

James T Morton

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.

43
papers

5,474
citations

26
h-index

48
g-index

48
ext. papers

8,048
ext. citations

14.3
avg, IF

5.47
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 43 | EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021 , 6, | 7.6 | 14 |
| 42 | Learned Embeddings from Deep Learning to Visualize and Predict Protein Sets. <i>Current Protocols</i> , 2021 , 1, e113 | | 15 |
| 41 | Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , 2021 , 39, 169-173 | 44.5 | 36 |
| 40 | 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 | 9.7 | 21 |
| 39 | Lower Airway Dysbiosis Affects Lung Cancer Progression. <i>Cancer Discovery</i> , 2021 , 11, 293-307 | 24.4 | 34 |
| 38 | Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021 , 39, 165-168 | 44.5 | 23 |
| 37 | Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , 2021 , 18, 40-41 | 11.6 | 2 |
| 36 | Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. <i>MSystems</i> , 2021 , 6, | 7.6 | 8 |
| 35 | Visualizing genomic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa023 | 3.7 | 48 |
| 34 | High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020 , 5, | 7.6 | 24 |
| 33 | Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. <i>MSystems</i> , 2020 , 5, | 7.6 | 8 |
| 32 | Establishing microbial composition measurement standards with reference frames. <i>Nature Communications</i> , 2019 , 10, 2719 | 17.4 | 220 |
| 31 | Red Sea SAR11 and Single-Cell Genomes Reflect Globally Distributed Pangenomes. <i>Applied and Environmental Microbiology</i> , 2019 , 85, | 4.8 | 7 |
| 30 | Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019 , 4, | 7.6 | 20 |
| 29 | Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. <i>ISME Journal</i> , 2019 , 13, 576-587 | 11.9 | 132 |
| 28 | 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 | 10.6 | 26 |
| 27 | Learning representations of microbe-metabolite interactions. <i>Nature Methods</i> , 2019 , 16, 1306-1314 | 21.6 | 79 |

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| 26 | A Novel Sparse Compositional Technique Reveals Microbial Perturbations. <i>MSystems</i> , 2019 , 4, | 7.6 | 137 |
| 25 | Phylofactorization: a graph partitioning algorithm to identify phylogenetic scales of ecological data. <i>Ecological Monographs</i> , 2019 , 89, e01353 | 9 | 33 |
| 24 | Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019 , 10, 5477 | 17.4 | 89 |
| 23 | Environmental radiation alters the gut microbiome of the bank vole <i>Myodes glareolus</i> . <i>ISME Journal</i> , 2018 , 12, 2801-2806 | 11.9 | 23 |
| 22 | Niche partitioning of a pathogenic microbiome driven by chemical gradients. <i>Science Advances</i> , 2018 , 4, eaau1908 | 14.3 | 21 |
| 21 | American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3, | 7.6 | 336 |
| 20 | Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018 , 16, 410-422 | 22.2 | 668 |
| 19 | Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018 , 3, 652-661 | 26.6 | 43 |
| 18 | Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017 , 2, | 7.6 | 177 |
| 17 | Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017 , 21, 7-10 | 23.4 | 44 |
| 16 | Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2, | 7.6 | 763 |
| 15 | Uncovering the Horseshoe Effect in Microbial Analyses. <i>MSystems</i> , 2017 , 2, | 7.6 | 41 |
| 14 | Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. <i>Movement Disorders</i> , 2017 , 32, 739-749 | 7 | 405 |
| 13 | An <i>Elegans</i> (t) Screen for Drug-Microbe Interactions. <i>Cell Host and Microbe</i> , 2017 , 21, 555-556 | 23.4 | 2 |
| 12 | A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463 | 50.4 | 1076 |
| 11 | Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. <i>MSystems</i> , 2017 , 2, | 7.6 | 44 |
| 10 | Mass Spectrometry-Based Chemical Cartography of a Cardiac Parasitic Infection. <i>Analytical Chemistry</i> , 2017 , 89, 10414-10421 | 7.8 | 20 |
| 9 | Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017 , 7, 15497 | 4.9 | 64 |

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|---|--|------|-----|
| 8 | The Microbiome in Posttraumatic Stress Disorder and Trauma-Exposed Controls: An Exploratory Study. <i>Psychosomatic Medicine</i> , 2017 , 79, 936-946 | 3.7 | 100 |
| 7 | Discrete False-Discovery Rate Improves Identification of Differentially Abundant Microbes. <i>MSystems</i> , 2017 , 2, | 7.6 | 48 |
| 6 | Rail-RNA: scalable analysis of RNA-seq splicing and coverage. <i>Bioinformatics</i> , 2017 , 33, 4033-4040 | 7.2 | 33 |
| 5 | Microbiome-wide association studies link dynamic microbial consortia to disease. <i>Nature</i> , 2016 , 535, 94-103 | 5.4 | 443 |
| 4 | 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 | 11.5 | 137 |
| 3 | SCOPE++: sequence classification of homoPolymer emissions. <i>Genomics</i> , 2014 , 104, 157-62 | 4.3 | |
| 2 | Protein Structural Alignments From Sequence | | 6 |
| 1 | Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment | | 3 |