## Annika C Mosier

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Relative abundance and diversity of ammoniaâ€oxidizing archaea and bacteria in the San Francisco Bay estuary. Environmental Microbiology, 2008, 10, 3002-3016.	3.8	342
2	Genome of a Low-Salinity Ammonia-Oxidizing Archaeon Determined by Single-Cell and Metagenomic Analysis. PLoS ONE, 2011, 6, e16626.	2.5	287
3	Core and Intact Polar Glycerol Dibiphytanyl Glycerol Tetraether Lipids of Ammonia-Oxidizing Archaea Enriched from Marine and Estuarine Sediments. Applied and Environmental Microbiology, 2011, 77, 3468-3477.	3.1	166
4	Denitrifier abundance and activity across the San Francisco Bay estuary. Environmental Microbiology Reports, 2010, 2, 667-676.	2.4	109
5	Spatial Variability in Nitrification Rates and Ammonia-Oxidizing Microbial Communities in the Agriculturally Impacted Elkhorn Slough Estuary, California. Applied and Environmental Microbiology, 2011, 77, 269-280.	3.1	98
6	Global Biodiversity of Aquatic Ammonia-Oxidizing Archaea is Partitioned by Habitat. Frontiers in Microbiology, 2012, 3, 252.	3.5	94
7	Metabolites Associated with Adaptation of Microorganisms to an Acidophilic, Metal-Rich Environment Identified by Stable-Isotope-Enabled Metabolomics. MBio, 2013, 4, e00484-12.	4.1	87
8	Genome Sequence of " <i>Candidatus</i> Nitrosopumilus salaria―BD31, an Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary. Journal of Bacteriology, 2012, 194, 2121-2122.	2.2	77
9	Ecophysiology of an Ammonia-Oxidizing Archaeon Adapted to Low-Salinity Habitats. Microbial Ecology, 2012, 64, 955-963.	2.8	76
10	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. Frontiers in Microbiology, 2016, 7, 238.	3.5	66
11	Microbiota within the perennial ice cover of Lake Vida, Antarctica. FEMS Microbiology Ecology, 2007, 59, 274-288.	2.7	63
12	Genome Sequence of " <i>Candidatus</i> Nitrosoarchaeum limnia―BG20, a Low-Salinity Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary. Journal of Bacteriology, 2012, 194, 2119-2120.	2.2	59
13	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. ISME Journal, 2015, 9, 180-194.	9.8	57
14	Spatiotemporal Relationships Between the Abundance, Distribution, and Potential Activities of Ammonia-Oxidizing and Denitrifying Microorganisms in Intertidal Sediments. Microbial Ecology, 2015, 69, 13-24.	2.8	49
15	<sup>15</sup> <scp>N</scp> ―and <sup>2</sup> <scp>H</scp> proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. Environmental Microbiology, 2014, 16, 3224-3237.	3.8	48
16	Seasonal <i>Synechococcus</i> and <i>Thaumarchaeal</i> population dynamics examined with high resolution with remote <i>in situ</i> instrumentation. ISME Journal, 2012, 6, 513-523.	9.8	46
17	Genomic profiling of four cultivated <i>Candidatus</i> Nitrotoga spp. predicts broad metabolic potential and environmental distribution. ISME Journal, 2018, 12, 2864-2882.	9.8	42
18	Expanded Diversity and Metabolic Versatility of Marine Nitrite-Oxidizing Bacteria Revealed by Cultivation- and Genomics-Based Approaches. Applied and Environmental Microbiology, 2020, 86, .	3.1	38

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19	Determining the Distribution of Marine and Coastal Ammonia-Oxidizing Archaea and Bacteria Using a Quantitative Approach. Methods in Enzymology, 2011, 486, 205-221.	1.0	30
20	Benthic ammonia oxidizers differ in community structure and biogeochemical potential across a riverine delta. Frontiers in Microbiology, 2014, 5, 743.	3.5	28
21	Honey bee microbiome associated with different hive and sample types over a honey production season. PLoS ONE, 2019, 14, e0223834.	2.5	25
22	Nitrifier Gene Abundance and Diversity in Sediments Impacted by Acid Mine Drainage. Frontiers in Microbiology, 2017, 8, 2136.	3.5	20
23	Community Composition ofÂNitrite Reductase Gene Sequences inÂanÂAcid Mine Drainage Environment. Microbial Ecology, 2020, 79, 562-575.	2.8	9
24	Physiology of the Nitrite-Oxidizing Bacterium Candidatus Nitrotoga sp. CP45 Enriched From a Colorado River. Frontiers in Microbiology, 2021, 12, 709371.	3.5	4