

Chengwei Luo

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

7,005
citations

377584

21
h-index

721071

23
g-index

23
all docs

23
docs citations

23
times ranked

13553
citing authors

#	ARTICLE	IF	CITATIONS
1	Iterative subtractive binning of freshwater chronoserries metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
2	Model-based Comparisons of the Abundance Dynamics of Bacterial Communities in Two Lakes. <i>Scientific Reports</i> , 2020, 10, 2423.	1.6	14
3	The Bacterial Symbionts of Closely Related Hydrothermal Vent Snails With Distinct Geochemical Habitats Show Broad Similarity in Chemoautotrophic Gene Content. <i>Frontiers in Microbiology</i> , 2019, 10, 1818.	1.5	21
4	Gut Microbiome Function Predicts Response to Anti-integrin Biologic Therapy in Inflammatory Bowel Diseases. <i>Cell Host and Microbe</i> , 2017, 21, 603-610.e3.	5.1	306
5	Ectopic colonization of oral bacteria in the intestine drives T _H 1 cell induction and inflammation. <i>Science</i> , 2017, 358, 359-365.	6.0	612
6	Indoleacrylic Acid Produced by Commensal Peptostreptococcus Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	5.1	523
7	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	54
8	Paneth cell defects in Crohn's disease patients promote dysbiosis. <i>JCI Insight</i> , 2016, 1, e86907.	2.3	91
9	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	1.5	66
10	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
11	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2872-2883.	1.4	102
12	ConStrains identifies microbial strains in metagenomic datasets. <i>Nature Biotechnology</i> , 2015, 33, 1045-1052.	9.4	235
13	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e93827.	1.1	508
14	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <i>Nucleic Acids Research</i> , 2014, 42, e73-e73.	6.5	445
15	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
16	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
17	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. <i>Environmental Microbiology Reports</i> , 2014, 6, 640-655.	1.0	36
18	Stability, genotypic and phenotypic diversity of <i>Sphaerobacter</i> in the redox transition zone of the Baltic Sea. <i>Environmental Microbiology</i> , 2014, 16, 1854-1866.	1.8	26

#	ARTICLE	IF	CITATIONS
19	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547.	0.4	28
20	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. <i>PLoS ONE</i> , 2012, 7, e30087.	1.1	360
21	Individual genome assembly from complex community short-read metagenomic datasets. <i>ISME Journal</i> , 2012, 6, 898-901.	4.4	106
22	Genome sequencing of environmental <i>Escherichia coli</i> expands understanding of the ecology and speciation of the model bacterial species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7200-7205.	3.3	279
23	Metagenomic Insights into the Evolution, Function, and Complexity of the Planktonic Microbial Community of Lake Lanier, a Temperate Freshwater Ecosystem. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6000-6011.	1.4	151