

Jongsik Chun

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

250
papers

26,465
citations

56
h-index

160
g-index

252
ext. papers

33,086
ext. citations

3.7
avg, IF

7.25
L-index

#	Paper	IF	Citations
250	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	2.2	4480
249	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	2.2	3649
248	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	2.2	1807
247	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	2.2	1657
246	OrthoANI: An improved algorithm and software for calculating average nucleotide identity. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016 , 66, 1100-1103	2.2	1338
245	A large-scale evaluation of algorithms to calculate average nucleotide identity. <i>Antonie Van Leeuwenhoek</i> , 2017 , 110, 1281-1286	2.1	1296
244	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	2.2	1279
243	UBCG: Up-to-date bacterial core gene set and pipeline for phylogenomic tree reconstruction. <i>Journal of Microbiology</i> , 2018 , 56, 280-285	3	505
242	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011 , 477, 462-5	50.4	492
241	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	2.2	327
240	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, 129-34	2.9	318
239	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, 15442-7	11.5	297
238	Genotypes associated with virulence in environmental isolates of <i>Vibrio cholerae</i> . <i>Applied and Environmental Microbiology</i> , 2001 , 67, 2421-9	4.8	261
237	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, 2202-8	4.8	220
236	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	2.2	200
235	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, 91-6	5.8	189
234	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	4.5	181

233	Tropical soil bacterial communities in Malaysia: pH dominates in the equatorial tropics too. <i>Microbial Ecology</i> , 2012 , 64, 474-84	4.4	173
232	Characterization of biofilm structure and its effect on membrane permeability in MBR for dye wastewater treatment. <i>Water Research</i> , 2006 , 40, 45-52	12.5	172
231	Phylogenetic study of the species within the family Streptomyetaceae. <i>Antonie Van Leeuwenhoek</i> , 2012 , 101, 73-104	2.1	162
230	jPHYDIT: a JAVA-based integrated environment for molecular phylogeny of ribosomal RNA sequences. <i>Bioinformatics</i> , 2005 , 21, 3171-3	7.2	158
229	Bacterial community analysis during fermentation of ten representative kinds of kimchi with barcoded pyrosequencing. <i>Food Microbiology</i> , 2012 , 30, 197-204	6	155
228	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, 123-7	2.1	150
227	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146
226	Population dynamics of chesapeake bay virioplankton: total-community analysis by pulsed-field gel electrophoresis. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 231-40	4.8	146
225	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	5.9	137
224	<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 Pt 5, 1909-1913	2.2	130
223	The complete genome sequence of <i>Thermococcus onnurineus</i> NA1 reveals a mixed heterotrophic and carboxydrotrophic metabolism. <i>Journal of Bacteriology</i> , 2008 , 190, 7491-9	3.5	119
222	A hump-backed trend in bacterial diversity with elevation on Mount Fuji, Japan. <i>Microbial Ecology</i> , 2012 , 63, 429-37	4.4	115
221	Distinctive phyllosphere bacterial communities in tropical trees. <i>Microbial Ecology</i> , 2012 , 63, 674-81	4.4	111
220	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	2.2	109
219	Analytical tools and databases for metagenomics in the next-generation sequencing era. <i>Genomics and Informatics</i> , 2013 , 11, 102-13	1.9	98
218	Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010 , 48, 284-9	3	97
217	Use of barcoded pyrosequencing and shared OTUs to determine sources of fecal bacteria in watersheds. <i>Environmental Science & Technology</i> , 2010 , 44, 7777-82	10.3	95
216	Rhodococcal systematics: problems and developments. <i>Antonie Van Leeuwenhoek</i> , 1998 , 74, 3-20	2.1	94

215	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, 1568-71	9.7	93
214	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , 2011 , 39, e140	20.1	93
213	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, 3524-33	3.5	87
212	Correlation between microbial community structure and biofouling in a laboratory scale membrane bioreactor with synthetic wastewater. <i>Desalination</i> , 2012 , 287, 209-215	10.3	85
211	The Effect of Probiotics on Gut Microbiota during the <i>Helicobacter pylori</i> Eradication: Randomized Controlled Trial. <i>Helicobacter</i> , 2016 , 21, 165-74	4.9	85
210	<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	2.2	83
209	<i>Leuconostoc kimchii</i> sp. nov., a new species from kimchi. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000 , 50 Pt 5, 1915-1919	2.2	83
208	<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	2.2	80
207	<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 Pt 4, 1495-1500	2.2	77
206	Identification of household bacterial community and analysis of species shared with human microbiome. <i>Current Microbiology</i> , 2013 , 67, 557-63	2.4	75
205	Bacterial community structure and soil properties of a subarctic tundra soil in Council, Alaska. <i>FEMS Microbiology Ecology</i> , 2014 , 89, 465-75	4.3	74
204	<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	2.2	74
203	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 Pt 1, 219-224	2.2	73
202	<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	2.2	72
201	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	3.2	67
200	Impact of enrofloxacin on the human intestinal microbiota revealed by comparative molecular analysis. <i>Anaerobe</i> , 2012 , 18, 310-20	2.8	64
199	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, 127-31		64
198	<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	2.2	64

197	<i>Nocardia salmonicida</i> nom. rev., a fish pathogen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999 , 49 Pt 2, 833-7	2.2	62
196	<i>Nocardioides ganghwensis</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 1295-1299	2.2	60
195	<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	2.2	57
194	Rapid phylogenetic dissection of prokaryotic community structure in tidal flat using pyrosequencing. <i>Journal of Microbiology</i> , 2008 , 46, 357-63	3	56
193	<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	2.2	56
192	Current status and future promise of the human microbiome. <i>Pediatric Gastroenterology, Hepatology and Nutrition</i> , 2013 , 16, 71-9	2.3	55
191	Complete genome sequence of <i>Vibrio vulnificus</i> MO6-24/O. <i>Journal of Bacteriology</i> , 2011 , 193, 2062-3	3.5	55
190	<i>Streptomyces seoulensis</i> sp. nov. <i>International Journal of Systematic Bacteriology</i> , 1997 , 47, 492-8		55
189	<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	2.2	55
188	Metagenomic insights into the bioaerosols in the indoor and outdoor environments of childcare facilities. <i>PLoS ONE</i> , 2015 , 10, e0126960	3.7	54
187	<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	2.2	54
186	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 Pt 4, 1641-1647	2.2	52
185	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	2.2	51
184	Profiling bacterial community in upper respiratory tracts. <i>BMC Infectious Diseases</i> , 2014 , 14, 583	4	48
183	<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	2.2	48
182	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	2.2	48
181	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	3.1	47
180	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	2.2	47

179	Use of a chiA probe for detection of chitinase genes in bacteria from the Chesapeake Bay(1). <i>FEMS Microbiology Ecology</i> , 2000 , 34, 63-71	4.3	46
178	<i>Nocardia crassostreae</i> sp. nov., the causal agent of nocardiosis in Pacific oysters. <i>International Journal of Systematic Bacteriology</i> , 1998 , 48 Pt 1, 237-46		46
177	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	3.3	46
176	Archaeal diversity in tidal flat sediment as revealed by 16S rDNA analysis. <i>Journal of Microbiology</i> , 2005 , 43, 144-51	3	46
175	Pyrosequencing-based molecular monitoring of the intestinal bacterial colonization in preterm infants. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , 2011 , 53, 512-9	2.8	45
174	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	3.7	44
173	Discovery of novel <i>Vibrio cholerae</i> VSP-II genomic islands using comparative genomic analysis. <i>FEMS Microbiology Letters</i> , 2010 , 308, 130-7	2.9	44
172	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	4.5	44
171	<i>Hymenobacter rigui</i> sp. nov., isolated from wetland freshwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2189-2192	2.2	44
170	<i>Nocardioides aestuarii</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 2151-2154	2.2	44
169	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	3.2	42
168	<i>Tenacibaculum litoreum</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 635-640	2.2	42
167	<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	2.2	42
166	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, 955-66	3.9	41
165	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, 21134-9	11.5	40
164	Genomic evolution of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , 2010 , 13, 646-51	7.9	39
163	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	11.5	38
162	<i>Glaciecola nitratireducens</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2185-2188	2.2	38

161	16S rRNA Gene-Based Identification of Bacteria and Archaea using the EzTaxon Server. <i>Methods in Microbiology</i> , 2014 , 41, 61-74	2.8	37
160	<i>Amycolatopsis japonicum</i> sp. nov., an Actinomycete Producing (S,S)-N,NSEthylenediaminedisuccinic Acid. <i>Systematic and Applied Microbiology</i> , 1997 , 20, 78-84	4.2	37
159	Genome sequence of <i>Escherichia coli</i> J53, a reference strain for genetic studies. <i>Journal of Bacteriology</i> , 2012 , 194, 3742-3	3.5	36
158	<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, 377-81	2.2	36
157	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, 1732-9	2.3	35
156	Complete Genome Sequence of Middle East Respiratory Syndrome Coronavirus KOR/KNIH/002_05_2015, Isolated in South Korea. <i>Genome Announcements</i> , 2015 , 3,		35
155	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	2.2	35
154	<i>Tsukamurella spumae</i> sp. nov., a novel actinomycete associated with foaming in activated sludge plants. <i>Systematic and Applied Microbiology</i> , 2003 , 26, 367-75	4.2	34
153	N-Acetylglucosaminidase activities in wetlands: a global survey. <i>Hydrobiologia</i> , 2005 , 532, 103-110	2.4	34
152	<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 Pt 4, 1369-73	2.2	34
151	<i>Thalassobius aestuarii</i> sp. nov., isolated from tidal flat sediment. <i>Journal of Microbiology</i> , 2006 , 44, 171-63		34
150	Activated sludge foaming: the true extent of actinomycete diversity. <i>Water Science and Technology</i> , 1998 , 37, 511-519	2.2	33
149	A vanillin derivative causes mitochondrial dysfunction and triggers oxidative stress in <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , 2014 , 9, e89122	3.7	32
148	rRNASelector: a computer program for selecting ribosomal RNA encoding sequences from metagenomic and metatranscriptomic shotgun libraries. <i>Journal of Microbiology</i> , 2011 , 49, 689-91	3	31
147	<i>Marinifilum fragile</i> gen. nov., sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009 , 59, 2241-6	2.2	31
146	<i>Nocardia flavorosea</i> sp. nov. <i>International Journal of Systematic Bacteriology</i> , 1998 , 48 Pt 3, 901-5		31
145	Improved pipeline for reducing erroneous identification by 16S rRNA sequences using the Illumina MiSeq platform. <i>Journal of Microbiology</i> , 2015 , 53, 60-9	3	30
144	Genome sequence of <i>Lactobacillus mucosae</i> LM1, isolated from piglet feces. <i>Journal of Bacteriology</i> , 2012 , 194, 4766	3.5	30

143	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	3.8	30
142	<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	2.2	30
141	<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 Pt 2, 753-8	2.2	29
140	Spatial scaling effects on soil bacterial communities in Malaysian tropical forests. <i>Microbial Ecology</i> , 2014 , 68, 247-58	4.4	28
139	<i>Maribacter arcticus</i> sp. nov., isolated from Arctic marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 1300-3	2.2	28
138	Multilocus sequence typing analysis of <i>Shigella flexneri</i> isolates collected in Asian countries. <i>Journal of Medical Microbiology</i> , 2007 , 56, 1460-1466	3.2	28
137	<i>Thalassomonas ganghwensis</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 377-380	2.2	28
136	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		28
135	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, 150-5	4.2	27
134	Draft genome sequence of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> BD(T). <i>Journal of Bacteriology</i> , 2012 , 194, 2756-7	3.5	27
133	<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, 2415-9	2.2	27
132	<i>Nocardioides dokdonensis</i> sp. nov., an actinomycete isolated from sand sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 2619-23	2.2	27
131	<i>Pseudoalteromonas byunsanensis</i> sp. nov., isolated from tidal flat sediment in Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005 , 55, 2519-2523	2.2	27
130	Phylogenetic analysis of the <i>nef</i> gene reveals a distinctive monophyletic clade in Korean HIV-1 cases. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1998 , 17, 58-68		27
129	<i>Actibacter sediminis</i> gen. nov., sp. nov., a marine bacterium of the family <i>Flavobacteriaceae</i> isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 139-43	2.2	26
128	Phylogeny of mycolic acid-containing actinomycetes. <i>Journal of Industrial Microbiology</i> , 1996 , 17, 205-213		26
127	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	3	25
126	TBC: a clustering algorithm based on prokaryotic taxonomy. <i>Journal of Microbiology</i> , 2012 , 50, 181-5	3	25

125	Classification of hybrid and altered <i>Vibrio cholerae</i> strains by CTX prophage and RS1 element structure. <i>Journal of Microbiology</i> , 2009 , 47, 783-8	3	25
124	<i>Luteimonas marina</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 2904-8	2.2	25
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	2.2	25
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