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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.

133 papers	13,071 citations	53 h-index	114 g-index
166 ext. papers	18,218 ext. citations	12.9 avg, IF	6.16 L-index

#	Paper	IF	Citations
133	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018 , 555, 210-215	50.4	1170
132	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016 , 352, 560-4	33.3	1120
131	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016 , 352, 565-9	33.3	929
130	Proton pump inhibitors affect the gut microbiome. <i>Gut</i> , 2016 , 65, 740-8	19.2	575
129	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019 , 4, 293-305	26.6	512
128	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016 , 167, 1125-1136	1136.4	497
127	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016 , 48, 1407-1412	36.3	434
126	The genetics of plant metabolism. <i>Nature Genetics</i> , 2006 , 38, 842-9	36.3	401
125	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. <i>Nature Genetics</i> , 2019 , 51, 600-605	36.3	378
124	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. <i>Circulation Research</i> , 2015 , 117, 817-24	15.7	368
123	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. <i>Gut</i> , 2018 , 67, 108-119	19.2	368
122	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
121	Regulatory network construction in Arabidopsis by using genome-wide gene expression quantitative trait loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 1708-13	11.5	269
120	Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. <i>PLoS Genetics</i> , 2011 , 7, e1002197	6	261
119	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010 , 42, 1068-76	36.3	249
118	Mapping determinants of gene expression plasticity by genetical genomics in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2006 , 2, e222	6	210
117	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. <i>PLoS Genetics</i> , 2013 , 9, e1003201	6	209

116	System-wide molecular evidence for phenotypic buffering in Arabidopsis. <i>Nature Genetics</i> , 2009 , 41, 1663-1667.	36.3	205
115	Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. <i>Nature Communications</i> , 2020 , 11, 362	17.4	188
114	Unraveling the regulatory mechanisms underlying tissue-dependent genetic variation of gene expression. <i>PLoS Genetics</i> , 2012 , 8, e1002431	6	163
113	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	159
112	Host Genetics and Gut Microbiome: Challenges and Perspectives. <i>Trends in Immunology</i> , 2017 , 38, 633-647.	14.4	149
111	Genetical genomics: spotlight on QTL hotspots. <i>PLoS Genetics</i> , 2008 , 4, e1000232	6	146
110	Interaction between drugs and the gut microbiome. <i>Gut</i> , 2020 , 69, 1510-1519	19.2	136
109	Structural variation in the gut microbiome associates with host health. <i>Nature</i> , 2019 , 568, 43-48	50.4	133
108	Analysis of HLA and non-HLA alleles can identify individuals at high risk for celiac disease. <i>Gastroenterology</i> , 2009 , 137, 834-40, 840.e1-3	13.3	103
107	A Proinflammatory Gut Microbiota Increases Systemic Inflammation and Accelerates Atherosclerosis. <i>Circulation Research</i> , 2019 , 124, 94-100	15.7	103
106	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019 , 4, 1727-1736	26.6	100
105	Role of gut microbiota in chronic low-grade inflammation as potential driver for atherosclerotic cardiovascular disease: a systematic review of human studies. <i>Obesity Reviews</i> , 2018 , 19, 1719-1734	10.6	98
104	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL, and CARD9. <i>Hepatology</i> , 2011 , 53, 1977-85	11.2	96
103	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. <i>BMC Genomics</i> , 2014 , 15, 860	4.5	90
102	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. <i>Gut Microbes</i> , 2017 , 8, 351-358	8.8	87
101	Analysis of SNPs with an effect on gene expression identifies UBE2L3 and BCL3 as potential new risk genes for Crohn's disease. <i>Human Molecular Genetics</i> , 2010 , 19, 3482-8	5.6	82
100	Integrative analyses of genetic variation in enzyme activities of primary carbohydrate metabolism reveal distinct modes of regulation in Arabidopsis thaliana. <i>Genome Biology</i> , 2008 , 9, R129	18.3	82
99	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81

98	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
97	Preparation of superhydrophobic/oleophilic copper mesh for oil-water separation. <i>Applied Surface Science</i> , 2017 , 412, 599-605	6.7	79
96	Are hypertriglyceridemia and low HDL causal factors in the development of insulin resistance?. <i>Atherosclerosis</i> , 2014 , 233, 130-8	3.1	78
95	Signal transduction of bone morphogenetic proteins in osteoblast differentiation. <i>Journal of Bone and Joint Surgery - Series A</i> , 2003 , 85-A Suppl 3, 34-8	5.6	78
94	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , 2019 , 124, 1808-1820	15.7	77
93	Intestinal microbiome composition and its relation to joint pain and inflammation. <i>Nature Communications</i> , 2019 , 10, 4881	17.4	73
92	Gut microbiota composition associated with stool consistency. <i>Gut</i> , 2016 , 65, 540-2	19.2	72
91	Shared gut, but distinct oral microbiota composition in primary Sjögren's syndrome and systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2019 , 97, 77-87	15.5	72
90	Pharmacomicrobiomics: a novel route towards personalized medicine?. <i>Protein and Cell</i> , 2018 , 9, 432-445	7.2	70
89	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019 , 10, 358-366	8.8	65
88	Relationship between gut microbiota and circulating metabolites in population-based cohorts. <i>Nature Communications</i> , 2019 , 10, 5813	17.4	63
87	Studying the gut virome in the metagenomic era: challenges and perspectives. <i>BMC Biology</i> , 2019 , 17, 84	7.3	62
86	A liver-specific long noncoding RNA with a role in cell viability is elevated in human nonalcoholic steatohepatitis. <i>Hepatology</i> , 2017 , 66, 794-808	11.2	61
85	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020 , 2, 1135-1148	14.6	61
84	Pleiotropic effects of lipid genes on plasma glucose, HbA1c, and HOMA-IR levels. <i>Diabetes</i> , 2014 , 63, 3149-58	0.9	54
83	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018 , 50, 1524-1532	36.3	54
82	Systems genetics: From GWAS to disease pathways. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014 , 1842, 1903-1909	6.9	53
81	Facile design of superhydrophobic and superoleophilic copper mesh assisted by candle soot for oil water separation. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2018 , 537, 294-302	5.1	51

80	Multi-ethnic studies in complex traits. <i>Human Molecular Genetics</i> , 2011 , 20, R206-13	5.6	51
79	Gut microbiome and lipid metabolism: from associations to mechanisms. <i>Current Opinion in Lipidology</i> , 2016 , 27, 216-24	4.4	51
78	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. <i>Biological Psychiatry</i> , 2020 , 87, 409-418	7.9	51
77	Common genetic variation near the phospholamban gene is associated with cardiac repolarisation: meta-analysis of three genome-wide association studies. <i>PLoS ONE</i> , 2009 , 4, e6138	3.7	50
76	Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Gut</i> , 2021 , 70, 1287-1298	19.2	50
75	Genetics of coronary artery disease: genome-wide association studies and beyond. <i>Atherosclerosis</i> , 2012 , 225, 1-10	3.1	48
74	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. <i>Genome Medicine</i> , 2015 , 7, 30	14.4	45
73	Understanding human immune function using the resources from the Human Functional Genomics Project. <i>Nature Medicine</i> , 2016 , 22, 831-3	50.5	43
72	Defining gene and QTL networks. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 241-6	9.9	40
71	The genome revolution and its role in understanding complex diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014 , 1842, 1889-1895	6.9	39
70	Plasma cholesteryl ester transfer protein is predominantly derived from Kupffer cells. <i>Hepatology</i> , 2015 , 62, 1710-22	11.2	37
69	Lactate Degradation Pattern Shifts in Rumen Acidosis Models. <i>Frontiers in Microbiology</i> , 2019 , 10, 162	5.7	37
68	The long-term genetic stability and individual specificity of the human gut microbiome. <i>Cell</i> , 2021 , 184, 2302-2315.e12	56.2	32
67	Lack of Association Between Genetic Variants at and Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. <i>Frontiers in Genetics</i> , 2020 , 11, 613	4.5	31
66	Dysbiosis of the buccal mucosa microbiome in primary Sjögren's syndrome patients. <i>Rheumatology</i> , 2018 , 57, 2225-2234	3.9	31
65	The immunity-diet-microbiota axis in the development of metabolic syndrome. <i>Current Opinion in Lipidology</i> , 2015 , 26, 73-81	4.4	30
64	Determining the association between adipokine expression in multiple tissues and phenotypic features of non-alcoholic fatty liver disease in obesity. <i>Nutrition and Diabetes</i> , 2015 , 5, e146	4.7	29
63	Optimal design and analysis of genetic studies on gene expression. <i>Genetics</i> , 2006 , 172, 1993-9	4	29

62	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018 , 6, e4303	3.1	28
61	Extraintestinal manifestations and complications in inflammatory bowel disease: from shared genetics to shared biological pathways. <i>Inflammatory Bowel Diseases</i> , 2014 , 20, 987-94	4.5	27
60	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. <i>Neurology</i> , 2019 , 92, e1899-e1911	6.5	26
59	MetaNetwork: a computational protocol for the genetic study of metabolic networks. <i>Nature Protocols</i> , 2007 , 2, 685-94	18.8	25
58	Gut microbial co-abundance networks show specificity in inflammatory bowel disease and obesity. <i>Nature Communications</i> , 2020 , 11, 4018	17.4	25
57	GWAS as a Driver of Gene Discovery in Cardiometabolic Diseases. <i>Trends in Endocrinology and Metabolism</i> , 2015 , 26, 722-732	8.8	24
56	A system biology perspective on environment-host-microbe interactions. <i>Human Molecular Genetics</i> , 2018 , 27, R187-R194	5.6	23
55	Anti-inflammatory Gut Microbial Pathways Are Decreased During Crohn's Disease Exacerbations. <i>Journal of Crohn's and Colitis</i> , 2019 , 13, 1439-1449	1.5	22
54	Genetic and Microbial Associations to Plasma and Fecal Bile Acids in Obesity Relate to Plasma Lipids and Liver Fat Content. <i>Cell Reports</i> , 2020 , 33, 108212	10.6	22
53	Apple or pear: size and shape matter. <i>Cell Metabolism</i> , 2015 , 21, 507-8	24.6	21
52	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug-metabolite atlas. <i>Nature Medicine</i> , 2020 , 26, 110-117	50.5	19
51	Environmental factors shaping the gut microbiome in a Dutch population.. <i>Nature</i> , 2022 ,	50.4	19
50	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. <i>PLoS ONE</i> , 2016 , 11, e0167519	3.7	18
49	Lipopolysaccharide Lowers Cholesteryl Ester Transfer Protein by Activating F4/80Clec4fVsig4Ly6C Kupffer Cell Subsets. <i>Journal of the American Heart Association</i> , 2018 , 7,	6	17
48	Correlation of genetic risk and messenger RNA expression in a Th17/IL23 pathway analysis in inflammatory bowel disease. <i>Inflammatory Bowel Diseases</i> , 2014 , 20, 777-82	4.5	16
47	Gut microbiome and bile acids in obesity-related diseases. <i>Best Practice and Research in Clinical Endocrinology and Metabolism</i> , 2021 , 35, 101493	6.5	14
46	ImmunoChip meta-analysis in European and Argentinian populations identifies two novel genetic loci associated with celiac disease. <i>European Journal of Human Genetics</i> , 2020 , 28, 313-323	5.3	14
45	A GWAS meta-analysis suggests roles for xenobiotic metabolism and ion channel activity in the biology of stool frequency. <i>Gut</i> , 2017 , 66, 756-758	19.2	12

44	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. <i>Hypertension</i> , 2020 , 76, 195-205	8.5	12
43	Association of Insulin Resistance and Type 2 Diabetes With Gut Microbial Diversity: A Microbiome-Wide Analysis From Population Studies. <i>JAMA Network Open</i> , 2021 , 4, e2118811	10.4	12
42	Cholangiopathy and Biliary Fibrosis in Cyp2c70-Deficient Mice Are Fully Reversed by Ursodeoxycholic Acid. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021 , 11, 1045-1069	7.9	11
41	Combining microarrays and genetic analysis. <i>Briefings in Bioinformatics</i> , 2005 , 6, 135-45	13.4	10
40	Limited evidence for parent-of-origin effects in inflammatory bowel disease associated loci. <i>PLoS ONE</i> , 2012 , 7, e45287	3.7	9
39	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
38	Whole exome sequencing analyses reveal gene-microbiota interactions in the context of IBD. <i>Gut</i> , 2021 , 70, 285-296	19.2	9
37	Healthy Cotwins Share Gut Microbiome Signatures With Their Inflammatory Bowel Disease Twins and Unrelated Patients. <i>Gastroenterology</i> , 2021 , 160, 1970-1985	13.3	8
36	Population-wide diversity and stability of serum antibody epitope repertoires against human microbiota. <i>Nature Medicine</i> , 2021 , 27, 1442-1450	50.5	8
35	SLC39A8 missense variant is associated with Crohn's disease but does not have a major impact on gut microbiome composition in healthy subjects. <i>PLoS ONE</i> , 2019 , 14, e0211328	3.7	7
34	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project.. <i>Nature Genetics</i> , 2022 , 54, 143-151	36.3	7
33	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. <i>BMC Bioinformatics</i> , 2009 , 10, 188	3.6	6
32	Challenges and future directions for studying effects of host genetics on the gut microbiome.. <i>Nature Genetics</i> , 2022 , 54, 100-106	36.3	6
31	Characterization of gut microbial structural variations as determinants of human bile acid metabolism. <i>Cell Host and Microbe</i> , 2021 , 29, 1802-1814.e5	23.4	6
30	The Dutch Microbiome Project defines factors that shape the healthy gut microbiome		6
29	Oral Microbiome in Relation to Periodontitis Severity and Systemic Inflammation. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	6
28	The Composition and Metabolic Potential of the Human Small Intestinal Microbiota Within the Context of Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2021 , 15, 1326-1338	1.5	6
27	Genomic evaluation of circulating proteins for drug target characterisation and precision medicine		5

26	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage		5
25	How government regulation of interbank financing impacts risk for Chinese commercial banks. <i>Journal of Asian Economics</i> , 2020 , 66, 101148	2.2	5
24	A systematic analysis of metabolic pathways in the human gut microbiota		5
23	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021 , 35, 109132	10.6	4
22	A Benchmark of Genetic Variant Calling Pipelines Using Metagenomic Short-Read Sequencing. <i>Frontiers in Genetics</i> , 2021 , 12, 648229	4.5	4
21	Optimal design of genetic studies of gene expression with two-color microarrays in outbred crosses. <i>Genetics</i> , 2008 , 180, 1691-8	4	3
20	Discovery, diversity, and functional associations of crAss-like phages in human gut metagenomes from four Dutch cohorts.. <i>Cell Reports</i> , 2022 , 38, 110204	10.6	3
19	Lack of association between genetic variants at ACE2 and TMPRSS2 genes involved in SARS-CoV-2 infection and human quantitative phenotypes		3
18	A cross-omics integrative study of metabolic signatures of chronic obstructive pulmonary disease. <i>BMC Pulmonary Medicine</i> , 2020 , 20, 193	3.5	3
17	Role of the gut microbiome in mediating lactose intolerance symptoms. <i>Gut</i> , 2022 , 71, 215-217	19.2	3
16	Long Non-Coding RNAs Involved in Progression of Non-Alcoholic Fatty Liver Disease to Steatohepatitis. <i>Cells</i> , 2021 , 10,	7.9	3
15	Systems genetics approach reveals cross-talk between bile acids and intestinal microbes. <i>PLoS Genetics</i> , 2019 , 15, e1008307	6	2
14	Hematopoietic Npc1 mutation shifts gut microbiota composition in Ldlr mice on a high-fat, high-cholesterol diet. <i>Scientific Reports</i> , 2019 , 9, 14956	4.9	2
13	Low production of 12hydroxylated bile acids prevents hepatic steatosis in Cyp2c70 mice by reducing fat absorption. <i>Journal of Lipid Research</i> , 2021 , 100134	6.3	2
12	Patient attitudes towards faecal sampling for gut microbiome studies and clinical care reveal positive engagement and room for improvement. <i>PLoS ONE</i> , 2021 , 16, e0249405	3.7	2
11	Is gut microbiota a relevant and competitive dietary target for cardio-metabolic health? Proceedings of an expert workshop. <i>Trends in Food Science and Technology</i> , 2018 , 81, 146-154	15.3	2
10	Inflammatory Protein Profiles in Plasma of Candidaemia Patients and the Contribution of Host Genetics to Their Variability. <i>Frontiers in Immunology</i> , 2021 , 12, 662171	8.4	2
9	A combination of fecal calprotectin and human beta-defensin 2 facilitates diagnosis and monitoring of inflammatory bowel disease. <i>Gut Microbes</i> , 2021 , 13, 1943288	8.8	2

8	Large HDL particles negatively associate with leukocyte counts independent of cholesterol efflux capacity: A cross sectional study in the population-based LifeLines DEEP cohort.. <i>Atherosclerosis</i> , 2022 , 343, 20-27	3.1	1
7	The role of the gut microbiome in graft fibrosis after pediatric liver transplantation. <i>Human Genetics</i> , 2021 , 140, 709-724	6.3	1
6	OP29 Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Journal of Crohns and Colitis</i> , 2021 , 15, S028-S029	1.5	0
5	OP01 In-depth characterisation of host genetics and gut microbiome unravels novel host-microbiome interactions in inflammatory bowel disease. <i>Journal of Crohns and Colitis</i> , 2019 , 13, S001-S001	1.5	
4	OP014 Analysis of 1792 gut metagenomes reveals microbial treatment targets for inflammatory bowel disease and irritable bowel syndrome. <i>Journal of Crohns and Colitis</i> , 2018 , 12, S010-S010	1.5	
3	PS13 - 7. Plasma cholesteryl ester transfer protein: a biomarker for hepatic macrophages. <i>Nederlands Tijdschrift Voor Diabetologie</i> , 2013 , 11, 195-195	0	
2	PS4 - 19. Expression of lipid genes, but not adipokine genes, in visceral adipose tissue is related to liver damage in obese individuals. <i>Nederlands Tijdschrift Voor Diabetologie</i> , 2011 , 9, 103-103	0	
1	P006 Host-genetics, dysbiosis, and clinical history explains fecal metabolic alterations in patients with Inflammatory Bowel Disease. <i>Journal of Crohns and Colitis</i> , 2021 , 15, S128-S128	1.5	