

Gavin M Douglas

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/78777/publications.pdf>

Version: 2024-02-01

24
papers

18,017
citations

430442

18
h-index

580395

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. <i>Nature Communications</i> , 2022, 13, 342.	5.8	286
2	Transcriptomic profiling of <i>Brassica napus</i> responses to <i>Pseudomonas aeruginosa</i> . <i>Innate Immunity</i> , 2021, 27, 143-157.	1.1	6
3	Genic Selection Within Prokaryotic Pangenomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	10
4	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	9.4	2,621
5	The human tumor microbiome is composed of tumor type-specific intracellular bacteria. <i>Science</i> , 2020, 368, 973-980.	6.0	1,077
6	Re-evaluating the relationship between missing heritability and the microbiome. <i>Microbiome</i> , 2020, 8, 87.	4.9	17
7	Detection of <i>Helicobacter pylori</i> Microevolution and Multiple Infection from Gastric Biopsies by Housekeeping Gene Amplicon Sequencing. <i>Pathogens</i> , 2020, 9, 97.	1.2	2
8	Metagenomic Functional Shifts to Plant Induced Environmental Changes. <i>Frontiers in Microbiology</i> , 2019, 10, 1682.	1.5	28
9	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
10	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. <i>Genome Biology and Evolution</i> , 2019, 11, 2750-2766.	1.1	70
11	Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. <i>Nature Communications</i> , 2019, 10, 89.	5.8	420
12	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. <i>Microbiome</i> , 2018, 6, 13.	4.9	94
13	Denoising the Denoisers: an independent evaluation of microbiome sequence error-correction approaches. <i>PeerJ</i> , 2018, 6, e5364.	0.9	278
14	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. <i>Methods in Molecular Biology</i> , 2018, 1849, 169-177.	0.4	155
15	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. <i>Methods in Molecular Biology</i> , 2018, 1849, 131-141.	0.4	5
16	Prediction of Cacao (<i>Theobroma cacao</i>) Resistance to <i>Moniliophthora</i> spp. Diseases via Genome-Wide Association Analysis and Genomic Selection. <i>Frontiers in Plant Science</i> , 2018, 9, 343.	1.7	43
17	Dissecting Community Structure in Wild Blueberry Root and Soil Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1187.	1.5	56
18	A Genome-Wide Association Study of Apple Quality and Scab Resistance. <i>Plant Genome</i> , 2018, 11, 170075.	1.6	61

#	ARTICLE	IF	CITATIONS
19	The coupling of taxonomy and function in microbiomes. <i>Biology and Philosophy</i> , 2017, 32, 1225-1243.	0.7	36
20	Variation in Bacterial and Eukaryotic Communities Associated with Natural and Managed Wild Blueberry Habitats. <i>Phytobiomes Journal</i> , 2017, 1, 102-113.	1.4	47
21	Decreased Transcription Factor Binding Levels Nearby Primate Pseudogenes Suggest Regulatory Degeneration. <i>Molecular Biology and Evolution</i> , 2016, 33, 1478-1485.	3.5	1
22	Hybrid origins and the earliest stages of diploidization in the highly successful recent polyploid <i>Capsella bursa-pastoris</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2806-2811.	3.3	128
23	Polymorphism Analysis Reveals Reduced Negative Selection and Elevated Rate of Insertions and Deletions in Intrinsically Disordered Protein Regions. <i>Genome Biology and Evolution</i> , 2015, 7, 1815-1826.	1.1	27
24	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6