

# Xochitl C Morgan

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/5393939/xochitl-c-morgan-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

49  
papers

7,823  
citations

26  
h-index

54  
g-index

54  
ext. papers

10,055  
ext. citations

10.7  
avg, IF

5.72  
L-index

#	Paper	IF	Citations
49	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , <b>2014</b> , 15, 382-392	23.4	1836
48	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , <b>2012</b> , 13, R79	18.3	1668
47	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , <b>2019</b> , 176, 649-662.e20	56.2	588
46	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , <b>2013</b> , 4, 2304	17.4	511
45	Relating the metatranscriptome and metagenome of the human gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E2329-38	11.5	410
44	Sequencing and beyond: integrating molecular $\omicron$ mics for microbial community profiling. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 360-72	22.2	394
43	Chapter 12: Human microbiome analysis. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002808	5	310
42	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. <i>ISME Journal</i> , <b>2014</b> , 8, 1403-17	11.9	275
41	Computational meta $\omicron$ mics for microbial community studies. <i>Molecular Systems Biology</i> , <b>2013</b> , 9, 666	12.2	216
40	Biogeography of the intestinal mucosal and luminal microbiome in the rhesus macaque. <i>Cell Host and Microbe</i> , <b>2015</b> , 17, 385-391	23.4	185
39	Biodiversity and functional genomics in the human microbiome. <i>Trends in Genetics</i> , <b>2013</b> , 29, 51-8	8.5	167
38	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , <b>2016</b> , 8, 17	14.4	127
37	Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. <i>Genome Biology</i> , <b>2015</b> , 16, 67	18.3	119
36	Meta $\omicron$ mic analytic techniques for studying the intestinal microbiome. <i>Gastroenterology</i> , <b>2014</b> , 146, 1437-1448.e16	13.4	116
35	bioBakery: a meta $\omicron$ mic analysis environment. <i>Bioinformatics</i> , <b>2018</b> , 34, 1235-1237	7.2	108
34	Mapping DNA-protein interactions in large genomes by sequence tag analysis of genomic enrichment. <i>Nature Methods</i> , <b>2005</b> , 2, 47-53	21.6	99
33	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , <b>2017</b> , 18, 228	18.3	87

32	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , <b>2016</b> , 1,	7.6	73
31	Microbial biogeography of 925 geothermal springs in New Zealand. <i>Nature Communications</i> , <b>2018</b> , 9, 2876	17.4	70
30	Determining microbial products and identifying molecular targets in the human microbiome. <i>Cell Metabolism</i> , <b>2014</b> , 20, 731-741	24.6	68
29	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , <b>2019</b> , 13, 2617-2632	11.9	54
28	Chthonomonas calidirosea gen. nov., sp. nov., an aerobic, pigmented, thermophilic micro-organism of a novel bacterial class, Chthonomonadetes classis nov., of the newly described phylum Armatimonadetes originally designated candidate division OP10. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2011</b> , 61, 2482-2490	2.2	50
27	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , <b>2013</b> , 5, 65	14.4	39
26	Pyrinomonas methylaliphatogenes gen. nov., sp. nov., a novel group 4 thermophilic member of the phylum Acidobacteria from geothermal soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2014</b> , 64, 220-227	2.2	35
25	Electing a candidate: a speculative history of the bacterial phylum OP10. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 3069-80	5.2	32
24	Genomic analysis of Chthonomonas calidirosea, the first sequenced isolate of the phylum Armatimonadetes. <i>ISME Journal</i> , <b>2014</b> , 8, 1522-33	11.9	30
23	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , <b>2019</b> , 7, e6160	3.1	22
22	A novel fatty acid, 12,17-dimethyloctadecanoic acid, from the extremophile Thermogemmatispora sp. (Strain T81). <i>Lipids</i> , <b>2012</b> , 47, 601-11	1.6	19
21	Phylogenetic delineation of the novel phylum Armatimonadetes (former candidate division OP10) and definition of two novel candidate divisions. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 2484-4.8	4.8	19
20	Eczema-protective probiotic alters infant gut microbiome functional capacity but not composition: sub-sample analysis from a RCT. <i>Beneficial Microbes</i> , <b>2019</b> , 10, 5-17	4.9	17
19	Complete genome sequence of the thermophilic Acidobacteria, Pyrinomonas methylaliphatogenes type strain K22(T). <i>Standards in Genomic Sciences</i> , <b>2015</b> , 10, 101		13
18	Predicting combinatorial binding of transcription factors to regulatory elements in the human genome by association rule mining. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 445	3.6	12
17	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , <b>2017</b> , 2,	7.6	11
16	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , <b>2015</b> , 3, e791	3.1	11
15	Fatty Acids of Chthonomonas calidirosea, of a novel class Chthonomonadetes from a recently described phylum Armatimonadetes. <i>Lipids</i> , <b>2011</b> , 46, 1155-61	1.6	6

14	Microbial biogeography of 1,000 geothermal springs in New Zealand		5
13	The Chthonomonas calidirosea Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's Taupō Volcanic Zone. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 3572-81	4.8	5
12	Mucosal-associated invariant T cells and V $\alpha$ 17 T cells in community acquired pneumonia: association of abundance in sputum with clinical severity and outcome. <i>Clinical and Experimental Immunology</i> , <b>2020</b> , 199, 201-215	6.2	5
11	Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant in New Zealand. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	3
10	Genomic Sequencing and Other Tools for Studying Microbial Communities. <i>Microbe Magazine</i> , <b>2015</b> , 10, 419-425		3
9	Invited Commentary: Improving the Accessibility of Human Microbiome Project Data Through Integration With R/Bioconductor. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1027-1030	3.8	2
8	Genetic evaluation of ESBL-producing urinary isolates in Otago, New Zealand. <i>JAC-Antimicrobial Resistance</i> , <b>2021</b> , 3, dlab147	2.9	1
7	Rectal swabs are a reliable method of assessing the colonic microbiome.. <i>International Journal of Medical Microbiology</i> , <b>2022</b> , 312, 151549	3.7	0
6	Complete Genome Sequences of sp. Strain XES5, sp. Strain XGS7, and sp. Strain XCS3, Isolated from Xenopus laevis Skin.. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0105021	1.3	0
5	Chthonomonadetes <b>2018</b> , 1-1		
4	Chthonomonadaceae <b>2018</b> , 1-1		
3	Chthonomonadales <b>2018</b> , 1-1		
2	Pyrinomonas <b>2018</b> , 1-8		
1	Chthonomonas <b>2018</b> , 1-6		