

Xochitl C Morgan

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.

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	Rectal swabs are a reliable method of assessing the colonic microbiome.. <i>International Journal of Medical Microbiology</i> , 2022 , 312, 151549	3.7	0
48	Genetic evaluation of ESBL-producing urinary isolates in Otago, New Zealand. <i>JAC-Antimicrobial Resistance</i> , 2021 , 3, dlab147	2.9	1
47	Complete Genome Sequences of sp. Strain XES5, sp. Strain XGS7, and sp. Strain XCS3, Isolated from <i>Xenopus laevis</i> Skin.. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0105021	1.3	0
46	Mucosal-associated invariant T cells and V α 17 T cells in community acquired pneumonia: association of abundance in sputum with clinical severity and outcome. <i>Clinical and Experimental Immunology</i> , 2020 , 199, 201-215	6.2	5
45	Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant in New Zealand. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	3
44	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019 , 13, 2617-2632	11.9	54
43	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019 , 7, e6160	3.1	22
42	Eczema-protective probiotic alters infant gut microbiome functional capacity but not composition: sub-sample analysis from a RCT. <i>Beneficial Microbes</i> , 2019 , 10, 5-17	4.9	17
41	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019 , 176, 649-662.e20	56.2	588
40	Invited Commentary: Improving the Accessibility of Human Microbiome Project Data Through Integration With R/Bioconductor. <i>American Journal of Epidemiology</i> , 2019 , 188, 1027-1030	3.8	2
39	bioBakery: a meta-genomic analysis environment. <i>Bioinformatics</i> , 2018 , 34, 1235-1237	7.2	108
38	Chthonomonadetes 2018 , 1-1		
37	Chthonomonadaceae 2018 , 1-1		
36	Chthonomonadales 2018 , 1-1		
35	Microbial biogeography of 925 geothermal springs in New Zealand. <i>Nature Communications</i> , 2018 , 9, 2876	17.4	70
34	Pyrinomonas 2018 , 1-8		
33	Chthonomonas 2018 , 1-6		

32	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017 , 18, 228	18.3	87
31	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017 , 2,	7.6	11
30	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016 , 8, 17	14.4	127
29	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , 2016 , 1,	7.6	73
28	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> , 2016 , 82, 3572-81	4.8	5
27	Biogeography of the intestinal mucosal and luminal microbiome in the rhesus macaque. <i>Cell Host and Microbe</i> , 2015 , 17, 385-391	23.4	185
26	Sequencing and beyond: integrating molecular omics for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015 , 13, 360-72	22.2	394
25	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> , 2015 , 16, 67	18.3	119
24	Complete genome sequence of the thermophilic Acidobacteria, Pyrinomonas methylaliphatogenes type strain K22(T). <i>Standards in Genomic Sciences</i> , 2015 , 10, 101		13
23	Genomic Sequencing and Other Tools for Studying Microbial Communities. <i>Microbe Magazine</i> , 2015 , 10, 419-425		3
22	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015 , 3, e791	3.1	11
21	Metagenomic analytic techniques for studying the intestinal microbiome. <i>Gastroenterology</i> , 2014 , 146, 1437-1448.e16	13.4	116
20	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , 2014 , 15, 382-392	23.4	1836
19	Relating the metatranscriptome and metagenome of the human gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E2329-38	11.5	410
18	Determining microbial products and identifying molecular targets in the human microbiome. <i>Cell Metabolism</i> , 2014 , 20, 731-741	24.6	68
17	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. <i>ISME Journal</i> , 2014 , 8, 1403-17	11.9	275
16	Genomic analysis of Chthonomonas calidirosea, the first sequenced isolate of the phylum Armatimonadetes. <i>ISME Journal</i> , 2014 , 8, 1522-33	11.9	30
15	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> , 2014 , 64, 220-227	2.2	35

14	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013 , 4, 2304	17.4	511
13	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013 , 5, 65	14.4	39
12	Biodiversity and functional genomics in the human microbiome. <i>Trends in Genetics</i> , 2013 , 29, 51-8	8.5	167
11	Computational metagenomics for microbial community studies. <i>Molecular Systems Biology</i> , 2013 , 9, 666	12.2	216
10	Phylogenetic delineation of the novel phylum Armatimonadetes (former candidate division OP10) and definition of two novel candidate divisions. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 2484-7	4.8	19
9	Electing a candidate: a speculative history of the bacterial phylum OP10. <i>Environmental Microbiology</i> , 2012 , 14, 3069-80	5.2	32
8	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , 2012 , 13, R79	18.3	1668
7	A novel fatty acid, 12,17-dimethyloctadecanoic acid, from the extremophile Thermogemmatispora sp. (Strain T81). <i>Lipids</i> , 2012 , 47, 601-11	1.6	19
6	Chapter 12: Human microbiome analysis. <i>PLoS Computational Biology</i> , 2012 , 8, e1002808	5	310
5	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> , 2011 , 61, 2482-2490	2.2	50
4	Fatty Acids of Chthonomonas calidirosea, of a novel class Chthonomonadetes from a recently described phylum Armatimonadetes. <i>Lipids</i> , 2011 , 46, 1155-61	1.6	6
3	Predicting combinatorial binding of transcription factors to regulatory elements in the human genome by association rule mining. <i>BMC Bioinformatics</i> , 2007 , 8, 445	3.6	12
2	Mapping DNA-protein interactions in large genomes by sequence tag analysis of genomic enrichment. <i>Nature Methods</i> , 2005 , 2, 47-53	21.6	99
1	Microbial biogeography of 1,000 geothermal springs in New Zealand		5