Youngik Yang

List of Publications by Year
in descending order

30 papers	1,094 citations	687363 13 h-index	677142 22 g-index
30 all docs	30 docs citations	30 times ranked	2106 citing authors

#	Article	IF	Citations
1	Chromosome-level genome assembly of the shuttles hoppfish, *Periophthalmus modestus*. GigaScience, 2022, 11, .	6.4	4
2	The complete mitochondrial genome of *Trichoderma simmonsii* (Hypocreales: Hypocreaceae) from the Southern Coast of Korea. Mitochondrial DNA Part B: Resources, 2022, 7, 640-641.	0.4	3
3	Telomere-to-telomere genome assembly of asparaginase-producing Trichoderma simmonsii. BMC Genomics, 2021, 22, 830.	2.8	9
4	First draft genome for the sand-hopper Trinorchestia longiramus. Scientific Data, 2020, 7, 85.	5.3	8
5	The Draft Genome Sequence of a New Land-Hopper Platorchestia hallaensis. Frontiers in Genetics, 2020, 11, 621301.	2.3	1
6	The complete mitochondrial genome of the sand-hopper Trinorchestia longiramus (Amphipoda:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54	0.4	2
7	GRASP2: fast and memory-efficient gene-centric assembly and homolog search for metagenomic sequencing data. BMC Bioinformatics, 2019, 20, 276.	2.6	5
8	Uncovering complex microbiome activities via metatranscriptomics during 24‰hours of oral biofilm assembly and maturation. Microbiome, 2018, 6, 217.	11.1	34
9	GRASP2: Fast and memory-efficient gene-centric assembly and homolog search. , 2017, , .		3
10	Metagenome and Metatranscriptome Analyses Using Protein Family Profiles. PLoS Computational Biology, 2016, 12, e1004991.	3.2	21
11	GRASPx: efficient homolog-search of short peptide metagenome database through simultaneous alignment and assembly. BMC Bioinformatics, 2016, 17, 283.	2.6	5
12	Meta-omics uncover temporal regulation of pathways across oral microbiome genera during *in vitro* sugar metabolism. ISME Journal, 2015, 9, 2605-2619.	9.8	63
13	SFA-SPA: a suffix array based short peptide assembler for metagenomic data. Bioinformatics, 2015, 31, 1833-1835.	4.1	10
14	Genomic and proteomic characterization of "*Candidatus* Nitrosopelagicus brevis" An ammonia-oxidizing archaeon from the open ocean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1173-1178.	7.1	278
15	Precision-guided antimicrobial peptide as a targeted modulator of human microbial ecology. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7569-7574.	7.1	135
16	GRASP: Guided Reference-based Assembly of Short Peptides. Nucleic Acids Research, 2015, 43, e18-e18.	14.5	25
17	An in vitrobiofilm model system maintaining a highly reproducible species and metabolic diversity approaching that of the human oral microbiome. Microbiome, 2013, 1, 25.	11.1	106
18	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2390-9.	7.1	192

#	ARTICLE	IF	CITATIONS
19	SPA: a short peptide assembler for metagenomic data. Nucleic Acids Research, 2013, 41, e91-e91.	14.5	15
20	A novel k-mer mixture logistic regression for methylation susceptibility modeling of CpG dinucleotides in human gene promoters. BMC Bioinformatics, 2012, 13, S15.	2.6	16
21	BioVLAB-MMIA: A Cloud Environment for microRNA and mRNA Integrated Analysis (MMIA) on Amazon EC2. IEEE Transactions on Nanobioscience, 2012, 11, 266-272.	3.3	24
22	BioVLAB-MMIA: A Reconfigurable Cloud Computing Environment for microRNA and mRNA Integrated Analysis. , 2011, , .		0
23	A novel K-mer mixture logistic regression for methylation susceptibility modeling of CpG dinucleotides in human gene promoters. , 2011, , .		0
24	A garter snake transcriptome: pyrosequencing, de novo assembly, and sex-specific differences. BMC Genomics, 2010, 11, 694.	2.8	60
25	Gene discovery in the horned beetle Onthophagus taurus. BMC Genomics, 2010, 11, 703.	2.8	40
26	Annotation confidence score for genome annotation: a genome comparison approach. Bioinformatics, 2010, 26, 22-29.	4.1	10
27	Experience report. , 2009, , .		0
28	BioVLAB-Microarray: Microarray Data Analysis in Virtual Environment. , 2008, , .		23
29	V-Lab-Protein: Virtual Collaborative Lab for protein sequence analysis. , 2007, , .		2
30	CGAS. Methods in Molecular Biology, 2007, , 133-146.	0.9	0