## Shibu Yooseph

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/278192/publications.pdf

Version: 2024-02-01

29 papers 4,449 citations

567281 15 h-index 26 g-index

31 all docs

31 does citations

times ranked

31

7241 citing authors

#	Article	IF	CITATIONS
1	Variational Approximation-Based Model Selection for Microbial Network Inference. Journal of Computational Biology, 2022, 29, 724-737.	1.6	1
2	De Novo Genome Assembly Highlights the Role of Lineage-Specific Gene Duplications in the Evolution of Venom in Fea's Viper ( <i>Azemiops feae</i> ). Genome Biology and Evolution, 2022, 14, .	2.5	5
3	Peroxidized Linoleic Acid, 13-HPODE, Alters Gene Expression Profile in Intestinal Epithelial Cells. Foods, 2021, 10, 314.	4.3	5
4	Identification of Nasal Gammaproteobacteria with Potent Activity against Staphylococcus aureus: Novel Insights into the "Noncarrier―State. MSphere, 2021, 6, .	2.9	8
5	Bacterial associations in the healthy human gut microbiome across populations. Scientific Reports, 2021, 11, 2828.	3.3	34
6	Bacterial community structure alterations within the colorectal cancer gut microbiome. BMC Microbiology, 2021, 21, 98.	3.3	26
7	Effect of 13-Hydroperoxyoctadecadienoic Acid (13-HPODE) Treatment on the Transcriptomic Profile of Poorly-Differentiated Caco-2 Cells. Applied Sciences (Switzerland), 2021, 11, 2678.	2.5	O
8	Pulmonary Microbiome of Patients Receiving Mechanical Ventilation: Changes Over Time. American Journal of Critical Care, 2021, 30, 128-132.	1.6	3
9	Microbial community structure and composition is associated with host species and sex in Sigmodon cotton rats. Animal Microbiome, 2021, 3, 29.	3 <b>.</b> 8	3
10	Linking Inflammatory Bowel Disease Symptoms to Changes in the Gut Microbiome Structure and Function. Frontiers in Microbiology, 2021, 12, 673632.	3 <b>.</b> 5	6
11	Metatranscriptomics to characterize respiratory virome, microbiome, and host response directly from clinical samples. Cell Reports Methods, 2021, 1, 100091.	2.9	19
12	Global ecotypes in the ubiquitous marine clade SAR86. ISME Journal, 2020, 14, 178-188.	9.8	49
13	Evaluation of the upper airway microbiome and immune response with nasal epithelial lining fluid absorption and nasal washes. Scientific Reports, 2020, 10, 20618.	3.3	4
14	Co-occurrence of Anaerobes in Human Chronic Wounds. Microbial Ecology, 2019, 77, 808-820.	2.8	40
15	Learning a mixture of microbial networks using minorization–maximization. Bioinformatics, 2019, 35, i23-i30.	4.1	15
16	GRASP2: fast and memory-efficient gene-centric assembly and homolog search for metagenomic sequencing data. BMC Bioinformatics, 2019, 20, 276.	2.6	5
17	Gut microbiota dependent anti-tumor immunity restricts melanoma growth in Rnf5â^'/â^' mice. Nature Communications, 2019, 10, 1492.	12.8	114
18	Uncovering complex microbiome activities via metatranscriptomics during 24 hours of oral biofilm assembly and maturation. Microbiome, 2018, 6, 217.	11.1	34

#	Article	IF	CITATIONS
19	Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. BMC Genomics, 2017, 18, 296.	2.8	21
20	Gut Microbiome-Based Metagenomic Signature for Non-invasive Detection of Advanced Fibrosis in Human Nonalcoholic Fatty Liver Disease. Cell Metabolism, 2017, 25, 1054-1062.e5.	16.2	748
21	Metaâ€omic analyses of Baltic Sea cyanobacteria: diversity, community structure and salt acclimation. Environmental Microbiology, 2017, 19, 673-686.	3.8	65
22	GRASP2: Fast and memory-efficient gene-centric assembly and homolog search. , 2017, , .		3
23	Global biogeography of <i>Prochlorococcus</i> genome diversity in the surface ocean. ISME Journal, 2016, 10, 1856-1865.	9.8	76
24	Library preparation methodology can influence genomic and functional predictions in human microbiome research. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14024-14029.	7.1	179
25	Diet and Feeding Pattern Affect the Diurnal Dynamics of the Gut Microbiome. Cell Metabolism, 2014, 20, 1006-1017.	16.2	655
26	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. ISME Journal, 2012, 6, 1186-1199.	9.8	511
27	From Bacterial to Microbial Ecosystems (Metagenomics). Methods in Molecular Biology, 2012, 804, 35-55.	0.9	21
28	Gene identification and protein classification in microbial metagenomic sequence data via incremental clustering. BMC Bioinformatics, 2008, 9, 182.	2.6	42
29	The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. PLoS Biology, 2007, 5, e77.	5.6	1,757