Ilnam Kang

List of Publications by Year
in descending order

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36 papers	829 citations	566801 15 h-index	525886 27 g-index
36 all docs	36 docs citations	36 times ranked	1025 citing authors

#	Article	IF	Citations
1	Genome of a SAR116 bacteriophage shows the prevalence of this phage type in the oceans. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12343-12348.	3.3	122
2	Complete Genome Sequence of â€œ Candidatus Puniceispirillum marinumâ€•IMCC1322, a Representative of the SAR116 Clade in the Alphaproteobacteria. Journal of Bacteriology, 2010, 192, 3240-3241.	1.0	106
3	Genome Sequence of â€œCandidatus Aquilunaâ€•sp. Strain IMCC13023, a Marine Member of the Actinobacteria Isolated from an Arctic Fjord. Journal of Bacteriology, 2012, 194, 3550-3551.	1.0	66
4	Expansion of Cultured Bacterial Diversity by Large-Scale Dilution-to-Extinction Culturing from a Single Seawater Sample. Microbial Ecology, 2016, 71, 29-43.	1.4	42
5	The first complete genome sequences of the acI lineage, the most abundant freshwater Actinobacteria, obtained by whole-genome-amplification of dilution-to-extinction cultures. Scientific Reports, 2017, 7, 42252.	1.6	42
6	Bacterial Communities of Surface Mixed Layer in the Pacific Sector of the Western Arctic Ocean during Sea-Ice Melting. PLoS ONE, 2014, 9, e86887.	1.1	40
7	Culturing the ubiquitous freshwater actinobacterial acI lineage by supplying a biochemical â€˜helperâ€™ catalase. ISME Journal, 2019, 13, 2252-2263.	4.4	37
8	Complete Genome Sequences of Two Persicivirga Bacteriophages, P12024S and P12024L. Journal of Virology, 2012, 86, 8907-8908.	1.5	29
9	Complete Genome Sequence of Celeribacter Bacteriophage P12053L. Journal of Virology, 2012, 86, 8339-8340.	1.5	27
10	Genome characteristics and environmental distribution of the first phage that infects the LD28 clade, aÂfreshwater methylotrophic bacterial group. Environmental Microbiology, 2017, 19, 4714-4727.	1.8	26
11	Complete genome sequences of bacteriophages P12002L and P12002S, two lytic phages that infect a marine Polaribacter strain. Standards in Genomic Sciences, 2015, 10, 82.	1.5	25
12	Complete Genome Sequence of Croceibacter Bacteriophage P2559S. Journal of Virology, 2012, 86, 8912-8913.	1.5	22
13	Genome Sequence of Fulvimarina pelagi HTCC2506 T , a Mn(II)-Oxidizing Alphaproteobacterium Possessing an Aerobic Anoxygenic Photosynthetic Gene Cluster and Xanthorhodopsin. Journal of Bacteriology, 2010, 192, 4798-4799.	1.0	21
14	Complete genome sequence of bacteriophage P2559Y, a marine phage that infects Croceibacter atlanticus HTCC2559. Marine Genomics, 2016, 29, 35-38.	0.4	20
15	Heme auxotrophy in abundant aquatic microbial lineages. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	20
16	Genomic and ecological study of two distinctive freshwater bacteriophages infecting a Comamonadaceae bacterium. Scientific Reports, 2018, 8, 7989.	1.6	19
17	Viral metagenomes of Lake Soyang, the largest freshwater lake in South Korea. Scientific Data, 2020, 7, 349.	2.4	16
18	Genome Sequence of Strain IMCC3088, a Proteorhodopsin-Containing Marine Bacterium Belonging to the OM60/NOR5 Clade. Journal of Bacteriology, 2011, 193, 3415-3416.	1.0	14

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19	Kordia antarctica sp. nov., isolated from Antarctic seawater. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 3617-3622.	0.8	14
20	High-throughput cultivation based on dilution-to-extinction with catalase supplementation and a case study of cultivating acI bacteria from Lake Soyang. Journal of Microbiology, 2020, 58, 893-905.	1.3	14
21	Complete Genome Sequence of Marinomonas Bacteriophage P12026. Journal of Virology, 2012, 86, 8909-8910.	1.5	11
22	Halioglobus maricola sp. nov., isolated from coastal seawater. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1868-1875.	0.8	11
23	Genome Sequence of the Marine Alphaproteobacterium HTCC2150, Assigned to the Roseobacter Clade. Journal of Bacteriology, 2010, 192, 6315-6316.	1.0	10
24	Formosa arctica sp. nov., isolated from Arctic seawater. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 78-82.	0.8	10
25	Genome Sequence of Strain HTCC2083, a Novel Member of the Marine Clade Roseobacter. Journal of Bacteriology, 2011, 193, 319-320.	1.0	9
26	Complete genome sequence of Celeribacter marinus IMCC12053T, the host strain of marine bacteriophage P12053L. Marine Genomics, 2016, 26, 5-7.	0.4	7
27	Genome characteristics of Kordia antarctica IMCC3317T and comparative genome analysis of the genus Kordia. Scientific Reports, 2020, 10, 14715.	1.6	7
28	Genome Sequence of Strain IMCC2047, a Novel Marine Member of the Gammaproteobacteria. Journal of Bacteriology, 2011, 193, 3688-3689.	1.0	6
29	Genome Sequence of Strain IMCC14465, Isolated from the East Sea, Belonging to the PS1 Clade of Alphaproteobacteria. Journal of Bacteriology, 2012, 194, 6952-6953.	1.0	6
30	Cultivation of Dominant Freshwater Bacterioplankton Lineages Using a High-Throughput Dilution-to-Extinction Culturing Approach Over a 1-Year Period. Frontiers in Microbiology, 2021, 12, 700637.	1.5	6
31	Epoxinnamide: An Epoxy Cinnamoyl-Containing Nonribosomal Peptide from an Intertidal Mudflat-Derived Streptomyces sp.. Marine Drugs, 2022, 20, 455.	2.2	6
32	Uliginosibacterium aquaticum sp. nov., Isolated from a Freshwater Lake. Current Microbiology, 2021, 78, 3381-3387.	1.0	5
33	Depth-Specific Distribution of the SAR116 Phages Revealed by Virome Binning. Journal of Microbiology and Biotechnology, 2014, 24, 592-596.	0.9	5
34	Permianibacter fluminis sp. nov., isolated from a freshwater stream. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	4
35	Taeanamides A and B, Nonribosomal Lipo-Decapeptides Isolated from an Intertidal-Mudflat-Derived Streptomyces sp.. Marine Drugs, 2022, 20, 400.	2.2	3
36	Complete genome sequence of bacteriophage P8625, the first lytic phage that infects Verrucomicrobia. Standards in Genomic Sciences, 2015, 10, 96.	1.5	1