

# 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

87843

38  
h-index

82499

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.	5.8	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.	4.4	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.	3.9	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.	0.6	4
5	Harnessing the plant microbiome to promote the growth of agricultural crops. <i>Microbiological Research</i> , 2021, 245, 126690.	2.5	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.	2.1	5
7	Identifying biases and their potential solutions in human microbiome studies. <i>Microbiome</i> , 2021, 9, 113.	4.9	82
8	A multi-OMIC characterisation of biodegradation and microbial community succession within the PET plastisphere. <i>Microbiome</i> , 2021, 9, 141.	4.9	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.	0.6	2
10	Transcriptomic profiling of <i>Brassica napus</i> responses to <i>Pseudomonas aeruginosa</i> . <i>Innate Immunity</i> , 2021, 27, 143-157.	1.1	6
11	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	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.	1.1	8
13	Assessing the Variation within the Oral Microbiome of Healthy Adults. <i>MSphere</i> , 2020, 5, .	1.3	49
14	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	9.4	2,621
15	The human tumor microbiome is composed of tumor type-specific intracellular bacteria. <i>Science</i> , 2020, 368, 973-980.	6.0	1,077
16	Re-evaluating the relationship between missing heritability and the microbiome. <i>Microbiome</i> , 2020, 8, 87.	4.9	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, .	1.3	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.	1.2	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.	0.9	35
20	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. <i>Blood</i> , 2020, 136, 40-41.	0.6	0
21	Metagenomic Functional Shifts to Plant Induced Environmental Changes. <i>Frontiers in Microbiology</i> , 2019, 10, 1682.	1.5	28
22	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	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.	1.1	70
24	Drivers of Regional Bacterial Community Structure and Diversity in the Northwest Atlantic Ocean. <i>Frontiers in Microbiology</i> , 2019, 10, 281.	1.5	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.	1.8	48
26	Enhancement of the gut barrier integrity by a microbial metabolite through the Nrf2 pathway. <i>Nature Communications</i> , 2019, 10, 89.	5.8	420
27	Polyphenol-based prebiotics and synbiotics: potential for cancer chemoprevention. <i>Current Opinion in Food Science</i> , 2018, 20, 51-57.	4.1	50
28	Exploring Linkages between Taxonomic and Functional Profiles of the Human Microbiome. <i>MSystems</i> , 2018, 3, .	1.7	69
29	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. <i>Microbiome</i> , 2018, 6, 13.	4.9	94
30	Denoising the Denoisers: an independent evaluation of microbiome sequence error-correction approaches. <i>PeerJ</i> , 2018, 6, e5364.	0.9	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.	1.3	33
32	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. <i>Methods in Molecular Biology</i> , 2018, 1849, 169-177.	0.4	155
33	Processing a 16S rRNA Sequencing Dataset with the Microbiome Helper Workflow. <i>Methods in Molecular Biology</i> , 2018, 1849, 131-141.	0.4	5
34	Selective sensitivity of the gut microbiome to iron chelators in polybacterial abdominal sepsis. <i>Medical Hypotheses</i> , 2018, 120, 68-71.	0.8	2
35	Dissecting Community Structure in Wild Blueberry Root and Soil Microbiome. <i>Frontiers in Microbiology</i> , 2018, 9, 1187.	1.5	56
36	Differences in adiposity and diet quality among individuals with inflammatory bowel disease in Eastern Canada. <i>PLoS ONE</i> , 2018, 13, e0200580.	1.1	14

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37	â€œAvailable upon requestâ€ not good enough for microbiome data!. <i>Microbiome</i> , 2018, 6, 8.	4.9	35
38	The impact of chemerin or chemokine-like receptor 1 loss on the mouse gut microbiome. <i>PeerJ</i> , 2018, 6, e5494.	0.9	10
39	Microbiome Helper: a Custom and Streamlined Workflow for Microbiome Research. <i>MSystems</i> , 2017, 2, .	1.7	558
40	The coupling of taxonomy and function in microbiomes. <i>Biology and Philosophy</i> , 2017, 32, 1225-1243.	0.7	36
41	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
42	Moderate Exercise Has Limited but Distinguishable Effects on the Mouse Microbiome. <i>MSystems</i> , 2017, 2, .	1.7	65
43	Taxonomic differences of gut microbiomes drive cellulolytic enzymatic potential within hind-gut fermenting mammals. <i>PLoS ONE</i> , 2017, 12, e0189404.	1.1	22
44	The Impact of Exclusive Enteral Nutrition (EEN) on the Gut Microbiome in Crohnâ€™s Disease: A Review. <i>Nutrients</i> , 2017, 9, 0447.	1.7	84
45	Genomic Analysis of a Serotype 5<i>Streptococcus pneumoniae</i> Outbreak in British Columbia, Canada, 2005â€“2009. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-7.	0.7	6
46	Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. <i>Poultry Science</i> , 2016, 95, 2250-2258.	1.5	11
47	GenomeD3Plot: a library for rich, interactive visualizations of genomic data in web applications: Fig. 1.. <i>Bioinformatics</i> , 2015, 31, 3348-3349.	1.8	13
48	IslandViewer 3: more flexible, interactive genomic island discovery, visualization and analysis: Figure 1.. <i>Nucleic Acids Research</i> , 2015, 43, W104-W108.	6.5	316
49	Frailty and the Microbiome. <i>Interdisciplinary Topics in Gerontology and Geriatrics</i> , 2015, 41, 54-65.	2.6	12
50	Fecal microbes, short chain fatty acids, and colorectal cancer across racial/ethnic groups. <i>World Journal of Gastroenterology</i> , 2015, 21, 2759.	1.4	64
51	Microbial shifts in the aging mouse gut. <i>Microbiome</i> , 2014, 2, 50.	4.9	354
52	Interactions in the microbiome: communities of organisms and communities of genes. <i>FEMS Microbiology Reviews</i> , 2014, 38, 90-118.	3.9	174
53	Which is more important for classifying microbial communities: whoâ€™s there or what they can do?. <i>ISME Journal</i> , 2014, 8, 2357-2359.	4.4	82
54	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049

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55	IslandViewer update: improved genomic island discovery and visualization. <i>Nucleic Acids Research</i> , 2013, 41, W129-W132.	6.5	87
56	GenGIS 2: Geospatial Analysis of Traditional and Genetic Biodiversity, with New Gradient Algorithms and an Extensible Plugin Framework. <i>PLoS ONE</i> , 2013, 8, e69885.	1.1	118
57	MicrobeDB: a locally maintainable database of microbial genomic sequences. <i>Bioinformatics</i> , 2012, 28, 1947-1948.	1.8	15
58	Sifting through genomes with iterative-sequence clustering produces a large, phylogenetically diverse protein-family resource. <i>BMC Bioinformatics</i> , 2012, 13, 264.	1.2	20
59	Functional Biogeography of Ocean Microbes Revealed through Non-Negative Matrix Factorization. <i>PLoS ONE</i> , 2012, 7, e43866.	1.1	60
60	Human Microbiome: A Genetic Bazaar for Microbes?. <i>Current Biology</i> , 2012, 22, R20-R22.	1.8	7
61	Sequencing of Seven Haloarchaeal Genomes Reveals Patterns of Genomic Flux. <i>PLoS ONE</i> , 2012, 7, e41389.	1.1	42
62	Detecting genomic islands using bioinformatics approaches. <i>Nature Reviews Microbiology</i> , 2010, 8, 373-382.	13.6	257
63	BioTorrents: A File Sharing Service for Scientific Data. <i>PLoS ONE</i> , 2010, 5, e10071.	1.1	29
64	Newly introduced genomic prophage islands are critical determinants of in vivo competitiveness in the Liverpool Epidemic Strain of <i>Pseudomonas aeruginosa</i> . <i>Genome Research</i> , 2009, 19, 12-23.	2.4	317
65	The Association of Virulence Factors with Genomic Islands. <i>PLoS ONE</i> , 2009, 4, e8094.	1.1	119
66	IslandViewer: an integrated interface for computational identification and visualization of genomic islands. <i>Bioinformatics</i> , 2009, 25, 664-665.	1.8	398
67	Bioinformatic detection of horizontally transferred DNA in bacterial genomes. <i>F1000 Biology Reports</i> , 2009, 1, 25.	4.0	9
68	Evaluation of genomic island predictors using a comparative genomics approach. <i>BMC Bioinformatics</i> , 2008, 9, 329.	1.2	255
69	MOBILE GENETIC ELEMENTS AND THEIR PREDICTION. <i>Series on Advances in Bioinformatics and Computational Biology</i> , 2008, , 113-135.	0.2	1
70	Parent genes of retrotransposition-generated gene duplicates in <i>Drosophila melanogaster</i> have distinct expression profiles. <i>Genomics</i> , 2007, 90, 334-343.	1.3	11
71	Data Standards for Flow Cytometry. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 209-214.	1.0	23
72	Color lesion boundary detection using live wire. , 2005, , .		24

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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