

Birte Svensson

List of Publications by Year in descending order

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288
papers

12,621
citations

22099

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39575

94
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297
all docs

297
docs citations

297
times ranked

8416
citing authors

#	ARTICLE	IF	CITATIONS
1	Relationship of sequence and structure to specificity in the $\hat{\alpha}$ -amylase family of enzymes. BBA - Proteins and Proteomics, 2001, 1546, 1-20.	2.1	554
2	Protein engineering in the β -amylase family: catalytic mechanism, substrate specificity, and stability. Plant Molecular Biology, 1994, 25, 141-157.	2.0	410
3	$\hat{\alpha}$ -Amylase: an enzyme specificity found in various families of glycoside hydrolases. Cellular and Molecular Life Sciences, 2014, 71, 1149-1170.	2.4	272
4	Starch- and glycogen-debranching and branching enzymes: Prediction of structural features of the catalytic (??)8-barrel domain and evolutionary relationship to other amylolytic enzymes. The Protein Journal, 1993, 12, 791-805.	1.1	258
5	Proteome Analysis of Grain Filling and Seed Maturation in Barley. Plant Physiology, 2002, 129, 1308-1319.	2.3	239
6	Crystal and Molecular Structure of Barley $\hat{\alpha}$ -Amylase. Journal of Molecular Biology, 1994, 239, 104-121.	2.0	236
7	The complete amino acid sequence of the glycoprotein, glucoamylase G1, from Aspergillus niger. Carlsberg Research Communications, 1983, 48, 529-544.	1.7	199
8	Molecular structure of a barley $\hat{\alpha}$ -amylase-inhibitor complex: implications for starch binding and catalysis. Journal of Molecular Biology, 1998, 278, 205-217.	2.0	177
9	Structure, specificity and function of cyclomaltodextrinase, a multispecific enzyme of the $\hat{\alpha}$ -amylase family. BBA - Proteins and Proteomics, 2000, 1478, 165-185.	2.1	175
10	Glucoamylase: structure/function relationships, and protein engineering. BBA - Proteins and Proteomics, 2000, 1543, 275-293.	2.1	170
11	The carbohydrate-binding module family " diversity, structure, and function. FEBS Journal, 2009, 276, 5006-5029.	2.2	168
12	Characterization of two forms of glucoamylase from aspergillus niger. Carlsberg Research Communications, 1982, 47, 55-69.	1.7	164
13	Domain Evolution in the $\hat{\alpha}$ -Amylase Family. Journal of Molecular Evolution, 1997, 45, 322-331.	0.8	157
14	Regional distant sequence homology between amylases, $\hat{\alpha}$ -glucosidases and transglucanoylases. FEBS Letters, 1988, 230, 72-76.	1.3	150
15	A circularly permuted $\hat{\alpha}$ -amylase-type $\hat{\alpha}/\hat{\beta}$ -barrel structure in glucan-synthesizing glucosyltransferases. FEBS Letters, 1996, 378, 263-266.	1.3	143
16	The Structure of Barley $\hat{\alpha}$ -Amylase Isozyme 1 Reveals a Novel Role of Domain C in Substrate Recognition and Binding. Structure, 2003, 11, 973-984.	1.6	142
17	Proteinaceous $\hat{\alpha}$ -amylase inhibitors. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1696, 145-156.	1.1	136
18	Barley $\hat{\alpha}$ -amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9 Å resolution. Structure, 1998, 6, 649-659.	1.6	129

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19	Characterization of a glucoamylase G2 from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 1986, 154, 497-502.	0.2	127
20	Recent development of phosphorylases possessing large potential for oligosaccharide synthesis. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 301-309.	2.8	122
21	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.	1.7	114
22	Plant alpha-glucosidases of the glycoside hydrolase family 31. Molecular properties, substrate specificity, reaction mechanism, and comparison with family members of different origin. , 1998, 37, 1-13.		112
23	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, 429-440.	1.6	112
24	Electrospray ionization and matrix assisted laser desorption/ionization mass spectrometry: Powerful analytical tools in recombinant protein chemistry. <i>Nature Biotechnology</i> , 1996, 14, 449-457.	9.4	110
25	Identification of Thioredoxin Disulfide Targets Using a Quantitative Proteomics Approach Based on Isotope-Coded Affinity Tags. <i>Journal of Proteome Research</i> , 2008, 7, 5270-5276.	1.8	109
26	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, 193-198.	1.0	108
27	Crystallographic Complexes of Glucoamylase with Maltooligosaccharide Analogs: A Relationship of Stereochemical Distortions at the Nonreducing End to the Catalytic Mechanism. <i>Biochemistry</i> , 1996, 35, 8319-8328.	1.2	102
28	Relation between domain evolution, specificity, and taxonomy of the α -amylase family members containing a C-terminal starch-binding domain. <i>FEBS Journal</i> , 2003, 270, 635-645.	0.2	102
29	Initial proteome analysis of mature barley seeds and malt. <i>Proteomics</i> , 2002, 2, 733-739.	1.3	101
30	Transcriptional and functional analysis of galactooligosaccharide uptake by <i>Lactobacillus acidophilus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17785-17790.	3.3	99
31	Barley seed proteomics from spots to structures. <i>Journal of Proteomics</i> , 2009, 72, 315-324.	1.2	94
32	Structural Basis for Target Protein Recognition by the Protein Disulfide Reductase Thioredoxin. <i>Structure</i> , 2006, 14, 1701-1710.	1.6	93
33	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.	1.1	90
34	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 γ -Carboxylate Group of Glutamic Acid 400. <i>Biochemistry</i> , 1994, 33, 13808-13816.	1.2	89
35	Starch-binding domains as CBM families: history, occurrence, structure, function and evolution. <i>Biotechnology Advances</i> , 2019, 37, 107451.	6.0	83
36	Expression of cDNAs encoding barley α -amylase 1 and 2 in yeast and characterization of the secreted proteins. <i>Gene</i> , 1990, 94, 173-179.	1.0	81

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37	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, 728-742.	1.3	81
38	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.	1.7	80
39	Barley malt- α -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.	2.1	79
40	Overexpression, Purification, and Characterization of Recombinant Barley α -Amylases 1 and 2 Secreted by the Methylophilic Yeast <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 1996, 8, 204-214.	0.6	79
41	Both binding sites of the starch-binding domain of <i>Aspergillus niger</i> glucoamylase are essential for inducing a conformational change in amylose 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 313, 1149-1159.	2.0	79
42	<i>Arabidopsis thaliana</i> AMY3 Is a Unique Redox-regulated Chloroplastic α -Amylase. <i>Journal of Biological Chemistry</i> , 2013, 288, 33620-33633.	1.6	79
43	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, 10191-10199.	1.2	77
44	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, 4528-4540.	1.3	72
45	Two Secondary Carbohydrate Binding Sites on the Surface of Barley α -Amylase 1 Have Distinct Functions and Display Synergy in Hydrolysis of Starch Granules. <i>Biochemistry</i> , 2009, 48, 7686-7697.	1.2	72
46	The NADPH-Dependent Thioredoxin Reductase/Thioredoxin System in Germinating Barley Seeds: Gene Expression, Protein Profiles, and Interactions between Isoforms of Thioredoxin <i>h</i> and Thioredoxin Reductase. <i>Plant Physiology</i> , 2008, 146, 323-324.	2.3	71
47	Transcriptional Analysis of Prebiotic Uptake and Catabolism by <i>Lactobacillus acidophilus</i> NCFM. <i>PLoS ONE</i> , 2012, 7, e44409.	1.1	71
48	Enzymology and Structure of the GH13_31 Glucan 1,6- α -Glucosidase That Confers Isomaltooligosaccharide Utilization in the Probiotic <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Bacteriology</i> , 2012, 194, 4249-4259.	1.0	69
49	Structure and function of α -glucan debranching enzymes. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2619-2641.	2.4	68
50	Oligosaccharide Binding to Barley α -Amylase 1. <i>Journal of Biological Chemistry</i> , 2005, 280, 32968-32978.	1.6	67
51	Mucin- and carbohydrate-stimulated adhesion and subproteome changes of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM. <i>Journal of Proteomics</i> , 2017, 163, 102-110.	1.2	66
52	Transcriptional analysis of oligosaccharide utilization by <i>Bifidobacterium lactis</i> BI-04. <i>BMC Genomics</i> , 2013, 14, 312.	1.2	65
53	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.	1.8	64
54	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, 7285-7291.	1.4	64

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55	GH62 arabinofuranosidases: Structure, function and applications. <i>Biotechnology Advances</i> , 2017, 35, 792-804.	6.0	64
56	Crystal Structure of Î±-Galactosidase from <i>Lactobacillus acidophilus</i> NCFM: Insight into Tetramer Formation and Substrate Binding. <i>Journal of Molecular Biology</i> , 2011, 412, 466-480.	2.0	63
57	A new clan of CBM families based on bioinformatics of starch-binding domains from families CBM20 and CBM21. <i>FEBS Journal</i> , 2005, 272, 5497-5513.	2.2	62
58	The "pair of sugar tongs" site on the non-catalytic domain C of barley Î±-amylase participates in substrate binding and activity. <i>FEBS Journal</i> , 2007, 274, 5055-5067.	2.2	61
59	Refined structure for the complex of d-gluco-dihydroacarbose 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.	1.3	60
60	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, 2503-2514.	1.3	60
61	On the mechanism of Î±-amylase. <i>FEBS Journal</i> , 2003, 270, 3871-3879.	0.2	59
62	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, 338-345.	3.6	59
63	Proteomes of the barley aleurone layer: A model system for plant signalling and protein secretion. <i>Proteomics</i> , 2011, 11, 1595-1605.	1.3	58
64	Structural basis for arabinoxylo-oligosaccharide capture by the probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BB-12. <i>Molecular Microbiology</i> , 2013, 90, 1100-1112.	1.2	58
65	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.	0.2	57
66	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, 1634-1644.	1.3	57
67	Partial amino acid sequences of Î±-amylase isozymes from barley malt. <i>Carlsberg Research Communications</i> , 1985, 50, 15-22.	1.7	56
68	Reaction mechanisms of Trp120 and Phe and wild-type glucoamylases from <i>Aspergillus niger</i> . Interactions with maltooligodextrins and acarbose. <i>Biochemistry</i> , 1993, 32, 9686-9693.	1.2	56
69	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.	1.7	56
70	Crystal Structure of an Essential Enzyme in Seed Starch Degradation: Barley Limit Dextrinase in Complex with Cyclodextrins. <i>Journal of Molecular Biology</i> , 2010, 403, 739-750.	2.0	55
71	Analysis of surface binding sites (SBSs) in carbohydrate active enzymes with focus on glycoside hydrolase families 13 and 77 - a mini-review. <i>Biologia (Poland)</i> , 2014, 69, 705-712.	0.8	55
72	Identification, cloning and characterization of two thioredoxin h isoforms, HvTrxh1 and HvTrxh2, from the barley seed proteome. <i>FEBS Journal</i> , 2003, 270, 2633-2643.	0.2	54

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73	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, 20220-20231.	1.6	54
74	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, 10162-10169.	1.2	53
75	Efficient chemoenzymatic oligosaccharide synthesis by reverse phosphorolysis using cellobiose phosphorylase and cellodextrin phosphorylase from <i>Clostridium thermocellum</i> . <i>Biochimie</i> , 2010, 92, 1818-1826.	1.3	53
76	The maltodextrin transport system and metabolism in <i>Lactobacillus acidophilus</i> NCFM and production of novel α -glucosides through reverse phosphorolysis by maltose phosphorylase. <i>FEBS Journal</i> , 2009, 276, 7353-7365.	2.2	52
77	Thermodynamics of Inhibitor Binding to Mutant Forms of Glucoamylase from <i>Aspergillus niger</i> Determined by Isothermal Titration Calorimetry. <i>Biochemistry</i> , 1995, 34, 10153-10161.	1.2	51
78	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. <i>Scientific Reports</i> , 2017, 7, 16483.	1.6	51
79	Isolation and characterization of the gene encoding the starch debranching enzyme limit dextrinase from germinating barley. <i>BBA - Proteins and Proteomics</i> , 1999, 1431, 538-546.	2.1	50
80	Barley α -amylase/subtilisin inhibitor: structure, biophysics and protein engineering. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1696, 157-164.	1.1	50
81	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.	1.1	48
82	Identification of tryptophanyl residues involved in binding of carbohydrate ligands to barley α -amylase 2. <i>Carlsberg Research Communications</i> , 1987, 52, 373-379.	1.7	47
83	Thermodynamics of Ligand Binding to the Starch-Binding Domain of Glucoamylase from <i>Aspergillus Niger</i> . <i>FEBS Journal</i> , 1994, 225, 133-141.	0.2	47
84	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, 159-170.	0.6	47
85	A CBM20 low-affinity starch-binding domain from glucan, water dikinase. <i>FEBS Letters</i> , 2009, 583, 1159-1163.	1.3	47
86	Recombinant production and characterisation of two related GH5 endo- α -1,4-mannanases from <i>Aspergillus nidulans</i> FGSC A4 showing distinctly different transglycosylation capacity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 1720-1729.	1.1	46
87	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, 777-784.	0.2	45
88	Location of repeat elements in glucan sucrases of <i>Leuconostoc</i> and <i>Streptococcus</i> species. <i>FEMS Microbiology Letters</i> , 2000, 192, 53-57.	0.7	45
89	Modulation of the Multisubstrate Specificity of <i>Thermus Maltogenic Amylase</i> by Truncation of the N-Terminal Domain and by a Salt-Induced Shift of the Monomer/Dimer Equilibrium. <i>Biochemistry</i> , 2001, 40, 14182-14190.	1.2	45
90	Kinetics and Energetics of the Binding between Barley α -Amylase/Subtilisin Inhibitor and Barley α -Amylase 2 Analyzed by Surface Plasmon Resonance and Isothermal Titration Calorimetry. <i>Biochemistry</i> , 2003, 42, 1478-1487.	1.2	45

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91	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, 277-284.	0.2	43
92	Purification, Enzymatic Characterization, and Nucleotide Sequence of a High-Isoelectric-Point Î±-Glucosidase from Barley Malt. <i>Plant Physiology</i> , 2000, 123, 275-286.	2.3	43
93	Identification of key amino acid residues in <i>Neisseria polysaccharea</i> amylase. <i>FEBS Letters</i> , 2000, 474, 33-37.	1.3	43
94	Proteome reference map of <i>Lactobacillus acidophilus</i> NCFM and quantitative proteomics towards understanding the prebiotic action of lactitol. <i>Proteomics</i> , 2011, 11, 3470-3481.	1.3	43
95	Involvement of Individual Subsites and Secondary Substrate Binding Sites in Multiple Attack on Amylose by Barley Î±-Amylase. <i>Biochemistry</i> , 2005, 44, 1824-1832.	1.2	42
96	The activity of barley Î±-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, 275-284.	1.1	42
97	Spatio-temporal profiling and degradation of Î±-amylase isozymes during barley seed germination. <i>FEBS Journal</i> , 2007, 274, 2552-2565.	2.2	42
98	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.	6.2	42
99	O/N/S-Specificity in Glycosyltransferase Catalysis: From Mechanistic Understanding to Engineering. <i>ACS Catalysis</i> , 2021, 11, 1810-1815.	5.5	42
100	Wheat ATIs: Characteristics and Role in Human Disease. <i>Frontiers in Nutrition</i> , 2021, 8, 667370.	1.6	42
101	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.	1.7	41
102	Plant redox proteomics. <i>Journal of Proteomics</i> , 2011, 74, 1450-1462.	1.2	41
103	Distinct substrate specificities of three glycoside hydrolase family 42 Î±-galactosidases from <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697. <i>Glycobiology</i> , 2014, 24, 208-216.	1.3	40
104	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, 225-236.	1.3	40
105	Serological assessment of neutrophil elastase activity on elastin during lung ECM remodeling. <i>BMC Pulmonary Medicine</i> , 2015, 15, 53.	0.8	40
106	Structural and functional aspects of mannuronic acidâ€“specific PL6 alginate lyase from the human gut microbe <i>Bacteroides cellulosilyticus</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 17915-17930.	1.6	40
107	A remote but significant sequence homology between glycoside hydrolase clan GH-H and family GH31. <i>FEBS Letters</i> , 2007, 581, 1261-1268.	1.3	39
108	Barley peroxidase isozymes. <i>International Journal of Mass Spectrometry</i> , 2007, 268, 244-253.	0.7	38

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109	<i>Aspergillus nidulans</i> Î±-galactosidase of glycoside hydrolase family 36 catalyses the formation of Î±-galactooligosaccharides by transglycosylation. FEBS Journal, 2010, 277, 3538-3551.	2.2	38
110	Starch-binding domains in the CBM45 family " low-affinity domains from glucan, water dikinase and Î±-amylase involved in plastidial starch metabolism. FEBS Journal, 2011, 278, 1175-1185.	2.2	38
111	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
112	Isozyme hybrids within the protruding third loop domain of the barley Î±-amylase (Î²/Î±)8-barrel implication for BASI sensitivity and substrate affinity. FEBS Letters, 1995, 363, 299-303.	1.3	37
113	Specific inhibition of barley Î±-amylase f2 by barley Î±-amylase/subtilisin inhibitor depends on charge interactions and can be conferred to isozyeme f1 by mutation. FEBS Journal, 2000, 267, 1019-1029.	0.2	37
114	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
115	The Role of Extracellular Matrix Quality in Pulmonary Fibrosis. Respiration, 2014, 88, 487-499.	1.2	36
116	Complementing DIGE proteomics and DNA subarray analyses to shed light on <i>Oenococcus oeni</i> adaptation to ethanol in wine-simulated conditions. Journal of Proteomics, 2015, 123, 114-127.	1.2	36
117	A Î²1â€³ galactosidase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> B l04 gives insight into substrate specificities of Î²-galactoside catabolism within <i>Bifidobacterium</i> . Molecular Microbiology, 2014, 94, 1024-1040.	1.2	35
118	The GH5 1,4-Î²-mannanase from <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Bl-04 possesses a low-affinity mannan-binding module and highlights the diversity of mannanolytic enzymes. BMC Biochemistry, 2015, 16, 26.	4.4	35
119	Structural biology of starch-degrading enzymes and their regulation. Current Opinion in Structural Biology, 2016, 40, 33-42.	2.6	35
120	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
121	Dietary Nutrients, Proteomes, and Adhesion of Probiotic Lactobacilli to Mucin and Host Epithelial Cells. Microorganisms, 2018, 6, 90.	1.6	35
122	Substrate Binding Mechanism of Glu180â†'Gln, Asp176â†'Asn, and Wild-Type Glucoamylases from <i>Aspergillus niger</i> . Biochemistry, 1996, 35, 15009-15018.	1.2	34
123	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
124	The exopolysaccharide properties and structures database: EPS-DB. Application to bacterial exopolysaccharides. Carbohydrate Polymers, 2019, 205, 565-570.	5.1	34
125	Modulation of activity and substrate binding modes by mutation of single and double subsites +1/+2 and 5/6 of barley Î±-amylase 1. FEBS Journal, 2001, 268, 6545-6558.	0.2	33
126	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 Î±-Amylase 1. Journal of Biological Chemistry, 2004, 279, 10093-10102.	1.6	33

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127	Oligosaccharide and Substrate Binding in the Starch Debranching Enzyme Barley Limit Dextrinase. <i>Journal of Molecular Biology</i> , 2015, 427, 1263-1277.	2.0	33
128	Functional and structural characterization of plastidic starch phosphorylase during barley endosperm development. <i>PLoS ONE</i> , 2017, 12, e0175488.	1.1	33
129	Environmental and transgene expression effects on the barley seed proteome. <i>Phytochemistry</i> , 2004, 65, 1619-1627.	1.4	32
130	Production of active, insect-specific scorpion neurotoxin in yeast. <i>FEBS Journal</i> , 1994, 223, 637-645.	0.2	31
131	Involvement of Gln937 of <i>Streptococcus downei</i> GTF-I glucansucrase in transition-state stabilization. <i>FEBS Journal</i> , 2000, 267, 4127-4136.	0.2	31
132	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.	1.5	31
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