

# 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	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. <i>Environment International</i> , 2022, 158, 106899.	4.8	40
2	The effect of gluten in adolescents and young adults with gastrointestinal symptoms: a blinded randomised cross-over trial. <i>Alimentary Pharmacology and Therapeutics</i> , 2022, 55, 1116-1127.	1.9	12
3	MIntO: A Modular and Scalable Pipeline For Microbiome Metagenomic and Metatranscriptomic Data Integration. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	5
4	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
5	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021, 13, 36.	3.6	31
6	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021, 13, 37.	3.6	34
7	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
8	Genomic diversity and ecology of human-associated <i>Akkermansia</i> species in the gut microbiome revealed by extensive metagenomic assembly. <i>Genome Biology</i> , 2021, 22, 209.	3.8	65
9	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
10	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021, 44, 511-518.	4.3	16
11	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	1.7	22
12	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
13	Trust is good, control is better: technical considerations in blood microbiome analysis. <i>Gut</i> , 2020, 69, 1362-1363.	6.1	28
14	Variation in Bile Microbiome by the Etiology of Cholestatic Liver Disease. <i>Liver Transplantation</i> , 2020, 26, 1652-1657.	1.3	8
15	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. <i>PLoS ONE</i> , 2020, 15, e0238648.	1.1	9
16	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
17	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
18	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167

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19	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
20	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. <i>Frontiers in Immunology</i> , 2019, 10, 69.	2.2	40
21	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
22	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
23	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. <i>Animal Microbiome</i> , 2019, 1, 11.	1.5	15
24	Correction: Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019, 37, 102-102.	9.4	0
25	The Role of the Mycobiota in the Gut-Liver Axis. , 2019, , 133-145.		1
26	The Role of the Bacterial Microbiota in Alcoholic and Non-alcoholic Fatty Liver Disease. , 2019, , 89-104.		0
27	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
28	Circulating microbiome in blood of different circulatory compartments. <i>Gut</i> , 2019, 68, 578-580.	6.1	120
29	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
30	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	5.9	483
31	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
32	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
33	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
34	Towards affordable diagnosis based on human gut microbiome: Colorectal cancer as a case study. <i>Toxicology Letters</i> , 2017, 280, S12.	0.4	0
35	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
36	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506

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37	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. <i>Scientific Reports</i> , 2016, 6, 26775.	1.6	164
38	Gut microbiome development along the colorectal adenomaâ€“carcinoma sequence. <i>Nature Communications</i> , 2015, 6, 6528.	5.8	1,062
39	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015, 33, 1103-1108.	9.4	422
40	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
41	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
42	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
43	Interplay between FGF21 and insulin action in the liver regulates metabolism. <i>Journal of Clinical Investigation</i> , 2014, 124, 515-527.	3.9	201
44	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
45	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
46	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013, 23, 1163-1169.	2.4	356
47	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
48	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
49	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013, 2, 120.	0.6	6
50	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
51	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	1.1	208
52	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e31386.	1.1	214
53	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
54	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

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55	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
56	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
57	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , 2010, 26, 2977-2978.	1.8	89
58	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010, 26, 2979-2980.	1.8	24
59	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. <i>Bioinformatics</i> , 2009, 25, 1587-1593.	1.8	6
60	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	6.0	394
61	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
62	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006, 7, S5.	13.9	15
63	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
64	Closing in on the <i>C. elegans</i> ORFeome by cloning TWINSCAN predictions. <i>Genome Research</i> , 2005, 15, 577-582.	2.4	39
65	Identification of Rat Genes by TWINSCAN Gene Prediction, RT-PCR, and Direct Sequencing. <i>Genome Research</i> , 2004, 14, 665-671.	2.4	31
66	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943