Morgan G I Langille

List of Publications by Year
in descending order

74 papers	30,380 citations	87723 38 h-index	82410 72 g-index
88 all docs	88 docs citations	88 times ranked	34243 citing authors

#	Article	IF	Citations
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
2	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	9.4	8,049
3	PICRUSt2 for prediction of metagenome functions. Nature Biotechnology, 2020, 38, 685-688.	9.4	2,621
4	The human tumor microbiome is composed of tumor typeâ€"specific intracellular bacteria. Science, 2020, 368, 973-980.	6.0	1,077
5	Microbiome Helper: a Custom and Streamlined Workflow for Microbiome Research. MSystems, 2017, 2, .	1.7	558
6	Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. Nature Communications, 2019, 10, 89.	5.8	420
7	IslandViewer: an integrated interface for computational identification and visualization of genomic islands. Bioinformatics, 2009, 25, 664-665.	1.8	398
8	Microbial shifts in the aging mouse gut. Microbiome, 2014, 2, 50.	4.9	354
9	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i>. Genome Research, 2009, 19, 12-23.	2.4	317
10	IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis: Figure 1.. Nucleic Acids Research, 2015, 43, W104-W108.	6.5	316
11	Microbiome differential abundance methods produce different results across 38 datasets. Nature Communications, 2022, 13, 342.	5.8	286
12	Denoising the Denoisers: an independent evaluation of microbiome sequence error-correction approaches. PeerJ, 2018, 6, e5364.	0.9	278
13	Detecting genomic islands using bioinformatics approaches. Nature Reviews Microbiology, 2010, 8, 373-382.	13.6	257
14	Evaluation of genomic island predictors using a comparative genomics approach. BMC Bioinformatics, 2008, 9, 329.	1.2	255
15	Interactions in the microbiome: communities of organisms and communities of genes. FEMS Microbiology Reviews, 2014, 38, 90-118.	3.9	174
16	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
17	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. Methods in Molecular Biology, 2018, 1849, 169-177.	0.4	155
18	The Association of Virulence Factors with Genomic Islands. PLoS ONE, 2009, 4, e8094.	1.1	119

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19	GenGIS 2: Geospatial Analysis of Traditional and Genetic Biodiversity, with New Gradient Algorithms and an Extensible Plugin Framework. PLoS ONE, 2013, 8, e69885.	1.1	118
20	Food or just a free ride? A meta-analysis reveals the global diversity of the Plastisphere. ISME Journal, 2021, 15, 789-806.	4.4	110
21	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. Microbiome, 2018, 6, 13.	4.9	94
22	IslandViewer update: improved genomic island discovery and visualization. Nucleic Acids Research, 2013, 41, W129-W132.	6.5	87
23	The Impact of Exclusive Enteral Nutrition (EEN) on the Gut Microbiome in Crohn's Disease: A Review. Nutrients, 2017, 9, 0447.	1.7	84
24	Harnessing the plant microbiome to promote the growth of agricultural crops. Microbiological Research, 2021, 245, 126690.	2.5	84
25	Which is more important for classifying microbial communities: who's there or what they can do?. ISME Journal, 2014, 8, 2357-2359.	4.4	82
26	Identifying biases and their potential solutions in human microbiome studies. Microbiome, 2021, 9, 113.	4.9	82
27	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. Genome Biology and Evolution, 2019, 11, 2750-2766.	1.1	70
28	Exploring Linkages between Taxonomic and Functional Profiles of the Human Microbiome. MSystems, 2018, 3, .	1.7	69
29	Moderate Exercise Has Limited but Distinguishable Effects on the Mouse Microbiome. MSystems, 2017, 2, .	1.7	65
30	Fecal microbes, short chain fatty acids, and colorectal cancer across racial/ethnic groups. World Journal of Gastroenterology, 2015, 21, 2759.	1.4	64
31	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. PLoS ONE, 2012, 7, e43866.	1.1	60
32	Dissecting Community Structure in Wild Blueberry Root and Soil Microbiome. Frontiers in Microbiology, 2018, 9, 1187.	1.5	56
33	Polyphenol-based prebiotics and synbiotics: potential for cancer chemoprevention. Current Opinion in Food Science, 2018, 20, 51-57.	4.1	50
34	Drivers of Regional Bacterial Community Structure and Diversity in the Northwest Atlantic Ocean. Frontiers in Microbiology, 2019, 10, 281.	1.5	50
35	Assessing the Variation within the Oral Microbiome of Healthy Adults. MSphere, 2020, 5, .	1.3	49
36	A multi-OMIC characterisation of biodegradation and microbial community succession within the PET plastisphere. Microbiome, 2021, 9, 141.	4.9	49

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37	Infectious Complications Are Associated With Alterations in the Gut Microbiome in Pediatric Patients With Acute Lymphoblastic Leukemia. Frontiers in Cellular and Infection Microbiology, 2019, 9, 28.	1.8	48
38	Variation in Bacterial and Eukaryotic Communities Associated with Natural and Managed Wild Blueberry Habitats. Phytobiomes Journal, 2017, 1, 102-113.	1.4	47
39	Age-Related Variation of Bacterial and Fungal Communities in Different Body Habitats across the Young, Elderly, and Centenarians in Sardinia. MSphere, 2020, 5, .	1.3	45
40	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS ONE, 2012, 7, e41389.	1.1	42
41	Microbial co-occurrence network analysis of soils receiving short- and long-term applications of alkaline treated biosolids. Science of the Total Environment, 2021, 751, 141687.	3.9	37
42	The coupling of taxonomy and function in microbiomes. Biology and Philosophy, 2017, 32, 1225-1243.	0.7	36
43	â€œAvailable upon requestâ€ not good enough for microbiome data!. Microbiome, 2018, 6, 8.	4.9	35
44	Bacterial Taxa and Functions Are Predictive of Sustained Remission Following Exclusive Enteral Nutrition in Pediatric Crohnâ€™s Disease. Inflammatory Bowel Diseases, 2020, 26, 1026-1037.	0.9	35
45	The Phosphate Binder Ferric Citrate Alters the Gut Microbiome in Rats with Chronic Kidney Disease. Journal of Pharmacology and Experimental Therapeutics, 2018, 367, 452-460.	1.3	33
46	BioTorrents: A File Sharing Service for Scientific Data. PLoS ONE, 2010, 5, e10071.	1.1	29
47	Metagenomic Functional Shifts to Plant Induced Environmental Changes. Frontiers in Microbiology, 2019, 10, 1682.	1.5	28
48	Color lesion boundary detection using live wire. , 2005, , .		24
49	3D live-wire-based semi-automatic segmentation of medical images. , 2005, 5747, 1597.		24
50	Data Standards for Flow Cytometry. OMICS A Journal of Integrative Biology, 2006, 10, 209-214.	1.0	23
51	Taxonomic differences of gut microbiomes drive cellulolytic enzymatic potential within hind-gut fermenting mammals. PLoS ONE, 2017, 12, e0189404.	1.1	22
52	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. BMC Bioinformatics, 2012, 13, 264.	1.2	20
53	Re-evaluating the relationship between missing heritability and the microbiome. Microbiome, 2020, 8, 87.	4.9	17
54	MicrobeDB: a locally maintainable database of microbial genomic sequences. Bioinformatics, 2012, 28, 1947-1948.	1.8	15

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55	Differences in adiposity and diet quality among individuals with inflammatory bowel disease in Eastern Canada. PLoS ONE, 2018, 13, e0200580.	1.1	14
56	GenomeD3Plot: a library for rich, interactive visualizations of genomic data in web applications: Fig. 1.. Bioinformatics, 2015, 31, 3348-3349.	1.8	13
57	Frailty and the Microbiome. Interdisciplinary Topics in Gerontology and Geriatrics, 2015, 41, 54-65.	2.6	12
58	Parent genes of retrotransposition-generated gene duplicates in Drosophila melanogaster have distinct expression profiles. Genomics, 2007, 90, 334-343.	1.3	11
59	Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. Poultry Science, 2016, 95, 2250-2258.	1.5	11
60	The impact of chemerin or chemokine-like receptor 1 loss on the mouse gut microbiome. PeerJ, 2018, 6, e5494.	0.9	10
61	Bioinformatic detection of horizontally transferred DNA in bacterial genomes. F1000 Biology Reports, 2009, 1, 25.	4.0	9
62	Investigation of the impact of commonly used medications on the oral microbiome of individuals living without major chronic conditions. PLoS ONE, 2021, 16, e0261032.	1.1	8
63	Human Microbiome: A Genetic Bazaar for Microbes?. Current Biology, 2012, 22, R20-R22.	1.8	7
64	Genomic Analysis of a Serotype 5 *Streptococcus pneumoniae* Outbreak in British Columbia, Canada, 2005–2009. Canadian Journal of Infectious Diseases and Medical Microbiology, 2016, 2016, 1-7.	0.7	6
65	Transcriptomic profiling of *Brassica napus* responses to *Pseudomonas aeruginosa*. Innate Immunity, 2021, 27, 143-157.	1.1	6
66	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6
67	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. Methods in Molecular Biology, 2018, 1849, 131-141.	0.4	5
68	An *in vivo* genome–wide shRNA screen identifies BCL6 as a targetable biomarker of paclitaxel resistance in breast cancer. Molecular Oncology, 2021, 15, 2046-2064.	2.1	5
69	Investigating the gut microbial community and genes in children with differing levels of change in serum asparaginase activity during pegaspargase treatment for acute lymphoblastic leukemia. Leukemia and Lymphoma, 2021, 62, 927-936.	0.6	4
70	Selective sensitivity of the gut microbiome to iron chelators in polybacterial abdominal sepsis. Medical Hypotheses, 2018, 120, 68-71.	0.8	2
71	Detection of Helicobacter pylori Microevolution and Multiple Infection from Gastric Biopsies by Housekeeping Gene Amplicon Sequencing. Pathogens, 2020, 9, 97.	1.2	2
72	Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. Leukemia and Lymphoma, 2021, 62, 1-12.	0.6	2

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73	MOBILE GENETIC ELEMENTS AND THEIR PREDICTION. Series on Advances in Bioinformatics and Computational Biology, 2008, , 113-135.	0.2	1
74	Investigating Gut Microbial Taxa and Asparaginase Related Genes in Children Showing Different Direction of Change in Serum Asparaginase Activity Levels during Pegasparaginase Treatment for Acute Lymphoblastic Leukemia. Blood, 2020, 136, 40-41.	0.6	0