Chenhao Li

List of Publications by Year
in descending order

16	1,550	623734	839539
papers	citations	14	18
		h-index	g-index

23	23	23	2804
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole metagenome profiling reveals skin microbiome-dependent susceptibility to atopic dermatitis flare. Nature Microbiology, 2016, 1, 16106.	13.3	298
2	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. Nature Biotechnology, 2019, 37, 937-944.	17.5	216
3	Genus-Wide Comparative Genomics of Malassezia Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. PLoS Genetics, 2015, 11, e1005614.	3.5	198
4	INC-Seq: accurate single molecule reads using nanopore sequencing. GigaScience, 2016, 5, 34.	6.4	133
5	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
6	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	30.7	130
7	Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. Nature Ecology and Evolution, 2020, 4, 1256-1267.	7.8	98
8	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202.	6.1	94
9	Determination of isoform-specific RNA structure with nanopore long reads. Nature Biotechnology, 2021, 39, 336-346.	17.5	72
10	Predicting microbial interactions through computational approaches. Methods, 2016, 102, 12-19.	3.8	49
11	@MInter: automated text-mining of microbial interactions. Bioinformatics, 2016, 32, 2981-2987.	4.1	30
12	An expectation-maximization algorithm enables accurate ecological modeling using longitudinal microbiome sequencing data. Microbiome, 2019, 7, 118.	11.1	28
13	Atopic dermatitis microbiomes stratify into ecologic dermotypes enabling microbial virulence and disease severity. Journal of Allergy and Clinical Immunology, 2021, 147, 1329-1340.	2.9	26
14	ConsensusDriver Improves upon Individual Algorithms for Predicting Driver Alterations in Different Cancer Types and Individual Patients. Cancer Research, 2018, 78, 290-301.	0.9	20
15	Single-virion sequencing of lamivudine-treated HBV populations reveal population evolution dynamics and demographic history. BMC Genomics, 2017, 18, 829.	2.8	6
16	BEEM-Static: Accurate inference of ecological interactions from cross-sectional microbiome data. PLoS Computational Biology, 2021, 17, e1009343.	3.2	2