Byung Kwon Kim

List of Publications by Year
in descending order

20 papers	2,725 citations	840776 11 h-index	752698 20 g-index
20 all docs	20 docs citations	20 times ranked	3224 citing authors

#	Article	IF	Citations
1	EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 2259-2261.	1.7	1,960
2	Differences in Gastric Mucosal Microbiota Profiling in Patients with Chronic Gastritis, Intestinal Metaplasia, and Gastric Cancer Using Pyrosequencing Methods. Helicobacter, 2014, 19, 407-416.	3.5	253
3	Assessment of soil fungal communities using pyrosequencing. Journal of Microbiology, 2010, 48, 284-289.	2.8	116
4	Genome Sequence of an Ammonia-Oxidizing Soil Archaeon, â€œCandidatus Nitrosoarchaeum koreensisâ€• MY1. Journal of Bacteriology, 2011, 193, 5539-5540.	2.2	111
5	Rapid phylogenetic dissection of prokaryotic community structure in tidal flat using pyrosequencing. Journal of Microbiology, 2008, 46, 357-363.	2.8	71
6	Sulfitobacter geojensis sp. nov., Sulfitobacter noctilucae sp. nov., and Sulfitobacter noctilucicola sp. nov., isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 3760-3767.	1.7	38
7	Complete Genome Sequence of the Endophytic Bacterium Burkholderia sp. Strain KJ006. Journal of Bacteriology, 2012, 194, 4432-4433.	2.2	35
8	PyroTrimmer: a software with GUI for pre-processing 454 amplicon sequences. Journal of Microbiology, 2012, 50, 766-769.	2.8	28
9	Complete genome of Kangiella geojedonensis KCTC 23420T, putative evidence for recent genome reduction in marine environments. Marine Genomics, 2015, 24, 215-217.	1.1	21
10	Genome Sequence of the Leaf-Colonizing Bacterium Bacillus sp. Strain 5B6, Isolated from a Cherry Tree. Journal of Bacteriology, 2012, 194, 3758-3759.	2.2	19
11	CLUSTOM: A Novel Method for Clustering 16S rRNA Next Generation Sequences by Overlap Minimization. PLoS ONE, 2013, 8, e62623.	2.5	18
12	Complete genome of the marine bacterium Wenzhouxiangella marina KCTC 42284T. Marine Genomics, 2015, 24, 277-280.	1.1	10
13	CLUSTOM-CLOUD: In-Memory Data Grid-Based Software for Clustering 16S rRNA Sequence Data in the Cloud Environment. PLoS ONE, 2016, 11, e0151064.	2.5	9
14	Draft Genome Sequence of the Antifungal-Producing Plant-Benefiting Bacterium Burkholderia pyrrocinia CH-67. Journal of Bacteriology, 2012, 194, 6649-6650.	2.2	8
15	Complete genome of a coastal marine bacterium Muricauda lutaonensis KCTC 22339T. Marine Genomics, 2015, 23, 51-53.	1.1	8
16	Complete genome of biodegradable plastics-decomposing Roseateles depolymerans KCTC 42856T (=61AT). Journal of Biotechnology, 2016, 220, 47-48.	3.8	7
17	Identification and characterization of metagenomic fragments from tidal flat sediment. Journal of Microbiology, 2009, 47, 402-410.	2.8	5
18	Complete genome of the multidrug-resistant Acinetobacter baumannii strain KBN10P02143 isolated from Korea. Memorias Do Instituto Oswaldo Cruz, 2016, 111, 355-358.	1.6	4

#	Article	IF	Citations
19	Proposal to transferFlavobacterium oceanosedimentumÃ¢Â€Âƒ Carty and Litchfield 1978 to the genusCurtobacteriumÃ¢Â€Âƒ asCurtobacterium oceanosedimentumcomb. nov.. FEMS Microbiology Letters, 2009, 296, 137-141.	1.8	3
20	Complete genome of brown algal polysaccharides-degrading Pseudoalteromonas issachenkonii KCTC 12958T (=KMM 3549T). Journal of Biotechnology, 2016, 219, 86-87.	3.8	1