Manimozhiyan Arumugam

List of Publications by Year
in descending order

66 papers	49,455 citations	76326 40 h-index	91884 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. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
2	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	27.8	9,342
3	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	27.8	5,800
4	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
5	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
6	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	17.5	1,664
7	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	27.8	1,627
8	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
9	Gut microbiome development along the colorectal adenoma–carcinoma sequence. Nature Communications, 2015, 6, 6528.	12.8	1,062
10	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909
11	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. Gut, 2017, 66, 70-78.	12.1	865
12	Genomic variation landscape of the human gut microbiome. Nature, 2013, 493, 45-50.	27.8	783
13	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. Nature Medicine, 2019, 25, 679-689.	30.7	734
14	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	13.3	717
15	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
16	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. Nature Medicine, 2019, 25, 667-678.	30.7	602
17	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. ISME Journal, 2012, 6, 1415-1426.	9.8	544
18	Recovery of gut microbiota of healthy adults following antibiotic exposure. Nature Microbiology, 2018, 3, 1255-1265.	13.3	483

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19	Metagenomic species profiling using universal phylogenetic marker genes. Nature Methods, 2013, 10, 1196-1199.	19.0	442
20	A catalog of the mouse gut metagenome. Nature Biotechnology, 2015, 33, 1103-1108.	17.5	422
21	Transcriptome Complexity in a Genome-Reduced Bacterium. Science, 2009, 326, 1268-1271.	12.6	394
22	Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 1163-1169.	5.5	356
23	Roux-en-Y gastric bypass surgery of morbidly obese patients induces swift and persistent changes of the individual gut microbiota. Genome Medicine, 2016, 8, 67.	8.2	260
24	Insight into Structure and Assembly of the Nuclear Pore Complex by Utilizing the Genome of a Eukaryotic Thermophile. Cell, 2011, 146, 277-289.	28.9	232
25	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. PLoS ONE, 2012, 7, e31386.	2.5	214
26	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. PLoS ONE, 2012, 7, e47656.	2.5	208
27	Interplay between FGF21 and insulin action in the liver regulates metabolism. Journal of Clinical Investigation, 2014, 124, 515-527.	8.2	201
28	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
29	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. Scientific Reports, 2016, 6, 26775.	3.3	164
30	Molecular Properties of Adult Mouse Gastric and Intestinal Epithelial Progenitors in Their Niches. Journal of Biological Chemistry, 2006, 281, 11292-11300.	3.4	149
31	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. Microbiome, 2017, 5, 43.	11.1	132
32	Circulating microbiome in blood of different circulatory compartments. Gut, 2019, 68, 578-580.	12.1	120
33	Butyrate producing colonic Clostridiales metabolise human milk oligosaccharides and cross feed on mucin via conserved pathways. Nature Communications, 2020, 11, 3285.	12.8	102
34	Utilizing the gut microbiome in decompensated cirrhosis and acute-on-chronic liver failure. Nature Reviews Gastroenterology and Hepatology, 2021, 18, 167-180.	17.8	97
35	SmashCommunity: a metagenomic annotation and analysis tool. Bioinformatics, 2010, 26, 2977-2978.	4.1	89
36	Genomic diversity and ecology of human-associated Akkermansia species in the gut microbiome revealed by extensive metagenomic assembly. Genome Biology, 2021, 22, 209.	8.8	65

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37	Consistent mutational paths predict eukaryotic thermostability. BMC Evolutionary Biology, 2013, 13, 7.	3.2	60
38	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. Frontiers in Immunology, 2019, 10, 69.	4.8	40
39	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. Environment International, 2022, 158, 106899.	10.0	40
40	Closing in on the C. elegans ORFeome by cloning TWINSCAN predictions. Genome Research, 2005, 15, 577-582.	5.5	39
41	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. Genome Medicine, 2021, 13, 37.	8.2	34
42	Identification of Rat Genes by TWINSCAN Gene Prediction, RT-PCR, and Direct Sequencing. Genome Research, 2004, 14, 665-671.	5.5	31
43	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. Genome Medicine, 2021, 13, 36.	8.2	31
44	Trust is good, control is better: technical considerations in blood microbiome analysis. Gut, 2020, 69, 1362-1363.	12.1	28
45	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. Bioinformatics, 2010, 26, 2979-2980.	4.1	24
46	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. Journal of Hepatology, 2019, 71, 594-602.	3.7	23
47	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. MSystems, 2021, 6, e0038221.	3.8	22
48	Perturbation of gut microbiota decreases susceptibility but does not modulate ongoing autoimmune neurological disease. Journal of Neuroinflammation, 2020, 17, 79.	7.2	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. Diabetes, 2021, 70, 2092-2106.	0.6	17
50	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. Diabetes Care, 2021, 44, 511-518.	8.6	16
51	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. Genome Biology, 2006, 7, S5.	9.6	15
52	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. Animal Microbiome, 2019, 1, 11.	3.8	15
53	Genes controlling the activation of natural killer lymphocytes are epigenetically remodeled in intestinal cells from germâ€free mice. FASEB Journal, 2019, 33, 2719-2731.	0.5	12
54	The effect of gluten in adolescents and young adults with gastrointestinal symptoms: a blinded randomised crossâ€over trial. Alimentary Pharmacology and Therapeutics, 2022, 55, 1116-1127.	3.7	12

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55	The Treeterbi and Parallel Treeterbi algorithms: efficient, optimal decoding for ordinary, generalized and pair HMMs. Bioinformatics, 2007, 23, 545-554.	4.1	9
56	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. PLoS ONE, 2020, 15, e0238648.	2.5	9
57	Variation in Bile Microbiome by the Etiology of Cholestatic Liver Disease. Liver Transplantation, 2020, 26, 1652-1657.	2.4	8
58	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. Bioinformatics, 2009, 25, 1587-1593.	4.1	6
59	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
60	Ecological Adaptation and Succession of Human Fecal Microbial Communities in an Automated *In Vitro* Fermentation System. MSystems, 2021, 6, e0023221.	3.8	5
61	MIntO: A Modular and Scalable Pipeline For Microbiome Metagenomic and Metatranscriptomic Data Integration. Frontiers in Bioinformatics, 2022, 2, .	2.1	5
62	Complete Genome Sequences of *emm111* Type Streptococcus pyogenes Strain GUR, with Antitumor Activity, and Its Derivative Strain GURSA1 with an Inactivated *emm* Gene. Genome Announcements, 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. Toxicology Letters, 2017, 280, S12.	0.8	0
65	Correction: Amendments: Author Correction: A catalog of the mouse gut metagenome. Nature Biotechnology, 2019, 37, 102-102.	17.5	0
66	The Role of the Bacterial Microbiota in Alcoholic and Non-alcoholic Fatty Liver Disease. , 2019, , 89-104.		0