

In-Geol Choi

List of Publications by Year in descending order

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147
papers

5,099
citations

71102

41
h-index

110387

64
g-index

154
all docs

154
docs citations

154
times ranked

6022
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. <i>New Phytologist</i> , 2022, 233, 1383-1400.	7.3	19
2	Soil environment reshapes microbiota of laboratory-maintained Collembola during host development. <i>Environmental Microbiomes</i> , 2022, 17, 16.	5.0	1
3	The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom <i>Schizophyllum commune</i> . <i>MBio</i> , 2022, 13, .	4.1	10
4	<i>Aurantiacibacter sediminis</i> sp. nov., a marine bacterium isolated from a tidal flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	4
5	Transcriptome Analysis Reveals the AhR, Smad2/3, and HIF-1 α Pathways as the Mechanism of Ochratoxin A Toxicity in Kidney Cells. <i>Toxins</i> , 2021, 13, 190.	3.4	21
6	A Novel Auxiliary Agarolytic Pathway Expands Metabolic Versatility in the Agar-Degrading Marine Bacterium <i>Colwellia echini</i> A3. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0023021.	3.1	9
7	Dietary sophorolipid accelerates growth by modulation of gut microbiota population and intestinal environments in broiler chickens. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 81.	5.3	11
8	<i>Novosphingobium aureum</i> sp. nov., a marine bacterium isolated from salt flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	10
9	Development of a Novel Cell Surface Attachment System to Display Multi-Protein Complex Using the Cohesin-Dockerin Binding Pair. <i>Journal of Microbiology and Biotechnology</i> , 2021, 31, 1183-1189.	2.1	0
10	Metabolism perturbation Caused by the overexpression of carbon monoxide dehydrogenase/Acetyl-CoA synthase gene complex accelerated gas to acetate conversion rate of <i>Eubacterium limosum</i> KIST612. <i>Bioresource Technology</i> , 2021, 341, 125879.	9.6	15
11	Evaluating Genetic Diversity of <i>Agaricus bisporus</i> Accessions through Phylogenetic Analysis Using Single-Nucleotide Polymorphism (SNP) Markers. <i>Mycobiology</i> , 2021, 49, 61-68.	1.7	4
12	Augmented CO ₂ tolerance by expressing a single H ⁺ -pump enables microalgal valorization of industrial flue gas. <i>Nature Communications</i> , 2021, 12, 6049.	12.8	34
13	SNP-Based Genetic Linkage Map and Quantitative Trait Locus Mapping Associated with the Agronomically Important Traits of <i>Hypsizygus marmoreus</i> . <i>Mycobiology</i> , 2021, 49, 589-598.	1.7	2
14	<i>Altererythrobacter lutimaris</i> sp. nov., a marine bacterium isolated from a tidal flat and reclassification of <i>Altererythrobacter deserti</i> , <i>Altererythrobacter estronivorus</i> and <i>Altererythrobacter muriae</i> as <i>Tsuneonella deserti</i> comb. nov., <i>Croceicoccus estronivorus</i> comb. nov. and <i>Alteripontixanthobacter muriae</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	20
15	Preparation of a ribosomally synthesized fungal peptide toxin precursor and its in-vitro cyclization. <i>Journal of Biotechnology</i> , 2020, 308, 124-129.	3.8	1
16	Structural insights into the psychrophilic germinal protease PaGPR and its autoinhibitory loop. <i>Journal of Microbiology</i> , 2020, 58, 772-779.	2.8	2
17	Novel Monomeric Fungal Subtilisin Inhibitor from a Plant-Pathogenic Fungus, <i>Choanephora cucurbitarum</i> : Isolation and Molecular Characterization. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	0
18	Genomic and transcriptomic perspectives on mycoremediation of polycyclic aromatic hydrocarbons. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6919-6928.	3.6	25

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19	A Multifunctional Polysaccharide Utilization Gene Cluster in <i>Colwellia echini</i> Encodes Enzymes for the Complete Degradation of Î²-Carrageenan, Î¹-Carrageenan, and Hybrid Î²/Î¹-Carrageenan. <i>MSphere</i> , 2020, 5, .	2.9	18
20	Biosensing and electrochemical properties of flavin adenine dinucleotide (FAD)-Dependent glucose dehydrogenase (GDH) fused to a gold binding peptide. <i>Biosensors and Bioelectronics</i> , 2020, 165, 112427.	10.1	21
21	Unusual genome expansion and transcription suppression in ectomycorrhizal <i>Tricholoma matsutake</i> by insertions of transposable elements. <i>PLoS ONE</i> , 2020, 15, e0227923.	2.5	15
22	Genetic engineering system for syngas-utilizing acetogen, <i>Eubacterium limosum</i> KIST612. <i>Bioresource Technology Reports</i> , 2020, 11, 100452.	2.7	17
23	<i>Muricauda ochracea</i> sp. nov., isolated from a tidal flat in the Republic of Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4555-4561.	1.7	11
24	<i>Marinobacter halodurans</i> sp. nov., a halophilic bacterium isolated from sediment of a salt flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6294-6300.	1.7	12
25	Characterization of two leaf rust-resistant <i>Aegilops tauschii</i> accessions for the synthetic wheat development. <i>Applied Biological Chemistry</i> , 2020, 63, .	1.9	3
26	Comprehensive genomic and transcriptomic analysis of polycyclic aromatic hydrocarbon degradation by a mycoremediation fungus, <i>Dentipellis</i> sp. KUC8613. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8145-8155.	3.6	41
27	Draft Genome Sequences of Two Glycoalkaloid-Degrading <i>Arthrobacter</i> Strains Isolated from Green Potato Peel. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
28	Practical Guide for Fungal Gene Prediction from Genome Assembly and RNA-Seq Reads by FunGAP. <i>Methods in Molecular Biology</i> , 2019, 1962, 53-64.	0.9	0
29	Whole-Genome Sequences of Five <i>Geobacillus stearothermophilus</i> Strains Isolated from Processing Lines of Powdered Infant Formula. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
30	Gene-Centric Metagenome Analysis Reveals Gene Clusters for Carbon Monoxide Conversion and Validates Isolation of a Clostridial Acetogen for C2 Chemical Production. <i>Biotechnology Journal</i> , 2019, 14, 1800471.	3.5	3
31	Significant enhancement of direct electric communication across enzyme-electrode interface via nano-patterning of synthetic glucose dehydrogenase on spatially tunable gold nanoparticle (AuNP)-modified electrode. <i>Biosensors and Bioelectronics</i> , 2019, 126, 170-177.	10.1	14
32	<i>Chryseobacterium phosphatilyticum</i> sp. nov., a phosphate-solubilizing endophyte isolated from cucumber (<i>Cucumis sativus</i> L.) root. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 610-615.	1.7	13
33	<i>Gemmobacter lutimaris</i> sp. nov., a marine bacterium isolated from a tidal flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1676-1681.	1.7	19
34	Transcriptome analysis and anaerobic C ₄ -dicarboxylate transport in <i>Actinobacillus succinogenes</i> . <i>MicrobiologyOpen</i> , 2018, 7, e00565.	3.0	11
35	High substrate specificity of 3,6-anhydro- l -galactose dehydrogenase indicates its essentiality in the agar catabolism of a marine bacterium. <i>Process Biochemistry</i> , 2018, 64, 130-135.	3.7	7
36	Draft Genome Sequence of a Novel <i>Serratia</i> sp. Strain with Antifungal Activity. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3

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37	Draft Genome Sequences of <i>Chryseobacterium lactis</i> NCTC11390 Isolated from Milk, <i>Chryseobacterium oncorhynchi</i> 701B-08 from Rainbow Trout, and <i>Chryseobacterium viscerum</i> 687B-08 from Diseased Fish. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
38	Genomic discovery of the hypsin gene and biosynthetic pathways for terpenoids in <i>Hypsizygus marmoreus</i> . <i>BMC Genomics</i> , 2018, 19, 789.	2.8	21
39	The obligate alkalophilic soda lake fungus <i>Sodiomyces alkalinus</i> has shifted to a protein diet. <i>Molecular Ecology</i> , 2018, 27, 4808-4819.	3.9	20
40	Comparative study of the airborne microbial communities and their functional composition in fine particulate matter (PM2.5) under non-extreme and extreme PM2.5 conditions. <i>Atmospheric Environment</i> , 2018, 194, 82-92.	4.1	46
41	Construction of Uniform Monolayer- and Orientation-Tunable Enzyme Electrode by a Synthetic Glucose Dehydrogenase without Electron-Transfer Subunit via Optimized Site-Specific Gold-Binding Peptide Capable of Direct Electron Transfer. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 28615-28626.	8.0	32
42	Draft Genome Sequences of <i>Bacillus megaterium</i> KU143, <i>Microbacterium testaceum</i> KU313, and <i>Pseudomonas protegens</i> AS15, Isolated from Stored Rice Grains. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
43	Draft Genome Sequence of Phosphate-Solubilizing <i>Chryseobacterium</i> sp. Strain ISE14, a Biocontrol and Plant Growth-Promoting Rhizobacterium Isolated from Cucumber. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
44	Model-Based Complete Enzymatic Production of 3,6-Anhydro-L-galactose from Red Algal Biomass. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 6814-6821.	5.2	11
45	<i>Zobellella maritima</i> sp. nov., a polycyclic aromatic hydrocarbon-degrading bacterium, isolated from beach sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2279-2284.	1.7	10
46	<i>Oceanimonas marisflavi</i> sp. nov., a polycyclic aromatic hydrocarbon-degrading marine bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2990-2995.	1.7	13
47	Transcriptional Response and Enhanced Intestinal Adhesion Ability of <i>Lactobacillus rhamnosus</i> GG after Acid Stress. <i>Journal of Microbiology and Biotechnology</i> , 2018, 28, 1604-1613.	2.1	24
48	<i>Maribacter litoralis</i> sp. nov. a marine bacterium isolated from seashore. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3471-3478.	1.7	8
49	Cellotriose-hydrolyzing activity conferred by truncating the carbohydrate-binding modules of Cel5 from <i>Hahella chejuensis</i> . <i>Bioprocess and Biosystems Engineering</i> , 2017, 40, 241-249.	3.4	5
50	Genome Analysis of a Zygomycete Fungus <i>Choanephora cucurbitarum</i> Elucidates Necrotrophic Features Including Bacterial Genes Related to Plant Colonization. <i>Scientific Reports</i> , 2017, 7, 40432.	3.3	9
51	Rapid and robust enzymatic sensing and quantitation of 3,6-Anhydro-L-galactose in a heterogeneous sugar mixture. <i>Carbohydrate Research</i> , 2017, 446-447, 13-18.	2.3	3
52	FunGAP: Fungal Genome Annotation Pipeline using evidence-based gene model evaluation. <i>Bioinformatics</i> , 2017, 33, 2936-2937.	4.1	70
53	Prokaryotic Contig Annotation Pipeline Server: Web Application for a Prokaryotic Genome Annotation Pipeline Based on the Shiny App Package. <i>Journal of Computational Biology</i> , 2017, 24, 917-922.	1.6	4
54	d-Stereoisomer preference of the OmpA-like domain of Pal in peptidoglycan of <i>Acinetobacter baumannii</i> . <i>Process Biochemistry</i> , 2017, 55, 110-115.	3.7	1

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55	Acetate-assisted increase of butyrate production by <i>Eubacterium limosum</i> KIST612 during carbon monoxide fermentation. <i>Bioresource Technology</i> , 2017, 245, 560-566.	9.6	36
56	Crystal structure analysis of 3,6-anhydro-L-galactonate cycloisomerase suggests emergence of novel substrate specificity in the enolase superfamily. <i>Biochemical and Biophysical Research Communications</i> , 2017, 491, 217-222.	2.1	1
57	Draft Genome Sequence of an Acid-Tolerant Yeast, <i>Candida zemplinina</i> NP2, a Potential Producer of Organic Acids. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
58	Enzymatic liquefaction of agarose above the sol-gel transition temperature using a thermostable endo-type α -agarase, Aga16B. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1111-1120.	3.6	38
59	3,6-Anhydro-L-galactonate cycloisomerase from <i>Vibriosp.</i> strain EY3: crystallization and X-ray crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 511-514.	0.8	3
60	<i>Chryseobacterium cucumeris</i> sp. nov., an endophyte isolated from cucumber (<i>Cucumis sativus</i> L.) root, and emended description of <i>Chryseobacterium arthrosphaerae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 610-616.	1.7	30
61	Olfactory receptor 544 reduces adiposity by steering fuel preference toward fats. <i>Journal of Clinical Investigation</i> , 2017, 127, 4118-4123.	8.2	81
62	Draft Genome Sequences of <i>Chryseobacterium artocarpi</i> UTM-3 ^T and <i>Chryseobacterium contaminans</i> C26 ^T , Isolated from Rhizospheres, and <i>Chryseobacterium arthrosphaerae</i> CC-VM-7 ^T , Isolated from the Feces of a Pill Millipede. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
63	Transcriptome landscape of <i>Synechococcus elongatus</i> PCC 7942 for nitrogen starvation responses using RNA-seq. <i>Scientific Reports</i> , 2016, 6, 30584.	3.3	28
64	Draft Genome Sequences of Two Ureolytic Bacteria Isolated from Concrete Block Waste. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
65	Draft Genome Sequence of <i>Chryseobacterium</i> sp. Strain GSE06, a Biocontrol Endophytic Bacterium Isolated from Cucumber (<i>Cucumis sativus</i>). <i>Genome Announcements</i> , 2016, 4, .	0.8	10
66	Draft Genome Sequence of a Biocontrol Rhizobacterium, <i>Chryseobacterium kwangjuense</i> Strain KJ1R5, Isolated from Pepper (<i>Capsicum annuum</i>). <i>Genome Announcements</i> , 2016, 4, .	0.8	6
67	Characterization of the biochemical properties of recombinant Xyn10C from a marine bacterium, <i>Saccharophagus degradans</i> 2-40. <i>Bioprocess and Biosystems Engineering</i> , 2016, 39, 677-684.	3.4	11
68	Pretreatment and saccharification of red macroalgae to produce fermentable sugars. <i>Bioresource Technology</i> , 2016, 199, 311-318.	9.6	87
69	Calcium Carbonate Precipitation by <i>Bacillus</i> and <i>Sporosarcina</i> Strains Isolated from Concrete and Analysis of the Bacterial Community of Concrete. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 540-548.	2.1	56
70	Structural studies of the virulence factor peptidoglycan-associated lipoprotein from a Gram-negative pathogen. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2016, 72, s218-s218.	0.1	0
71	Red macroalgae as a sustainable resource for bio-based products. <i>Trends in Biotechnology</i> , 2015, 33, 247-249.	9.3	68
72	Crystal structure analysis of a bacterial aryl acylamidase belonging to the amidase signature enzyme family. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 268-274.	2.1	23

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73	Enhanced tolerance of <i>Saccharomyces cerevisiae</i> to multiple lignocellulose-derived inhibitors through modulation of spermidine contents. <i>Metabolic Engineering</i> , 2015, 29, 46-55.	7.0	77
74	Genome sequence of a white rot fungus <i>Schizophora paradoxa</i> KUC8140 for wood decay and mycoremediation. <i>Journal of Biotechnology</i> , 2015, 211, 42-43.	3.8	21
75	Transcriptome analysis of acetic-acid-treated yeast cells identifies a large set of genes whose overexpression or deletion enhances acetic acid tolerance. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6391-6403.	3.6	31
76	Energy Conservation Model Based on Genomic and Experimental Analyses of a Carbon Monoxide-Utilizing, Butyrate-Forming Acetogen, <i>Eubacterium limosum</i> KIST612. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4782-4790.	3.1	69
77	Optimization of synergism of a recombinant auxiliary activity 9 from <i>Chaetomium globosum</i> with cellulase in cellulose hydrolysis. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8537-8547.	3.6	54
78	Tolerance to acetic acid is improved by mutations of the <i>TATA</i> -binding protein gene. <i>Environmental Microbiology</i> , 2015, 17, 656-669.	3.8	18
79	The novel catabolic pathway of 3,6-anhydro- β -galactose, the main component of red macroalgae, in a marine bacterium. <i>Environmental Microbiology</i> , 2015, 17, 1677-1688.	3.8	106
80	Saccharification of agar using hydrothermal pretreatment and enzymes supplemented with agarolytic β -galactosidase. <i>Process Biochemistry</i> , 2015, 50, 1629-1633.	3.7	28
81	Loss of <i>Dfg5</i> glycosylphosphatidylinositol-anchored membrane protein confers enhanced heat tolerance in <i>Saccharomyces cerevisiae</i> . <i>Environmental Microbiology</i> , 2015, 17, 2721-2734.	3.8	16
82	Selection of parental monokaryons from Korean <i>Hypsizygus marmoreus</i> by protoplast regeneration. <i>Journal of Mushrooms</i> , 2015, 13, 270-273.	0.3	0
83	Selection of <i>Agaricus bitorquis</i> hybrid strains based on RAPD analysis. <i>Journal of Mushrooms</i> , 2015, 13, 243-249.	0.3	0
84	Development of a new brown button mushroom cultivar 'Hogam'. <i>Journal of Mushrooms</i> , 2015, 13, 237-242.	0.3	1
85	Previously Undescribed Plasmids Recovered from Activated Sludge Confer Tetracycline Resistance and Phenotypic Changes to <i>Acinetobacter oleivorans</i> DR1. <i>Microbial Ecology</i> , 2014, 67, 369-379.	2.8	12
86	Metabolically engineered glucose-utilizing <i>Shewanella</i> strains under anaerobic conditions. <i>Bioresource Technology</i> , 2014, 154, 59-66.	9.6	60
87	Synergistic proteins for the enhanced enzymatic hydrolysis of cellulose by cellulase. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 8469-8480.	3.6	92
88	A Novel Agarolytic β -Galactosidase Acts on Agarooligosaccharides for Complete Hydrolysis of Agarose into Monomers. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5965-5973.	3.1	78
89	Feasibility test of utilizing <i>Saccharophagus degradans</i> 2-40T as the source of crude enzyme for the saccharification of lignocellulose. <i>Bioprocess and Biosystems Engineering</i> , 2014, 37, 707-710.	3.4	6
90	Genomics of wood-degrading fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 82-90.	2.1	103

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91	Characteristic evaluation of collected strains of <i>Agaricus</i> spp. based on ITS rDNA sequence. <i>Journal of Mushrooms</i> , 2014, 12, 244-250.	0.3	0
92	High temperature and low acid pretreatment and agarase treatment of agarose for the production of sugar and ethanol from red seaweed biomass. <i>Bioresource Technology</i> , 2013, 136, 582-587.	9.6	55
93	Enzymatic production of 3,6-anhydro-l-galactose from agarose and its purification and in vitro skin whitening and anti-inflammatory activities. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 2961-2970.	3.6	96
94	An expansin from the marine bacterium <i>Hahella chejuensis</i> acts synergistically with xylanase and enhances xylan hydrolysis. <i>Bioresource Technology</i> , 2013, 149, 516-519.	9.6	20
95	Binding characteristics of a bacterial expansin (BsEXLX1) for various types of pretreated lignocellulose. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 5381-5388.	3.6	39
96	Characteristics of the binding of a bacterial expansin (<i>BsEXLX1</i>) to microcrystalline cellulose. <i>Biotechnology and Bioengineering</i> , 2013, 110, 401-407.	3.3	26
97	Functional Cell Surface Display and Controlled Secretion of Diverse Agarolytic Enzymes by <i>Escherichia coli</i> with a Novel Ligation-Independent Cloning Vector Based on the Autotransporter YfaL. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3051-3058.	3.1	16
98	Genome Sequence of <i>Janthinobacterium</i> sp. Strain PAMC 25724, Isolated from Alpine Glacier Cryoconite. <i>Journal of Bacteriology</i> , 2012, 194, 2096-2096.	2.2	33
99	Genome Sequence of a Novel Member of the Genus <i>Psychrobacter</i> Isolated from Antarctic Soil. <i>Journal of Bacteriology</i> , 2012, 194, 2403-2403.	2.2	34
100	Genome Sequence of <i>Vibrio</i> sp. Strain EJY3, an Agarolytic Marine Bacterium Metabolizing 3,6-Anhydro-L-Galactose as a Sole Carbon Source. <i>Journal of Bacteriology</i> , 2012, 194, 2773-2774.	2.2	34
101	Exploring the human diseasesome: the human disease network. <i>Briefings in Functional Genomics</i> , 2012, 11, 533-542.	2.7	118
102	Aqueous ammonia pretreatment, saccharification, and fermentation evaluation of oil palm fronds for ethanol production. <i>Bioprocess and Biosystems Engineering</i> , 2012, 35, 1497-1503.	3.4	32
103	Characterization of a recombinant endo-type alginate lyase (Alg7D) from <i>Saccharophagus degradans</i> . <i>Biotechnology Letters</i> , 2012, 34, 1087-1092.	2.2	60
104	The complete enzymatic saccharification of agarose and its application to simultaneous saccharification and fermentation of agarose for ethanol production. <i>Bioresource Technology</i> , 2012, 107, 301-306.	9.6	72
105	Depolymerization of alginate into a monomeric sugar acid using Alg17C, an exo-oligoalginate lyase cloned from <i>Saccharophagus degradans</i> 2-40. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 2233-2239.	3.6	90
106	Production of p-acetaminophenol by whole-cell catalysis using <i>Escherichia coli</i> overexpressing bacterial aryl acylamidase. <i>Biotechnology Letters</i> , 2012, 34, 677-682.	2.2	4
107	Genome Sequence of the Abyssomicin- and Proximicin-Producing Marine Actinomycete <i>Verrucosipora maris</i> AB-18-032. <i>Journal of Bacteriology</i> , 2011, 193, 3391-3392.	2.2	24
108	Complete Genome Sequence of a Carbon Monoxide-Utilizing Acetogen, <i>Eubacterium limosum</i> KIST612. <i>Journal of Bacteriology</i> , 2011, 193, 307-308.	2.2	68

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109	Crystal structure of a key enzyme in the agarolytic pathway, β -D-neoagarobiose hydrolase from <i>Saccharophagus degradans</i> 2-40. <i>Biochemical and Biophysical Research Communications</i> , 2011, 412, 238-244.	2.1	76
110	Aqueous ammonia pretreatment of oil palm empty fruit bunches for ethanol production. <i>Bioresource Technology</i> , 2011, 102, 9806-9809.	9.6	74
111	Ethanol production from oil palm trunks treated with aqueous ammonia and cellulase. <i>Bioresource Technology</i> , 2011, 102, 7307-7312.	9.6	52
112	Production of 3,6-anhydro-l-galactose from agarose by agarolytic enzymes of <i>Saccharophagus degradans</i> 2-40. <i>Process Biochemistry</i> , 2011, 46, 88-93.	3.7	44
113	Complete Genome Sequencing of <i>Lactobacillus acidophilus</i> 30SC, Isolated from Swine Intestine. <i>Journal of Bacteriology</i> , 2011, 193, 2882-2883.	2.2	18
114	Overexpression and molecular characterization of Aga50D from <i>Saccharophagus degradans</i> 2-40: an α -D-galactosidase producing neoagarobiose. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 227-234.	3.6	127
115	An Expansin-Like Protein from <i>Hahella chejuensis</i> Binds Cellulose and Enhances Cellulase Activity. <i>Molecules and Cells</i> , 2010, 29, 379-386.	2.6	59
116	Molecular Characterization of a Novel Bacterial Aryl Acylamidase Belonging to the Amidase Signature Enzyme Family. <i>Molecules and Cells</i> , 2010, 29, 485-492.	2.6	23
117	Global metabolic profiling of plant cell wall polysaccharide degradation by <i>Saccharophagus degradans</i> . <i>Biotechnology and Bioengineering</i> , 2010, 105, 477-488.	3.3	32
118	Biological pretreatment of rice straw by fermenting with <i>Dichomitus squalens</i> . <i>New Biotechnology</i> , 2010, 27, 424-434.	4.4	53
119	Global metabolite profiling of agarose degradation by <i>Saccharophagus degradans</i> 2-40. <i>New Biotechnology</i> , 2010, 27, 156-168.	4.4	26
120	Modification of mesenchymal stem cells for cardiac regeneration. <i>Expert Opinion on Biological Therapy</i> , 2010, 10, 309-319.	3.1	97
121	Functional characterization of a bacterial expansin from <i>Bacillus subtilis</i> for enhanced enzymatic hydrolysis of cellulose. <i>Biotechnology and Bioengineering</i> , 2009, 102, 1342-1353.	3.3	142
122	Fungal pretreatment of lignocellulose by <i>Phanerochaete chrysosporium</i> to produce ethanol from rice straw. <i>Biotechnology and Bioengineering</i> , 2009, 104, 471-482.	3.3	176
123	Crystallization and preliminary X-ray analysis of neoagarobiose hydrolase from <i>Saccharophagus degradans</i> 2-40. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1299-1301.	0.7	20
124	Improved enzymatic hydrolysis yield of rice straw using electron beam irradiation pretreatment. <i>Bioresource Technology</i> , 2009, 100, 1285-1290.	9.6	202
125	Optimal production of a novel endo-acting β -D-1,4-xylanase cloned from <i>Saccharophagus degradans</i> 2-40 into <i>Escherichia coli</i> BL21(DE3). <i>New Biotechnology</i> , 2009, 26, 157-164.	4.4	18
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