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	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
2	Complete genome of biodegradable plastics-decomposing Roseateles depolymerans KCTC 42856T (=61AT). Journal of Biotechnology, 2016, 220, 47-48.	3.8	7
3	Complete genome of brown algal polysaccharides-degrading Pseudoalteromonas issachenkonii KCTC 12958T (=KMM 3549T). Journal of Biotechnology, 2016, 219, 86-87.	3.8	1
4	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
5	Complete genome of a coastal marine bacterium Muricauda lutaonensis KCTC 22339T. Marine Genomics, 2015, 23, 51-53.	1.1	8
6	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
7	Complete genome of the marine bacterium Wenzhouxiangella marina KCTC 42284T. Marine Genomics, 2015, 24, 277-280.	1.1	10
8	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
9	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
10	CLUSTOM: A Novel Method for Clustering 16S rRNA Next Generation Sequences by Overlap Minimization. PLoS ONE, 2013, 8, e62623.	2.5	18
11	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
12	Draft Genome Sequence of the Antifungal-Producing Plant-Benefiting Bacterium Burkholderia pyrrocinia CH-67. Journal of Bacteriology, 2012, 194, 6649-6650.	2.2	8
13	Complete Genome Sequence of the Endophytic Bacterium Burkholderia sp. Strain KJ006. Journal of Bacteriology, 2012, 194, 4432-4433.	2.2	35
14	PyroTrimmer: a software with GUI for pre-processing 454 amplicon sequences. Journal of Microbiology, 2012, 50, 766-769.	2.8	28
15	Genome Sequence of an Ammonia-Oxidizing Soil Archaeon, "Candidatus Nitrosoarchaeum koreensis" MY1. Journal of Bacteriology, 2011, 193, 5539-5540.	2.2	111
16	Assessment of soil fungal communities using pyrosequencing. Journal of Microbiology, 2010, 48, 284-289.	2.8	116
17	Identification and characterization of metagenomic fragments from tidal flat sediment. Journal of Microbiology, 2009, 47, 402-410.	2.8	5
18	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

#	Article	IF	Citations
19	Rapid phylogenetic dissection of prokaryotic community structure in tidal flat using pyrosequencing. Journal of Microbiology, 2008, 46, 357-363.	2.8	71
20	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