

Morgan G I Langille

List of Publications by Year in descending order

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Version: 2024-02-01

74

papers

30,380

citations

87888

38

h-index

82547

72

g-index

88

all docs

88

docs citations

88

times ranked

34243

citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiome differential abundance methods produce different results across 38 datasets. <i>Nature Communications</i> , 2022, 13, 342.	12.8	286
2	Food or just a free ride? A meta-analysis reveals the global diversity of the Plastisphere. <i>ISME Journal</i> , 2021, 15, 789-806.	9.8	110
3	Microbial co-occurrence network analysis of soils receiving short- and long-term applications of alkaline treated biosolids. <i>Science of the Total Environment</i> , 2021, 751, 141687.	8.0	37
4	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. <i>Leukemia and Lymphoma</i> , 2021, 62, 927-936.	1.3	4
5	Harnessing the plant microbiome to promote the growth of agricultural crops. <i>Microbiological Research</i> , 2021, 245, 126690.	5.3	84
6	An <i>in vivo</i> genome-wide shRNA screen identifies BCL6 as a targetable biomarker of paclitaxel resistance in breast cancer. <i>Molecular Oncology</i> , 2021, 15, 2046-2064.	4.6	5
7	Identifying biases and their potential solutions in human microbiome studies. <i>Microbiome</i> , 2021, 9, 113.	11.1	82
8	A multi-OMIC characterisation of biodegradation and microbial community succession within the PET plastisphere. <i>Microbiome</i> , 2021, 9, 141.	11.1	49
9	Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2021, 62, 1-12.	1.3	2
10	Transcriptomic profiling of <i>Brassica napus</i> responses to <i>Pseudomonas aeruginosa</i> . <i>Innate Immunity</i> , 2021, 27, 143-157.	2.4	6
11	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
12	Investigation of the impact of commonly used medications on the oral microbiome of individuals living without major chronic conditions. <i>PLoS ONE</i> , 2021, 16, e0261032.	2.5	8
13	Assessing the Variation within the Oral Microbiome of Healthy Adults. <i>MSphere</i> , 2020, 5, .	2.9	49
14	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	17.5	2,621
15	The human tumor microbiome is composed of tumor type-specific intracellular bacteria. <i>Science</i> , 2020, 368, 973-980.	12.6	1,077
16	Re-evaluating the relationship between missing heritability and the microbiome. <i>Microbiome</i> , 2020, 8, 87.	11.1	17
17	Age-Related Variation of Bacterial and Fungal Communities in Different Body Habitats across the Young, Elderly, and Centenarians in Sardinia. <i>MSphere</i> , 2020, 5, .	2.9	45
18	Detection of <i>Helicobacter pylori</i> Microevolution and Multiple Infection from Gastric Biopsies by Housekeeping Gene Amplicon Sequencing. <i>Pathogens</i> , 2020, 9, 97.	2.8	2

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19	Bacterial Taxa and Functions Are Predictive of Sustained Remission Following Exclusive Enteral Nutrition in Pediatric Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 1026-1037.	1.9	35
20	Investigating Gut Microbial Taxa and Asparaginase Related Genes in Children Showing Different Direction of Change in Serum Asparaginase Activity Levels during Pegasparginase Treatment for Acute Lymphoblastic Leukemia. <i>Blood</i> , 2020, 136, 40-41.	1.4	0
21	Metagenomic Functional Shifts to Plant Induced Environmental Changes. <i>Frontiers in Microbiology</i> , 2019, 10, 1682.	3.5	28
22	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
23	Current and Promising Approaches to Identify Horizontal Gene Transfer Events in Metagenomes. <i>Genome Biology and Evolution</i> , 2019, 11, 2750-2766.	2.5	70
24	Drivers of Regional Bacterial Community Structure and Diversity in the Northwest Atlantic Ocean. <i>Frontiers in Microbiology</i> , 2019, 10, 281.	3.5	50
25	Infectious Complications Are Associated With Alterations in the Gut Microbiome in Pediatric Patients With Acute Lymphoblastic Leukemia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 28.	3.9	48
26	Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. <i>Nature Communications</i> , 2019, 10, 89.	12.8	420
27	Polyphenol-based prebiotics and synbiotics: potential for cancer chemoprevention. <i>Current Opinion in Food Science</i> , 2018, 20, 51-57.	8.0	50
28	Exploring Linkages between Taxonomic and Functional Profiles of the Human Microbiome. <i>MSystems</i> , 2018, 3, .	3.8	69
29	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. <i>Microbiome</i> , 2018, 6, 13.	11.1	94
30	Denoising the Denoisers: an independent evaluation of microbiome sequence error-correction approaches. <i>PeerJ</i> , 2018, 6, e5364.	2.0	278
31	The Phosphate Binder Ferric Citrate Alters the Gut Microbiome in Rats with Chronic Kidney Disease. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2018, 367, 452-460.	2.5	33
32	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. <i>Methods in Molecular Biology</i> , 2018, 1849, 169-177.	0.9	155
33	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. <i>Methods in Molecular Biology</i> , 2018, 1849, 131-141.	0.9	5
34	Selective sensitivity of the gut microbiome to iron chelators in polybacterial abdominal sepsis. <i>Medical Hypotheses</i> , 2018, 120, 68-71.	1.5	2
35	Dissecting Community Structure in Wild Blueberry Root and Soil Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1187.	3.5	56
36	Differences in adiposity and diet quality among individuals with inflammatory bowel disease in Eastern Canada. <i>PLoS ONE</i> , 2018, 13, e0200580.	2.5	14

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37	“Available upon request” not good enough for microbiome data!. Microbiome, 2018, 6, 8.	11.1	35
38	The impact of chemerin or chemokine-like receptor 1 loss on the mouse gut microbiome. PeerJ, 2018, 6, e5494.	2.0	10
39	Microbiome Helper: a Custom and Streamlined Workflow for Microbiome Research. MSystems, 2017, 2, .	3.8	558
40	The coupling of taxonomy and function in microbiomes. Biology and Philosophy, 2017, 32, 1225-1243.	1.4	36
41	Variation in Bacterial and Eukaryotic Communities Associated with Natural and Managed Wild Blueberry Habitats. Phytobiomes Journal, 2017, 1, 102-113.	2.7	47
42	Moderate Exercise Has Limited but Distinguishable Effects on the Mouse Microbiome. MSystems, 2017, 2, .	3.8	65
43	Taxonomic differences of gut microbiomes drive cellulolytic enzymatic potential within hind-gut fermenting mammals. PLoS ONE, 2017, 12, e0189404.	2.5	22
44	The Impact of Exclusive Enteral Nutrition (EEN) on the Gut Microbiome in Crohn’s Disease: A Review. Nutrients, 2017, 9, 0447.	4.1	84
45	Genomic Analysis of a Serotype 5<i>Streptococcus pneumoniae</i> Outbreak in British Columbia, Canada, 2005–2009. Canadian Journal of Infectious Diseases and Medical Microbiology, 2016, 2016, 1-7.	1.9	6
46	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.	3.4	11
47	GenomeD3Plot: a library for rich, interactive visualizations of genomic data in web applications: Fig. 1.. Bioinformatics, 2015, 31, 3348-3349.	4.1	13
48	IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis: Figure 1.. Nucleic Acids Research, 2015, 43, W104-W108.	14.5	316
49	Frailty and the Microbiome. Interdisciplinary Topics in Gerontology and Geriatrics, 2015, 41, 54-65.	2.6	12
50	Fecal microbes, short chain fatty acids, and colorectal cancer across racial/ethnic groups. World Journal of Gastroenterology, 2015, 21, 2759.	3.3	64
51	Microbial shifts in the aging mouse gut. Microbiome, 2014, 2, 50.	11.1	354
52	Interactions in the microbiome: communities of organisms and communities of genes. FEMS Microbiology Reviews, 2014, 38, 90-118.	8.6	174
53	Which is more important for classifying microbial communities: who’s there or what they can do?. ISME Journal, 2014, 8, 2357-2359.	9.8	82
54	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	17.5	8,049

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55	IslandViewer update: improved genomic island discovery and visualization. Nucleic Acids Research, 2013, 41, W129-W132.	14.5	87
56	GenGIS 2: Geospatial Analysis of Traditional and Genetic Biodiversity, with New Gradient Algorithms and an Extensible Plugin Framework. PLoS ONE, 2013, 8, e69885.	2.5	118
57	MicrobeDB: a locally maintainable database of microbial genomic sequences. Bioinformatics, 2012, 28, 1947-1948.	4.1	15
58	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. BMC Bioinformatics, 2012, 13, 264.	2.6	20
59	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. PLoS ONE, 2012, 7, e43866.	2.5	60
60	Human Microbiome: A Genetic Bazaar for Microbes?. Current Biology, 2012, 22, R20-R22.	3.9	7
61	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. PLoS ONE, 2012, 7, e41389.	2.5	42
62	Detecting genomic islands using bioinformatics approaches. Nature Reviews Microbiology, 2010, 8, 373-382.	28.6	257
63	BioTorrents: A File Sharing Service for Scientific Data. PLoS ONE, 2010, 5, e10071.	2.5	29
64	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.	5.5	317
65	The Association of Virulence Factors with Genomic Islands. PLoS ONE, 2009, 4, e8094.	2.5	119
66	IslandViewer: an integrated interface for computational identification and visualization of genomic islands. Bioinformatics, 2009, 25, 664-665.	4.1	398
67	Bioinformatic detection of horizontally transferred DNA in bacterial genomes. F1000 Biology Reports, 2009, 1, 25.	4.0	9
68	Evaluation of genomic island predictors using a comparative genomics approach. BMC Bioinformatics, 2008, 9, 329.	2.6	255
69	MOBILE GENETIC ELEMENTS AND THEIR PREDICTION. Series on Advances in Bioinformatics and Computational Biology, 2008, , 113-135.	0.2	1
70	Parent genes of retrotransposition-generated gene duplicates in <i>Drosophila melanogaster</i> have distinct expression profiles. Genomics, 2007, 90, 334-343.	2.9	11
71	Data Standards for Flow Cytometry. OMICS A Journal of Integrative Biology, 2006, 10, 209-214.	2.0	23
72	Color lesion boundary detection using live wire. , 2005, , .		24

#	ARTICLE	IF	CITATIONS
73	3D live-wire-based semi-automatic segmentation of medical images. , 2005, 5747, 1597.		24
74	A primer and discussion on DNA-based microbiome data and related bioinformatics analyses. , 0, 1, .		6