

# James T Morton

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8707686/publications.pdf>

Version: 2024-02-01

42  
papers

9,723  
citations

136950

32  
h-index

276875

41  
g-index

48  
all docs

48  
docs citations

48  
times ranked

14407  
citing authors

#	ARTICLE	IF	CITATIONS
1	Auto-deconvolution and molecular networking of gas chromatography–mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	17.5	78
2	Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. <i>Genome Research</i> , 2021, 31, 64-74.	5.5	59
3	Lower Airway Dysbiosis Affects Lung Cancer Progression. <i>Cancer Discovery</i> , 2021, 11, 293-307.	9.4	139
4	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	17.5	61
5	Reply to: Examining microbe–metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	19.0	6
6	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021, 6, .	3.8	19
7	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	3.8	36
8	Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. <i>Current Protocols</i> , 2021, 1, e113.	2.9	61
9	Microbe-Metabolite Associations Linked to the Rebounding Murine Gut Microbiome Postcolonization with Vancomycin-Resistant <i>Enterococcus faecium</i> . <i>MSystems</i> , 2020, 5, .	3.8	3
10	Visualizing –omic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa023.	3.2	97
11	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	3.8	47
12	Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. <i>MSystems</i> , 2020, 5, .	3.8	12
13	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019, 13, 576-587.	9.8	236
14	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	6.2	46
15	Learning representations of microbe–metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314.	19.0	184
16	Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019, 10, 2719.	12.8	428
17	Red Sea SAR11 and <i>Prochlorococcus</i> Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	11
18	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	3.8	28

#	ARTICLE	IF	CITATIONS
19	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019, 4, .	3.8	295
20	Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. <i>Ecological Monographs</i> , 2019, 89, e01353.	5.4	52
21	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	197
22	Niche partitioning of a pathogenic microbiome driven by chemical gradients. <i>Science Advances</i> , 2018, 4, eaau1908.	10.3	40
23	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
24	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	28.6	1,138
25	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	13.3	68
26	Environmental radiation alters the gut microbiome of the bank vole <i>Myodes glareolus</i> . <i>ISME Journal</i> , 2018, 12, 2801-2806.	9.8	44
27	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. <i>Bioinformatics</i> , 2017, 33, 4033-4040.	4.1	57
28	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	3.8	284
29	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017, 21, 7-10.	11.0	95
30	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	3.8	1,339
31	Uncovering the Horseshoe Effect in Microbial Analyses. <i>MSystems</i> , 2017, 2, .	3.8	67
32	Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. <i>Movement Disorders</i> , 2017, 32, 739-749.	3.9	649
33	An ELEGANT Screen for Drug-Microbe Interactions. <i>Cell Host and Microbe</i> , 2017, 21, 555-556.	11.0	2
34	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
35	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. <i>MSystems</i> , 2017, 2, .	3.8	116
36	Mass Spectrometry-Based Chemical Cartography of a Cardiac Parasitic Infection. <i>Analytical Chemistry</i> , 2017, 89, 10414-10421.	6.5	35

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37	Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017, 7, 15497.	3.3	112
38	The Microbiome in Posttraumatic Stress Disorder and Trauma-Exposed Controls: An Exploratory Study. <i>Psychosomatic Medicine</i> , 2017, 79, 936-946.	2.0	153
39	Discrete False-Discovery Rate Improves Identification of Differentially Abundant Microbes. <i>MSystems</i> , 2017, 2, .	3.8	73
40	Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016, 535, 94-103.	27.8	595
41	Immunization with a heat-killed preparation of the environmental bacterium <i>Mycobacterium vaccae</i> promotes stress resilience in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3130-9.	7.1	186
42	SCOPE++: Sequence Classification Of homoPolymer Emissions. <i>Genomics</i> , 2014, 104, 157-162.	2.9	0