to the starch-binding domain of glucoamylase from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , <b>1994</b> , 225, 133-41		43
208	Identification of key amino acid residues in <i>Neisseria polysaccharea</i> amylosucrase. <i>FEBS Letters</i> , <b>2000</b> , 474, 33-7	3.8	42
207	The maltodextrin transport system and metabolism in <i>Lactobacillus acidophilus</i> NCFM and production of novel alpha-glucosides through reverse phosphorylation by maltose phosphorylase. <i>FEBS Journal</i> , <b>2009</b> , 276, 7353-65	5.7	41
206	Proteome reference map of <i>Lactobacillus acidophilus</i> NCFM and quantitative proteomics towards understanding the prebiotic action of lactitol. <i>Proteomics</i> , <b>2011</b> , 11, 3470-81	4.8	40
205	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> , <b>2007</b> , 5, 158-70	2	40
204	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> , <b>1994</b> , 221, 277-84		40
203	Stopped-flow fluorescence and steady-state kinetic studies of ligand-binding reactions of glucoamylase from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , <b>1992</b> , 209, 777-84		40
202	Recombinant production and characterisation of two related GH5 endo- $\alpha$ 1,4-mannanases from <i>Aspergillus nidulans</i> FGSC A4 showing distinctly different transglycosylation capacity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2011</b> , 1814, 1720-9	4	39
201	Proteomes of the barley aleurone layer: A model system for plant signalling and protein secretion. <i>Proteomics</i> , <b>2011</b> , 11, 1595-605	4.8	39
200	Modulation of the multisubstrate specificity of <i>Thermus maltogenic</i> amylase by truncation of the N-terminal domain and by a salt-induced shift of the monomer/dimer equilibrium. <i>Biochemistry</i> , <b>2001</b> , 40, 14182-90	3.2	39
199	Plant redox proteomics. <i>Journal of Proteomics</i> , <b>2011</b> , 74, 1450-62	3.9	38



198	Spatio-temporal profiling and degradation of alpha-amylase isozymes during barley seed germination. <i>FEBS Journal</i> , <b>2007</b> , 274, 2552-65	5.7	38
197	A remote but significant sequence homology between glycoside hydrolase clan GH-H and family GH31. <i>FEBS Letters</i> , <b>2007</b> , 581, 1261-8	3.8	38
196	Location of repeat elements in glucanases of <i>Leuconostoc</i> and <i>Streptococcus</i> species. <i>FEMS Microbiology Letters</i> , <b>2000</b> , 192, 53-7	2.9	38
195	Starch-binding domains in the CBM45 family--low-affinity domains from glucan, water dikinase and <del>amylase</del> amylase involved in plastidial starch metabolism. <i>FEBS Journal</i> , <b>2011</b> , 278, 1175-85	5.7	37
194	<i>Aspergillus nidulans</i> alpha-galactosidase of glycoside hydrolase family 36 catalyses the formation of alpha-galacto-oligosaccharides by transglycosylation. <i>FEBS Journal</i> , <b>2010</b> , 277, 3538-51	5.7	37
193	A CBM20 low-affinity starch-binding domain from glucan, water dikinase. <i>FEBS Letters</i> , <b>2009</b> , 583, 1159-63	3.8	37
192	Involvement of individual subsites and secondary substrate binding sites in multiple attack on amylose by barley alpha-amylase. <i>Biochemistry</i> , <b>2005</b> , 44, 1824-32	3.2	37
191	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> , <b>2006</b> , 1764, 275-84	4	37
190	Purification, enzymatic characterization, and nucleotide sequence of a high-isoelectric-point alpha-glucosidase from barley malt. <i>Plant Physiology</i> , <b>2000</b> , 123, 275-86	6.6	37
189	GH62 arabinofuranosidases: Structure, function and applications. <i>Biotechnology Advances</i> , <b>2017</b> , 35, 792-804	6.0	36
188	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. <i>Scientific Reports</i> , <b>2017</b> , 7, 16483	4.9	35
187	Barley peroxidase isozymes. <i>International Journal of Mass Spectrometry</i> , <b>2007</b> , 268, 244-253	1.9	33
186	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> , <b>2006</b> , 86, 1573-1586	4.3	33
185	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> , <b>2000</b> , 267, 1019-29		33
184	Lytic polysaccharide monooxygenases and other oxidative enzymes are abundantly secreted by <i>Aspergillus nidulans</i> grown on different starches. <i>Biotechnology for Biofuels</i> , <b>2016</b> , 9, 187	7.8	33
183	An ATP Binding Cassette Transporter Mediates the Uptake of $\beta(1,6)$ -Linked Dietary Oligosaccharides in <i>Bifidobacterium</i> and Correlates with Competitive Growth on These Substrates. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 20220-31	5.4	32
182	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> , <b>2004</b> , 279, 10093-102	5.4	32
181	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> , <b>1995</b> , 363, 299-303	3.8	32

180	Substrate binding mechanism of Glu180-->Gln, Asp176-->Asn, and wild-type glucoamylases from <i>Aspergillus niger</i> . <i>Biochemistry</i> , <b>1996</b> , 35, 15009-18	3.2	32
179	Distinct substrate specificities of three glycoside hydrolase family 42 $\beta$ -galactosidases from <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697. <i>Glycobiology</i> , <b>2014</b> , 24, 208-16	5.8	31
178	Serological assessment of neutrophil elastase activity on elastin during lung ECM remodeling. <i>BMC Pulmonary Medicine</i> , <b>2015</b> , 15, 53	3.5	31
177	Environmental and transgene expression effects on the barley seed proteome. <i>Phytochemistry</i> , <b>2004</b> , 65, 1619-27	4	31
176	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> , <b>2001</b> , 268, 6545-58		31
175	Involvement of Gln937 of <i>Streptococcus downei</i> GTF-I glucanase in transition-state stabilization. <i>FEBS Journal</i> , <b>2000</b> , 267, 4127-36		30
174	The GH5 1,4- $\beta$ -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> , <b>2015</b> , 16, 26	4.8	29
173	Production of active, insect-specific scorpion neurotoxin in yeast. <i>FEBS Journal</i> , <b>1994</b> , 223, 637-45		29
172	The role of extracellular matrix quality in pulmonary fibrosis. <i>Respiration</i> , <b>2014</b> , 88, 487-99	3.7	28
171	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> , <b>2013</b> , 288, 28581-98	5.4	28
170	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> , <b>1999</b> , 38, 6300-10	3.2	28
169	Functional and structural characterization of plastidic starch phosphorylase during barley endosperm development. <i>PLoS ONE</i> , <b>2017</b> , 12, e0175488	3.7	26
168	A $\beta$ -6/ $\beta$ -3 galactosidase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BI-04 gives insight into sub-specificities of $\beta$ -galactoside catabolism within <i>Bifidobacterium</i> . <i>Molecular Microbiology</i> , <b>2014</b> , 94, 1024	4.1	26
167	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> , <b>2014</b> , 90, 225-36	4.3	26
166	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> , <b>2008</b> , 17, 1015-24	6.3	26
165	$\alpha$ -amylases: structure and function. <i>Carbohydrate Polymers</i> , <b>1993</b> , 21, 137-146	10.3	26
164	Oligosaccharide and substrate binding in the starch debranching enzyme barley limit dextrinase. <i>Journal of Molecular Biology</i> , <b>2015</b> , 427, 1263-1277	6.5	25
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34	New Insight into Structure/Function Relationships in Plant $\alpha$ -Amylase Family GH13 Members. <i>Journal of Applied Glycoscience</i> (1999), <b>2010</b> , 57, 157-162	1	3
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31	Data regarding the growth of NCFM on different carbohydrates and recombinant production of elongation factor G and pyruvate kinase. <i>Data in Brief</i> , <b>2017</b> , 14, 118-122	1.2	2
30	Distinct effects of different $\alpha$ -amylases on cross-linked tapioca starch and gel-improving mechanism. <i>Food Hydrocolloids</i> , <b>2022</b> , 128, 107580	10.6	2
29	Mechanistic basis for understanding the dual activities of the bifunctional mannuronan C-5 epimerase and alginate lyase AlgE7. <i>Applied and Environmental Microbiology</i> , <b>2021</b> , AEM0183621	4.8	2
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