

# Laura A Hug

## List of Publications by Year in descending order

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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	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	13.3	1,823
2	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	27.8	1,050
3	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
4	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
5	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
6	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic "supergroups". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3859-3864.	7.1	444
7	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. <i>ELife</i> , 2013, 2, e01102.	6.0	355
8	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. <i>MBio</i> , 2013, 4, e00708-13.	4.1	298
9	Overview of organohalide-respiring bacteria and a proposal for a classification system for reductive dehalogenases. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120322.	4.0	266
10	AnnoTree: visualization and exploration of a functionally annotated microbial tree of life. <i>Nucleic Acids Research</i> , 2019, 47, 4442-4448.	14.5	220
11	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO <sub>2</sub> concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	3.8	212
12	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
13	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	9.8	170
14	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
15	The Impact of Fossils and Taxon Sampling on Ancient Molecular Dating Analyses. <i>Molecular Biology and Evolution</i> , 2007, 24, 1889-1897.	8.9	137
16	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	5.5	121
17	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
18	Comparative metagenomics of three Dehalococcoides-containing enrichment cultures: the role of the non-dechlorinating community. <i>BMC Genomics</i> , 2012, 13, 327.	2.8	109

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19	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
20	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
21	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	9.8	88
22	Phylogenetic Distributions and Histories of Proteins Involved in Anaerobic Pyruvate Metabolism in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2010, 27, 311-324.	8.9	81
23	Distribution of reactive oxygen species defense mechanisms across domain bacteria. <i>Free Radical Biology and Medicine</i> , 2019, 140, 93-102.	2.9	70
24	Site-Specific Mobilization of Vinyl Chloride Respiration Islands by a Mechanism Common in <i>Dehalococcoides</i> . <i>BMC Genomics</i> , 2011, 12, 287.	2.8	55
25	Discovery of a <i>trans</i> -Dichloroethene-Respiring <i>Dehalogenimonas</i> Species in the 1,1,2,2-Tetrachloroethane-Dechlorinating WBC-2 Consortium. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5280-5287.	3.1	54
26	Novel Hydrogenosomes in the Microaerophilic Jakobid <i>Stygiella incarcerata</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 2318-2336.	8.9	52
27	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
28	Diversity of reductive dehalogenase genes from environmental samples and enrichment cultures identified with degenerate primer PCR screens. <i>Frontiers in Microbiology</i> , 2013, 4, 341.	3.5	44
29	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
30	Design and Verification of a Pangenome Microarray Oligonucleotide Probe Set for <i>Dehalococcoides</i> spp. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5361-5369.	3.1	34
31	Transcriptional Analysis of a <i>Dehalococcoides</i> -Containing Microbial Consortium Reveals Prophage Activation. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1178-1186.	3.1	34
32	It Takes a Village: Microbial Communities Thrive through Interactions and Metabolic Handoffs. <i>MSystems</i> , 2018, 3, .	3.8	34
33	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
34	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
35	The phylogenetic and global distribution of bacterial polyhydroxyalkanoate bioplastic-degrading genes. <i>Environmental Microbiology</i> , 2021, 23, 1717-1731.	3.8	25
36	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

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37	New Insights into Dehalococcoides mccartyi Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of D. mccartyi Transcriptomes. PLoS ONE, 2014, 9, e94808.	2.5	14
38	Sizing Up the Uncultured Microbial Majority. MSystems, 2018, 3, .	3.8	13
39	Diversity, Evolution, and Environmental Distribution of Reductive Dehalogenase Genes. , 2016, , 377-393.		12
40	Widespread Antibiotic, Biocide, and Metal Resistance in Microbial Communities Inhabiting a Municipal Waste Environment and Anthropogenically Impacted River. MSphere, 2018, 3, .	2.9	12
41	Environmental Potential for Microbial 1,4-Dioxane Degradation Is Sparse despite Mobile Elements Playing a Role in Trait Distribution. Applied and Environmental Microbiology, 2022, 88, e0209121.	3.1	8
42	Cloacimonadota metabolisms include adaptations in engineered environments that are reflected in the evolutionary history of the phylum. Environmental Microbiology Reports, 2022, 14, 520-529.	2.4	8
43	Substrate-restricted methanogenesis and limited volatile organic compound degradation in highly diverse and heterogeneous municipal landfill microbial communities. ISME Communications, 2022, 2, .	4.2	8
44	Prediction, enrichment and isolation identify a responsive, competitive community of cellulolytic microorganisms from a municipal landfill. FEMS Microbiology Ecology, 2021, 97, .	2.7	3
45	Subsampled Assemblies and Hybrid Nucleotide Composition/Differential Coverage Binning for Genome-Resolved Metagenomics. Methods in Molecular Biology, 2018, 1849, 215-225.	0.9	2
46	A Need for Improved Cellulase Identification from Metagenomic Sequence Data. Applied and Environmental Microbiology, 2020, 87, .	3.1	2
47	Research Needs for Bioaugmentation. , 2013, , 333-361.		1
48	Adapting Macroecology to Microbiology: Using Occupancy Modeling To Assess Functional Profiles across Metagenomes. MSystems, 2021, 6, e0079021.	3.8	1