Gavin M Douglas

List of Publications by Year
in descending order

24 papers	18,017 citations	430874 18 h-index	580821 25 g-index
34 all docs	34 docs citations	34 times ranked	19987 citing authors

#	Article	IF	Citations
1	Microbiome differential abundance methods produce different results across 38 datasets. Nature Communications, 2022, 13, 342.	12.8	286
2	Transcriptomic profiling of *Brassica napus* responses to *Pseudomonas aeruginosa*. Innate Immunity, 2021, 27, 143-157.	2.4	6
3	Genic Selection Within Prokaryotic Pangenomes. Genome Biology and Evolution, 2021, 13, .	2.5	10
4	PICRUSt2 for prediction of metagenome functions. Nature Biotechnology, 2020, 38, 685-688.	17.5	2,621
5	The human tumor microbiome is composed of tumor type–specific intracellular bacteria. Science, 2020, 368, 973-980.	12.6	1,077
6	Re-evaluating the relationship between missing heritability and the microbiome. Microbiome, 2020, 8, 87.	11.1	17
7	Detection of Helicobacter pylori Microevolution and Multiple Infection from Gastric Biopsies by Housekeeping Gene Amplicon Sequencing. Pathogens, 2020, 9, 97.	2.8	2
8	Metagenomic Functional Shifts to Plant Induced Environmental Changes. Frontiers in Microbiology, 2019, 10, 1682.	3.5	28
9	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
10	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. Genome Biology and Evolution, 2019, 11, 2750-2766.	2.5	70
11	Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. Nature Communications, 2019, 10, 89.	12.8	420
12	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. Microbiome, 2018, 6, 13.	11.1	94
13	Denoising the Denoisers: an independent evaluation of microbiome sequence error-correction approaches. PeerJ, 2018, 6, e5364.	2.0	278
14	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. Methods in Molecular Biology, 2018, 1849, 169-177.	0.9	155
15	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. Methods in Molecular Biology, 2018, 1849, 131-141.	0.9	5
16	Prediction of Cacao (Theobroma cacao) Resistance to Moniliophthora spp. Diseases via Genome-Wide Association Analysis and Genomic Selection. Frontiers in Plant Science, 2018, 9, 343.	3.6	43
17	Dissecting Community Structure in Wild Blueberry Root and Soil Microbiome. Frontiers in Microbiology, 2018, 9, 1187.	3.5	56
18	A Genome‐Wide Association Study of Apple Quality and Scab Resistance. Plant Genome, 2018, 11, 170075.	2.8	61

#	Article	IF	Citations
19	The coupling of taxonomy and function in microbiomes. Biology and Philosophy, 2017, 32, 1225-1243.	1.4	36
20	Variation in Bacterial and Eukaryotic Communities Associated with Natural and Managed Wild Blueberry Habitats. Phytobiomes Journal, 2017, 1, 102-113.	2.7	47
21	Decreased Transcription Factor Binding Levels Nearby Primate Pseudogenes Suggest Regulatory Degeneration. Molecular Biology and Evolution, 2016, 33, 1478-1485.	8.9	1
22	Hybrid origins and the earliest stages of diploidization in the highly successful recent polyploid <i>Capsella bursa-pastoris</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2806-2811.	7.1	128
23	Polymorphism Analysis Reveals Reduced Negative Selection and Elevated Rate of Insertions and Deletions in Intrinsically Disordered Protein Regions. Genome Biology and Evolution, 2015, 7, 1815-1826.	2.5	27
24	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6