

# Jongsik Chun

## List of Publications by Year in descending order

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248  
papers

37,212  
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15466

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times ranked

23509  
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#	ARTICLE	IF	CITATIONS
1	Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1613-1617.	0.8	5,862
2	Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 716-721.	0.8	4,898
3	Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 346-351.	0.8	2,463
4	A large-scale evaluation of algorithms to calculate average nucleotide identity. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1281-1286.	0.7	2,461
5	Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 461-466.	0.8	2,359
6	OrthoANI: An improved algorithm and software for calculating average nucleotide identity. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1100-1103.	0.8	2,209
7	EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2259-2261.	0.8	1,960
8	UBCG: Up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. <i>Journal of Microbiology</i> , 2018, 56, 280-285.	1.3	1,010
9	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011, 477, 462-465.	13.7	649
10	Integrating genomics into the taxonomy and systematics of the Bacteria and Archaea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 316-324.	0.8	483
11	A novel electrochemically active and Fe(III)-reducing bacterium phylogenetically related to <i>Aeromonas hydrophila</i> , isolated from a microbial fuel cell. <i>FEMS Microbiology Letters</i> , 2003, 223, 129-134.	0.7	381
12	ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 2053-2057.	0.8	377
13	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15442-15447.	3.3	351
14	Genotypes Associated with Virulence in Environmental Isolates of <i>Vibrio cholerae</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 2421-2429.	1.4	317
15	Tropical Soil Bacterial Communities in Malaysia: pH Dominates in the Equatorial Tropics Too. <i>Microbial Ecology</i> , 2012, 64, 474-484.	1.4	258
16	Analysis of 16S-23S rRNA Intergenic Spacer Regions of <i>Vibrio cholerae</i> and <i>Vibrio mimicus</i> . <i>Applied and Environmental Microbiology</i> , 1999, 65, 2202-2208.	1.4	231
17	Phylogenetic study of the species within the family Streptomycetaceae. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 73-104.	0.7	225
18	Characterization of microbiome in bronchoalveolar lavage fluid of patients with lung cancer comparing with benign mass like lesions. <i>Lung Cancer</i> , 2016, 102, 89-95.	0.9	223

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19	Bacterial community structure in kimchi, a Korean fermented vegetable food, as revealed by 16S rRNA gene analysis. <i>International Journal of Food Microbiology</i> , 2005, 103, 91-96.	2.1	221
20	The analysis of oral microbial communities of wild-type and toll-like receptor 2-deficient mice using a 454 GS FLX Titanium pyrosequencer. <i>BMC Microbiology</i> , 2010, 10, 101.	1.3	204
21	Bacterial community analysis during fermentation of ten representative kinds of kimchi with barcoded pyrosequencing. <i>Food Microbiology</i> , 2012, 30, 197-204.	2.1	198
22	Phylogenetic analysis of <i>Bacillus subtilis</i> and related taxa based on partial <i>gyrA</i> gene sequences. <i>Antonie Van Leeuwenhoek</i> , 2000, 78, 123-127.	0.7	193
23	Characterization of biofilm structure and its effect on membrane permeability in MBR for dye wastewater treatment. <i>Water Research</i> , 2006, 40, 45-52.	5.3	190
24	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
25	jPHYDIT: a JAVA-based integrated environment for molecular phylogeny of ribosomal RNA sequences. <i>Bioinformatics</i> , 2005, 21, 3171-3173.	1.8	185
26	Population Dynamics of Chesapeake Bay Virioplankton: Total-Community Analysis by Pulsed-Field Gel Electrophoresis. <i>Applied and Environmental Microbiology</i> , 1999, 65, 231-240.	1.4	181
27	A Hump-Backed Trend in Bacterial Diversity with Elevation on Mount Fuji, Japan. <i>Microbial Ecology</i> , 2012, 63, 429-437.	1.4	166
28	Introducing EzAAI: a pipeline for high throughput calculations of prokaryotic average amino acid identity. <i>Journal of Microbiology</i> , 2021, 59, 476-480.	1.3	155
29	Distinctive Phyllosphere Bacterial Communities in Tropical Trees. <i>Microbial Ecology</i> , 2012, 63, 674-681.	1.4	154
30	<i>Nocardiopsis kunsanensis</i> sp. nov., a moderately halophilic actinomycete isolated from a saltern.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 1909-1913.	0.8	150
31	EzEditor: a versatile sequence alignment editor for both rRNA- and protein-coding genes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 689-691.	0.8	139
32	The Complete Genome Sequence of <i>Thermococcus onnurineus</i> NA1 Reveals a Mixed Heterotrophic and Carboxydrotrophic Metabolism. <i>Journal of Bacteriology</i> , 2008, 190, 7491-7499.	1.0	136
33	The Effect of Probiotics on Gut Microbiota during the <i>Helicobacter pylori</i> Eradication: Randomized Controlled Trial. <i>Helicobacter</i> , 2016, 21, 165-174.	1.6	124
34	Rhodococcal systematics: problems and developments. <i>Antonie Van Leeuwenhoek</i> , 1998, 74, 3-20.	0.7	122
35	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. <i>FEMS Microbiology Ecology</i> , 2014, 89, 465-475.	1.3	121
36	Analytical Tools and Databases for Metagenomics in the Next-Generation Sequencing Era. <i>Genomics and Informatics</i> , 2013, 11, 102.	0.4	117

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37	Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010, 48, 284-289.	1.3	116
38	Use of Barcoded Pyrosequencing and Shared OTUs To Determine Sources of Fecal Bacteria in Watersheds. <i>Environmental Science &amp; Technology</i> , 2010, 44, 7777-7782.	4.6	108
39	Cholera Outbreaks Caused by an Altered <i>Vibrio cholerae</i> O1 El Tor Biotype Strain Producing Classical Cholera Toxin B in Vietnam in 2007 to 2008. <i>Journal of Clinical Microbiology</i> , 2009, 47, 1568-1571.	1.8	104
40	<i>Leuconostoc kimchii</i> sp. nov., a new species from kimchi.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 1915-1919.	0.8	103
41	<i>Hahella chejuensis</i> gen. nov., sp. nov., an extracellular-polysaccharide-producing marine bacterium.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2001, 51, 661-666.	0.8	103
42	Genome Sequence of Hybrid <i>Vibrio cholerae</i> O1 MJ-1236, B-33, and CIRS101 and Comparative Genomics with <i>V. cholerae</i> . <i>Journal of Bacteriology</i> , 2010, 192, 3524-3533.	1.0	101
43	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , 2011, 39, e140-e140.	6.5	100
44	<i>Paenibacillus koreensis</i> sp. nov., a new species that produces an iturin-like antifungal compound.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 1495-1500.	0.8	99
45	Correlation between microbial community structure and biofouling in a laboratory scale membrane bioreactor with synthetic wastewater. <i>Desalination</i> , 2012, 287, 209-215.	4.0	98
46	A proposal for the reclassification of <i>Bdellovibrio stolpii</i> and <i>Bdellovibrio starrii</i> into a new genus, <i>Bacteriovorax</i> gen. nov. as <i>Bacteriovorax stolpii</i> comb. nov. and <i>Bacteriovorax starrii</i> comb. nov., respectively.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 219-224.	0.8	94
47	<i>Kordia algicida</i> gen. nov., sp. nov., an algicidal bacterium isolated from red tide. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 675-680.	0.8	94
48	<i>Flavobacterium antarcticum</i> sp. nov., a novel psychrotolerant bacterium isolated from the Antarctic. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 637-641.	0.8	94
49	<i>Demequina aestuarii</i> gen. nov., sp. nov., a novel actinomycete of the suborder Micrococccineae, and reclassification of <i>Cellulomonas fermentans</i> Bagnara et al. 1985 as <i>Actinotalea fermentans</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 151-156.	0.8	90
50	Identification of Household Bacterial Community and Analysis of Species Shared with Human Microbiome. <i>Current Microbiology</i> , 2013, 67, 557-563.	1.0	88
51	A Proposal To Reclassify <i>Nocardia pinensis</i> Blackall et al. as <i>Skermania piniformis</i> gen. nov., comb. nov.. <i>International Journal of Systematic Bacteriology</i> , 1997, 47, 127-131.	2.8	87
52	Comparison of the Gut Microbiota of Centenarians in Longevity Villages of South Korea with Those of Other Age Groups. <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 429-440.	0.9	87
53	<i>Nocardia salmonicida</i> nom. rev., a fish pathogen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 833-837.	0.8	85
54	<i>Serinicoccus marinus</i> gen. nov., sp. nov., a novel actinomycete with l-ornithine and l-serine in the peptidoglycan. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1585-1589.	0.8	84

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55	UBCG2: Up-to-date bacterial core genes and pipeline for phylogenomic analysis. <i>Journal of Microbiology</i> , 2021, 59, 609-615.	1.3	83
56	Application of the Whole Genome-Based Bacterial Identification System, TrueBac ID, Using Clinical Isolates That Were Not Identified With Three Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) Systems. <i>Annals of Laboratory Medicine</i> , 2019, 39, 530-536.	1.2	82
57	Metagenomic Insights into the Bioaerosols in the Indoor and Outdoor Environments of Childcare Facilities. <i>PLoS ONE</i> , 2015, 10, e0126960.	1.1	75
58	Multilocus sequence typing (MLST) analysis of <i>Vibrio cholerae</i> O1 El Tor isolates from Mozambique that harbour the classical CTX prophage. <i>Journal of Medical Microbiology</i> , 2006, 55, 165-170.	0.7	74
59	Impact of enrofloxacin on the human intestinal microbiota revealed by comparative molecular analysis. <i>Anaerobe</i> , 2012, 18, 310-320.	1.0	74
60	Current Status and Future Promise of the Human Microbiome. <i>Pediatric Gastroenterology, Hepatology and Nutrition</i> , 2013, 16, 71.	0.4	74
61	<i>Tsukamurella pseudospumae</i> sp. nov., a novel actinomycete isolated from activated sludge foam. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1209-1212.	0.8	71
62	Rapid phylogenetic dissection of prokaryotic community structure in tidal flat using pyrosequencing. <i>Journal of Microbiology</i> , 2008, 46, 357-363.	1.3	71
63	<i>Hongiella mannitolivorans</i> gen. nov., sp. nov., <i>Hongiella halophila</i> sp. nov. and <i>Hongiella ornithinivorans</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 157-162.	0.8	68
64	<i>Sejongia antarctica</i> gen. nov., sp. nov. and <i>Sejongia jeonii</i> sp. nov., isolated from the Antarctic. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 409-416.	0.8	68
65	<i>Streptomyces seoulensis</i> sp. nov.. <i>International Journal of Systematic Bacteriology</i> , 1997, 47, 492-498.	2.8	67
66	<i>Zooshikella ganghwensis</i> gen. nov., sp. nov., isolated from tidal flat sediments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1013-1018.	0.8	67
67	<i>Nocardia crassostreae</i> sp. nov., the causal agent of nocardiosis in Pacific oysters. <i>International Journal of Systematic Bacteriology</i> , 1998, 48, 237-246.	2.8	66
68	Profiling bacterial community in upper respiratory tracts. <i>BMC Infectious Diseases</i> , 2014, 14, 583.	1.3	66
69	<i>Nocardioides ganghwensis</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1295-1299.	0.8	65
70	Taxonomic evaluation of the genera <i>Ruegeria</i> and <i>Silicibacter</i> : a proposal to transfer the genus <i>Silicibacter</i> Petursdottir and Kristjansson 1999 to the genus <i>Ruegeria</i> Uchino et al. 1999. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 815-819.	0.8	65
71	Reassessment of the systematics of the suborder Pseudonocardineae: transfer of the genera within the family Actinosynnemataceae Labeda and Kroppenstedt 2000 emend. Zhi et al. 2009 into an emended family Pseudonocardiaceae Embley et al. 1989 emend. Zhi et al. 2009. <i>International Journal of Systematic and Evolutionary Microbiology</i> . 2011, 61, 1259-1264.	0.8	65
72	16S rRNA Gene-Based Identification of Bacteria and Archaea using the EzTaxon Server. <i>Methods in Microbiology</i> , 2014, 41, 61-74.	0.4	64

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73	<i>Aestuariibacter salexigens</i> gen. nov., sp. nov. and <i>Aestuariibacter halophilus</i> sp. nov., isolated from tidal flat sediment, and emended description of <i>Alteromonas macleodii</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 571-576.	0.8	63
74	Discovery of novel <i>Vibrio cholerae</i> VSP-II genomic islands using comparative genomic analysis. <i>FEMS Microbiology Letters</i> , 2010, 308, no-no.	0.7	63
75	Unification of the genera <i>Nonlabens</i> , <i>Persicivirga</i> , <i>Sandarakinotalea</i> and <i>Stenothermobacter</i> into a single emended genus, <i>Nonlabens</i> , and description of <i>Nonlabens agnitus</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2012, 35, 150-155.	1.2	63
76	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2813-9.	3.3	63
77	Polyphasic assignment of an aromatic-degrading <i>Pseudomonas</i> sp., strain DJ77, in the genus <i>Sphingomonas</i> as <i>Sphingomonas chungbukensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000, 50, 1641-1647.	0.8	61
78	<i>Flavobacterium weaverense</i> sp. nov. and <i>Flavobacterium segetis</i> sp. nov., novel psychrophiles isolated from the Antarctic. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1239-1244.	0.8	59
79	Complete Genome Sequence of <i>Vibrio vulnificus</i> MO6-24/O. <i>Journal of Bacteriology</i> , 2011, 193, 2062-2063.	1.0	59
80	Genome Sequence of <i>Escherichia coli</i> J53, a Reference Strain for Genetic Studies. <i>Journal of Bacteriology</i> , 2012, 194, 3742-3743.	1.0	58
81	Use of a <i>chiA</i> probe for detection of chitinase genes in bacteria from the Chesapeake Bay1. <i>FEMS Microbiology Ecology</i> , 2000, 34, 63-71.	1.3	56
82	The Genome Sequence of <i>Mycobacterium massiliense</i> ™ Strain CIP 108297 Suggests the Independent Taxonomic Status of the <i>Mycobacterium abscessus</i> Complex at the Subspecies Level. <i>PLoS ONE</i> , 2013, 8, e81560.	1.1	54
83	<i>Nocardioides aestuarii</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 2151-2154.	0.8	53
84	Pyrosequencing-based Molecular Monitoring of the Intestinal Bacterial Colonization in Preterm Infants. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2011, 53, 512-519.	0.9	53
85	Phylogenetic analysis of the genera <i>Streptomyces</i> and <i>Kitasatospora</i> based on partial RNA polymerase $\beta$ -subunit gene ( <i>rpoB</i> ) sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 593-598.	0.8	52
86	<i>Hymenobacter rigui</i> sp. nov., isolated from wetland freshwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2189-2192.	0.8	52
87	Comparative genomics of clinical and environmental <i>Vibrio mimicus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21134-21139.	3.3	52
88	<i>Comamonas koreensis</i> sp. nov., a non-motile species from wetland in Woopo, Korea.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 377-381.	0.8	51
89	Analysis of Thermophilic Clades within the Genus <i>Streptomyces</i> by 16S Ribosomal DNA Sequence Comparisons. <i>International Journal of Systematic Bacteriology</i> , 1996, 46, 581-587.	2.8	50
90	<i>Amycolatopsis japonicum</i> sp. nov., an Actinomycete Producing (S,S)-N,N'-Ethylenediaminedisuccinic Acid. <i>Systematic and Applied Microbiology</i> , 1997, 20, 78-84.	1.2	50

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91	Comparative genomic analysis reveals evidence of two novel <i>Vibrio</i> species closely related to <i>V. cholerae</i> . <i>BMC Microbiology</i> , 2010, 10, 154.	1.3	50
92	Genomic evolution of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , 2010, 13, 646-651.	2.3	50
93	Phylogeny of mycolic acid-containing actinomycetes. <i>Journal of Industrial Microbiology</i> , 1996, 17, 205-213.	0.9	49
94	<i>Tenacibaculum litoreum</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 635-640.	0.8	49
95	Archaeal diversity in tidal flat sediment as revealed by 16S rDNA analysis. <i>Journal of Microbiology</i> , 2005, 43, 144-51.	1.3	49
96	A defect in iron uptake enhances the susceptibility of <i>Cryptococcus neoformans</i> to azole antifungal drugs. <i>Fungal Genetics and Biology</i> , 2012, 49, 955-966.	0.9	48
97	Vertical distribution of bacterial community is associated with the degree of soil organic matter decomposition in the active layer of moist acidic tundra. <i>Journal of Microbiology</i> , 2016, 54, 713-723.	1.3	48
98	Large-Scale Genomics Reveals the Genetic Characteristics of Seven Species and Importance of Phylogenetic Distance for Estimating Pan-Genome Size. <i>Frontiers in Microbiology</i> , 2019, 10, 834.	1.5	48
99	Transfer of <i>Hongia koreensis</i> Lee et al. 2000 to the genus <i>Kribbella</i> Park et al. 1999 as <i>Kribbella koreensis</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1005-1007.	0.8	47
100	rRNASelector: A computer program for selecting ribosomal RNA encoding sequences from metagenomic and metatranscriptomic shotgun libraries. <i>Journal of Microbiology</i> , 2011, 49, 689-691.	1.3	45
101	<i>Amycolatopsis thermoflava</i> sp. nov., a novel soil actinomycete from Hainan Island, China. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 1369-1373.	0.8	44
102	<i>Glaciecola nitratireducens</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2185-2188.	0.8	44
103	Phylogeny Trumps Chemotaxonomy: A Case Study Involving <i>Turicella otitidis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 834.	1.5	44
104	Multilocus variable-number tandem repeat analysis of <i>Vibrio cholerae</i> O1 El Tor strains harbouring classical toxin B. <i>Journal of Medical Microbiology</i> , 2010, 59, 763-769.	0.7	43
105	<i>Marinifilum fragile</i> gen. nov., sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2241-2246.	0.8	42
106	A Vanillin Derivative Causes Mitochondrial Dysfunction and Triggers Oxidative Stress in <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , 2014, 9, e89122.	1.1	42
107	Spatial Scaling Effects on Soil Bacterial Communities in Malaysian Tropical Forests. <i>Microbial Ecology</i> , 2014, 68, 247-258.	1.4	42
108	Complete Genome Sequence of Middle East Respiratory Syndrome Coronavirus KOR/KNIH/002_05_2015, Isolated in South Korea. <i>Genome Announcements</i> , 2015, 3, .	0.8	42



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109	<i>Kitasatospora cheerisanensis</i> sp. nov., a new species of the genus <i>Kitasatospora</i> that produces an antifungal agent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 753-758.	0.8	41
110	<i>Tsukamurella spumae</i> sp. nov., A Novel Actinomycete Associated with Foaming in Activated Sludge Plants. <i>Systematic and Applied Microbiology</i> , 2003, 26, 367-375.	1.2	41
111	Improved pipeline for reducing erroneous identification by 16S rRNA sequences using the Illumina MiSeq platform. <i>Journal of Microbiology</i> , 2015, 53, 60-69.	1.3	41
112	<i>Photobacterium ganghwense</i> sp. nov., a halophilic bacterium isolated from sea water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 745-749.	0.8	41
113	<i>Sphingopyxis marina</i> sp. nov. and <i>Sphingopyxis litoris</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2415-2419.	0.8	40
114	<i>Nocardioides dokdonensis</i> sp. nov., an actinomycete isolated from sand sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2619-2623.	0.8	39
115	An eco-friendly treatment of tannery wastewater using bioaugmentation with a novel microbial consortium. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2013, 48, 1732-1739.	0.9	39
116	<i>Dehalogenimonas formicexedens</i> sp. nov., a chlorinated alkane-respiring bacterium isolated from contaminated groundwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1366-1373.	0.8	39
117	<i>Nocardia flavorosea</i> sp. nov.. <i>International Journal of Systematic Bacteriology</i> , 1998, 48, 901-905.	2.8	38
118	<i>Lacinutrix jangbogonensis</i> sp. nov., a psychrophilic bacterium isolated from Antarctic marine sediment and emended description of the genus <i>Lacinutrix</i> . <i>Antonie Van Leeuwenhoek</i> , 2014, 106, 527-533.	0.7	38
119	Genomic characterization of <i>Nocardia seriolae</i> strains isolated from diseased fish. <i>MicrobiologyOpen</i> , 2019, 8, e00656.	1.2	38
120	Activated sludge foaming: the true extent of actinomycete diversity. <i>Water Science and Technology</i> , 1998, 37, 511-519.	1.2	37
121	<i>Thalassobius aestuarii</i> sp. nov., isolated from tidal flat sediment. <i>Journal of Microbiology</i> , 2006, 44, 171-6.	1.3	37
122	N-Acetylglucosaminidase activities in wetlands: a global survey. <i>Hydrobiologia</i> , 2005, 532, 103-110.	1.0	36
123	<i>Anaerosporobacter mobilis</i> gen. nov., sp. nov., isolated from forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 1784-1787.	0.8	36
124	<i>Actibacter sediminis</i> gen. nov., sp. nov., a marine bacterium of the family Flavobacteriaceae isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 139-143.	0.8	36
125	Genome Sequence of <i>Lactobacillus mucosae</i> LM1, Isolated from Piglet Feces. <i>Journal of Bacteriology</i> , 2012, 194, 4766-4766.	1.0	35
126	Genomic Insight Into the Predominance of Candidate Phylum Atribacteria JS1 Lineage in Marine Sediments. <i>Frontiers in Microbiology</i> , 2018, 9, 2909.	1.5	35



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