

Jongsik Chun

List of Publications by Year in descending order

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Version: 2024-02-01

248
papers

37,212
citations

15466

65
h-index

3173

186
g-index

252
all docs

252
docs citations

252
times ranked

23509
citing authors

#	ARTICLE	IF	CITATIONS
1	AMDB: a database of animal gut microbial communities with manually curated metadata. <i>Nucleic Acids Research</i> , 2022, 50, D729-D735.	6.5	11
2	Genome insights into the pharmaceutical and plant growth promoting features of the novel species <i>Nocardia alni</i> sp. nov. <i>BMC Genomics</i> , 2022, 23, 70.	1.2	10
3	Proposal of a health gut microbiome index based on a meta-analysis of Korean and global population datasets. <i>Journal of Microbiology</i> , 2022, 60, 533-549.	1.3	7
4	Epidemiologic Linkage of COVID-19 Outbreaks at Two University-affiliated Hospitals in the Seoul Metropolitan Area in March 2020. <i>Journal of Korean Medical Science</i> , 2021, 36, e38.	1.1	5
5	Characterization of Gut Microbiome in Korean Patients with Metabolic Associated Fatty Liver Disease. <i>Nutrients</i> , 2021, 13, 1013.	1.7	18
6	Taxonomic composition and variation in the gut microbiota of laboratory mice. <i>Mammalian Genome</i> , 2021, 32, 297-310.	1.0	9
7	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
8	UBCG2: Up-to-date bacterial core genes and pipeline for phylogenomic analysis. <i>Journal of Microbiology</i> , 2021, 59, 609-615.	1.3	83
9	VicPred: A <i>Vibrio cholerae</i> Genotype Prediction Tool. <i>Frontiers in Microbiology</i> , 2021, 12, 691895.	1.5	12
10	NASCUP: Nucleic Acid Sequence Classification by Universal Probability. <i>IEEE Access</i> , 2021, 9, 162779-162791.	2.6	0
11	Emotional well-being and gut microbiome profiles by enterotype. <i>Scientific Reports</i> , 2020, 10, 20736.	1.6	35
12	Metagenomic Association Analysis of Gut Symbiont <i>Limosilactobacillus reuteri</i> Without Host-Specific Genome Isolation. <i>Frontiers in Microbiology</i> , 2020, 11, 585622.	1.5	4
13	Comparative analysis of the tonsillar microbiota in IgA nephropathy and other glomerular diseases. <i>Scientific Reports</i> , 2020, 10, 16206.	1.6	14
14	Changes in the Intestinal Microbiota of Patients with Inflammatory Bowel Disease with Clinical Remission during an 8-Week Infliximab Infusion Cycle. <i>Microorganisms</i> , 2020, 8, 874.	1.6	16
15	Improved Metagenomic Taxonomic Profiling Using a Curated Core Gene-Based Bacterial Database Reveals Unrecognized Species in the Genus <i>Streptococcus</i> . <i>Pathogens</i> , 2020, 9, 204.	1.2	15
16	Characterization of intratissue bacterial communities and isolation of <i>Escherichia coli</i> from oral lichen planus lesions. <i>Scientific Reports</i> , 2020, 10, 3495.	1.6	21
17	Genome-based reclassification of <i>Paenibacillus jamilae</i> Aguilera et al. 2001 as a later heterotypic synonym of <i>Paenibacillus polymyxa</i> (Prazmowski 1880) Ash et al. 1994. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3134-3138.	0.8	10
18	Genomic characterization of <i>Nocardia seriolae</i> strains isolated from diseased fish. <i>MicrobiologyOpen</i> , 2019, 8, e00656.	1.2	38

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19	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
20	Introducing Murine Microbiome Database (MMDB): A Curated Database with Taxonomic Profiling of the Healthy Mouse Gastrointestinal Microbiome. <i>Microorganisms</i> , 2019, 7, 480.	1.6	19
21	Comparative Genomic and Phylogenomic Analyses Clarify Relationships Within and Between <i>Bacillus cereus</i> and <i>Bacillus thuringiensis</i> : Proposal for the Recognition of Two <i>Bacillus thuringiensis</i> Genomovars. <i>Frontiers in Microbiology</i> , 2019, 10, 1978.	1.5	33
22	Comparative Genomic Analysis of the 2016 <i>Vibrio cholerae</i> Outbreak in South Korea. <i>Frontiers in Public Health</i> , 2019, 7, 228.	1.3	10
23	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
24	VCGIDB: A Database and Web Resource for the Genomic Islands from <i>Vibrio cholerae</i> . <i>Pathogens</i> , 2019, 8, 261.	1.2	5
25	Genome-based reclassification of <i>Weissella jogaejeotgali</i> as a later heterotypic synonym of <i>Weissella thailandensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3672-3675.	0.8	10
26	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
27	hc-OTU: A Fast and Accurate Method for Clustering Operational Taxonomic Units Based on Homopolymer Compaction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 441-451.	1.9	10
28	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
29	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
30	Genome sequence of <i>Mycobacterium yongonense</i> RT 955-2015 isolate from a patient misdiagnosed with multidrug-resistant tuberculosis: First clinical detection in Tanzania. <i>International Journal of Infectious Diseases</i> , 2018, 71, 82-88.	1.5	5
31	Phylogeny Trumps Chemotaxonomy: A Case Study Involving <i>Turicella otitidis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 834.	1.5	44
32	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
33	A large-scale evaluation of algorithms to calculate average nucleotide identity. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 1281-1286.	0.7	2,461
34	Replication of <i>Vibrio cholerae</i> classical CTX phage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2343-2348.	3.3	27
35	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
36	<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

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37	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
38	Rejection of reclassification of <i>Lactobacillus kimchii</i> and <i>Lactobacillus bobalius</i> as later subjective synonyms of <i>Lactobacillus paralimentarius</i> using comparative genomics. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 4515-4517.	0.8	7
39	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
40	Genome sequence of the organohalide-respiring <i>Dehalogenimonas alkenigignens</i> type strain (IP3-3T). <i>Standards in Genomic Sciences</i> , 2016, 11, 44.	1.5	10
41	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
42	A single gene of a commensal microbe affects host susceptibility to enteric infection. <i>Nature Communications</i> , 2016, 7, 11606.	5.8	31
43	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
44	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
45	Complete genome sequence of <i>Mycobacterium tuberculosis</i> K from a Korean high school outbreak, belonging to the Beijing family. <i>Standards in Genomic Sciences</i> , 2015, 10, 78.	1.5	26
46	Metagenomic Insights into the Bioaerosols in the Indoor and Outdoor Environments of Childcare Facilities. <i>PLoS ONE</i> , 2015, 10, e0126960.	1.1	75
47	Draft genome sequence of the psychrophilic bacterium <i>Lacinutrix jangbogonensis</i> PAMC 27137T. <i>Marine Genomics</i> , 2015, 23, 31-32.	0.4	3
48	<i>Paenibacillus xanthinilyticus</i> sp. nov., isolated from agricultural soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 2937-2942.	0.8	13
49	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
50	Telomere maintenance through recruitment of internal genomic regions. <i>Nature Communications</i> , 2015, 6, 8189.	5.8	26
51	<i>Neisseria weaveri</i> Andersen et al. 1993 is a later heterotypic synonym of <i>Neisseria weaveri</i> Holmes et al. 1993. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 463-464.	0.8	9
52	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
53	Large-scale evaluation of experimentally determined DNA G+C contents with whole genome sequences of prokaryotes. <i>Systematic and Applied Microbiology</i> , 2015, 38, 79-83.	1.2	18
54	<i>Burkholderia megalochromosomata</i> sp. nov., isolated from grassland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 959-964.	0.8	14

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55	Comparison of the genome profiles between head and body lice. <i>Journal of Asia-Pacific Entomology</i> , 2015, 18, 377-382.	0.4	8
56	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
57	<i>Burkholderia monticola</i> sp. nov., isolated from mountain soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 504-509.	0.8	14
58	Report on 14 unrecorded bacterial species in Korea that belong to the phyla Bacteroidetes and Deinococcus-Thermus. <i>Journal of Species Research</i> , 2015, 4, 137-144.	0.1	1
59	The Genus <i>Vibrio</i> and Related Genera. , 2015, , 371-382.		0
60	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
61	Profiling bacterial community in upper respiratory tracts. <i>BMC Infectious Diseases</i> , 2014, 14, 583.	1.3	66
62	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
63	Clonality and Resistome Analysis of KPC-Producing <i>Klebsiella pneumoniae</i> Strain Isolated in Korea Using Whole Genome Sequencing. <i>BioMed Research International</i> , 2014, 2014, 1-6.	0.9	30
64	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. <i>PLoS Biology</i> , 2014, 12, e1001920.	2.6	190
65	Draft Genome Sequence of <i>Kitasatospora cheerisanensis</i> KCTC 2395, Which Produces Plecomacrolide against Phytopathogenic Fungi. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
66	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
67	Genome sequence of type strain of <i>Staphylococcus aureus</i> subsp. <i>aureus</i> . <i>Gut Pathogens</i> , 2014, 6, 6.	1.6	16
68	Genomic insights into the taxonomic status of the three subspecies of <i>Bacillus subtilis</i> . <i>Systematic and Applied Microbiology</i> , 2014, 37, 95-99.	1.2	24
69	Bacterial community of sediments from the Australian-Antarctic ridge. <i>Polar Biology</i> , 2014, 37, 587-593.	0.5	10
70	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
71	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
72	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

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73	Lacinutrix jangbogonensis sp. nov., a psychrophilic bacterium isolated from Antarctic marine sediment and emended description of the genus Lacinutrix. Antonie Van Leeuwenhoek, 2014, 106, 527-533.	0.7	38
74	Spatial Scaling Effects on Soil Bacterial Communities in Malaysian Tropical Forests. Microbial Ecology, 2014, 68, 247-258.	1.4	42
75	Draft genome sequence of Pseudomonas sp. strain G5, isolated from a traditional indigo fermentation dye vat. Journal of the Korean Society for Applied Biological Chemistry, 2013, 56, 339-341.	0.9	2
76	Identification of Household Bacterial Community and Analysis of Species Shared with Human Microbiome. Current Microbiology, 2013, 67, 557-563.	1.0	88
77	An eco-friendly treatment of tannery wastewater using bioaugmentation with a novel microbial consortium. Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering, 2013, 48, 1732-1739.	0.9	39
78	Comparison of a culture-based and a PCR-based methods for estimating bacterial abundance on eggshells, with comments on statistical analyses. Journal of Field Ornithology, 2013, 84, 304-315.	0.3	10
79	Structure of soil bacterial communities in relation to environmental variables in a semi-arid region of Mongolia. Journal of Arid Environments, 2013, 89, 38-44.	1.2	18
80	Fretibacter rubidus gen. nov., sp. nov., isolated from seawater. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4633-4638.	0.8	15
81	Analytical Tools and Databases for Metagenomics in the Next-Generation Sequencing Era. Genomics and Informatics, 2013, 11, 102.	0.4	117
82	Flavobacterium limnosediminis sp. nov., isolated from sediment of a freshwater lake. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4784-4789.	0.8	17
83	Genome sequence of the moderately halophilic bacterium Salinicoccus carniancra type strain CrmT (= DSM 23852T). Standards in Genomic Sciences, 2013, 8, 255-263.	1.5	11
84	Genome sequence of the chromate-resistant bacterium Leucobacter salsicius type strain M1-8T. Standards in Genomic Sciences, 2013, 9, 495-504.	1.5	9
85	Current Status and Future Promise of the Human Microbiome. Pediatric Gastroenterology, Hepatology and Nutrition, 2013, 16, 71.	0.4	74
86	The Genome Sequence of <i>Mycobacterium massiliense</i> ™ Strain CIP 108297 Suggests the Independent Taxonomic Status of the Mycobacterium abscessus Complex at the Subspecies Level. PLoS ONE, 2013, 8, e81560.	1.1	54
87	Production of Hydrogen and Volatile Fatty Acid by Enterobacter sp. T4384 Using Organic Waste Materials. Journal of Microbiology and Biotechnology, 2013, 23, 189-194.	0.9	4
88	Transcriptomic Analysis of Genes Modulated by Cyclo(L-Phenylalanine-L-Proline) in Vibrio vulnificus. Journal of Microbiology and Biotechnology, 2013, 23, 1791-1801.	0.9	14
89	Complete Genome Sequence of Mycobacterium intracellulare Clinical Strain MOTT-36Y, Belonging to the INT5 Genotype. Journal of Bacteriology, 2012, 194, 4141-4142.	1.0	13
90	Genome Sequence of Lactobacillus mucosae LM1, Isolated from Piglet Feces. Journal of Bacteriology, 2012, 194, 4766-4766.	1.0	35

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91	Flavivirga jejuensis gen. nov., sp. nov., and Flavivirga amylovorans sp. nov., new members of the family Flavobacteriaceae isolated from seawater, and emended descriptions of the genera Psychroserpens and Lacinutrix. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 1061-1068.	0.8	28
92	Genome Sequence of Extracellular-Protease-Producing Alishewanella jeotgali Isolated from Traditional Korean Fermented Seafood. Journal of Bacteriology, 2012, 194, 2097-2097.	1.0	15
93	Genome Sequence of Escherichia coli J53, a Reference Strain for Genetic Studies. Journal of Bacteriology, 2012, 194, 3742-3743.	1.0	58
94	Draft Genome Sequence of Escherichia coli W26, an Enteric Strain Isolated from Cow Feces. Journal of Bacteriology, 2012, 194, 5149-5150.	1.0	5
95	Draft Genome Sequence of Mycobacterium abscessus subsp. bolletii BDT. Journal of Bacteriology, 2012, 194, 2756-2757.	1.0	30
96	Genome Sequence of Pectin-Degrading Alishewanella aestuarii Strain B11 ^T , Isolated from Tidal Flat Sediment. Journal of Bacteriology, 2012, 194, 5476-5476.	1.0	12
97	Complete Genome Sequence of Mycobacterium intracellulare Clinical Strain MOTT-02. Journal of Bacteriology, 2012, 194, 2771-2771.	1.0	17
98	Toll-like receptor 9 mediates oral bacteria-induced IL-8 expression in gingival epithelial cells. Immunology and Cell Biology, 2012, 90, 655-663.	1.0	26
99	Genome Sequence of Pectin-Degrading Alishewanella agri, Isolated from Landfill Soil. Journal of Bacteriology, 2012, 194, 5135-5136.	1.0	11
100	Draft Genome Sequencing of Bacillus sp. Strain M2-6, Isolated from the Roots of Korean Ginseng, Panax ginseng C. A. Meyer, after High-Hydrostatic-Pressure Processing. Journal of Bacteriology, 2012, 194, 7003-7004.	1.0	2
101	Draft Genome Sequence of Klebsiella pneumoniae subsp. pneumoniae DSM 30104 ^T . Journal of Bacteriology, 2012, 194, 5722-5723.	1.0	3
102	Draft Genome Sequence of Weissella koreensis KCTC 3621 T. Journal of Bacteriology, 2012, 194, 5711-5712.	1.0	9
103	Complete Genome Sequence of Mycobacterium intracellulare Strain ATCC 13950T. Journal of Bacteriology, 2012, 194, 2750-2750.	1.0	25
104	Draft Genome Sequence of Staphylococcus saprophyticus subsp. saprophyticus M1-1, Isolated from the Gills of a Korean Rockfish, Sebastes schlegeli Hilgendorf, after High Hydrostatic Pressure Processing. Journal of Bacteriology, 2012, 194, 4441-4442.	1.0	5
105	Genome Sequence of the Halotolerant Staphylococcus sp. Strain OJ82, Isolated from Korean Traditional Salt-Fermented Seafood. Journal of Bacteriology, 2012, 194, 6353-6354.	1.0	7
106	Draft Genome Sequence of Escherichia coli A127, a Porcine Isolate Belonging to Phylogenetic Group B1. Journal of Bacteriology, 2012, 194, 6640-6641.	1.0	1
107	A defect in iron uptake enhances the susceptibility of Cryptococcus neoformans to azole antifungal drugs. Fungal Genetics and Biology, 2012, 49, 955-966.	0.9	48
108	Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 716-721.	0.8	4,898

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109	TBC: A clustering algorithm based on prokaryotic taxonomy. <i>Journal of Microbiology</i> , 2012, 50, 181-185.	1.3	26
110	Tropical Soil Bacterial Communities in Malaysia: pH Dominates in the Equatorial Tropics Too. <i>Microbial Ecology</i> , 2012, 64, 474-484.	1.4	258
111	Comparative genomics of <i>Neisseria weaveri</i> clarifies the taxonomy of this species and identifies genetic determinants that may be associated with virulence. <i>FEMS Microbiology Letters</i> , 2012, 328, 100-105.	0.7	12
112	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
113	Impact of enrofloxacin on the human intestinal microbiota revealed by comparative molecular analysis. <i>Anaerobe</i> , 2012, 18, 310-320.	1.0	74
114	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
115	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
116	A Hump-Backed Trend in Bacterial Diversity with Elevation on Mount Fuji, Japan. <i>Microbial Ecology</i> , 2012, 63, 429-437.	1.4	166
117	Distinctive Phyllosphere Bacterial Communities in Tropical Trees. <i>Microbial Ecology</i> , 2012, 63, 674-681.	1.4	154
118	Phylogenetic study of the species within the family Streptomycetaceae. <i>Antonie Van Leeuwenhoek</i> , 2012, 101, 73-104.	0.7	225
119	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 Pseudonocardaceae 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
120	<i>Aquimarina addita</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2445-2449.	0.8	30
121	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
122	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011, 477, 462-465.	13.7	649
123	Comparative approach to capture bacterial diversity of coastal waters. <i>Journal of Microbiology</i> , 2011, 49, 729-740.	1.3	25
124	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
125	<i>Snuella lapsa</i> gen. nov., sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2469-2474.	0.8	12
126	Genome Sequence of <i>Lactobacillus ruminis</i> SPM0211, Isolated from a Fecal Sample from a Healthy Korean. <i>Journal of Bacteriology</i> , 2011, 193, 5034-5034.	1.0	6

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127	Genome Sequence of <i>Escherichia coli</i> AA86, Isolated from Cow Feces. <i>Journal of Bacteriology</i> , 2011, 193, 3681-3681.	1.0	9
128	Draft Genome Sequence of <i>Shewanella</i> sp. Strain HN-41, Which Produces Arsenic-Sulfide Nanotubes. <i>Journal of Bacteriology</i> , 2011, 193, 5039-5040.	1.0	8
129	<i>Pontirhabdus pectinivorans</i> gen. nov., sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2475-2481.	0.8	18
130	Genome Sequence of <i>Lactobacillus johnsonii</i> PF01, Isolated from Piglet Feces. <i>Journal of Bacteriology</i> , 2011, 193, 5030-5031.	1.0	16
131	Complete Genome Sequence of <i>Vibrio vulnificus</i> MO6-24/O. <i>Journal of Bacteriology</i> , 2011, 193, 2062-2063.	1.0	59
132	Draft Genome Sequence of <i>Methylophaga aminisulfidivorans</i> MP ^T . <i>Journal of Bacteriology</i> , 2011, 193, 4265-4265.	1.0	12
133	Genome Sequence of <i>Lactobacillus salivarius</i> GJ-24, a Probiotic Strain Isolated from Healthy Adult Intestine. <i>Journal of Bacteriology</i> , 2011, 193, 5021-5022.	1.0	12
134	<i>Zobellella aerophila</i> sp. nov., isolated from seashore sand, and emended description of the genus <i>Zobellella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2491-2495.	0.8	14
135	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , 2011, 39, e140-e140.	6.5	100
136	Occurrence of the <i>Vibrio cholerae</i> Seventh Pandemic VSP-I Island and a New Variant. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 1-7.	1.0	33
137	Designing primers from multiple sequences using matchup program to improve detection of hepatitis B virus by polymerase chain reaction. <i>Journal of Microbiology</i> , 2010, 48, 111-116.	1.3	1
138	Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010, 48, 284-289.	1.3	116
139	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
140	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
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