## Chengwei Luo

List of Publications by Year in descending order

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

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331642 642715 7,005 23 21 23 h-index citations g-index papers 23 23 23 12349 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. Cell Host and Microbe, 2014, 15, 382-392.	11.0	2,582
2	Ectopic colonization of oral bacteria in the intestine drives T <sub>H</sub> 1 cell induction and inflammation. Science, 2017, 358, 359-365.	12.6	612
3	Indoleacrylic Acid Produced by Commensal Peptostreptococcus Species Suppresses Inflammation. Cell Host and Microbe, 2017, 22, 25-37.e6.	11.0	<b>52</b> 3
4	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. PLoS ONE, 2014, 9, e93827.	2.5	508
5	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. Nucleic Acids Research, 2014, 42, e73-e73.	14.5	445
6	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. PLoS ONE, 2012, 7, e30087.	2.5	360
7	Gut Microbiome Function Predicts Response to Anti-integrin Biologic Therapy in Inflammatory Bowel Diseases. Cell Host and Microbe, 2017, 21, 603-610.e3.	11.0	306
8	Genome sequencing of environmental <i>Escherichia coli</i> expands understanding of the ecology and speciation of the model bacterial species. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7200-7205.	7.1	279
9	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. Nature Climate Change, 2016, 6, 595-600.	18.8	260
10	ConStrains identifies microbial strains in metagenomic datasets. Nature Biotechnology, 2015, 33, 1045-1052.	17.5	235
11	Metagenomic Insights into the Evolution, Function, and Complexity of the Planktonic Microbial Community of Lake Lanier, a Temperate Freshwater Ecosystem. Applied and Environmental Microbiology, 2011, 77, 6000-6011.	3.1	151
12	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. Applied and Environmental Microbiology, 2014, 80, 1777-1786.	3.1	131
13	Individual genome assembly from complex community short-read metagenomic datasets. ISME Journal, 2012, 6, 898-901.	9.8	106
14	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. Applied and Environmental Microbiology, 2016, 82, 2872-2883.	3.1	102
15	Paneth cell defects in Crohn's disease patients promote dysbiosis. JCl Insight, 2016, 1, e86907.	5.0	91
16	Iterative subtractive binning of freshwater chronoseries metagenomes identifies over 400 novel species and their ecologic preferences. Environmental Microbiology, 2020, 22, 3394-3412.	3.8	69
17	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. Frontiers in Microbiology, 2016, 7, 579.	3.5	66
18	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. Applied and Environmental Microbiology, 2017, 83, .	3.1	54

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#	Article	IF	CITATION
19	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. Environmental Microbiology Reports, 2014, 6, 640-655.	2.4	36
20	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. Methods in Enzymology, 2013, 531, 525-547.	1.0	28
21	Stability, genotypic and phenotypic diversity of <scp><i>S</i></scp> <i>hewanella baltica</i> in the redox transition zone of the <scp>B</scp> altic <scp>S</scp> ea. Environmental Microbiology, 2014, 16, 1854-1866.	3.8	26
22	The Bacterial Symbionts of Closely Related Hydrothermal Vent Snails With Distinct Geochemical Habitats Show Broad Similarity in Chemoautotrophic Gene Content. Frontiers in Microbiology, 2019, 10, 1818.	3.5	21
23	Model-based Comparisons of the Abundance Dynamics of Bacterial Communities in Two Lakes. Scientific Reports, 2020, 10, 2423.	3.3	14