

Laura A Hug

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/466607/publications.pdf>

Version: 2024-02-01

48
papers

8,714
citations

172457

29
h-index

223800

46
g-index

57
all docs

57
docs citations

57
times ranked

9640
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 detection from the built environment and wastewater and its use for hospital surveillance. <i>Facets</i> , 2022, 7, 82-97.	2.4	15
2	Environmental Potential for Microbial 1,4-Dioxane Degradation Is Sparse despite Mobile Elements Playing a Role in Trait Distribution. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0209121.	3.1	8
3	Clacimonadota metabolisms include adaptations in engineered environments that are reflected in the evolutionary history of the phylum. <i>Environmental Microbiology Reports</i> , 2022, 14, 520-529.	2.4	8
4	Substrate-restricted methanogenesis and limited volatile organic compound degradation in highly diverse and heterogeneous municipal landfill microbial communities. <i>ISME Communications</i> , 2022, 2, .	4.2	8
5	Composition of the North American Wood Frog (<i>Rana sylvatica</i>) Bacterial Skin Microbiome and Seasonal Variation in Community Structure. <i>Microbial Ecology</i> , 2021, 81, 78-92.	2.8	25
6	The phylogenetic and global distribution of bacterial polyhydroxyalkanoate bioplastic-degrading genes. <i>Environmental Microbiology</i> , 2021, 23, 1717-1731.	3.8	25
7	Prediction, enrichment and isolation identify a responsive, competitive community of cellulolytic microorganisms from a municipal landfill. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	3
8	New approaches for the characterization of plastic-associated microbial communities and the discovery of plastic-degrading microorganisms and enzymes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6191-6200.	4.1	28
9	Adapting Macroecology to Microbiology: Using Occupancy Modeling To Assess Functional Profiles across Metagenomes. <i>MSystems</i> , 2021, 6, e0079021.	3.8	1
10	A Need for Improved Cellulase Identification from Metagenomic Sequence Data. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	2
11	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. <i>ISME Journal</i> , 2020, 14, 2907-2922.	9.8	51
12	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
13	High functional diversity among <i>Nitrospira</i> populations that dominate rotating biological contactor microbial communities in a municipal wastewater treatment plant. <i>ISME Journal</i> , 2020, 14, 1857-1872.	9.8	91
14	Distribution of reactive oxygen species defense mechanisms across domain bacteria. <i>Free Radical Biology and Medicine</i> , 2019, 140, 93-102.	2.9	70
15	AnnoTree: visualization and exploration of a functionally annotated microbial tree of life. <i>Nucleic Acids Research</i> , 2019, 47, 4442-4448.	14.5	220
16	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. <i>MSphere</i> , 2018, 3, .	2.9	12
17	Sizing Up the Uncultured Microbial Majority. <i>MSystems</i> , 2018, 3, .	3.8	13
18	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. <i>Methods in Molecular Biology</i> , 2018, 1849, 215-225.	0.9	2

#	ARTICLE	IF	CITATIONS
19	It Takes a Village: Microbial Communities Thrive through Interactions and Metabolic Handoffs. <i>MSystems</i> , 2018, 3, .	3.8	34
20	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	3.8	212
21	Diversity, Evolution, and Environmental Distribution of Reductive Dehalogenase Genes. , 2016, , 377-393.		12
22	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
23	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	13.3	1,823
24	Novel Hydrogenosomes in the Microaerophilic Jakobid <i>Stygiella incarcerata</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2318-2336.	8.9	52
25	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016, 18, 159-173.	3.8	164
26	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	5.5	121
27	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	9.8	88
28	Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. <i>Current Biology</i> , 2015, 25, 690-701.	3.9	522
29	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	27.8	1,050
30	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
31	New Insights into <i>Dehalococcoides mccartyi</i> Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of <i>D. mccartyi</i> Transcriptomes. <i>PLoS ONE</i> , 2014, 9, e94808.	2.5	14
32	Metatranscriptome of an Anaerobic Benzene-Degrading, Nitrate-Reducing Enrichment Culture Reveals Involvement of Carboxylation in Benzene Ring Activation. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4095-4107.	3.1	99
33	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	9.8	170
34	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
35	Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. <i>Microbiome</i> , 2013, 1, 22.	11.1	493
36	Research Needs for Bioaugmentation. , 2013, , 333-361.		1

#	ARTICLE	IF	CITATIONS
37	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. MBio, 2013, 4, e00708-13.	4.1	298
38	Overview of organohalide-respiring bacteria and a proposal for a classification system for reductive dehalogenases. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120322.	4.0	266
39	Diversity of reductive dehalogenase genes from environmental samples and enrichment cultures identified with degenerate primer PCR screens. Frontiers in Microbiology, 2013, 4, 341.	3.5	44
40	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. ELife, 2013, 2, e01102.	6.0	355
41	Discovery of a <i>trans</i> -Dichloroethene-Respiring Dehalogenimonas Species in the 1,1,2,2-Tetrachloroethane-Dechlorinating WBC-2 Consortium. Applied and Environmental Microbiology, 2012, 78, 5280-5287.	3.1	54
42	Transcriptional Analysis of a Dehalococcoides-Containing Microbial Consortium Reveals Prophage Activation. Applied and Environmental Microbiology, 2012, 78, 1178-1186.	3.1	34
43	Comparative metagenomics of three Dehalococcoides-containing enrichment cultures: the role of the non-dechlorinating community. BMC Genomics, 2012, 13, 327.	2.8	109
44	Site-Specific Mobilization of Vinyl Chloride Respiration Islands by a Mechanism Common in Dehalococcoides. BMC Genomics, 2011, 12, 287.	2.8	55
45	Design and Verification of a Pangenome Microarray Oligonucleotide Probe Set for Dehalococcoides spp. Applied and Environmental Microbiology, 2011, 77, 5361-5369.	3.1	34
46	Phylogenetic Distributions and Histories of Proteins Involved in Anaerobic Pyruvate Metabolism in Eukaryotes. Molecular Biology and Evolution, 2010, 27, 311-324.	8.9	81
47	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic "supergroups". Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3859-3864.	7.1	444
48	The Impact of Fossils and Taxon Sampling on Ancient Molecular Dating Analyses. Molecular Biology and Evolution, 2007, 24, 1889-1897.	8.9	137