In-Geol Choi

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Ethanol production from rice straw using optimized aqueous-ammonia soaking pretreatment and simultaneous saccharification and fermentation processes. Bioresource Technology, 2009, 100, 4374-4380.	9.6	247
2	Improved enzymatic hydrolysis yield of rice straw using electron beam irradiation pretreatment. Bioresource Technology, 2009, 100, 1285-1290.	9.6	202
3	Fungal pretreatment of lignocellulose by <i>Phanerochaete chrysosporium</i> to produce ethanol from rice straw. Biotechnology and Bioengineering, 2009, 104, 471-482.	3.3	176
4	Global extent of horizontal gene transfer. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4489-4494.	7.1	142
5	Functional characterization of a bacterial expansin from <i>Bacillus subtilis</i> for enhanced enzymatic hydrolysis of cellulose. Biotechnology and Bioengineering, 2009, 102, 1342-1353.	3.3	142
6	Overexpression and molecular characterization of Aga50D from Saccharophagus degradans 2-40: an exo-type β-agarase producing neoagarobiose. Applied Microbiology and Biotechnology, 2010, 86, 227-234.	3.6	127
7	Exploring the human diseasome: the human disease network. Briefings in Functional Genomics, 2012, 11, 533-542.	2.7	118
8	The novel catabolic pathway of 3,6â€anhydroâ€ <scp>L</scp> â€galactose, the main component of red macroalgae, in a marine bacterium. Environmental Microbiology, 2015, 17, 1677-1688.	3.8	106
9	Genomics of wood-degrading fungi. Fungal Genetics and Biology, 2014, 72, 82-90.	2.1	103
10	Crystal structure of an intracellular protease from Pyrococcus horikoshii at 2-A resolution. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14079-14084.	7.1	97
11	Modification of mesenchymal stem cells for cardiac regeneration. Expert Opinion on Biological Therapy, 2010, 10, 309-319.	3.1	97
12	Enzymatic production of 3,6-anhydro-l-galactose from agarose and its purification and in vitro skin whitening and anti-inflammatory activities. Applied Microbiology and Biotechnology, 2013, 97, 2961-2970.	3.6	96
13	Synergistic proteins for the enhanced enzymatic hydrolysis of cellulose by cellulase. Applied Microbiology and Biotechnology, 2014, 98, 8469-8480.	3.6	92
14	Depolymerization of alginate into a monomeric sugar acid using Alg17C, an exo-oligoalginate lyase cloned from Saccharophagus degradans 2-40. Applied Microbiology and Biotechnology, 2012, 93, 2233-2239.	3.6	90
15	Pretreatment and saccharification of red macroalgae to produce fermentable sugars. Bioresource Technology, 2016, 199, 311-318.	9.6	87
16	Olfactory receptor 544 reduces adiposity by steering fuel preference toward fats. Journal of Clinical Investigation, 2017, 127, 4118-4123.	8.2	81
17	A Novel Agarolytic β-Galactosidase Acts on Agarooligosaccharides for Complete Hydrolysis of Agarose into Monomers. Applied and Environmental Microbiology, 2014, 80, 5965-5973.	3.1	78
18	Enhanced tolerance of Saccharomyces cerevisiae to multiple lignocellulose-derived inhibitors through modulation of spermidine contents. Metabolic Engineering, 2015, 29, 46-55.	7.0	77

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19	Crystal structure of a key enzyme in the agarolytic pathway, α-neoagarobiose hydrolase from Saccharophagus degradans 2–40. Biochemical and Biophysical Research Communications, 2011, 412, 238-244.	2.1	76
20	Local feature frequency profile: A method to measure structural similarity in proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3797-3802.	7.1	74
21	Aqueous ammonia pretreatment of oil palm empty fruit bunches for ethanol production. Bioresource Technology, 2011, 102, 9806-9809.	9.6	74
22	Evolution of protein structural classes and protein sequence families. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14056-14061.	7.1	72
23	The complete enzymatic saccharification of agarose and its application to simultaneous saccharification and fermentation of agarose for ethanol production. Bioresource Technology, 2012, 107, 301-306.	9.6	72
24	FunGAP: Fungal Genome Annotation Pipeline using evidence-based gene model evaluation. Bioinformatics, 2017, 33, 2936-2937.	4.1	70
25	Energy Conservation Model Based on Genomic and Experimental Analyses of a Carbon Monoxide-Utilizing, Butyrate-Forming Acetogen, Eubacterium limosum KIST612. Applied and Environmental Microbiology, 2015, 81, 4782-4790.	3.1	69
26	Complete Genome Sequence of a Carbon Monoxide-Utilizing Acetogen, <i>Eubacterium limosum</i> KIST612. Journal of Bacteriology, 2011, 193, 307-308.	2.2	68
27	Red macroalgae as a sustainable resource for bio-based products. Trends in Biotechnology, 2015, 33, 247-249.	9.3	68
28	Structure-based functional inference in structural genomics. Journal of Structural and Functional Genomics, 2003, 4, 129-135.	1.2	60
29	Characterization of a recombinant endo-type alginate lyase (Alg7D) from Saccharophagus degradans. Biotechnology Letters, 2012, 34, 1087-1092.	2.2	60
30	Metabolically engineered glucose-utilizing Shewanella strains under anaerobic conditions. Bioresource Technology, 2014, 154, 59-66.	9.6	60
31	An Expansin-Like Protein from Hahella chejuensis Binds Cellulose and Enhances Cellulase Activity. Molecules and Cells, 2010, 29, 379-386.	2.6	59
32	Calcium Carbonate Precipitation by Bacillus and Sporosarcina Strains Isolated from Concrete and Analysis of the Bacterial Community of Concrete. Journal of Microbiology and Biotechnology, 2016, 26, 540-548.	2.1	56
33	High temperature and low acid pretreatment and agarase treatment of agarose for the production of sugar and ethanol from red seaweed biomass. Bioresource Technology, 2013, 136, 582-587.	9.6	55
34	Optimization of synergism of a recombinant auxiliary activity 9 from Chaetomium globosum with cellulase in cellulose hydrolysis. Applied Microbiology and Biotechnology, 2015, 99, 8537-8547.	3.6	54
35	Biological pretreatment of rice straw by fermenting with Dichomitus squalens. New Biotechnology, 2010, 27, 424-434.	4.4	53
36	Ethanol production from oil palm trunks treated with aqueous ammonia and cellulase. Bioresource Technology, 2011, 102, 7307-7312.	9.6	52

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37	Analysis of survival rates and cellular fatty acid profiles of Listeria monocytogenes treated with supercritical carbon dioxide under the influence of cosolvents. Journal of Microbiological Methods, 2008, 75, 47-54.	1.6	46
38	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. Atmospheric Environment, 2018, 194, 82-92.	4.1	46
39	Protein conformational space in higher order Â-Â maps. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 618-621.	7.1	45
40	Chemicals that modulate stem cell differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7467-7471.	7.1	45
41	Production of 3,6-anhydro-l-galactose from agarose by agarolytic enzymes of Saccharophagus degradans 2-40. Process Biochemistry, 2011, 46, 88-93.	3.7	44
42	Comprehensive genomic and transcriptomic analysis of polycyclic aromatic hydrocarbon degradation by a mycoremediation fungus, Dentipellis sp. KUC8613. Applied Microbiology and Biotechnology, 2019, 103, 8145-8155.	3.6	41
43	Binding characteristics of a bacterial expansin (BsEXLX1) for various types of pretreated lignocellulose. Applied Microbiology and Biotechnology, 2013, 97, 5381-5388.	3.6	39
44	Enzymatic liquefaction of agarose above the sol–gel transition temperature using a thermostable endo-type β-agarase, Aga16B. Applied Microbiology and Biotechnology, 2017, 101, 1111-1120.	3.6	38
45	Cloning and expression of superoxide dismutase fromAquifex pyrophilus, a hyperthermophilic bacterium. FEBS Letters, 1997, 406, 142-146.	2.8	36
46	Acetate-assisted increase of butyrate production by Eubacterium limosum KIST612 during carbon monoxide fermentation. Bioresource Technology, 2017, 245, 560-566.	9.6	36
47	Extremely Thermostable Serine-type Protease fromAquifex pyrophilus. Journal of Biological Chemistry, 1999, 274, 881-888.	3.4	34
48	Genome Sequence of a Novel Member of the Genus Psychrobacter Isolated from Antarctic Soil. Journal of Bacteriology, 2012, 194, 2403-2403.	2.2	34
49	Genome Sequence of Vibrio sp. Strain EJY3, an Agarolytic Marine Bacterium Metabolizing 3,6-Anhydro-L-Galactose as a Sole Carbon Source. Journal of Bacteriology, 2012, 194, 2773-2774.	2.2	34
50	Augmented CO2 tolerance by expressing a single H+-pump enables microalgal valorization of industrial flue gas. Nature Communications, 2021, 12, 6049.	12.8	34
51	Genome Sequence of Janthinobacterium sp. Strain PAMC 25724, Isolated from Alpine Glacier Cryoconite. Journal of Bacteriology, 2012, 194, 2096-2096.	2.2	33
52	Structure of OsmC fromEscherichia coli: a salt-shock-induced protein. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 903-911.	2.5	32
53	Global metabolic profiling of plant cell wall polysaccharide degradation by <i>Saccharophagus degradans</i> . Biotechnology and Bioengineering, 2010, 105, 477-488.	3.3	32
54	Aqueous ammonia pretreatment, saccharification, and fermentation evaluation of oil palm fronds for ethanol production. Bioprocess and Biosystems Engineering, 2012, 35, 1497-1503.	3.4	32

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55	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. ACS Applied Materials & Interfaces, 2018, 10, 28615-28626.	8.0	32
56	Transcriptome analysis of acetic-acid-treated yeast cells identifies a large set of genes whose overexpression or deletion enhances acetic acid tolerance. Applied Microbiology and Biotechnology, 2015, 99, 6391-6403.	3.6	31
57	Chryseobacterium cucumeris sp. nov., an endophyte isolated from cucumber (Cucumis sativus L.) root, and emended description of Chryseobacterium arthrosphaerae. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 610-616.	1.7	30
58	Structural Genomics of Minimal Organisms and Protein Fold Space. Journal of Structural and Functional Genomics, 2005, 6, 63-70.	1.2	29
59	Saccharification of agar using hydrothermal pretreatment and enzymes supplemented with agarolytic β-galactosidase. Process Biochemistry, 2015, 50, 1629-1633.	3.7	28
60	Transcriptome landscape of Synechococcus elongatus PCC 7942 for nitrogen starvation responses using RNA-seq. Scientific Reports, 2016, 6, 30584.	3.3	28
61	Structure-based inference of molecular functions of proteins of unknown function from Berkeley Structural Genomics Center. Journal of Structural and Functional Genomics, 2007, 8, 99-105.	1.2	26
62	Global metabolite profiling of agarose degradation by Saccharophagus degradans 2-40. New Biotechnology, 2010, 27, 156-168.	4.4	26
63	Characteristics of the binding of a bacterial expansin (<i>Bs</i> EXLX1) to microcrystalline cellulose. Biotechnology and Bioengineering, 2013, 110, 401-407.	3.3	26
64	Effect of propofol on calcium homeostasis in hypoxia-reoxygenated neonatal rat cardiomyocytes. European Journal of Pharmacology, 2008, 594, 139-145.	3.5	25
65	Genomic and transcriptomic perspectives on mycoremediation of polycyclic aromatic hydrocarbons. Applied Microbiology and Biotechnology, 2020, 104, 6919-6928.	3.6	25
66	Genome Sequence of the Abyssomicin- and Proximicin-Producing Marine Actinomycete Verrucosispora maris AB-18-032. Journal of Bacteriology, 2011, 193, 3391-3392.	2.2	24
67	Transcriptional Response and Enhanced Intestinal Adhesion Ability of Lactobacillus rhamnosus GG after Acid Stress. Journal of Microbiology and Biotechnology, 2018, 28, 1604-1613.	2.1	24
68	Molecular Characterization of a Novel Bacterial Aryl Acylamidase Belonging to the Amidase Signature Enzyme Family. Molecules and Cells, 2010, 29, 485-492.	2.6	23
69	Crystal structure analysis of a bacterial aryl acylamidase belonging to the amidase signature enzyme family. Biochemical and Biophysical Research Communications, 2015, 467, 268-274.	2.1	23
70	Molecular cloning, expression, and characterization of a thermostable glutamate racemase from a hyperthermophilic bacterium, Aquifex pyrophilus. Extremophiles, 1999, 3, 175-183.	2.3	21
71	Genome sequence of a white rot fungus Schizopora paradoxa KUC8140 for wood decay and mycoremediation. Journal of Biotechnology, 2015, 211, 42-43.	3.8	21
72	Genomic discovery of the hypsin gene and biosynthetic pathways for terpenoids in Hypsizygus marmoreus. BMC Genomics, 2018, 19, 789.	2.8	21

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73	Biosensing and electrochemical properties of flavin adenine dinucleotide (FAD)-Dependent glucose dehydrogenase (GDH) fused to a gold binding peptide. Biosensors and Bioelectronics, 2020, 165, 112427.	10.1	21
74	Transcriptome Analysis Reveals the AhR, Smad2/3, and HIF-1α Pathways as the Mechanism of Ochratoxin A Toxicity in Kidney Cells. Toxins, 2021, 13, 190.	3.4	21
75	Crystallization and preliminary X-ray analysis of neoagarobiose hydrolase from <i>Saccharophagus degradans</i> 2-40. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1299-1301.	0.7	20
76	An expansin from the marine bacterium Hahella chejuensis acts synergistically with xylanase and enhances xylan hydrolysis. Bioresource Technology, 2013, 149, 516-519.	9.6	20
77	The obligate alkalophilic soda″ake fungus Sodiomyces alkalinus has shifted to a protein diet. Molecular Ecology, 2018, 27, 4808-4819.	3.9	20
78	Altererythrobacter lutimaris sp. nov., a marine bacterium isolated from a tidal flat and reclassification of Altererythrobacter deserti, Altererythrobacter estronivorus and Altererythrobacter muriae as Tsuneonella deserti comb. nov., Croceicoccus estronivorus comb. nov. and Alteripontixanthobacter muriae comb. nov International Journal of Systematic and Evolutionary Microbiology 2021, 71	1.7	20
79	Gemmobacter lutimaris sp. nov., a marine bacterium isolated from a tidal flat. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1676-1681.	1.7	19
80	Evolutionary innovations through gain and loss of genes in the ectomycorrhizal Boletales. New Phytologist, 2022, 233, 1383-1400.	7.3	19
81	Optimal production of a novel endo-acting β-1,4-xylanase cloned from Saccharophagus degradans 2-40 into Escherichia coli BL21(DE3). New Biotechnology, 2009, 26, 157-164.	4.4	18
82	Complete Genome Sequencing of Lactobacillus acidophilus 30SC, Isolated from Swine Intestine. Journal of Bacteriology, 2011, 193, 2882-2883.	2.2	18
83	Tolerance to acetic acid is improved by mutations of the <scp>TATA</scp> â€binding protein gene. Environmental Microbiology, 2015, 17, 656-669.	3.8	18
84	A Multifunctional Polysaccharide Utilization Gene Cluster in <i>Colwellia echini</i> Encodes Enzymes for the Complete Degradation of κ-Carrageenan, Î1-Carrageenan, and Hybrid β/κ-Carrageenan. MSphere, 2020, 5, .	2.9	18
85	Interaction and Assembly of HBV Structural Proteins: Novel Target Sites of Anti-HBV Agents. Infectious Disorders - Drug Targets, 2007, 7, 251-256.	0.8	17
86	Genetic engineering system for syngas-utilizing acetogen, Eubacterium limosum KIST612. Bioresource Technology Reports, 2020, 11, 100452.	2.7	17
87	Functional Cell Surface Display and Controlled Secretion of Diverse Agarolytic Enzymes by Escherichia coli with a Novel Ligation-Independent Cloning Vector Based on the Autotransporter YfaL. Applied and Environmental Microbiology, 2012, 78, 3051-3058.	3.1	16
88	Loss of <scp>D</scp> fg5 glycosylphosphatidylinositolâ€anchored membrane protein confers enhanced heat tolerance in <scp><i>S</i></scp> <i>accharomyces cerevisiae</i> . Environmental Microbiology, 2015, 17, 2721-2734.	3.8	16
89	Unusual genome expansion and transcription suppression in ectomycorrhizal Tricholoma matsutake by insertions of transposable elements. PLoS ONE, 2020, 15, e0227923.	2.5	15
90	Metabolism perturbation Caused by the overexpression of carbon monoxide dehydrogenase/Acetyl-CoA synthase gene complex accelerated gas to acetate conversion rate ofEubacterium limosumKIST612. Bioresource Technology, 2021, 341, 125879.	9.6	15

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91	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. Biosensors and Bioelectronics, 2019, 126, 170-177.	10.1	14
92	Crystal structure of a stress inducible protein from Mycoplasma pneumoniae at 2.85 A resolution. Journal of Structural and Functional Genomics, 2003, 4, 31-34.	1.2	13
93	Oceanimonas marisflavi sp. nov., a polycyclic aromatic hydrocarbon-degrading marine bacterium. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2990-2995.	1.7	13
94	Chryseobacterium phosphatilyticum sp. nov., a phosphate-solubilizing endophyte isolated from cucumber (Cucumis sativus L.) root. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 610-615.	1.7	13
95	Previously Undescribed Plasmids Recovered from Activated Sludge Confer Tetracycline Resistance and Phenotypic Changes to Acinetobacter oleivorans DR1. Microbial Ecology, 2014, 67, 369-379.	2.8	12
96	Marinobacter halodurans sp. nov., a halophilic bacterium isolated from sediment of a salt flat. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 6294-6300.	1.7	12
97	Random sequence analysis of genomic DNA of a hyperthermophile: Aquifex pyrophilus. Extremophiles, 1997, 1, 125-134.	2.3	11
98	Characterization of the biochemical properties of recombinant Xyn10C from a marine bacterium, Saccharophagus degradans 2-40. Bioprocess and Biosystems Engineering, 2016, 39, 677-684.	3.4	11
99	Transcriptome analysis and anaerobic C ₄ â€dicarboxylate transport in <i>Actinobacillus succinogenes</i> . MicrobiologyOpen, 2018, 7, e00565.	3.0	11
100	Model-Based Complete Enzymatic Production of 3,6-Anhydro- <scp>l</scp> -galactose from Red Algal Biomass. Journal of Agricultural and Food Chemistry, 2018, 66, 6814-6821.	5.2	11
101	Dietary sophorolipid accelerates growth by modulation of gut microbiota population and intestinal environments in broiler chickens. Journal of Animal Science and Biotechnology, 2021, 12, 81.	5.3	11
102	Muricauda ochracea sp. nov., isolated from a tidal flat in the Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 4555-4561.	1.7	11
103	Draft Genome Sequence of Chryseobacterium sp. Strain GSE06, a Biocontrol Endophytic Bacterium Isolated from Cucumber (Cucumis sativus). Genome Announcements, 2016, 4, .	0.8	10
104	Novosphingobium aureum sp. nov., a marine bacterium isolated from salt flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	10
105	Zobellella maritima sp. nov., a polycyclic aromatic hydrocarbon-degrading bacterium, isolated from beach sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2279-2284.	1.7	10
106	The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom <i>Schizophyllum commune</i> . MBio, 2022, 13, .	4.1	10
107	Genome Analysis of a Zygomycete Fungus Choanephora cucurbitarum Elucidates Necrotrophic Features Including Bacterial Genes Related to Plant Colonization. Scientific Reports, 2017, 7, 40432.	3.3	9
108	A Novel Auxiliary Agarolytic Pathway Expands Metabolic Versatility in the Agar-Degrading Marine Bacterium Colwellia echini A3 ^T . Applied and Environmental Microbiology, 2021, 87, e0023021.	3.1	9

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109	Draft Genome Sequences of Chryseobacterium lactis NCTC11390 ^T Isolated from Milk, Chryseobacterium oncorhynchi 701B-08 ^T from Rainbow Trout, and Chryseobacterium viscerum 687B-08 ^T from Diseased Fish. Genome Announcements, 2018, 6, .	0.8	8
110	Draft Genome Sequence of Phosphate-Solubilizing Chryseobacterium sp. Strain ISE14, a Biocontrol and Plant Growth-Promoting Rhizobacterium Isolated from Cucumber. Genome Announcements, 2018, 6, .	0.8	8
111	Maribacter litoralis sp. nov. a marine bacterium isolated from seashore. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3471-3478.	1.7	8
112	High substrate specificity of 3,6-anhydro- l -galactose dehydrogenase indicates its essentiality in the agar catabolism of a marine bacterium. Process Biochemistry, 2018, 64, 130-135.	3.7	7
113	Feasibility test of utilizing Saccharophagus degradans 2-40T as the source of crude enzyme for the saccharification of lignocellulose. Bioprocess and Biosystems Engineering, 2014, 37, 707-710.	3.4	6
114	Draft Genome Sequence of a Biocontrol Rhizobacterium, <i>Chryseobacterium kwangjuense</i> Strain KJ1R5, Isolated from Pepper (<i>Capsicum annuum</i>). Genome Announcements, 2016, 4, .	0.8	6
115	Cellotriose-hydrolyzing activity conferred by truncating the carbohydrate-binding modules of Cel5 from Hahella chejuensis. Bioprocess and Biosystems Engineering, 2017, 40, 241-249.	3.4	5
116	Target Selection for Structural Genomics: A Single Genome Approach. OMICS A Journal of Integrative Biology, 2002, 6, 349-362.	2.0	4
117	Production of p-acetaminophenol by whole-cell catalysis using Escherichia coli overexpressing bacterial aryl acylamidase. Biotechnology Letters, 2012, 34, 677-682.	2.2	4
118	Draft Genome Sequences of Chryseobacterium artocarpi UTM-3 ^T and Chryseobacterium contaminans C26 ^T , Isolated from Rhizospheres, and Chryseobacterium arthrosphaerae CC-VM-7 ^T , Isolated from the Feces of a Pill Millipede. Genome Announcements, 2016, 4, .	0.8	4
119	Prokaryotic Contig Annotation Pipeline Server: Web Application for a Prokaryotic Genome Annotation Pipeline Based on the Shiny App Package. Journal of Computational Biology, 2017, 24, 917-922.	1.6	4
120	Draft Genome Sequence of an Acid-Tolerant Yeast, Candida zemplinina NP2, a Potential Producer of Organic Acids. Genome Announcements, 2017, 5, .	0.8	4
121	Draft Genome Sequences of Two Glycoalkaloid-Degrading Arthrobacter Strains Isolated from Green Potato Peel. Microbiology Resource Announcements, 2019, 8, .	0.6	4
122	Evaluating Genetic Diversity of Agaricus bisporus Accessions through Phylogenetic Analysis Using Single-Nucleotide Polymorphism (SNP) Markers. Mycobiology, 2021, 49, 61-68.	1.7	4
123	Aurantiacibacter sediminis sp. nov., a marine bacterium isolated from a tidal flat. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	4
124	Rapid and robust enzymatic sensing and quantitation of 3,6-Anhydro-L-galactose in a heterogeneous sugar mixture. Carbohydrate Research, 2017, 446-447, 13-18.	2.3	3
125	3,6-Anhydro-L-galactonate cycloisomerase fromVibriosp. strain EJY3: crystallization and X-ray crystallographic analysis. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 511-514.	0.8	3
126	Draft Genome Sequence of a Novel <i>Serratia</i> sp. Strain with Antifungal Activity. Microbiology Resource Announcements, 2018, 7, .	0.6	3

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127	Draft Genome Sequences of Bacillus megaterium KU143, Microbacterium testaceum KU313, and Pseudomonas protegens AS15, Isolated from Stored Rice Grains. Genome Announcements, 2018, 6, .	0.8	3
128	Geneâ€Centric Metagenome Analysis Reveals Gene Clusters for Carbon Monoxide Conversion and Validates Isolation of a Clostridial Acetogen for C2 Chemical Production. Biotechnology Journal, 2019, 14, 1800471.	3.5	3
129	Characterization of two leaf rust-resistant Aegilops tauschii accessions for the synthetic wheat development. Applied Biological Chemistry, 2020, 63, .	1.9	3
130	Whole-Genome Sequences of Five Geobacillus stearothermophilus Strains Isolated from Processing Lines of Powdered Infant Formula. Microbiology Resource Announcements, 2019, 8, .	0.6	2
131	Structural insights into the psychrophilic germinal protease PaGPR and its autoinhibitory loop. Journal of Microbiology, 2020, 58, 772-779.	2.8	2
132	SNP-Based Genetic Linkage Map and Quantitative Trait Locus Mapping Associated with the Agronomically Important Traits of <i>Hypsizygus marmoreus</i> . Mycobiology, 2021, 49, 589-598.	1.7	2
133	Overexpression and characterization of recombinant agarases from Saccharophagus degradans strains 2–40. Journal of Biotechnology, 2008, 136, S589.	3.8	1
134	Draft Genome Sequences of Two Ureolytic Bacteria Isolated from Concrete Block Waste. Genome Announcements, 2016, 4, .	0.8	1
135	d -Stereoisomer preference of the OmpA-like domain of Pal in peptidoglycan of Acinetobacter baumannii. Process Biochemistry, 2017, 55, 110-115.	3.7	1
136	Crystal structure analysis of 3,6-anhydro- l -galactonate cycloisomerase suggests emergence of novel substrate specificity in the enolase superfamily. Biochemical and Biophysical Research Communications, 2017, 491, 217-222.	2.1	1
137	Preparation of a ribosomally synthesized fungal peptide toxin precursor and its in-vitro cyclization. Journal of Biotechnology, 2020, 308, 124-129.	3.8	1
138	Development of a new brown button mushroom cultivar 'Hogam'. Journal of Mushrooms, 2015, 13, 237-242.	0.3	1
139	Soil environment reshapes microbiota of laboratory-maintained Collembola during host development. Environmental Microbiomes, 2022, 17, 16.	5.0	1
140	Characterization of recombinant xylanases from Sacchrophagus degradans strains 2–40 for bioconversion of lignocellulosic biomass. Journal of Biotechnology, 2008, 136, S601.	3.8	0
141	Practical Guide for Fungal Gene Prediction from Genome Assembly and RNA-Seq Reads by FunGAP. Methods in Molecular Biology, 2019, 1962, 53-64.	0.9	0
142	Novel Monomeric Fungal Subtilisin Inhibitor from a Plant-Pathogenic Fungus, Choanephora cucurbitarum: Isolation and Molecular Characterization. Applied and Environmental Microbiology, 2020, 86, .	3.1	0
143	Development of a Novel Cell Surface Attachment System to Display Multi-Protein Complex Using the Cohesin-Dockerin Binding Pair. Journal of Microbiology and Biotechnology, 2021, 31, 1183-1189.	2.1	0
144	Characteristic evaluation of collected strains of Agaricus spp. based on ITS rDNA sequence. Journal of Mushrooms, 2014, 12, 244-250.	0.3	0

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145	Selection of parental monokaryons from Korean Hypsizigus marmoreus by protoplast regeneration. Journal of Mushrooms, 2015, 13, 270-273.	0.3	0
146	Selection of Agaricus bitorquis hybrid strains based on RAPD analysis. Journal of Mushrooms, 2015, 13, 243-249.	0.3	0
147	Structural studies of the virulence factor peptidoglycan-associated lipoprotein from a Gram-negative pathogen. Acta Crystallographica Section A: Foundations and Advances, 2016, 72, s218-s218.	0.1	0