

# Youngik Yang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Genomic and proteomic characterization of <i>Candidatus Nitrosopelagicus brevis</i> : An ammonia-oxidizing archaeon from the open ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1173-1178.	7.1	278
2	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2390-9.	7.1	192
3	Precision-guided antimicrobial peptide as a targeted modulator of human microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7569-7574.	7.1	135
4	An in vitro biofilm model system maintaining a highly reproducible species and metabolic diversity approaching that of the human oral microbiome. <i>Microbiome</i> , 2013, 1, 25.	11.1	106
5	Meta-omics uncover temporal regulation of pathways across oral microbiome genera during <i>in vitro</i> sugar metabolism. <i>ISME Journal</i> , 2015, 9, 2605-2619.	9.8	63
6	A garter snake transcriptome: pyrosequencing, de novo assembly, and sex-specific differences. <i>BMC Genomics</i> , 2010, 11, 694.	2.8	60
7	Gene discovery in the horned beetle <i>Onthophagus taurus</i> . <i>BMC Genomics</i> , 2010, 11, 703.	2.8	40
8	Uncovering complex microbiome activities via metatranscriptomics during 24-hour oral biofilm assembly and maturation. <i>Microbiome</i> , 2018, 6, 217.	11.1	34
9	GRASP: Guided Reference-based Assembly of Short Peptides. <i>Nucleic Acids Research</i> , 2015, 43, e18-e18.	14.5	25
10	BioVLAB-MMIA: A Cloud Environment for microRNA and mRNA Integrated Analysis (MMIA) on Amazon EC2. <i>IEEE Transactions on Nanobioscience</i> , 2012, 11, 266-272.	3.3	24
11	BioVLAB-Microarray: Microarray Data Analysis in Virtual Environment. , 2008, , .		23
12	Metagenome and Metatranscriptome Analyses Using Protein Family Profiles. <i>PLoS Computational Biology</i> , 2016, 12, e1004991.	3.2	21
13	A novel k-mer mixture logistic regression for methylation susceptibility modeling of CpG dinucleotides in human gene promoters. <i>BMC Bioinformatics</i> , 2012, 13, S15.	2.6	16
14	SPA: a short peptide assembler for metagenomic data. <i>Nucleic Acids Research</i> , 2013, 41, e91-e91.	14.5	15
15	Annotation confidence score for genome annotation: a genome comparison approach. <i>Bioinformatics</i> , 2010, 26, 22-29.	4.1	10
16	SFA-SPA: a suffix array based short peptide assembler for metagenomic data. <i>Bioinformatics</i> , 2015, 31, 1833-1835.	4.1	10
17	Telomere-to-telomere genome assembly of asparaginase-producing <i>Trichoderma simmonsii</i> . <i>BMC Genomics</i> , 2021, 22, 830.	2.8	9
18	First draft genome for the sand-hopper <i>Trinorchestia longiramus</i> . <i>Scientific Data</i> , 2020, 7, 85.	5.3	8

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19	GRASPx: efficient homolog-search of short peptide metagenome database through simultaneous alignment and assembly. BMC Bioinformatics, 2016, 17, 283.	2.6	5
20	GRASP2: fast and memory-efficient gene-centric assembly and homolog search for metagenomic sequencing data. BMC Bioinformatics, 2019, 20, 276.	2.6	5
21	Chromosome-level genome assembly of the shuttles hopppfish, <i>Periophthalmus modestus</i> . GigaScience, 2022, 11, .	6.4	4
22	GRASP2: Fast and memory-efficient gene-centric assembly and homolog search. , 2017, , .		3
23	The complete mitochondrial genome of <i>Trichoderma simmonsii</i> (Hypocreales: Hypocreaceae) from the Southern Coast of Korea. Mitochondrial DNA Part B: Resources, 2022, 7, 640-641.	0.4	3
24	V-Lab-Protein: Virtual Collaborative Lab for protein sequence analysis. , 2007, , .		2
25	The complete mitochondrial genome of the sand-hopper <i>Trinorchestia longiramus</i> (Amphipoda: Tj ETQq1 1 0.784314 rgBT /Overlock 0,4 2		2
26	The Draft Genome Sequence of a New Land-Hopper <i>Platorchestia hallaensis</i> . Frontiers in Genetics, 2020, 11, 621301.	2.3	1
27	Experience report. , 2009, , .		0
28	BioVLAB-MMIA: A Reconfigurable Cloud Computing Environment for microRNA and mRNA Integrated Analysis. , 2011, , .		0
29	A novel K-mer mixture logistic regression for methylation susceptibility modeling of CpG dinucleotides in human gene promoters. , 2011, , .		0
30	CGAS. Methods in Molecular Biology, 2007, , 133-146.	0.9	0