

Manimozhiyan Arumugam

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67

papers

30,640

citations

38

h-index

79

g-index

79

ext. papers

41,481

ext. citations

20.9

avg, IF

5.72

L-index

#	Paper	IF	Citations
67	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
66	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
65	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
64	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
63	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
62	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
61	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
60	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016 , 535, 376-81	50.4	977
59	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
58	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015 , 6, 6528	17.4	614
57	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
56	Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. <i>Gut</i> , 2017 , 66, 70-78	19.2	488
55	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
54	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012 , 6, 1415-26	11.9	416
53	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
52	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019 , 25, 679-689	50.5	353
51	Transcriptome complexity in a genome-reduced bacterium. <i>Science</i> , 2009 , 326, 1268-71	33.3	341

50	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
49	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015 , 33, 1103-8	44.5	295
48	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	50.5	289
47	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013 , 23, 1163-9	9.7	269
46	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018 , 3, 1255-1265	26.6	246
45	Insight into structure and assembly of the nuclear pore complex by utilizing the genome of a eukaryotic thermophile. <i>Cell</i> , 2011 , 146, 277-89	56.2	198
44	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	14.4	187
43	Interplay between FGF21 and insulin action in the liver regulates metabolism. <i>Journal of Clinical Investigation</i> , 2014 , 124, 515-27	15.9	163
42	Assessment of metagenomic assembly using simulated next generation sequencing data. <i>PLoS ONE</i> , 2012 , 7, e31386	3.7	157
41	MOCAT: a metagenomics assembly and gene prediction toolkit. <i>PLoS ONE</i> , 2012 , 7, e47656	3.7	143
40	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
39	Molecular properties of adult mouse gastric and intestinal epithelial progenitors in their niches. <i>Journal of Biological Chemistry</i> , 2006 , 281, 11292-300	5.4	137
38	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. <i>Scientific Reports</i> , 2016 , 6, 26775	4.9	101
37	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
36	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017 , 5, 43	16.6	77
35	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , 2010 , 26, 2977-8	7.2	77
34	Circulating microbiome in blood of different circulatory compartments. <i>Gut</i> , 2019 , 68, 578-580	19.2	65
33	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013 , 13, 7	3	47

32	Butyrate producing colonic Clostridiales metabolise human milk oligosaccharides and cross feed on mucin via conserved pathways. <i>Nature Communications</i> , 2020 , 11, 3285	17.4	41
31	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
30	Closing in on the <i>C. elegans</i> ORFeome by cloning TWINSCAN predictions. <i>Genome Research</i> , 2005 , 15, 577-82	9.7	34
29	Identification of rat genes by TWINSCAN gene prediction, RT-PCR, and direct sequencing. <i>Genome Research</i> , 2004 , 14, 665-71	9.7	29
28	Utilizing the gut microbiome in decompensated cirrhosis and acute-on-chronic liver failure. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2021 , 18, 167-180	24.2	28
27	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. <i>Frontiers in Immunology</i> , 2019 , 10, 69	8.4	23
26	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010 , 26, 2979-80	7.2	21
25	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
24	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	18.3	14
23	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S5.1-18.3	18.3	13
22	Trust is good, control is better: technical considerations in blood microbiome analysis. <i>Gut</i> , 2020 , 69, 1362-1363	19.2	13
21	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021 , 13, 36	14.4	13
20	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021 , 13, 37	14.4	12
19	Perturbation of gut microbiota decreases susceptibility but does not modulate ongoing autoimmune neurological disease. <i>Journal of Neuroinflammation</i> , 2020 , 17, 79	10.1	11
18	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	13.4	10
17	The Treeterbi and Parallel Treeterbi algorithms: efficient, optimal decoding for ordinary, generalized and pair HMMs. <i>Bioinformatics</i> , 2007 , 23, 545-54	7.2	9
16	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. <i>Bioinformatics</i> , 2009 , 25, 1587-93	7.2	6
15	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021 , 44, 511-518	14.6	6

14	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	0.9	6
13	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. <i>Animal Microbiome</i> , 2019 , 1, 11	4.1	5
12	Variation in Bile Microbiome by the Etiology of Cholestatic Liver Disease. <i>Liver Transplantation</i> , 2020 , 26, 1652-1657	4.5	4
11	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	0.9	4
10	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. <i>Environment International</i> , 2021 , 158, 106899	12.9	4
9	Implementations of the chemical structural and compositional similarity metric in R and Python		1
8	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013 , 2, 120	0.8	1
7	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. <i>PLoS ONE</i> , 2020 , 15, e0238648	3.7	1
6	The Role of the Mycobiota in the Gut-Liver Axis 2019 , 133-145		1
5	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs		1
4	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021 , 6, e0038221	7.6	0
3	Ecological Adaptation and Succession of Human Fecal Microbial Communities in an Automated Fermentation System. <i>MSystems</i> , 2021 , 6, e0023221	7.6	0
2	Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019 , 37, 102	44.5	
1	The Role of the Bacterial Microbiota in Alcoholic and Non-alcoholic Fatty Liver Disease 2019 , 89-104		