

Xochitl C Morgan

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

11,347
citations

201658

27
h-index

214788

47
g-index

54
all docs

54
docs citations

54
times ranked

17819
citing authors

#	ARTICLE	IF	CITATIONS
1	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.0	2,582
2	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , 2012, 13, R79.	9.6	2,258
3	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.	28.9	1,087
4	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013, 4, 2304.	12.8	797
5	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.	7.1	552
6	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	28.6	544
7	Chapter 12: Human Microbiome Analysis. <i>PLoS Computational Biology</i> , 2012, 8, e1002808.	3.2	408
8	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. <i>ISME Journal</i> , 2014, 8, 1403-1417.	9.8	352
9	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	11.0	273
10	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	7.2	253
11	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	4.1	241
12	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	8.2	219
13	Biodiversity and functional genomics in the human microbiome. <i>Trends in Genetics</i> , 2013, 29, 51-58.	6.7	207
14	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.	8.8	166
15	Microbial biogeography of 925 geothermal springs in New Zealand. <i>Nature Communications</i> , 2018, 9, 2876.	12.8	163
16	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	8.8	143
17	Meta'omic Analytic Techniques for Studying the Intestinal Microbiome. <i>Gastroenterology</i> , 2014, 146, 1437-1448.e1.	1.3	137
18	Diverse hydrogen production and consumption pathways influence methane production in ruminants. <i>ISME Journal</i> , 2019, 13, 2617-2632.	9.8	132

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19	Mapping DNA-protein interactions in large genomes by sequence tag analysis of genomic enrichment. <i>Nature Methods</i> , 2005, 2, 47-53.	19.0	108
20	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , 2016, 1, .	3.8	107
21	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. <i>Cell Metabolism</i> , 2014, 20, 731-741.	16.2	82
22	<i>Chthonomonas calidirosea</i> gen. nov., sp. nov., an aerobic, pigmented, thermophilic micro-organism of a novel bacterial class, <i>Chthonomonadetes classis</i> nov., of the newly described phylum <i>Armatimonadetes</i> originally designated candidate division OP10. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2482-2490.	1.7	75
23	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	8.2	61
24	<i>Pyrinomonas methylaliphatogenes</i> gen. nov., sp. nov., a novel group 4 thermophilic member of the phylum <i>Acidobacteria</i> from geothermal soils. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 220-227.	1.7	44
25	Genomic analysis of <i>Chthonomonas calidirosea</i> , the first sequenced isolate of the phylum <i>Armatimonadetes</i> . <i>ISME Journal</i> , 2014, 8, 1522-1533.	9.8	39
26	Electing a candidate: a speculative history of the bacterial phylum OP10. <i>Environmental Microbiology</i> , 2012, 14, 3069-3080.	3.8	34
27	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019, 7, e6160.	2.0	34
28	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.	2.4	31
29	A Novel Fatty Acid, 12,17-Dimethyloctadecanoic Acid, from the Extremophile <i>Thermogemmatispora</i> sp. (Strain T81). <i>Lipids</i> , 2012, 47, 601-611.	1.7	21
30	Phylogenetic Delineation of the Novel Phylum <i>Armatimonadetes</i> (Former Candidate Division OP10) and Definition of Two Novel Candidate Divisions. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2484-2487.	3.1	21
31	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017, 2, .	3.8	18
32	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	4.1	18
33	Predicting combinatorial binding of transcription factors to regulatory elements in the human genome by association rule mining. <i>BMC Bioinformatics</i> , 2007, 8, 445.	2.6	17
34	Complete genome sequence of the thermophilic <i>Acidobacteria</i> , <i>Pyrinomonas methylaliphatogenes</i> type strain K22T. <i>Standards in Genomic Sciences</i> , 2015, 10, 101.	1.5	17
35	Mucosal metabolites fuel the growth and virulence of <i>E. coli</i> linked to Crohn's disease. <i>JCI Insight</i> , 2022, 7, .	5.0	17
36	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015, 3, e791.	2.0	12

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37	Type I CRISPR-Cas provides robust immunity but incomplete attenuation of phage-induced cellular stress. <i>Nucleic Acids Research</i> , 2022, 50, 160-174.	14.5	12
38	Agricultural Origins of a Highly Persistent Lineage of Vancomycin-Resistant <i>Enterococcus faecalis</i> in New Zealand. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	11
39	Mucosal-associated invariant T cells and V α 2+ γ 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.	2.6	11
40	The <i>Chthonomonas calidirosea</i> Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's Taup \acute{a} Volcanic Zone. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3572-3581.	3.1	9
41	Rectal swabs are a reliable method of assessing the colonic microbiome. <i>International Journal of Medical Microbiology</i> , 2022, 312, 151549.	3.6	7
42	Fatty Acids of <i>Chthonomonas calidirosea</i> , of a Novel Class Chthonomonadetes from a Recently Described Phylum Armatimonadetes. <i>Lipids</i> , 2011, 46, 1155-1161.	1.7	6
43	OUP accepted manuscript. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab147.	2.1	4
44	Genomic Sequencing and Other Tools for Studying Microbial Communities. <i>Microbe Magazine</i> , 2015, 10, 419-425.	0.4	4
45	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.	3.4	3
46	Manipulating the microbiome alters regenerative outcomes in <i>Xenopus laevis</i> tadpoles via lipopolysaccharide signalling. <i>Wound Repair and Regeneration</i> , 2022, 30, 636-651.	3.0	3
47	Complete Genome Sequences of <i>Kinneretia</i> sp. Strain XES5, <i>Shinella</i> sp. Strain XGS7, and <i>Vogesella</i> sp. Strain XCS3, Isolated from <i>Xenopus laevis</i> Skin. <i>Microbiology Resource Announcements</i> , 2021, 10, e0105021.	0.6	2