

Jongsik Chun

List of Publications by Year in Descending Order

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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	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	4.5	4
249	Proposal of a health gut microbiome index based on a meta-analysis of Korean and global population datasets.. <i>Journal of Microbiology</i> , 2022 , 1	3	0
248	AMDB: a database of animal gut microbial communities with manually curated metadata. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
247	NASCUP: Nucleic Acid Sequence Classification by Universal Probability. <i>IEEE Access</i> , 2021 , 9, 162779-162791	3.1	1
246	Characterization of Gut Microbiome in Korean Patients with Metabolic Associated Fatty Liver Disease. <i>Nutrients</i> , 2021 , 13,	6.7	4
245	Taxonomic composition and variation in the gut microbiota of laboratory mice. <i>Mammalian Genome</i> , 2021 , 32, 297-310	3.2	1
244	Introducing EzAAI: a pipeline for high throughput calculations of prokaryotic average amino acid identity. <i>Journal of Microbiology</i> , 2021 , 59, 476-480	3	23
243	UBCG2: Up-to-date bacterial core genes and pipeline for phylogenomic analysis. <i>Journal of Microbiology</i> , 2021 , 59, 609-615	3	15
242	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	4.7	1
241	VicPred: A Genotype Prediction Tool. <i>Frontiers in Microbiology</i> , 2021 , 12, 691895	5.7	2
240	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,	4.9	8
239	Improved Metagenomic Taxonomic Profiling Using a Curated Core Gene-Based Bacterial Database Reveals Unrecognized Species in the Genus. <i>Pathogens</i> , 2020 , 9,	4.5	3
238	Characterization of intratissue bacterial communities and isolation of <i>Escherichia coli</i> from oral lichen planus lesions. <i>Scientific Reports</i> , 2020 , 10, 3495	4.9	8
237	Genome-based reclassification of <i>Aguilera</i> . 2001 as a later heterotypic synonym of (<i>Prazmowski</i> 1880) <i>Ash</i> . 1994. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 3134-3138	2.2	3
236	Emotional well-being and gut microbiome profiles by enterotype. <i>Scientific Reports</i> , 2020 , 10, 20736	4.9	10
235	Metagenomic Association Analysis of Gut Symbiont Without Host-Specific Genome Isolation. <i>Frontiers in Microbiology</i> , 2020 , 11, 585622	5.7	2
234	Comparative analysis of the tonsillar microbiota in IgA nephropathy and other glomerular diseases. <i>Scientific Reports</i> , 2020 , 10, 16206	4.9	8

233	Comparative Genomic and Phylogenomic Analyses Clarify Relationships Within and Between and : Proposal for the Recognition of Two Genomovars. <i>Frontiers in Microbiology</i> , 2019 , 10, 1978	5.7	19
232	Comparative Genomic Analysis of the 2016 Outbreak in South Korea. <i>Frontiers in Public Health</i> , 2019 , 7, 228	6	6
231	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	5.7	16
230	Genomic characterization of <i>Nocardia seriolae</i> strains isolated from diseased fish. <i>MicrobiologyOpen</i> , 2019 , 8, e00656	3.4	18
229	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
228	Introducing Murine Microbiome Database (MMDB): A Curated Database with Taxonomic Profiling of the Healthy Mouse Gastrointestinal Microbiome. <i>Microorganisms</i> , 2019 , 7,	4.9	9
227	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
226	Genome-based reclassification of as a later heterotypic synonym of. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019 , 69, 3672-3675	2.2	2
225	VCGIDB: A Database and Web Resource for the Genomic Islands from. <i>Pathogens</i> , 2019 , 8,	4.5	4
224	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	3	7
223	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
222	Phylogeny Trumps Chemotaxonomy: A Case Study Involving. <i>Frontiers in Microbiology</i> , 2018 , 9, 834	5.7	22
221	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
220	Genomic Insight Into the Predominance of Candidate Phylum Atribacteria JS1 Lineage in Marine Sediments. <i>Frontiers in Microbiology</i> , 2018 , 9, 2909	5.7	18
219	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	10.5	3
218	A large-scale evaluation of algorithms to calculate average nucleotide identity. <i>Antonie Van Leeuwenhoek</i> , 2017 , 110, 1281-1286	2.1	1296
217	Replication of classical CTX phage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2343-2348	11.5	15
216	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

215	Dehalogenimonas formicexedens sp. nov., a chlorinated alkane-respiring bacterium isolated from contaminated groundwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017 , 67, 1366-1373	2.2	22
214	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
213	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	2.2	4
212	Genome sequence of the organohalide-respiring <i>Dehalogenimonas alkenignens</i> type strain (IP3-3(T)). <i>Standards in Genomic Sciences</i> , 2016 , 11, 44		8
211	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
210	A single gene of a commensal microbe affects host susceptibility to enteric infection. <i>Nature Communications</i> , 2016 , 7, 11606	17.4	23
209	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
208	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
207	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
206	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	4.2	14
205	<i>Burkholderia megalochromosomata</i> sp. nov., isolated from grassland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 959-964	2.2	8
204	Comparison of the genome profiles between head and body lice. <i>Journal of Asia-Pacific Entomology</i> , 2015 , 18, 377-382	1.4	6
203	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
202	<i>Burkholderia monticola</i> sp. nov., isolated from mountain soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 504-509	2.2	10
201	Sejongia 2015 , 1-6		
200	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		21
199	Metagenomic insights into the bioaerosols in the indoor and outdoor environments of childcare facilities. <i>PLoS ONE</i> , 2015 , 10, e0126960	3.7	54
198	Draft genome sequence of the psychrophilic bacterium <i>Lacinutrix jangbogonensis</i> PAMC 27137(T). <i>Marine Genomics</i> , 2015 , 23, 31-2	1.9	2

197	Paenibacillus xanthinilyticus sp. nov., isolated from agricultural soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 2937-2942	2.2	5
196	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
195	Telomere maintenance through recruitment of internal genomic regions. <i>Nature Communications</i> , 2015 , 6, 8189	17.4	17
194	Neisseria weaveri Andersen et al. 1993 is a later heterotypic synonym of Neisseria weaveri Holmes et al. 1993. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 463-464	2.2	5
193	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
192	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		1
191	The Genus Vibrio and Related Genera 2015 , 371-382		
190	Bacterial community of sediments from the Australian-Antarctic ridge. <i>Polar Biology</i> , 2014 , 37, 587-593	2	6
189	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
188	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
187	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
186	Lacinutrix jangbogonensis sp. nov., a psychrophilic bacterium isolated from Antarctic marine sediment and emended description of the genus Lacinutrix. <i>Antonie Van Leeuwenhoek</i> , 2014 , 106, 527-33 ^{2,1}		22
185	Spatial scaling effects on soil bacterial communities in Malaysian tropical forests. <i>Microbial Ecology</i> , 2014 , 68, 247-58	4.4	28
184	A vanillin derivative causes mitochondrial dysfunction and triggers oxidative stress in Cryptococcus neoformans. <i>PLoS ONE</i> , 2014 , 9, e89122	3.7	32
183	Profiling bacterial community in upper respiratory tracts. <i>BMC Infectious Diseases</i> , 2014 , 14, 583	4	48
182	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
181	Clonality and Resistome analysis of KPC-producing Klebsiella pneumoniae strain isolated in Korea using whole genome sequencing. <i>BioMed Research International</i> , 2014 , 2014, 352862	3	21
180	Genomic encyclopedia of bacteria and archaea: sequencing a myriad of type strains. <i>PLoS Biology</i> , 2014 , 12, e1001920	9.7	146

179	Draft Genome Sequence of <i>Kitasatospora cheerisanensis</i> KCTC 2395, Which Produces Plecomacrolide against Phytopathogenic Fungi. <i>Genome Announcements</i> , 2014 , 2,		5
178	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
177	Genome sequence of type strain of <i>Staphylococcus aureus</i> subsp. <i>aureus</i> . <i>Gut Pathogens</i> , 2014 , 6, 6	5.4	13
176	Genomic insights into the taxonomic status of the three subspecies of <i>Bacillus subtilis</i> . <i>Systematic and Applied Microbiology</i> , 2014 , 37, 95-9	4.2	19
175	Genome sequence of the chromate-resistant bacterium <i>Leucobacter salsicius</i> type strain M1-8(T). <i>Standards in Genomic Sciences</i> , 2014 , 9, 495-504		7
174	Draft genome sequence of <i>Pseudomonas</i> sp. strain G5, isolated from a traditional indigo fermentation dye vat 2013 , 56, 339-341		1
173	Identification of household bacterial community and analysis of species shared with human microbiome. <i>Current Microbiology</i> , 2013 , 67, 557-63	2.4	75
172	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
171	Comparison of a culture-based and a PCR-based methods for estimating bacterial abundance on eggshells, with comments on statistical analyses. <i>Journal of Field Ornithology</i> , 2013 , 84, 304-315	0.9	8
170	Structure of soil bacterial communities in relation to environmental variables in a semi-arid region of Mongolia. <i>Journal of Arid Environments</i> , 2013 , 89, 38-44	2.5	16
169	<i>Fretibacter rubidus</i> gen. nov., sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 4633-4638	2.2	7
168	Analytical tools and databases for metagenomics in the next-generation sequencing era. <i>Genomics and Informatics</i> , 2013 , 11, 102-13	1.9	98
167	<i>Flavobacterium limnosediminis</i> sp. nov., isolated from sediment of a freshwater lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013 , 63, 4784-4789	2.2	13
166	Genome sequence of the moderately halophilic bacterium <i>Salinicoccus carnicancri</i> type strain Crm(T) (= DSM 23852(T)). <i>Standards in Genomic Sciences</i> , 2013 , 8, 255-63		6
165	Current status and future promise of the human microbiome. <i>Pediatric Gastroenterology, Hepatology and Nutrition</i> , 2013 , 16, 71-9	2.3	55
164	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
163	Production of hydrogen and volatile fatty acid by <i>Enterobacter</i> sp. T4384 using organic waste materials. <i>Journal of Microbiology and Biotechnology</i> , 2013 , 23, 189-94	3.3	3
162	Transcriptomic analysis of genes modulated by cyclo(L-phenylalanine-L-proline) in <i>Vibrio vulnificus</i> . <i>Journal of Microbiology and Biotechnology</i> , 2013 , 23, 1791-801	3.3	10

161	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
160	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
159	A hump-backed trend in bacterial diversity with elevation on Mount Fuji, Japan. <i>Microbial Ecology</i> , 2012 , 63, 429-37	4.4	115
158	Distinctive phyllosphere bacterial communities in tropical trees. <i>Microbial Ecology</i> , 2012 , 63, 674-81	4.4	111
157	Phylogenetic study of the species within the family Streptomycetaceae. <i>Antonie Van Leeuwenhoek</i> , 2012 , 101, 73-104	2.1	162
156	Draft Genome sequence of <i>Escherichia coli</i> AI27, a porcine isolate belonging to phylogenetic group B1. <i>Journal of Bacteriology</i> , 2012 , 194, 6640-1	3.5	1
155	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
154	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
153	TBC: a clustering algorithm based on prokaryotic taxonomy. <i>Journal of Microbiology</i> , 2012 , 50, 181-5	3	25
152	Tropical soil bacterial communities in Malaysia: pH dominates in the equatorial tropics too. <i>Microbial Ecology</i> , 2012 , 64, 474-84	4.4	173
151	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, 100-5 ^{2.9}		11
150	Bacterial community analysis during fermentation of ten representative kinds of kimchi with barcoded pyrosequencing. <i>Food Microbiology</i> , 2012 , 30, 197-204	6	155
149	Impact of enrofloxacin on the human intestinal microbiota revealed by comparative molecular analysis. <i>Anaerobe</i> , 2012 , 18, 310-20	2.8	64
148	Complete genome sequence of <i>Mycobacterium intracellulare</i> clinical strain MOTT-36Y, belonging to the INT5 genotype. <i>Journal of Bacteriology</i> , 2012 , 194, 4141-2	3.5	11
147	Genome sequence of <i>Lactobacillus mucosae</i> LM1, isolated from piglet feces. <i>Journal of Bacteriology</i> , 2012 , 194, 4766	3.5	30
146	<i>Flavivirga jejuensis</i> gen. nov., sp. nov., and <i>Flavivirga amylovorans</i> sp. nov., new members of the family Flavobacteriaceae isolated from seawater, and emended descriptions of the genera <i>Psychroserpens</i> and <i>Lacinutrix</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012 , 62, 1061-1068	2.2	12
145	Genome sequence of extracellular-protease-producing <i>Alishewanella jeotgali</i> isolated from traditional Korean fermented seafood. <i>Journal of Bacteriology</i> , 2012 , 194, 2097	3.5	13
144	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

143	Draft genome sequence of <i>Escherichia coli</i> W26, an enteric strain isolated from cow feces. <i>Journal of Bacteriology</i> , 2012 , 194, 5149-50	3.5	4
142	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
141	Genome sequence of pectin-degrading <i>Alishewanella aestuarii</i> strain B11(T), isolated from tidal flat sediment. <i>Journal of Bacteriology</i> , 2012 , 194, 5476	3.5	6
140	Complete genome sequence of <i>Mycobacterium intracellulare</i> clinical strain MOTT-02. <i>Journal of Bacteriology</i> , 2012 , 194, 2771	3.5	16
139	Toll-like receptor 9 mediates oral bacteria-induced IL-8 expression in gingival epithelial cells. <i>Immunology and Cell Biology</i> , 2012 , 90, 655-63	5	16
138	Genome sequence of pectin-degrading <i>Alishewanella agri</i> , isolated from landfill soil. <i>Journal of Bacteriology</i> , 2012 , 194, 5135-6	3.5	8
137	Draft genome sequencing of <i>Bacillus</i> sp. strain M2-6, isolated from the roots of Korean ginseng, <i>Panax ginseng</i> C. A. Meyer, after high-hydrostatic-pressure processing. <i>Journal of Bacteriology</i> , 2012 , 194, 7003-4	3.5	2
136	Draft genome sequence of <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> DSM 30104T. <i>Journal of Bacteriology</i> , 2012 , 194, 5722-3	3.5	0
135	Draft genome sequence of <i>Weissella koreensis</i> KCTC 3621T. <i>Journal of Bacteriology</i> , 2012 , 194, 5711-2	3.5	8
134	Complete genome sequence of <i>Mycobacterium intracellulare</i> strain ATCC 13950(T). <i>Journal of Bacteriology</i> , 2012 , 194, 2750	3.5	22
133	Draft genome sequence of <i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i> M1-1, isolated from the gills of a Korean rockfish, <i>Sebastes schlegeli</i> Hilgendorf, after high hydrostatic pressure processing. <i>Journal of Bacteriology</i> , 2012 , 194, 4441-2	3.5	5
132	Genome sequence of the halotolerant <i>Staphylococcus</i> sp. strain OJ82, isolated from Korean traditional salt-fermented seafood. <i>Journal of Bacteriology</i> , 2012 , 194, 6353-4	3.5	5
131	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
130	<i>Aquimarina addita</i> sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 2445-2449	2.2	24
129	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
128	Evidence for several waves of global transmission in the seventh cholera pandemic. <i>Nature</i> , 2011 , 477, 462-5	50.4	492
127	Comparative approach to capture bacterial diversity of coastal waters. <i>Journal of Microbiology</i> , 2011 , 49, 729-40	3	18
126	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

125	Snuella lapsa gen. nov., sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 2469-2474	2.2	6
124	Genome sequence of Lactobacillus ruminis SPM0211, isolated from a fecal sample from a healthy Korean. <i>Journal of Bacteriology</i> , 2011 , 193, 5034	3.5	5
123	Genome sequence of Escherichia coli AA86, isolated from cow feces. <i>Journal of Bacteriology</i> , 2011 , 193, 3681	3.5	7
122	Draft genome sequence of Shewanella sp. strain HN-41, which produces arsenic-sulfide nanotubes. <i>Journal of Bacteriology</i> , 2011 , 193, 5039-40	3.5	3
121	Pontirhabdus pectinivorans gen. nov., sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 2475-2481	2.2	12
120	Genome sequence of Lactobacillus johnsonii PF01, isolated from piglet feces. <i>Journal of Bacteriology</i> , 2011 , 193, 5030-1	3.5	13
119	Complete genome sequence of Vibrio vulnificus MO6-24/O. <i>Journal of Bacteriology</i> , 2011 , 193, 2062-3	3.5	55
118	Draft genome sequence of Methylophaga aminisulfidivorans MP T. <i>Journal of Bacteriology</i> , 2011 , 193, 4265	3.5	9
117	Genome sequence of Lactobacillus salivarius GJ-24, a probiotic strain isolated from healthy adult intestine. <i>Journal of Bacteriology</i> , 2011 , 193, 5021-2	3.5	12
116	Zobellella aerophila sp. nov., isolated from seashore sand, and emended description of the genus Zobellella. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011 , 61, 2491-2495	2.2	8
115	Duplex-specific nuclease efficiently removes rRNA for prokaryotic RNA-seq. <i>Nucleic Acids Research</i> , 2011 , 39, e140	20.1	93
114	Discovery of novel Vibrio cholerae VSP-II genomic islands using comparative genomic analysis. <i>FEMS Microbiology Letters</i> , 2010 , 308, 130-7	2.9	44
113	Multilocus variable-number tandem repeat analysis of Vibrio cholerae O1 El Tor strains harbouring classical toxin B. <i>Journal of Medical Microbiology</i> , 2010 , 59, 763-769	3.2	42
112	Comparative genomics of clinical and environmental Vibrio mimicus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 21134-9	11.5	40
111	Genome sequence of hybrid Vibrio cholerae O1 MJ-1236, B-33, and CIRS101 and comparative genomics with V. cholerae. <i>Journal of Bacteriology</i> , 2010 , 192, 3524-33	3.5	87
110	Classical RS1 and environmental RS1 elements in Vibrio cholerae O1 El Tor strains harbouring a tandem repeat of CTX prophage: revisiting Mozambique in 2005. <i>Journal of Medical Microbiology</i> , 2010 , 59, 302-308	3.2	18
109	Complete genome sequence analysis of Leuconostoc kimchii IMSNU 11154. <i>Journal of Bacteriology</i> , 2010 , 192, 3844-5	3.5	23
108	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

107	Genomic evolution of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , 2010 , 13, 646-51	7.9	39
106	The pre-seventh pandemic <i>Vibrio cholerae</i> BX 330286 El Tor genome: evidence for the environment as a genome reservoir. <i>Environmental Microbiology Reports</i> , 2010 , 2, 208-16	3.7	3
105	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
104	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, 111-6	3	1
103	Assessment of soil fungal communities using pyrosequencing. <i>Journal of Microbiology</i> , 2010 , 48, 284-9	3	97
102	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
101	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
100	<i>Vitellibacter aestuarii</i> sp. nov., isolated from tidal-flat sediment, and an emended description of the genus <i>Vitellibacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010 , 60, 1989-1992 ²	2.2	16
99	<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
98	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
97	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
96	Genomic analysis of a novel integrative conjugative element in <i>Vibrio cholerae</i> . <i>FEBS Letters</i> , 2009 , 583, 3630-6	3.8	19
95	Identification and characterization of metagenomic fragments from tidal flat sediment. <i>Journal of Microbiology</i> , 2009 , 47, 402-10	3	3
94	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
93	Proposal to transfer <i>Flavobacterium oceanosedimentum</i> Carty and Litchfield 1978 to the genus <i>Curtobacterium</i> as <i>Curtobacterium oceanosedimentum</i> comb. nov. <i>FEMS Microbiology Letters</i> , 2009 , 296, 137-41	2.9	2
92	<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
91	Characteristics of a pandemic clone of O3 : K6 and O4 : K68 <i>Vibrio parahaemolyticus</i> isolated in Beira, Mozambique. <i>Journal of Medical Microbiology</i> , 2008 , 57, 1502-1507	3.2	19
90	<i>Sanguibacter antarcticus</i> sp. nov., isolated from Antarctic sea sand. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 50-2	2.2	23

89	Nocardioides dokdonensis sp. nov., an actinomycete isolated from sand sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 2619-23	2.2	27
88	The complete genome sequence of Thermococcus onnurineus NA1 reveals a mixed heterotrophic and carboxydrotrophic metabolism. <i>Journal of Bacteriology</i> , 2008 , 190, 7491-9	3.5	119
87	Luteimonas marina sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 2904-8	2.2	25
86	Maribacter arcticus sp. nov., isolated from Arctic marine sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 1300-3	2.2	28
85	Actibacter sediminis 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, 139-23	2.2	26
84	Rapid phylogenetic dissection of prokaryotic community structure in tidal flat using pyrosequencing. <i>Journal of Microbiology</i> , 2008 , 46, 357-63	3	56
83	Diversity of bacterial community in freshwater of Woopo wetland. <i>Journal of Microbiology</i> , 2008 , 46, 647-55	3	23
82	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
81	Multilocus sequence typing analysis of Shigella flexneri isolates collected in Asian countries. <i>Journal of Medical Microbiology</i> , 2007 , 56, 1460-1466	3.2	28
80	Clostridium aestuarii sp. nov., from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007 , 57, 1315-1317	2.2	15
79	Anaerosporobacter mobilis gen. nov., sp. nov., isolated from forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007 , 57, 1784-1787	2.2	25
78	Reclassification of Flavobacterium resinovorum Delaporte and Daste 1956 as Novosphingobium resinovorum comb. nov., with Novosphingobium subarcticum (Nohynek et al. 1996) Takeuchi et al. 2001 as a later heterotypic synonym. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007 , 57, 1806-1808	2.2	21
77	Demequina aestuarii gen. nov., sp. nov., a novel actinomycete of the suborder Micrococccineae, and reclassification of Cellulomonas fermentans Bagnara et al. 1985 as Actinotalea fermentans gen. nov., comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007 , 57, 151-156	2.2	64
76	Taxonomic evaluation of the genera Ruegeria and Silicibacter: a proposal to transfer the genus Silicibacter Petursdottir and Kristjansson 1999 to the genus Ruegeria Uchino et al. 1999. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007 , 57, 815-819	2.2	48
75	Pseudomonas segetis sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2593-2595	2.2	11
74	Hymenobacter rigui sp. nov., isolated from wetland freshwater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2189-2192	2.2	44
73	Glaciecola nitratireducens sp. nov., isolated from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2185-2188	2.2	38
72	Jannaschia seosinensis sp. nov., isolated from hypersaline water of a solar saltern in Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 45-9	2.2	24

71	<i>Clostridium ganghwense</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 691-693	2.2	15
70	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
69	<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
68	<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
67	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
66	<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
65	Isolation of <i>Salmonella enterica</i> subspecies <i>enterica</i> serovar Paratyphi B dT+, or <i>Salmonella</i> Java, from Indonesia and alteration of the d-tartrate fermentation phenotype by disrupting the ORF STM 3356. <i>Journal of Medical Microbiology</i> , 2006 , 55, 1661-1665	3.2	8
64	<i>Thalassobius aestuarii</i> sp. nov., isolated from tidal flat sediment. <i>Journal of Microbiology</i> , 2006 , 44, 171-63		34
63	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
62	N-Acetylglucosaminidase activities in wetlands: a global survey. <i>Hydrobiologia</i> , 2005 , 532, 103-110	2.4	34
61	<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
60	<i>Hahella ganghwensis</i> sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005 , 55, 681-684	2.2	14
59	jPHYDIT: a JAVA-based integrated environment for molecular phylogeny of ribosomal RNA sequences. <i>Bioinformatics</i> , 2005 , 21, 3171-3	7.2	158
58	<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
57	<i>Pseudomonas panacis</i> sp. nov., isolated from the surface of rusty roots of Korean ginseng. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005 , 55, 1721-1724	2.2	20
56	<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
55	Archaeal diversity in tidal flat sediment as revealed by 16S rDNA analysis. <i>Journal of Microbiology</i> , 2005 , 43, 144-51	3	46
54	<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

53	Nocardioides ganghwensis sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 1295-1299	2.2	60
52	Kribbella solani sp. nov. and Kribbella jejuensis sp. nov., isolated from potato tuber and soil in Jeju, Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 1345-1348	2.2	22
51	Nocardioides aestuarii sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 2151-2154	2.2	44
50	Thalassomonas ganghwensis sp. nov., isolated from tidal flat sediment. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 377-380	2.2	28
49	Phylogenetic analysis of the genera Streptomyces and Kitasatospora based on partial RNA polymerase beta-subunit gene (rpoB) sequences. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 593-598	2.2	47
48	Clostridium jejuense sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 1465-1468	2.2	21
47	Serinicoccus marinus 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
46	Kordia algicida 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
45	Tsukamurella pseudospumae 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
44	Phylogenetic characterization of Legionella-like endosymbiotic X-bacteria in Amoeba proteus: a proposal for Candidatus Legionella jeonii Ssp. nov. <i>Environmental Microbiology</i> , 2004 , 6, 1252-63	5.2	25
43	Aestuariibacter salexigens gen. nov., sp. nov. and Aestuariibacter halophilus sp. nov., isolated from tidal flat sediment, and emended description of Alteromonas macleodii. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004 , 54, 571-576	2.2	42
42	A method for comparing multiple bacterial community structures from 16S rDNA clone library sequences. <i>Journal of Microbiology</i> , 2004 , 42, 9-13	3	23
41	Tsukamurella spumae 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
40	A novel electrochemically active and Fe(III)-reducing bacterium phylogenetically related to Aeromonas hydrophila, isolated from a microbial fuel cell. <i>FEMS Microbiology Letters</i> , 2003 , 223, 129-34	2.9	318
39	Transfer of Hongia koreensis Lee et al. 2000 to the genus Kribbella Park et al. 1999 as Kribbella koreensis comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003 , 53, 1005-1007	2.2	35
38	Zooshikella ganghwensis 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
37	Analysis of 16S-23S rRNA intergenic spacer of Vibrio cholerae and Vibrio mimicus for detection of these species. <i>Methods in Molecular Biology</i> , 2002 , 179, 171-8	1.4	6
36	Transfer of Tsukamurella wratislaviensis Goodfellow et al. 1995 to the genus Rhodococcus as Rhodococcus wratislaviensis comb. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002 , 52, 749-755	2.2	17

35	Comamonas koreensis 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
34	Metschnikowia koreensis sp. nov., a novel yeast species isolated from flowers in Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2001 , 51, 1927-1931	2.2	21
33	Hahella chejuensis 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
32	Genotypes associated with virulence in environmental isolates of Vibrio cholerae. <i>Applied and Environmental Microbiology</i> , 2001 , 67, 2421-9	4.8	261
31	Arthrobacter siderocapsulatus Dubinina and Zhdanov 1975AL is a later subjective synonym of Pseudomonas putida (Trevisan 1889) Migula 1895AL. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2001 , 51, 169-170	2.2	11
30	Detection of luciferase gene sequences in nonluminescent bacteria from the Chesapeake Bay. <i>FEMS Microbiology Ecology</i> , 2000 , 33, 27-34	4.3	15
29	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
28	Phylogenetic analysis of Bacillus subtilis and related taxa based on partial gyrA gene sequences. <i>Antonie Van Leeuwenhoek</i> , 2000 , 78, 123-7	2.1	150
27	Leuconostoc kimchii 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
26	Polyphasic assignment of an aromatic-degrading Pseudomonas sp., strain DJ77, in the genus Sphingomonas as Sphingomonas chungbukensis sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000 , 50 Pt 4, 1641-1647	2.2	52
25	A proposal for the reclassification of Bdellovibrio stolpii and Bdellovibrio starrii into a new genus, Bacteriovorax gen. nov. as Bacteriovorax stolpii comb. nov. and Bacteriovorax starrii comb. nov., respectively. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2000 , 50 Pt 1, 219-224	2.2	73
24	Paenibacillus koreensis 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
23	Nocardiopsis kunsanensis 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
22	Analysis of 16S-23S rRNA intergenic spacer regions of Vibrio cholerae and Vibrio mimicus. <i>Applied and Environmental Microbiology</i> , 1999 , 65, 2202-8	4.8	220
21	Amycolatopsis thermoflava 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
20	Nocardia uniformis nom. rev. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999 , 49 Pt 3, 1227-30	2.2	13
19	Nocardia salmonicida nom. rev., a fish pathogen. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999 , 49 Pt 2, 833-7	2.2	62
18	Kitasatospora cheerisanensis sp. nov., a new species of the genus Kitasatospora that produces an antifungal agent. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999 , 49 Pt 2, 753-8	2.2	29

17	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
16	Rhodococcal systematics: problems and developments. <i>Antonie Van Leeuwenhoek</i> , 1998 , 74, 3-20	2.1	94
15	Activated sludge foaming: The true extent of actinomycete diversity. <i>Water Science and Technology</i> , 1998 , 37, 511	2.2	13
14	<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
13	<i>Nocardia flavorosea</i> sp. nov. <i>International Journal of Systematic Bacteriology</i> , 1998 , 48 Pt 3, 901-5		31
12	Phylogenetic analysis of the nef gene reveals a distinctive monophyletic clade in Korean HIV-1 cases. <i>Journal of Acquired Immune Deficiency Syndromes</i> , 1998 , 17, 58-68		27
11	Activated sludge foaming: the true extent of actinomycete diversity. <i>Water Science and Technology</i> , 1998 , 37, 511-519	2.2	33
10	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
9	<i>Streptomyces seoulensis</i> sp. nov. <i>International Journal of Systematic Bacteriology</i> , 1997 , 47, 492-8		55
8	Long-term identification of streptomycetes using pyrolysis mass spectrometry and artificial neural networks. <i>Zentralblatt Fur Bakteriologie: International Journal of Medical Microbiology</i> , 1997 , 285, 258-66		5
7	<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
6	Phylogeny of mycolic acid-containing actinomycetes. <i>Journal of Industrial Microbiology</i> , 1996 , 17, 205-213		26
5	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
4	Transfer of <i>Nocardia amarae</i> Lechevalier and Lechevalier 1974 to the genus <i>Gordona</i> as <i>Gordona amarae</i> comb. nov. <i>Letters in Applied Microbiology</i> , 1994 , 19, 401-5	2.9	9
3	Curie Point Pyrolysis Mass Spectrometry and Its Application to Bacterial Systematics 1994 , 87-104		7
2	Rapid identification of streptomycetes by artificial neural network analysis of pyrolysis mass spectra. <i>FEMS Microbiology Letters</i> , 1993 , 114, 115-9	2.9	24
1	Metagenomic association analysis of gut symbiont <i>Lactobacillus reuteri</i> without host-specific genome isolation		1