

# Chengwei Luo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11963236/publications.pdf>

Version: 2024-02-01

23  
papers

7,005  
citations

331642  
21  
h-index

642715  
23  
g-index

23  
all docs

23  
docs citations

23  
times ranked

12349  
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.	3.8	69
2	Model-based Comparisons of the Abundance Dynamics of Bacterial Communities in Two Lakes. <i>Scientific Reports</i> , 2020, 10, 2423.	3.3	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.	3.5	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.	11.0	306
5	Ectopic colonization of oral bacteria in the intestine drives T <sub>H</sub> 1 cell induction and inflammation. <i>Science</i> , 2017, 358, 359-365.	12.6	612
6	Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	11.0	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, .	3.1	54
8	Paneth cell defects in Crohn's disease patients promote dysbiosis. <i>JCI Insight</i> , 2016, 1, e86907.	5.0	91
9	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	3.5	66
10	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	18.8	260
11	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2872-2883.	3.1	102
12	ConStrains identifies microbial strains in metagenomic datasets. <i>Nature Biotechnology</i> , 2015, 33, 1045-1052.	17.5	235
13	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e93827.	2.5	508
14	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <i>Nucleic Acids Research</i> , 2014, 42, e73-e73.	14.5	445
15	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.0	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.	3.1	131
17	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. <i>Environmental Microbiology Reports</i> , 2014, 6, 640-655.	2.4	36
18	Stability, genotypic and phenotypic diversity of <i>S. hewanella baltica</i> in the redox transition zone of the Baltic Sea. <i>Environmental Microbiology</i> , 2014, 16, 1854-1866.	3.8	26

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19	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547.	1.0	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.	2.5	360
21	Individual genome assembly from complex community short-read metagenomic datasets. <i>ISME Journal</i> , 2012, 6, 898-901.	9.8	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.	7.1	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.	3.1	151