

Manimozhiyan Arumugam

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

49,455
citations

76196

40
h-index

91712

69
g-index

79
all docs

79
docs citations

79
times ranked

51052
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
3	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
4	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
5	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
6	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
7	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
8	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
9	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	5.8	1,062
10	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
11	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017, 66, 70-78.	6.1	865
12	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
13	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
14	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
15	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
16	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. <i>Nature Medicine</i> , 2019, 25, 667-678.	15.2	602
17	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012, 6, 1415-1426.	4.4	544
18	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	5.9	483

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19	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
20	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	9.4	422
21	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	6.0	394
22	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013, 23, 1163-1169.	2.4	356
23	Roux-en-Y gastric bypass surgery of morbidly obese patients induces swift and persistent changes of the individual gut microbiota. <i>Genome Medicine</i> , 2016, 8, 67.	3.6	260
24	Insight into Structure and Assembly of the Nuclear Pore Complex by Utilizing the Genome of a Eukaryotic Thermophile. <i>Cell</i> , 2011, 146, 277-289.	13.5	232
25	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e31386.	1.1	214
26	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	1.1	208
27	Interplay between FGF21 and insulin action in the liver regulates metabolism. <i>Journal of Clinical Investigation</i> , 2014, 124, 515-527.	3.9	201
28	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
29	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. <i>Scientific Reports</i> , 2016, 6, 26775.	1.6	164
30	Molecular Properties of Adult Mouse Gastric and Intestinal Epithelial Progenitors in Their Niches. <i>Journal of Biological Chemistry</i> , 2006, 281, 11292-11300.	1.6	149
31	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017, 5, 43.	4.9	132
32	Circulating microbiome in blood of different circulatory compartments. <i>Gut</i> , 2019, 68, 578-580.	6.1	120
33	Butyrate producing colonic Clostridiales metabolise human milk oligosaccharides and cross feed on mucin via conserved pathways. <i>Nature Communications</i> , 2020, 11, 3285.	5.8	102
34	Utilizing the gut microbiome in decompensated cirrhosis and acute-on-chronic liver failure. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2021, 18, 167-180.	8.2	97
35	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , 2010, 26, 2977-2978.	1.8	89
36	Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. <i>Genome Biology</i> , 2021, 22, 209.	3.8	65

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37	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
38	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. <i>Frontiers in Immunology</i> , 2019, 10, 69.	2.2	40
39	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. <i>Environment International</i> , 2022, 158, 106899.	4.8	40
40	Closing in on the <i>C. elegans</i> ORFeome by cloning TWINSCAN predictions. <i>Genome Research</i> , 2005, 15, 577-582.	2.4	39
41	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021, 13, 37.	3.6	34
42	Identification of Rat Genes by TWINSCAN Gene Prediction, RT-PCR, and Direct Sequencing. <i>Genome Research</i> , 2004, 14, 665-671.	2.4	31
43	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021, 13, 36.	3.6	31
44	Trust is good, control is better: technical considerations in blood microbiome analysis. <i>Gut</i> , 2020, 69, 1362-1363.	6.1	28
45	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010, 26, 2979-2980.	1.8	24
46	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. <i>Journal of Hepatology</i> , 2019, 71, 594-602.	1.8	23
47	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	1.7	22
48	Perturbation of gut microbiota decreases susceptibility but does not modulate ongoing autoimmune neurological disease. <i>Journal of Neuroinflammation</i> , 2020, 17, 79.	3.1	19
49	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. <i>Diabetes</i> , 2021, 70, 2092-2106.	0.3	17
50	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021, 44, 511-518.	4.3	16
51	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006, 7, S5.	13.9	15
52	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. <i>Animal Microbiome</i> , 2019, 1, 11.	1.5	15
53	Genes controlling the activation of natural killer lymphocytes are epigenetically remodeled in intestinal cells from germ-free mice. <i>FASEB Journal</i> , 2019, 33, 2719-2731.	0.2	12
54	The effect of gluten in adolescents and young adults with gastrointestinal symptoms: a blinded randomised crossover trial. <i>Alimentary Pharmacology and Therapeutics</i> , 2022, 55, 1116-1127.	1.9	12

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55	The Treeterbi and Parallel Treeterbi algorithms: efficient, optimal decoding for ordinary, generalized and pair HMMs. <i>Bioinformatics</i> , 2007, 23, 545-554.	1.8	9
56	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. <i>PLoS ONE</i> , 2020, 15, e0238648.	1.1	9
57	Variation in Bile Microbiome by the Etiology of Cholestatic Liver Disease. <i>Liver Transplantation</i> , 2020, 26, 1652-1657.	1.3	8
58	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. <i>Bioinformatics</i> , 2009, 25, 1587-1593.	1.8	6
59	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013, 2, 120.	0.6	6
60	Ecological Adaptation and Succession of Human Fecal Microbial Communities in an Automated <i>In Vitro</i> Fermentation System. <i>MSystems</i> , 2021, 6, e0023221.	1.7	5
61	MIntO: A Modular and Scalable Pipeline For Microbiome Metagenomic and Metatranscriptomic Data Integration. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	5
62	Complete Genome Sequences of <i>emm111</i> Type <i>Streptococcus pyogenes</i> Strain GUR, with Antitumor Activity, and Its Derivative Strain GURSA1 with an Inactivated <i>emm</i> Gene. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
63	The Role of the Mycobiota in the Gut-Liver Axis. , 2019, , 133-145.		1
64	Towards affordable diagnosis based on human gut microbiome: Colorectal cancer as a case study. <i>Toxicology Letters</i> , 2017, 280, S12.	0.4	0
65	Correction: Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019, 37, 102-102.	9.4	0
66	The Role of the Bacterial Microbiota in Alcoholic and Non-alcoholic Fatty Liver Disease. , 2019, , 89-104.		0