

# Chenhao Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7746992/publications.pdf>

Version: 2024-02-01

16  
papers

1,550  
citations

623734

14  
h-index

839539

18  
g-index

23  
all docs

23  
docs citations

23  
times ranked

2804  
citing authors

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