

Tjaard Pijning

List of Publications by Year in descending order

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59
papers

2,597
citations

159585

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h-index

189892

50
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all docs

60
docs citations

60
times ranked

2273
citing authors

#	ARTICLE	IF	CITATIONS
1	Enzymatic glucosylation of polyphenols using glucansucrases and branching sucrases of glycoside hydrolase family 70. <i>Critical Reviews in Food Science and Nutrition</i> , 2023, 63, 5247-5267.	10.3	4
2	Mutations in Amino Acid Residues of <i>Limosilactobacillus reuteri</i> 121 GtfB 4,6- α -Glucanotransferase that Affect Reaction and Product Specificity. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 1952-1961.	5.2	3
3	Crystal Structure of Levansucrase from the Gram-Negative Bacterium <i>Brenneria</i> Provides Insights into Its Product Size Specificity. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 5095-5105.	5.2	7
4	Using Mutability Landscapes To Guide Enzyme Thermostabilization. <i>ChemBioChem</i> , 2021, 22, 170-175.	2.6	6
5	Crystal structure of an inulosucrase from <i>Halalkalicoccus jeotgali</i> B3T, a halophilic archaeal strain. <i>FEBS Journal</i> , 2021, 288, 5723-5736.	4.7	8
6	Insights into Broad-Specificity Starch Modification from the Crystal Structure of <i>Limosilactobacillus Reuteri</i> NCC 2613 4,6- α -Glucanotransferase GtfB. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 13235-13245.	5.2	14
7	Enantioselective Synthesis of Pharmaceutically Active β -Aminobutyric Acids Using a Tailor-Made Artificial Michaelase in One-Pot Cascade Reactions. <i>ACS Catalysis</i> , 2019, 9, 1503-1513.	11.2	53
8	Identification of <i>Thermotoga maritima</i> MSB8 GH57 α -amylase AmyC as a glycogen-branching enzyme with high hydrolytic activity. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 6141-6151.	3.6	12
9	Biochemical characterization of two GH70 family 4,6- α -glucanotransferases with distinct product specificity from <i>Lactobacillus aviarius</i> subsp. <i>aviarius</i> DSM 20655. <i>Food Chemistry</i> , 2018, 253, 236-246.	8.2	26
10	Biotechnological potential of novel glycoside hydrolase family 70 enzymes synthesizing α -glucans from starch and sucrose. <i>Biotechnology Advances</i> , 2018, 36, 196-207.	11.7	68
11	Mutational Analysis of the Role of the Glucansucrase Gtf180- α N Active Site Residues in Product and Linkage Specificity with Lactose as Acceptor Substrate. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 12544-12554.	5.2	6
12	Biochemical characterization of a GH70 protein from <i>Lactobacillus kunkeei</i> DSM 12361 with two catalytic domains involving branching sucrose activity. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7935-7950.	3.6	22
13	Biochemical and genetic characterization of fungal proline hydroxylase in echinocandin biosynthesis. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7877-7890.	3.6	14
14	4,3- α -Glucanotransferase, a novel reaction specificity in glycoside hydrolase family 70 and clan GH-H. <i>Scientific Reports</i> , 2017, 7, 39761.	3.3	42
15	Crystal Structure of 4,6- α -Glucanotransferase Supports Diet-Driven Evolution of GH70 Enzymes from α -Amylases in Oral Bacteria. <i>Structure</i> , 2017, 25, 231-242.	3.3	45
16	Engineering of the <i>Bacillus circulans</i> β -Galactosidase Product Specificity. <i>Biochemistry</i> , 2017, 56, 704-711.	2.5	30
17	A new group of glycoside hydrolase family 13 α -amylases with an aberrant catalytic triad. <i>Scientific Reports</i> , 2017, 7, 44230.	3.3	32
18	A general mechanism of ribosome dimerization revealed by single-particle cryo-electron microscopy. <i>Nature Communications</i> , 2017, 8, 722.	12.8	49

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19	Mining novel starch-converting Glycoside Hydrolase 70 enzymes from the Nestl� Culture Collection genome database: The <i>Lactobacillus reuteri</i> NCC 2613 GtfB. <i>Scientific Reports</i> , 2017, 7, 9947.	3.3	27
20	Characterization of the glucansucrase GTF180 W1065 mutant enzymes producing polysaccharides and oligosaccharides with altered linkage composition. <i>Food Chemistry</i> , 2017, 217, 81-90.	8.2	33
21	Biochemical Characterization of the Functional Roles of Residues in the Active Site of the β -Galactosidase from <i>Bacillus circulans</i> ATCC 31382. <i>Biochemistry</i> , 2017, 56, 3109-3118.	2.5	12
22	Structural determinants of alternating (α 1 \rightarrow 4) and (α 1 \rightarrow 6) linkage specificity in reuteransucrase of <i>Lactobacillus reuteri</i> . <i>Scientific Reports</i> , 2016, 6, 35261.	3.3	17
23	Structure-function relationships of family GH70 glucansucrase and 4,6- α -glucanotransferase enzymes, and their evolutionary relationships with family GH13 enzymes. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2681-2706.	5.4	64
24	The <i>Exiguobacterium sibiricum</i> 255-15 GtfC Enzyme Represents a Novel Glycoside Hydrolase 70 Subfamily of 4,6- α -Glucanotransferase Enzymes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 756-766.	3.1	38
25	<i>Lactobacillus reuteri</i> Strains Convert Starch and Maltodextrins into Homoexopolysaccharides Using an Extracellular and Cell-Associated 4,6- α -Glucanotransferase. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 2941-2952.	5.2	27
26	Synthesis of New Hyperbranched α -Glucans from Sucrose by <i>Lactobacillus reuteri</i> 180 Glucansucrase Mutants. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 433-442.	5.2	25
27	Truncation of domain V of the multidomain glucansucrase GTF180 of <i>Lactobacillus reuteri</i> 180 heavily impairs its polysaccharide-synthesizing ability. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5885-5894.	3.6	26
28	Biochemical Characterization of the <i>Lactobacillus reuteri</i> Glycoside Hydrolase Family 70 GTFB Type of 4,6- α -Glucanotransferase Enzymes That Synthesize Soluble Dietary Starch Fibers. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7223-7232.	3.1	54
29	Characterization of the Functional Roles of Amino Acid Residues in Acceptor-binding Subsite +1 in the Active Site of the Glucansucrase GTF180 from <i>Lactobacillus reuteri</i> 180. <i>Journal of Biological Chemistry</i> , 2015, 290, 30131-30141.	3.4	31
30	Residue Leu940 Has a Crucial Role in the Linkage and Reaction Specificity of the Glucansucrase GTF180 of the Probiotic Bacterium <i>Lactobacillus reuteri</i> 180. <i>Journal of Biological Chemistry</i> , 2014, 289, 32773-32782.	3.4	33
31	Flexibility of truncated and full-length glucansucrase GTF180 enzymes from <i>Lactobacillus reuteri</i> 180. <i>FEBS Journal</i> , 2014, 281, 2159-2171.	4.7	21
32	Improved activity and pH stability of <i>E. coli</i> ATCC 11105 penicillin acylase by error-prone PCR. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4467-4477.	3.6	17
33	4,6- α -Glucanotransferase activity occurs more widespread in <i>Lactobacillus</i> strains and constitutes a separate GH70 subfamily. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 181-193.	3.6	52
34	Glucansucrases: Three-dimensional structures, reactions, mechanism, α -glucan analysis and their implications in biotechnology and food applications. <i>Journal of Biotechnology</i> , 2013, 163, 250-272.	3.8	250
35	Improved activity and thermostability of <i>Bacillus pumilus</i> lipase by directed evolution. <i>Journal of Biotechnology</i> , 2013, 164, 123-129.	3.8	73
36	Functional and Structural Characterization of α -(1 \rightarrow 2) Branching Sucrase Derived from DSR-E Glucansucrase. <i>Journal of Biological Chemistry</i> , 2012, 287, 7915-7924.	3.4	78

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37	Glycosidic bond specificity of glucansucrases: on the role of acceptor substrate binding residues. <i>Biocatalysis and Biotransformation</i> , 2012, 30, 366-376.	2.0	53
38	The role of conserved inulosucrase residues in the reaction and product specificity of <i>Lactobacillus reuteri</i> inulosucrase. <i>FEBS Journal</i> , 2012, 279, 3612-3621.	4.7	23
39	Structure of the α -1,6/ α -1,4-specific glucansucrase GTFA from <i>Lactobacillus reuteri</i> 121. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1448-1454.	0.7	47
40	Biophysical characterization of mutants of <i>Bacillus subtilis</i> lipase evolved for thermostability: Factors contributing to increased activity retention. <i>Protein Science</i> , 2012, 21, 487-497.	7.6	49
41	Crystal Structure of Inulosucrase from <i>Lactobacillus</i> : Insights into the Substrate Specificity and Product Specificity of GH68 Fructansucrases. <i>Journal of Molecular Biology</i> , 2011, 412, 80-93.	4.2	63
42	<i>Thermus thermophilus</i> Glycoside Hydrolase Family 57 Branching Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 3520-3530.	3.4	88
43	Crystal structure of a 117 kDa glucansucrase fragment provides insight into evolution and product specificity of GH70 enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21406-21411.	7.1	140
44	Crystal Structure of the Leucine Aminopeptidase from <i>Pseudomonas putida</i> Reveals the Molecular Basis for its Enantioselectivity and Broad Substrate Specificity. <i>Journal of Molecular Biology</i> , 2010, 398, 703-714.	4.2	28
45	The crystal structure of a hyperthermoactive exopolygalacturonase from <i>Thermotoga maritima</i> reveals a unique tetramer. <i>FEBS Letters</i> , 2009, 583, 3665-3670.	2.8	27
46	A Novel Genetic Selection System for Improved Enantioselectivity of <i>Bacillus subtilis</i> Lipase A. <i>ChemBioChem</i> , 2008, 9, 1110-1115.	2.6	60
47	Loop Grafting of <i>Bacillus subtilis</i> Lipase A: Inversion of Enantioselectivity. <i>Chemistry and Biology</i> , 2008, 15, 782-789.	6.0	35
48	Biochemical and crystallographic characterization of a glucansucrase from <i>Lactobacillus reuteri</i> 180. <i>Biocatalysis and Biotransformation</i> , 2008, 26, 12-17.	2.0	31
49	A crystallographic study of Cys69Ala flavodoxin II from <i>Azotobacter vinelandii</i> : Structural determinants of redox potential. <i>Protein Science</i> , 2005, 14, 2284-2295.	7.6	48
50	Crystal Structure and Carbohydrate-binding Properties of the Human Cartilage Glycoprotein-39. <i>Journal of Biological Chemistry</i> , 2003, 278, 37753-37760.	3.4	183
51	Crystal Structure of the Copper-Containing Quercetin 2,3-Dioxygenase from <i>Aspergillus japonicus</i> . <i>Structure</i> , 2002, 10, 259-268.	3.3	216
52	The structure of the <i>Escherichia coli</i> phosphotransferase IIA _m annitol reveals a novel fold with two conformations of the active site. <i>Structure</i> , 1998, 6, 377-388.	3.3	49
53	The three-dimensional structure of the nitrogen regulatory protein IIA _{Ntr} from <i>Escherichia coli</i> 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1998, 279, 245-255.	4.2	30
54	The structure of an energy-coupling protein from bacteria, IIB _c ellobiose, reveals similarity to eukaryotic protein tyrosine phosphatases. <i>Structure</i> , 1997, 5, 217-225.	3.3	43

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55	Crystallization of Enzyme IIB of the Cellobiose-specific Phosphotransferase System of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1994, 239, 588-590.	4.2	8
56	The sinusoidal efflux of dibromosulphophthalein from rat liver is stimulated by albumin, ligandin and fatty acid binding protein but not by other dibromosulphophthalein binding proteins. <i>Journal of Hepatology</i> , 1994, 21, 29-36.	3.7	3
57	Structure of the complex between trypanosomal triosephosphate isomerase and <i>N</i> -hydroxy-4-phosphono-L-butanamide: Binding at the active site despite an "open" flexible loop conformation. <i>Protein Science</i> , 1992, 1, 1578-1584.	7.6	30
58	Influence of albumin on the net sinusoidal efflux of the organic anion dibromosulphophthalein from rat liver. <i>Hepatology</i> , 1992, 15, 302-309.	7.3	12
59	Mechanistic aspects of uptake and sinusoidal efflux of dibromosulphophthalein in the isolated perfused rat liver. <i>Biochemical Pharmacology</i> , 1991, 42, 1997-2002.	4.4	11