

Hui Peng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1680026/publications.pdf>

Version: 2024-02-01

17
papers

286
citations

933447

10
h-index

888059

17
g-index

18
all docs

18
docs citations

18
times ranked

366
citing authors

#	ARTICLE	IF	CITATIONS
1	A putative α -D-glucanase-encoding gene <i>AOL_s00076g207</i> regulates the development and pathogenicity of <i>Arthrotrypa oligospora</i> . <i>Journal of Basic Microbiology</i> , 2022, 62, 74-81.	3.3	8
2	Specific hydrolysis of curdlan with a novel glycoside hydrolase family 128 β -1,3-endoglucanase containing a carbohydrate-binding module. <i>Carbohydrate Polymers</i> , 2021, 253, 117276.	10.2	10
3	Using a novel hyperthermophilic amylopullulanase to simplify resistant starch preparation from rice starches. <i>Journal of Functional Foods</i> , 2021, 80, 104429.	3.4	12
4	Complex Structure of <i>Pseudomonas aeruginosa</i> Arginine Rhamnosyltransferase EarP with Its Acceptor Elongation Factor P. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	16
5	Extensive hydrolysis of raw rice starch by a chimeric α -amylase engineered with α -amylase (AmyP) and a starch-binding domain from <i>Cryptococcus</i> sp. S-2. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 743-750.	3.6	12
6	Efficient Hydrolysis of Raw Microalgae Starch by an α -Amylase (AmyP) of Glycoside Hydrolase Subfamily GH13_37. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 12748-12755.	5.2	10
7	Ligand Induced Folding of the First Identified CBM69 Starch Binding Domain AmyP-SBD. <i>Protein and Peptide Letters</i> , 2018, 25, 362-367.	0.9	4
8	Changes in the membrane fatty acid composition in <i>Anoxybacillus flavithermus</i> subsp. <i>yunnanensis</i> E13T as response to solvent stress. <i>Archives of Microbiology</i> , 2017, 199, 1-8.	2.2	16
9	Crystal structure of a raw-starch-degrading bacterial α -amylase belonging to subfamily 37 of the glycoside hydrolase family GH13. <i>Scientific Reports</i> , 2017, 7, 44067.	3.3	15
10	Increased enzymatic hydrolysis of sugarcane bagasse by a novel glucose- and xylose-stimulated β -D-glucosidase from <i>Anoxybacillus flavithermus</i> subsp. <i>yunnanensis</i> E13T. <i>BMC Biochemistry</i> , 2017, 18, 4.	4.4	19
11	Identification and characterization of a novel raw-starch-degrading α -amylase (AmyASS) from the marine fish pathogen <i>Aeromonas salmonicida</i> ssp. <i>salmonicida</i> . <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2015, 119, 71-77.	1.8	19
12	A starch-binding domain identified in α -amylase (AmyP) represents a new family of carbohydrate-binding modules that contribute to enzymatic hydrolysis of soluble starch. <i>FEBS Letters</i> , 2014, 588, 1161-1167.	2.8	51
13	Non-contiguous finished genome sequence of <i>Anoxybacillus flavithermus</i> subsp. <i>yunnanensis</i> type strain (E13T), a strictly thermophilic and organic solvent-tolerant bacterium. <i>Standards in Genomic Sciences</i> , 2014, 9, 735-743.	1.5	7
14	α -Amylase (AmyP) of glycoside hydrolase subfamily GH13_37 is resistant to various toxic compounds. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2013, 98, 114-118.	1.8	8
15	Phylogenetic analysis of bacterial community in the gut of American cockroach (<i>Periplaneta</i>) Tj ETQq1 1 0.784314 α -D-glucanase /Overlock 10	0.2	3
16	Preferential and rapid degradation of raw rice starch by an α -amylase of glycoside hydrolase subfamily GH13_37. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 1577-1584.	3.6	40
17	Identification and Phylogenetic Characterization of a New Subfamily of α -Amylase Enzymes from Marine Microorganisms. <i>Marine Biotechnology</i> , 2012, 14, 253-260.	2.4	35