

# Sarah M Owens

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

28  
papers

9,207  
citations

19  
h-index

30  
g-index

30  
ext. papers

12,290  
ext. citations

11.1  
avg, IF

5.34  
L-index

#	Paper	IF	Citations
28	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , <b>2021</b> , 16, e0237556	3.7	1
27	Reducing host DNA contamination in 16S rRNA gene surveys of anthozoan microbiomes using PNA clamps. <i>Coral Reefs</i> , <b>2020</b> , 39, 1817-1827	4.2	3
26	Microbiome characterization by high-throughput transfer RNA sequencing and modification analysis. <i>Nature Communications</i> , <b>2018</b> , 9, 5353	17.4	31
25	Enteric infection coupled with chronic Notch pathway inhibition alters colonic mucus composition leading to dysbiosis, barrier disruption and colitis. <i>PLoS ONE</i> , <b>2018</b> , 13, e0206701	3.7	13
24	Size, Composition, and Source Profiles of Inhalable Bioaerosols from Colorado Dairies. <i>Environmental Science &amp; Technology</i> , <b>2017</b> , 51, 6430-6440	10.3	23
23	Identifying the plant-associated microbiome across aquatic and terrestrial environments: the effects of amplification method on taxa discovery. <i>Molecular Ecology Resources</i> , <b>2017</b> , 17, 931-942	8.4	19
22	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , <b>2017</b> , 551, 457-463	50.4	1076
21	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. <i>MSphere</i> , <b>2017</b> , 2,	5	36
20	Parallelized, Aerobic, Single Carbon-Source Enrichments from Different Natural Environments Contain Divergent Microbial Communities. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2321	5.7	14
19	Divergent responses of viral and bacterial communities in the gut microbiome to dietary disturbances in mice. <i>ISME Journal</i> , <b>2016</b> , 10, 1217-27	11.9	58
18	Metagenomic Design and Sequencing <b>2016</b> , 291-312		
17	Spatial scale drives patterns in soil bacterial diversity. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 2039-51	5.2	131
16	The soil microbiome influences grapevine-associated microbiota. <i>MBio</i> , <b>2015</b> , 6,	7.8	465
15	Athletic equipment microbiota are shaped by interactions with human skin. <i>Microbiome</i> , <b>2015</b> , 3, 25	16.6	31
14	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , <b>2014</b> , 8, 841-53	11.9	111
13	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , <b>2014</b> , 345, 1048-52	33.3	543
12	Dinitrogen fixation associated with shoots of aquatic carnivorous plants: is it ecologically important?. <i>Annals of Botany</i> , <b>2014</b> , 114, 125-33	4.1	12

11	Saliva from obese individuals suppresses the release of aroma compounds from wine. <i>PLoS ONE</i> , <b>2014</b> , 9, e85611	3.7	70
10	Understanding cultivar-specificity and soil determinants of the cannabis microbiome. <i>PLoS ONE</i> , <b>2014</b> , 9, e99641	3.7	45
9	DNA extraction protocols cause differences in 16S rRNA amplicon sequencing efficiency but not in community profile composition or structure. <i>MicrobiologyOpen</i> , <b>2014</b> , 3, 910-21	3.4	64
8	Reconstructing the microbial diversity and function of pre-agricultural tallgrass prairie soils in the United States. <i>Science</i> , <b>2013</b> , 342, 621-4	33.3	324
7	Restricted streptomycin use in apple orchards did not adversely alter the soil bacteria communities. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 383	5.7	22
6	Metagenome sequencing of prokaryotic microbiota collected from Byron Glacier, Alaska. <i>Genome Announcements</i> , <b>2013</b> , 1, e0009913		12
5	Investigating the impact of storage conditions on microbial community composition in soil samples. <i>PLoS ONE</i> , <b>2013</b> , 8, e70460	3.7	86
4	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 21390-5	11.5	956
3	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , <b>2012</b> , 6, 1621-4	11.9	5059
2	Bacterial community composition and dynamics spanning five years in freshwater bog lakes		1
1	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota		1