

# Olivia U Mason

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3845340/publications.pdf>

Version: 2024-02-01

36  
papers

4,112  
citations

394390

19  
h-index

345203

36  
g-index

41  
all docs

41  
docs citations

41  
times ranked

4304  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. <i>Science</i> , 2010, 330, 204-208.	12.6	1,109
2	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	9.8	547
3	Succession of Hydrocarbon-Degrading Bacteria in the Aftermath of the <i>Deepwater Horizon</i> Oil Spill in the Gulf of Mexico. <i>Environmental Science &amp; Technology</i> , 2013, 47, 10860-10867.	10.0	344
4	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	9.8	325
5	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	3.8	275
6	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012, 6, 451-460.	9.8	240
7	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 130.	3.5	172
8	First Investigation of the Microbiology of the Deepest Layer of Ocean Crust. <i>PLoS ONE</i> , 2010, 5, e15399.	2.5	142
9	Prokaryotic diversity, distribution, and insights into their role in biogeochemical cycling in marine basalts. <i>ISME Journal</i> , 2009, 3, 231-242.	9.8	137
10	Single-cell genomics reveals features of a <i>Colwellia</i> species that was dominant during the Deepwater Horizon oil spill. <i>Frontiers in Microbiology</i> , 2014, 5, 332.	3.5	106
11	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <i>MBio</i> , 2017, 8, .	4.1	80
12	The microbial nitrogen cycling potential is impacted by polyaromatic hydrocarbon pollution of marine sediments. <i>Frontiers in Microbiology</i> , 2014, 5, 108.	3.5	76
13	The phylogeny of endolithic microbes associated with marine basalts. <i>Environmental Microbiology</i> , 2007, 9, 2539-2550.	3.8	74
14	Assessing impacts of unconventional natural gas extraction on microbial communities in headwater stream ecosystems in Northwestern Pennsylvania. <i>Frontiers in Microbiology</i> , 2014, 5, 522.	3.5	58
15	Archaeal enrichment in the hypoxic zone in the northern Gulf of Mexico. <i>Environmental Microbiology</i> , 2015, 17, 3847-3856.	3.8	51
16	Mississippi River Plume Enriches Microbial Diversity in the Northern Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2016, 7, 1048.	3.5	43
17	Comparison of Archaeal and Bacterial Diversity in Methane Seep Carbonate Nodules and Host Sediments, Eel River Basin and Hydrate Ridge, USA. <i>Microbial Ecology</i> , 2015, 70, 766-784.	2.8	40
18	Carbon fixation and energy metabolisms of a seafloor olivine biofilm. <i>ISME Journal</i> , 2019, 13, 1737-1749.	9.8	39

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19	Methane and microbial dynamics in the Gulf of Mexico water column. <i>Frontiers in Marine Science</i> , 2015, 2, .	2.5	25
20	Deep Crustal Communities of the Juan de Fuca Ridge Are Governed by Mineralogy. <i>Geomicrobiology Journal</i> , 2017, 34, 147-156.	2.0	21
21	Microbial Community Analysis Provides Insights into the Effects of Tetrahydrofuran on 1,4-Dioxane Biodegradation. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	20
22	Effects of a Ciliate Protozoa Predator on Microbial Communities in Pitcher Plant ( <i>Sarracenia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 622 T	2.5	20
23	Amino acid treatment enhances protein recovery from sediment and soils for metaproteomic studies. <i>Proteomics</i> , 2013, 13, 2776-2785.	2.2	18
24	Predator identity more than predator richness structures aquatic microbial assemblages in <i>Sarracenia purpurea</i> leaves. <i>Ecology</i> , 2018, 99, 652-660.	3.2	17
25	Elevated nutrient inputs to marshes differentially impact carbon and nitrogen cycling in two northern Gulf of Mexico saltmarsh plants. <i>Biogeochemistry</i> , 2020, 149, 1-16.	3.5	16
26	Extent of the annual Gulf of Mexico hypoxic zone influences microbial community structure. <i>PLoS ONE</i> , 2019, 14, e0209055.	2.5	15
27	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico "Dead Zone". <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	14
28	Investigating promising substrates for promoting 1,4-dioxane biodegradation: effects of ethane and tetrahydrofuran on microbial consortia. <i>Biodegradation</i> , 2020, 31, 171-182.	3.0	14
29	Host and environmental determinants of microbial community structure in the marine phyllosphere. <i>PLoS ONE</i> , 2020, 15, e0235441.	2.5	12
30	Enrichment of potential pathogens in marine microbiomes with different degrees of anthropogenic activity. <i>Environmental Pollution</i> , 2021, 268, 115757.	7.5	12
31	New Insights Into the Influence of Plant and Microbial Diversity on Denitrification Rates in a Salt Marsh. <i>Wetlands</i> , 2021, 41, 1.	1.5	12
32	Composition of seagrass phyllosphere microbial communities suggests rapid environmental regulation of community structure. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	11
33	Ditching Nutrients: Roadside Drainage Networks are Hotspots for Microbial Nitrogen Removal. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2021, 126, e2020JG006115.	3.0	9
34	Metagenomic analysis of microbial communities across a transect from low to highly hydrocarbon-contaminated soils in King George Island, Maritime Antarctica. <i>Geobiology</i> , 2022, 20, 98-111.	2.4	9
35	Environmental stressors alter the composition of seagrass phyllosphere microbial communities. <i>Climate Change Ecology</i> , 2021, 2, 100042.	1.9	4
36	Marine microbiology: Community clean up. <i>Nature Microbiology</i> , 2016, 1, 16102.	13.3	1