

# Matthew A Jackson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6171997/publications.pdf>

Version: 2024-02-01

27  
papers

5,931  
citations

304368

22  
h-index

525886

27  
g-index

33  
all docs

33  
docs citations

33  
times ranked

9490  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	5.1	831
2	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016, 65, 749-756.	6.1	682
3	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
4	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
5	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	9.4	482
6	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018, 9, 2655.	5.8	411
7	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	3.6	297
8	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.	1.6	268
9	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3.	2.9	261
10	Hippurate as a metabolomic marker of gut microbiome diversity: Modulation by diet and relationship to metabolic syndrome. <i>Scientific Reports</i> , 2017, 7, 13670.	1.6	193
11	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
12	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.	1.6	174
13	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.	15.2	117
14	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	4.9	109
15	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. <i>PLoS Genetics</i> , 2016, 12, e1006179.	1.5	94
16	Socioeconomic Status and the Gut Microbiome: A TwinsUK Cohort Study. <i>Microorganisms</i> , 2019, 7, 17.	1.6	93
17	Use of dietary indices to control for diet in human gut microbiota studies. <i>Microbiome</i> , 2018, 6, 77.	4.9	85
18	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.	1.6	68

#	ARTICLE	IF	CITATIONS
19	An Investigation Into Physical Frailty as a Link Between the Gut Microbiome and Cognitive Health. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 398.	1.7	51
20	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	0.9	48
21	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018, 9, 61-67.	4.3	41
22	A heritability-based comparison of methods used to cluster 16S rRNA gene sequences into operational taxonomic units. <i>PeerJ</i> , 2016, 4, e2341.	0.9	41
23	Accurate identification and quantification of commensal microbiota bound by host immunoglobulins. <i>Microbiome</i> , 2021, 9, 33.	4.9	29
24	A large genomic island allows <i>N. eisseria meningitidis</i> to utilize propionic acid, with implications for colonization of the human nasopharynx. <i>Molecular Microbiology</i> , 2014, 93, 346-355.	1.2	26
25	Endocannabinoid system mediates the association between gut-microbial diversity and anhedonia/amotivation in a general population cohort. <i>Molecular Psychiatry</i> , 2021, 26, 6269-6276.	4.1	24
26	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.	3.9	11
27	Response to: Population-Based Gut Microbiome Associations With Hypertension. <i>Circulation Research</i> , 2018, 123, 1188-1189.	2.0	0