

Cameron Martino

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2076118/publications.pdf>

Version: 2024-02-01

27
papers

2,304
citations

394421

19
h-index

526287

27
g-index

34
all docs

34
docs citations

34
times ranked

4277
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Infection Depends on Cellular Heparan Sulfate and ACE2. <i>Cell</i> , 2020, 183, 1043-1057.e15.	28.9	860
2	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019, 4, .	3.8	295
3	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
4	Visualizing TM omic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa023.	3.2	97
5	Air pollution exposure is associated with the gut microbiome as revealed by shotgun metagenomic sequencing. <i>Environment International</i> , 2020, 138, 105604.	10.0	97
6	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	3.8	81
7	Engineering the microbiome for animal health and conservation. <i>Experimental Biology and Medicine</i> , 2019, 244, 494-504.	2.4	65
8	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	17.5	61
9	Gut bacteria responding to dietary change encode sialidases that exhibit preference for red meat-associated carbohydrates. <i>Nature Microbiology</i> , 2019, 4, 2082-2089.	13.3	56
10	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	8.8	47
11	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , 2021, 9, 92.	11.1	40
12	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	11.1	37
13	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	4.4	37
14	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	3.8	36
15	Context-aware deconvolution of cell-cell communication with Tensor-cell2cell. <i>Nature Communications</i> , 2022, 13, .	12.8	32
16	Diet and feeding pattern modulate diurnal dynamics of the ileal microbiome and transcriptome. <i>Cell Reports</i> , 2022, 40, 111008.	6.4	32
17	Intermittent Hypoxia and Hypercapnia Alter Diurnal Rhythms of Luminal Gut Microbiome and Metabolome. <i>MSystems</i> , 2021, 6, e0011621.	3.8	27
18	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021, 6, e0069121.	3.8	27

#	ARTICLE	IF	CITATIONS
19	A comparison of six DNA extraction protocols for 16S, ITS and shotgun metagenomic sequencing of microbial communities. <i>BioTechniques</i> , 2022, 73, 34-46.	1.8	25
20	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	17.5	25
21	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , 2020, 5, .	2.9	20
22	Influence of Intermittent Hypoxia/Hypercapnia on Atherosclerosis, Gut Microbiome, and Metabolome. <i>Frontiers in Physiology</i> , 2021, 12, 663950.	2.8	20
23	A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. <i>BioTechniques</i> , 2021, 70, 149-159.	1.8	17
24	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	10
25	Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, 30.	6.4	7
26	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. <i>MSystems</i> , 2022, 7, e0005022.	3.8	4
27	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. <i>MSystems</i> , 2022, 7, e0137821.	3.8	3