

# Clarisse Marotz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3123519/publications.pdf>

Version: 2024-02-01

26  
papers

14,665  
citations

566801

15  
h-index

552369

26  
g-index

39  
all docs

39  
docs citations

39  
times ranked

18198  
citing authors

#	ARTICLE	IF	CITATIONS
1	Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) screening among symptom-free healthcare workers. <i>Infection Control and Hospital Epidemiology</i> , 2022, 43, 657-660.	1.0	9
2	Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 30.	2.9	7
3	Nitrite Generating and Depleting Capacity of the Oral Microbiome and Cardiometabolic Risk: Results from ORIGINS. <i>Journal of the American Heart Association</i> , 2022, 11, e023038.	1.6	10
4	Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. <i>Methods in Molecular Biology</i> , 2021, 2327, 87-92.	0.4	1
5	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , 2021, 9, 25.	4.9	13
6	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021, 6, .	1.7	19
7	A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. <i>BioTechniques</i> , 2021, 70, 149-159.	0.8	17
8	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	1.7	22
9	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
10	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	4.9	37
11	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	2.2	37
12	Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021, 184, 4939-4952.e15.	13.5	31
13	Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. <i>MSystems</i> , 2021, 6, e0113621.	1.7	14
14	Handwashing and Detergent Treatment Greatly Reduce SARS-CoV-2 Viral Load on Halloween Candy Handled by COVID-19 Patients. <i>MSystems</i> , 2020, 5, .	1.7	11
15	Linking metabolic phenotypes to pathogenic traits among <i>Candidatus Liberibacter asiaticus</i> and its hosts. <i>Npj Systems Biology and Applications</i> , 2020, 6, 24.	1.4	20
16	Differing salivary microbiome diversity, community and diurnal rhythmicity in association with affective state and peripheral inflammation in adults. <i>Brain, Behavior, and Immunity</i> , 2020, 87, 591-602.	2.0	11
17	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
18	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	5.8	428

#	ARTICLE	IF	CITATIONS
19	redbiom: a Rapid Sample Discovery and Feature Characterization System. MSystems, 2019, 4, .	1.7	35
20	Triplicate PCR reactions for 16S rRNA gene amplicon sequencing are unnecessary. BioTechniques, 2019, 67, 29-32.	0.8	48
21	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. Trends in Microbiology, 2019, 27, 105-117.	3.5	652
22	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	1.7	604
23	Are microbiome studies ready for hypothesis-driven research?. Current Opinion in Microbiology, 2018, 44, 61-69.	2.3	27
24	The Microbiome and Human Biology. Annual Review of Genomics and Human Genetics, 2017, 18, 65-86.	2.5	266
25	DNA extraction for streamlined metagenomics of diverse environmental samples. BioTechniques, 2017, 62, 290-293.	0.8	178
26	Culturing: Looking it up in our gut. Nature Microbiology, 2016, 1, 16169.	5.9	1