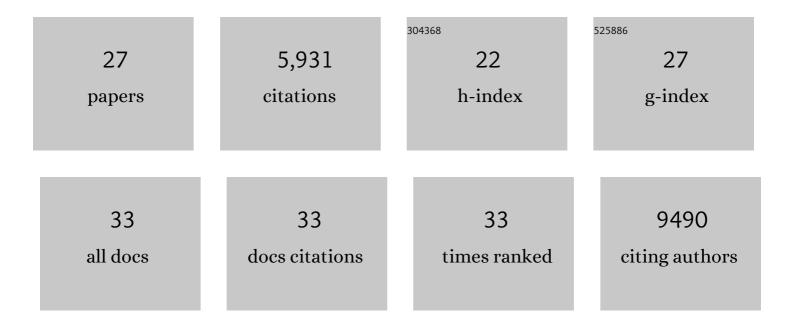
Matthew A Jackson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6171997/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genetic Determinants of the Gut Microbiome in UK Twins. Cell Host and Microbe, 2016, 19, 731-743.	5.1	831
2	Proton pump inhibitors alter the composition of the gut microbiota. Gut, 2016, 65, 749-756.	6.1	682
3	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
4	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	1.7	604
5	The fecal metabolome as a functional readout of the gut microbiome. Nature Genetics, 2018, 50, 790-795.	9.4	482
6	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. Nature Communications, 2018, 9, 2655.	5.8	411
7	Signatures of early frailty in the gut microbiota. Genome Medicine, 2016, 8, 8.	3.6	297
8	Gut microbiome diversity and high-fibre intake are related to lower long-term weight gain. International Journal of Obesity, 2017, 41, 1099-1105.	1.6	268
9	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. Cell Systems, 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. Scientific Reports, 2017, 7, 13670.	1.6	193
11	Heritable components of the human fecal microbiome are associated with visceral fat. Genome Biology, 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. Scientific Reports, 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. Nature Medicine, 2021, 27, 1970-1981.	15.2	117
14	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. Microbiome, 2018, 6, 101.	4.9	109
15	Recombination Rate Heterogeneity within Arabidopsis Disease Resistance Genes. PLoS Genetics, 2016, 12, e1006179.	1.5	94
16	Socioeconomic Status and the Gut Microbiome: A TwinsUK Cohort Study. Microorganisms, 2019, 7, 17.	1.6	93
17	Use of dietary indices to control for diet in human gut microbiota studies. Microbiome, 2018, 6, 77.	4.9	85
18	Untangling the relationship between diet and visceral fat mass through blood metabolomics and gut microbiome profiling. International Journal of Obesity, 2017, 41, 1106-1113.	1.6	68

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#	Article	IF	CITATIONS
19	An Investigation Into Physical Frailty as a Link Between the Gut Microbiome and Cognitive Health. Frontiers in Aging Neuroscience, 2018, 10, 398.	1.7	51
20	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. PeerJ, 2018, 6, e4303.	0.9	48
21	Heritable components of the human fecal microbiome are associated with visceral fat. Gut Microbes, 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. PeerJ, 2016, 4, e2341.	0.9	41
23	Accurate identification and quantification of commensal microbiota bound by host immunoglobulins. Microbiome, 2021, 9, 33.	4.9	29
24	A large genomic island allows N eisseria meningitidis to utilize propionic acid, with implications for colonization of the human nasopharynx. Molecular Microbiology, 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. Molecular Psychiatry, 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. Science of the Total Environment, 2020, 739, 139697.	3.9	11
27	Response to: Population-Based Gut Microbiome Associations With Hypertension. Circulation Research, 2018, 123, 1188-1189.	2.0	0