

Manimozhiyan Arumugam

List of Publications by Year in Descending Order

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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	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
66	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , 2021 , 44, 511-518	14.6	6
65	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021 , 6, e0038221	7.6	0
64	Trans-ethnic gut microbiota signatures of type 2 diabetes in Denmark and India. <i>Genome Medicine</i> , 2021 , 13, 37	14.4	12
63	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
62	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
61	Trans-ethnic gut microbial signatures of prediabetic subjects from India and Denmark. <i>Genome Medicine</i> , 2021 , 13, 36	14.4	13
60	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
59	Ecological Adaptation and Succession of Human Fecal Microbial Communities in an Automated Fermentation System. <i>MSystems</i> , 2021 , 6, e0023221	7.6	0
58	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs. <i>Environment International</i> , 2021 , 158, 106899	12.9	4
57	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
56	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
55	Variation in Bile Microbiome by the Etiology of Cholestatic Liver Disease. <i>Liver Transplantation</i> , 2020 , 26, 1652-1657	4.5	4
54	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. <i>PLoS ONE</i> , 2020 , 15, e0238648	3.7	1
53	Trust is good, control is better: technical considerations in blood microbiome analysis. <i>Gut</i> , 2020 , 69, 1362-1363	19.2	13
52	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
51	Compartmentalization of Immune Response and Microbial Translocation in Decompensated Cirrhosis. <i>Frontiers in Immunology</i> , 2019 , 10, 69	8.4	23

50	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
49	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
48	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
47	Impaired glucose metabolism and altered gut microbiome despite calorie restriction of ob/ob mice. <i>Animal Microbiome</i> , 2019 , 1, 11	4.1	5
46	Amendments: Author Correction: A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2019 , 37, 102	44.5	
45	The Role of the Mycobiota in the Gut-Liver Axis 2019 , 133-145		1
44	The Role of the Bacterial Microbiota in Alcoholic and Non-alcoholic Fatty Liver Disease 2019 , 89-104		
43	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
42	Circulating microbiome in blood of different circulatory compartments. <i>Gut</i> , 2019 , 68, 578-580	19.2	65
41	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018 , 3, 8-16	26.6	387
40	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
39	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018 , 3, 1255-1265	26.6	246
38	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
37	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
36	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016 , 535, 376-81	50.4	977
35	An Improved Method for High Quality Metagenomics DNA Extraction from Human and Environmental Samples. <i>Scientific Reports</i> , 2016 , 6, 26775	4.9	101
34	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
33	Gut microbiome development along the colorectal adenoma-carcinoma sequence. <i>Nature Communications</i> , 2015 , 6, 6528	17.4	614

32	A catalog of the mouse gut metagenome. <i>Nature Biotechnology</i> , 2015 , 33, 1103-8	44.5	295
31	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
30	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
29	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
28	Interplay between FGF21 and insulin action in the liver regulates metabolism. <i>Journal of Clinical Investigation</i> , 2014 , 124, 515-27	15.9	163
27	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
26	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
25	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013 , 23, 1163-9	9.7	269
24	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
23	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013 , 13, 7	3	47
22	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013 , 2, 120	0.8	1
21	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
20	MOCAT: a metagenomics assembly and gene prediction toolkit. <i>PLoS ONE</i> , 2012 , 7, e47656	3.7	143
19	Assessment of metagenomic assembly using simulated next generation sequencing data. <i>PLoS ONE</i> , 2012 , 7, e31386	3.7	157
18	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
17	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
16	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
15	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044

14	SmashCommunity: a metagenomic annotation and analysis tool. <i>Bioinformatics</i> , 2010 , 26, 2977-8	7.2	77
13	SmashCell: a software framework for the analysis of single-cell amplified genome sequences. <i>Bioinformatics</i> , 2010 , 26, 2979-80	7.2	21
12	Pairagon: a highly accurate, HMM-based cDNA-to-genome aligner. <i>Bioinformatics</i> , 2009 , 25, 1587-93	7.2	6
11	Transcriptome complexity in a genome-reduced bacterium. <i>Science</i> , 2009 , 326, 1268-71	33.3	34 ¹
10	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
9	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
8	Pairagon+N-SCAN_EST: a model-based gene annotation pipeline. <i>Genome Biology</i> , 2006 , 7 Suppl 1, S5.1-10.3	10.3	13
7	Closing in on the <i>C. elegans</i> ORFeome by cloning TWINSCAN predictions. <i>Genome Research</i> , 2005 , 15, 577-82	9.7	34
6	Identification of rat genes by TWINSCAN gene prediction, RT-PCR, and direct sequencing. <i>Genome Research</i> , 2004 , 14, 665-71	9.7	29
5	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
4	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
3	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
2	Implementations of the chemical structural and compositional similarity metric in R and Python		1
1	Metagenomic evidence for co-occurrence of antibiotic, biocide and metal resistance genes in pigs		1