List of Publications by Year in descending order

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Снамс-Ши Сна

#	Article	IF	CITATIONS
1	Biology of Acinetobacter baumannii: Pathogenesis, Antibiotic Resistance Mechanisms, and Prospective Treatment Options. Frontiers in Cellular and Infection Microbiology, 2017, 7, 55.	3.9	671
2	Antimicrobial Resistance of Hypervirulent Klebsiella pneumoniae: Epidemiology, Hypervirulence-Associated Determinants, and Resistance Mechanisms. Frontiers in Cellular and Infection Microbiology, 2017, 7, 483.	3.9	299
3	Biotransformation of Malachite Green by the Fungus <i>Cunninghamella elegans</i> . Applied and Environmental Microbiology, 2001, 67, 4358-4360.	3.1	241
4	Bacterial community analysis during fermentation of ten representative kinds of kimchi with barcoded pyrosequencing. Food Microbiology, 2012, 30, 197-204.	4.2	198
5	A master regulator ÏfBgoverns osmotic and oxidative response as well as differentiation via a network of sigma factors inStreptomycesâ€fcoelicolor. Molecular Microbiology, 2005, 57, 1252-1264.	2.5	159
6	Freshwater viral metagenome reveals novel and functional phage-borne antibiotic resistance genes. Microbiome, 2020, 8, 75.	11.1	118
7	Antibiotic resistome from the One-Health perspective: understanding and controlling antimicrobial resistance transmission. Experimental and Molecular Medicine, 2021, 53, 301-309.	7.7	113
8	Identification of proteins induced by polycyclic aromatic hydrocarbon inMycobacterium vanbaalenii PYR-1 using two-dimensional polyacrylamide gel electrophoresis andde novo sequencing methods. Proteomics, 2004, 4, 3899-3908.	2.2	90
9	Mobile resistome of human gut and pathogen drives anthropogenic bloom of antibiotic resistance. Microbiome, 2020, 8, 2.	11.1	80
10	<i>Escherichia coli</i> ribonuclease III activity is downregulated by osmotic stress: consequences for the degradation of <i>bdm</i> mRNA in biofilm formation. Molecular Microbiology, 2010, 75, 413-425.	2.5	71
11	Changes in human gut microbiota influenced by probiotic fermented milk ingestion. Journal of Dairy Science, 2015, 98, 3568-3576.	3.4	60
12	A novel sulfonamide resistance mechanism by two-component flavin-dependent monooxygenase system in sulfonamide-degrading actinobacteria. Environment International, 2019, 127, 206-215.	10.0	53
13	Purification and characterization of an erythromycin esterase from an erythromycin-resistantPseudomonassp FEMS Microbiology Letters, 2002, 210, 239-244.	1.8	50
14	Purification and characterization of thermostable β-glucosidase from the brown-rot basidiomycete Fomitopsis palustris grown on microcrystalline cellulose. Journal of Microbiology, 2008, 46, 51-55.	2.8	47
15	Degradation of cellulose by the major endoglucanase produced from the brown-rot fungus Fomitopsis pinicola. Biotechnology Letters, 2008, 30, 1373-1378.	2.2	45
16	Lysobacter panacisoli sp. nov., isolated from ginseng soil. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2193-2197.	1.7	39
17	Actibacter sediminis gen. nov., sp. nov., a marine bacterium of the family Flavobacteriaceae isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 139-143.	1.7	36
18	The brown-rot basidiomycete Fomitopsis palustris has the endo-glucanases capable of degrading microcrystalline cellulose. Journal of Microbiology and Biotechnology, 2007, 17, 800-5.	2.1	32

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19	Synthesis of Î <sup>3</sup> -glutamylcysteine as a major low-molecular-weight thiol in lactic acid bacteria Leuconostoc spp Biochemical and Biophysical Research Communications, 2008, 369, 1047-1051.	2.1	31
20	Genomic insights into the taxonomic status of the three subspecies of Bacillus subtilis. Systematic and Applied Microbiology, 2014, 37, 95-99.	2.8	24
21	Heterogeneous rRNAs are differentially expressed during the morphological development of <i>Streptomyces coelicolor</i> . FEMS Microbiology Letters, 2007, 275, 146-152.	1.8	21
22	Brevibacillus fluminis sp. nov., isolated from sediment of estuarine wetland. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 1595-1599.	1.7	21
23	Paenibacillus aestuarii sp. nov., isolated from an estuarine wetland. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 644-647.	1.7	20
24	Comparative genomic analysis of pyrene-degrading Mycobacterium species: Genomic islands and ring-hydroxylating dioxygenases involved in pyrene degradation. Journal of Microbiology, 2018, 56, 798-804.	2.8	20
25	Polymorphism of antibiotic-inactivating enzyme driven by ecology expands the environmental resistome. ISME Journal, 2018, 12, 267-276.	9.8	19
26	Impact of sulfamethoxazole on a riverine microbiome. Water Research, 2021, 201, 117382.	11.3	19
27	Fate of antibiotic resistant E. coli and antibiotic resistance genes during full scale conventional and advanced anaerobic digestion of sewage sludge. PLoS ONE, 2020, 15, e0237283.	2.5	18
28	Identification of genes for mycothiol biosynthesis in Streptomyces coelicolor A3(2). Journal of Microbiology, 2006, 44, 121-5.	2.8	18
29	Ecological processes underpinning microbial community structure during exposure to subinhibitory level of triclosan. Scientific Reports, 2019, 9, 4598.	3.3	17
30	The Modified β-Ketoadipate Pathway in <i>Rhodococcus rhodochrous</i> N75: Enzymology of 3-Methylmuconolactone Metabolism. Journal of Bacteriology, 1998, 180, 6668-6673.	2.2	17
31	Purification and characterization of a glutathioneS-transferase from the fungusCunninghamella elegans. FEMS Microbiology Letters, 2001, 203, 257-261.	1.8	16
32	Genome sequence of type strain of Staphylococcus aureus subsp. aureus. Gut Pathogens, 2014, 6, 6.	3.4	16
33	Bifidobacterium faecale sp. nov., isolated from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 3134-3139.	1.7	16
34	Functional characterization of a thermostable endoglucanase belonging to glycoside hydrolase family 45 from Fomitopsis palustris. Applied Microbiology and Biotechnology, 2018, 102, 6515-6523.	3.6	16
35	Overview of bioinformatic methods for analysis of antibiotic resistome from genome and metagenome data. Journal of Microbiology, 2021, 59, 270-280.	2.8	16
36	Lactobacillus alvi sp. nov., isolated from the intestinal tract of chicken. FEMS Microbiology Letters, 2011, 323, 83-87.	1.8	14

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37	Bacillus panacisoli sp. nov., isolated from ginseng soil. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 901-906.	1.7	14
38	Cohnella saccharovorans sp. nov., isolated from ginseng soil. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1713-1717.	1.7	14
39	Ramlibacter alkalitolerans sp. nov., alkali-tolerant bacterium isolated from soil of ginseng. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 4619-4623.	1.7	14
40	Chryseobacterium rigui sp. nov., isolated from an estuarine wetland. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 1062-1067.	1.7	13
41	Gordonia alkaliphila sp. nov., an actinomycete isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 327-331.	1.7	13
42	Flavihumibacter sediminis sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4310-4314.	1.7	13
43	Biotransformation of Plant Secondary Metabolite Decursin by Mycobacterium sp. PYR1001. Journal of Agricultural and Food Chemistry, 2010, 58, 2931-2934.	5.2	12
44	Stakelama sediminis sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 560-564.	1.7	12
45	Effects of biochar addition on the fate of ciprofloxacin and its associated antibiotic tolerance in an activated sludge microbiome. Environmental Pollution, 2022, 306, 119407.	7.5	12
46	Flavobacterium foetidum sp. nov., isolated from ginseng soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 616-622.	1.7	11
47	Chryseobacterium aureum sp. nov., isolated from the Han River, Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1628-1633.	1.7	10
48	Identification and functional analysis of a gene encoding β-glucosidase from the brown-rot basidiomycete Fomitopsis palustris. Journal of Microbiology, 2010, 48, 808-813.	2.8	9
49	Upregulation of RNase E activity by mutation of a site that uncompetitively interferes with RNA binding. RNA Biology, 2011, 8, 1022-1034.	3.1	9
50	Functional analysis of a gene encoding endoglucanase that belongs to glycosyl hydrolase family 12 from the brown-rot basidiomycete Fomitopsis palustris. Journal of Microbiology and Biotechnology, 2008, 18, 404-9.	2.1	9
51	Paenibacillus translucens sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 936-941.	1.7	8
52	Comamonas fluminis sp. nov., isolated from the Han River, Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	8
53	Genetic Analysis of the Invariant Residue G791 in <i>Escherichia coli</i> 16S rRNA Implicates RelA in Ribosome Function. Journal of Bacteriology, 2009, 191, 2042-2050.	2.2	7
54	Genome Sequence of Lactobacillus salivarius NIAS840, Isolated from Chicken Intestine. Journal of Bacteriology, 2011, 193, 5551-5552.	2.2	7

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55	Ferrimonas gelatinilytica sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4309-4314.	1.7	7
56	Paenibacillus limicola sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 423-426.	1.7	7
57	Marinitalea sucinacia gen. nov., sp. nov., a marine bacterium of the family Flavobacteriaceae isolated from tidal flat sediment. FEMS Microbiology Letters, 2011, 314, 89-94.	1.8	6
58	2-Nitrobenzoate 2-Nitroreductase (NbaA) Switches Its Substrate Specificity from 2-Nitrobenzoic Acid to 2,4-Dinitrobenzoic Acid under Oxidizing Conditions. Journal of Bacteriology, 2013, 195, 180-192.	2.2	6
59	Unique Features of <i>Aeromonas</i> Plasmid pAC3 and Expression of the Plasmid-Mediated Quinolone Resistance Genes. MSphere, 2017, 2, .	2.9	5
60	Myroides fluvii sp. nov., isolated from the Han River, Republic of Korea. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	5
61	Revisiting Polymorphic Diversity of Aminoglycoside N-Acetyltransferase AAC(6′)-lb Based on Bacterial Genomes of Human, Animal, and Environmental Origins. Frontiers in Microbiology, 2018, 9, 1831.	3.5	4
62	Functional analysis of the invariant residue G791 of Escherichia coli 16S rRNA. Journal of Microbiology, 2007, 45, 418-21.	2.8	4
63	Interspecies Interaction of Signal Peptide PapR Secreted by Bacillus cereus and Its Effect on Production of Antimicrobial Peptide. Applied Biochemistry and Biotechnology, 2012, 166, 700-710.	2.9	3
64	ldentification of Microorganisms, Cladosporium sp. and Sterigmatomyces sp., Proliferated on the Surface of Traditional Soy Sauce, and the Effect of NaCl Concentration on Their Enzymatic Activity. Korean Journal of Food Science and Technology, 2012, 44, 488-492.	0.3	2
65	Pedobacter aquae sp. nov., a multi-drug resistant bacterium isolated from fresh water. Antonie Van Leeuwenhoek, 2022, 115, 445-457.	1.7	2
66	Fungal β-Glycosidase Belonging to Subfamily 4 of Glycoside Hydrolase Family 30 with Transglycosylation Activity. Journal of Agricultural and Food Chemistry, 2021, 69, 15261-15267.	5.2	2
67	Report on 14 unrecorded bacterial species in Korea that belong to the phyla Bacteroidetes and Deinococcus-Thermus. Journal of Species Research, 2015, 4, 137-144.	0.1	1
68	A report of 10 unrecorded bacterial species of Korea, belonging to the phylum Firmicutes. Journal of Species Research, 2016, 5, 235-240.	0.1	1
69	Report on 31 unrecorded bacterial species in Korea that belong to the phylum Actinobacteria. Journal of Species Research, 2016, 5, 1-13.	0.1	1
70	A report on 33 unrecorded bacterial species of Korea isolated in 2014, belonging to the class Gammaproteobacteria. Journal of Species Research, 2016, 5, 241-253.	0.1	1
71	Stereo- and regiospecificcis,cis-muconate cycloisomerization byRhodococcus rhodochrousN75. FEMS Microbiology Letters, 2003, 224, 29-34.	1.8	0
72	Report on 24 unrecorded bacterial species of Korea belonging to the phylum Firmicutes. Journal of Species Research, 2015, 4, 127-136.	0.1	0

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73	A report of 39 unrecorded bacterial species in Korea, belonging to the Betaproteobacteria and Gammaproteobacteria. Journal of Species Research, 2015, 4, 109-126.	0.1	0
74	A report of 29 unrecorded bacterial species in Korea, belonging to the Alphaproteobacteria. Journal of Species Research, 2015, 4, 97-108.	0.1	0
75	A report of 31 unrecorded bacterial species in South Korea belonging to the class Gammaproteobacteria. Journal of Species Research, 2016, 5, 188-200.	0.1	0
76	A report of 21 unreported bacterial species in Korea, belonging to the Betaproteobacteria. Journal of Species Research, 2016, 5, 179-187.	0.1	0
77	A report of 26 unrecorded bacterial species in Korea, belonging to the Bacteroidetes and Firmicutes. Journal of Species Research, 2016, 5, 166-178.	0.1	0
78	A report of 38 unrecorded bacterial species in Korea, belonging to the phylum Actinobacteria. Journal of Species Research, 2016, 5, 223-234.	0.1	0
79	A report of 42 unrecorded bacterial species belonging to the Alphaproteobacteria in Korea. Journal of Species Research, 2016, 5, 206-219.	0.1	Ο
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