

Matthew A Jackson

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.

29
papers

3,258
citations

21
h-index

33
g-index

33
ext. papers

4,647
ext. citations

13.7
avg, IF

5
L-index

#	Paper	IF	Citations
29	IL-1-driven stromal-neutrophil interactions define a subset of patients with inflammatory bowel disease that does not respond to therapies. <i>Nature Medicine</i> , 2021 , 27, 1970-1981	50.5	11
28	Endocannabinoid system mediates the association between gut-microbial diversity and anhedonia/amotivation in a general population cohort. <i>Molecular Psychiatry</i> , 2021 ,	15.1	5
27	Accurate identification and quantification of commensal microbiota bound by host immunoglobulins. <i>Microbiome</i> , 2021 , 9, 33	16.6	8
26	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
25	Associations between UK tap water and gut microbiota composition suggest the gut microbiome as a potential mediator of health differences linked to water quality. <i>Science of the Total Environment</i> , 2020 , 739, 139697	10.2	6
24	Socioeconomic Status and the Gut Microbiome: A TwinsUK Cohort Study. <i>Microorganisms</i> , 2019 , 7,	4.9	49
23	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018 , 6, 101	16.6	53
22	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018 , 9, 2655	17.4	225
21	Use of dietary indices to control for diet in human gut microbiota studies. <i>Microbiome</i> , 2018 , 6, 77	16.6	61
20	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018 , 6, e4303	3.1	28
19	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018 , 9, 61-67	8.8	27
18	An Investigation Into Physical Frailty as a Link Between the Gut Microbiome and Cognitive Health. <i>Frontiers in Aging Neuroscience</i> , 2018 , 10, 398	5.3	27
17	Response to: Population-Based Gut Microbiome Associations With Hypertension. <i>Circulation Research</i> , 2018 , 123, 1188-1189	15.7	
16	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018 , 50, 790-795	36.3	262
15	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
14	Gut microbiome diversity and high-fibre intake are related to lower long-term weight gain. <i>International Journal of Obesity</i> , 2017 , 41, 1099-1105	5.5	174
13	Untangling the relationship between diet and visceral fat mass through blood metabolomics and gut microbiome profiling. <i>International Journal of Obesity</i> , 2017 , 41, 1106-1113	5.5	41

12	Hippurate as a metabolomic marker of gut microbiome diversity: Modulation by diet and relationship to metabolic syndrome. <i>Scientific Reports</i> , 2017 , 7, 13670	4.9	110
11	Omega-3 fatty acids correlate with gut microbiome diversity and production of N-carbamylglutamate in middle aged and elderly women. <i>Scientific Reports</i> , 2017 , 7, 11079	4.9	124
10	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016 , 8, 8	14.4	200
9	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016 , 65, 749-56	19.2	454
8	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. <i>PLoS Genetics</i> , 2016 , 12, e1006179	6	69
7	A heritability-based comparison of methods used to cluster 16S rRNA gene sequences into operational taxonomic units. <i>PeerJ</i> , 2016 , 4, e2341	3.1	23
6	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016 , 3, 572-584.e3	10.6	172
5	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016 , 19, 731-43	23.4	547
4	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016 , 17, 189	18.3	124
3	A large genomic island allows <i>Neisseria meningitidis</i> to utilize propionic acid, with implications for colonization of the human nasopharynx. <i>Molecular Microbiology</i> , 2014 , 93, 346-55	4.1	18
2	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
1	IL-1-driven stromal-neutrophil interaction in deep ulcers defines a pathotype of therapy non-responsive inflammatory bowel disease		1