

Jingyuan Fu

List of Publications by Year in descending order

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Version: 2024-02-01

142
papers

22,698
citations

19636

61
h-index

13365

130
g-index

166
all docs

166
docs citations

166
times ranked

30100
citing authors

#	ARTICLE	IF	CITATIONS
1	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018, 555, 210-215.	13.7	1,958
2	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	6.0	1,716
3	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398
4	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	5.9	1,094
5	Proton pump inhibitors affect the gut microbiome. <i>Gut</i> , 2016, 65, 740-748.	6.1	885
6	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. <i>Nature Genetics</i> , 2019, 51, 600-605.	9.4	854
7	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	13.5	806
8	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
9	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016, 48, 1407-1412.	9.4	672
10	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. <i>Gut</i> , 2018, 67, 108-119.	6.1	590
11	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. <i>Circulation Research</i> , 2015, 117, 817-824.	2.0	534
12	The genetics of plant metabolism. <i>Nature Genetics</i> , 2006, 38, 842-849.	9.4	454
13	Interaction between drugs and the gut microbiome. <i>Gut</i> , 2020, 69, 1510-1519.	6.1	451
14	Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. <i>Nature Communications</i> , 2020, 11, 362.	5.8	416
15	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
16	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	351
17	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, 1708-1713.	3.3	329
18	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327

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19	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.	1.5	324
20	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010, 42, 1068-1076.	9.4	308
21	Mapping Determinants of Gene Expression Plasticity by Genetical Genomics in <i>C. elegans</i> . <i>PLoS Genetics</i> , 2006, 2, e222.	1.5	269
22	System-wide molecular evidence for phenotypic buffering in <i>Arabidopsis</i> . <i>Nature Genetics</i> , 2009, 41, 166-167.	9.4	249
23	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. <i>PLoS Genetics</i> , 2013, 9, e1003201.	1.5	247
24	Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Gut</i> , 2021, 70, 1287-1298.	6.1	246
25	Structural variation in the gut microbiome associates with host health. <i>Nature</i> , 2019, 568, 43-48.	13.7	244
26	Environmental factors shaping the gut microbiome in a Dutch population. <i>Nature</i> , 2022, 604, 732-739.	13.7	239
27	A Proinflammatory Gut Microbiota Increases Systemic Inflammation and Accelerates Atherosclerosis. <i>Circulation Research</i> , 2019, 124, 94-100.	2.0	226
28	Host Genetics and Gut Microbiome: Challenges and Perspectives. <i>Trends in Immunology</i> , 2017, 38, 633-647.	2.9	219
29	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. <i>PLoS Genetics</i> , 2012, 8, e1002431.	1.5	194
30	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
31	Intestinal microbiome composition and its relation to joint pain and inflammation. <i>Nature Communications</i> , 2019, 10, 4881.	5.8	176
32	Genetical Genomics: Spotlight on QTL Hotspots. <i>PLoS Genetics</i> , 2008, 4, e1000232.	1.5	172
33	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.	3.1	169
34	Relationship between gut microbiota and circulating metabolites in population-based cohorts. <i>Nature Communications</i> , 2019, 10, 5813.	5.8	168
35	The long-term genetic stability and individual specificity of the human gut microbiome. <i>Cell</i> , 2021, 184, 2302-2315.e12.	13.5	166
36	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.	3.0	147

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37	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , 2019, 124, 1808-1820.	2.0	137
38	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. <i>Gut Microbes</i> , 2017, 8, 351-358.	4.3	136
39	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.	9.4	132
40	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.	0.7	129
41	Pharmacomicrobiomics: a novel route towards personalized medicine?. <i>Protein and Cell</i> , 2018, 9, 432-445.	4.8	128
42	Analysis of HLA and Non-HLA Alleles Can Identify Individuals at High Risk for Celiac Disease. <i>Gastroenterology</i> , 2009, 137, 834-840.e3.	0.6	126
43	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. <i>BMC Genomics</i> , 2014, 15, 860.	1.2	124
44	Association of Insulin Resistance and Type 2 Diabetes With Gut Microbial Diversity. <i>JAMA Network Open</i> , 2021, 4, e2118811.	2.8	119
45	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019, 10, 358-366.	4.3	118
46	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	1.5	115
47	Are hypertriglyceridemia and low HDL causal factors in the development of insulin resistance?. <i>Atherosclerosis</i> , 2014, 233, 130-138.	0.4	114
48	Studying the gut virome in the metagenomic era: challenges and perspectives. <i>BMC Biology</i> , 2019, 17, 84.	1.7	113
49	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for <i>IL2</i> , <i>REL</i> , and <i>CARD9</i> . <i>Hepatology</i> , 2011, 53, 1977-1985.	3.6	110
50	Preparation of superhydrophobic/oleophilic copper mesh for oil-water separation. <i>Applied Surface Science</i> , 2017, 412, 599-605.	3.1	106
51	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	9.4	97
52	Gut microbiota composition associated with stool consistency. <i>Gut</i> , 2016, 65, 540-542.	6.1	95
53	Analysis of SNPs with an effect on gene expression identifies <i>UBE2L3</i> and <i>BCL3</i> as potential new risk genes for Crohn's disease. <i>Human Molecular Genetics</i> , 2010, 19, 3482-3488.	1.4	92
54	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. <i>Genome Medicine</i> , 2015, 7, 30.	3.6	91

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55	Megasphaera elsdenii Lactate Degradation Pattern Shifts in Rumen Acidosis Models. <i>Frontiers in Microbiology</i> , 2019, 10, 162.	1.5	91
56	Integrative analyses of genetic variation in enzyme activities of primary carbohydrate metabolism reveal distinct modes of regulation in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008, 9, R129.	13.9	90
57	SIGNAL TRANSDUCTION OF BONE MORPHOGENETIC PROTEINS IN OSTEOBLAST DIFFERENTIATION. <i>Journal of Bone and Joint Surgery - Series A</i> , 2003, 85, 34-38.	1.4	90
58	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.	3.6	80
59	Gut microbial co-abundance networks show specificity in inflammatory bowel disease and obesity. <i>Nature Communications</i> , 2020, 11, 4018.	5.8	80
60	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.	2.3	79
61	Gut microbiome and lipid metabolism. <i>Current Opinion in Lipidology</i> , 2016, 27, 216-224.	1.2	72
62	Systems genetics: From GWAS to disease pathways. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014, 1842, 1903-1909.	1.8	67
63	Multi-ethnic studies in complex traits. <i>Human Molecular Genetics</i> , 2011, 20, R206-R213.	1.4	64
64	Understanding human immune function using the resources from the Human Functional Genomics Project. <i>Nature Medicine</i> , 2016, 22, 831-833.	15.2	63
65	Pleiotropic Effects of Lipid Genes on Plasma Glucose, HbA1c, and HOMA-IR Levels. <i>Diabetes</i> , 2014, 63, 3149-3158.	0.3	61
66	Plasma cholesteryl ester transfer protein is predominantly derived from Kupffer cells. <i>Hepatology</i> , 2015, 62, 1710-1722.	3.6	60
67	Genetics of coronary artery disease: Genome-wide association studies and beyond. <i>Atherosclerosis</i> , 2012, 225, 1-10.	0.4	59
68	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.	2.9	55
69	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug-metabolite atlas. <i>Nature Medicine</i> , 2020, 26, 110-117.	15.2	54
70	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.	1.1	53
71	Gut microbiome and bile acids in obesity-related diseases. <i>Best Practice and Research in Clinical Endocrinology and Metabolism</i> , 2021, 35, 101493.	2.2	52
72	The genome revolution and its role in understanding complex diseases. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014, 1842, 1889-1895.	1.8	48

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73	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	0.9	48
74	Dysbiosis of the buccal mucosa microbiome in primary Sjögren's syndrome patients. <i>Rheumatology</i> , 2018, 57, 2225-2234.	0.9	47
75	Defining gene and QTL networks. <i>Current Opinion in Plant Biology</i> , 2009, 12, 241-246.	3.5	46
76	Challenges and future directions for studying effects of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2022, 54, 100-106.	9.4	46
77	Lack of Association Between Genetic Variants at ACE2 and TMPRSS2 Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. <i>Frontiers in Genetics</i> , 2020, 11, 613.	1.1	45
78	Characterization of gut microbial structural variations as determinants of human bile acid metabolism. <i>Cell Host and Microbe</i> , 2021, 29, 1802-1814.e5.	5.1	43
79	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. <i>Neurology</i> , 2019, 92, e1899-e1911.	1.5	42
80	The immunity-diet-microbiota axis in the development of metabolic syndrome. <i>Current Opinion in Lipidology</i> , 2015, 26, 73-81.	1.2	41
81	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-e146.	1.5	40
82	Anti-inflammatory Gut Microbial Pathways Are Decreased During Crohn's Disease Exacerbations. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 1439-1449.	0.6	39
83	Oral Microbiome in Relation to Periodontitis Severity and Systemic Inflammation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5876.	1.8	38
84	Population-wide diversity and stability of serum antibody epitope repertoires against human microbiota. <i>Nature Medicine</i> , 2021, 27, 1442-1450.	15.2	38
85	A system biology perspective on environmental-host-microbe interactions. <i>Human Molecular Genetics</i> , 2018, 27, R187-R194.	1.4	37
86	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021, 35, 109132.	2.9	34
87	Identification, Heritability, and Relation With Gene Expression of Novel DNA Methylation Loci for Blood Pressure. <i>Hypertension</i> , 2020, 76, 195-205.	1.3	33
88	Optimal Design and Analysis of Genetic Studies on Gene Expression. <i>Genetics</i> , 2006, 172, 1993-1999.	1.2	32
89	Extraintestinal Manifestations and Complications in Inflammatory Bowel Disease. <i>Inflammatory Bowel Diseases</i> , 2014, 20, 1.	0.9	31
90	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.	2.3	31

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91	Healthy Cotwins Share Gut Microbiome Signatures With Their Inflammatory Bowel Disease Twins and Unrelated Patients. <i>Gastroenterology</i> , 2021, 160, 1970-1985.	0.6	31
92	MetaNetwork: a computational protocol for the genetic study of metabolic networks. <i>Nature Protocols</i> , 2007, 2, 685-694.	5.5	30
93	Discovery, diversity, and functional associations of crAss-like phages in human gut metagenomes from four Dutch cohorts. <i>Cell Reports</i> , 2022, 38, 110204.	2.9	30
94	GWAS as a Driver of Gene Discovery in Cardiometabolic Diseases. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 722-732.	3.1	29
95	Apple or Pear: Size and Shape Matter. <i>Cell Metabolism</i> , 2015, 21, 507-508.	7.2	29
96	Lipopolysaccharide Lowers Cholesteryl Ester Transfer Protein by Activating F4/80 ⁺ Clec4f ⁺ Vsig4 ⁺ Ly6C ^{hi} Kupffer Cell Subsets. <i>Journal of the American Heart Association</i> , 2018, 7, .	1.6	27
97	Whole exome sequencing analyses reveal gene-microbiota interactions in the context of IBD. <i>Gut</i> , 2021, 70, gutjnl-2019-319706.	6.1	26
98	Genetic, parental and lifestyle factors influence telomere length. <i>Communications Biology</i> , 2022, 5, .	2.0	23
99	Inter-Tissue Gene Co-Expression Networks between Metabolically Healthy and Unhealthy Obese Individuals. <i>PLoS ONE</i> , 2016, 11, e0167519.	1.1	21
100	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.	1.4	21
101	The Gut Microbiome Composition Is Altered in Long-standing Type 1 Diabetes and Associates With Glycemic Control and Disease-Related Complications. <i>Diabetes Care</i> , 2022, 45, 2084-2094.	4.3	21
102	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, 777-782.	0.9	20
103	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.	0.6	18
104	Role of the gut microbiome in mediating lactose intolerance symptoms. <i>Gut</i> , 2022, 71, 215-217.	6.1	18
105	A cross-omics integrative study of metabolic signatures of chronic obstructive pulmonary disease. <i>BMC Pulmonary Medicine</i> , 2020, 20, 193.	0.8	15
106	A Benchmark of Genetic Variant Calling Pipelines Using Metagenomic Short-Read Sequencing. <i>Frontiers in Genetics</i> , 2021, 12, 648229.	1.1	15
107	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.	6.1	14
108	Long Non-Coding RNAs Involved in Progression of Non-Alcoholic Fatty Liver Disease to Steatohepatitis. <i>Cells</i> , 2021, 10, 1883.	1.8	14

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109	iMeta: Integrated meta-omics for biology and environments. , 2022, 1, .		13
110	Combining microarrays and genetic analysis. Briefings in Bioinformatics, 2005, 6, 135-145.	3.2	12
111	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. BMC Bioinformatics, 2009, 10, 188.	1.2	10
112	Limited Evidence for Parent-of-Origin Effects in Inflammatory Bowel Disease Associated Loci. PLoS ONE, 2012, 7, e45287.	1.1	10
113	SLC39A8 missense variant is associated with Crohn's disease but does not have a major impact on gut microbiome composition in healthy subjects. PLoS ONE, 2019, 14, e0211328.	1.1	10
114	How government regulation of interbank financing impacts risk for Chinese commercial banks. Journal of Asian Economics, 2020, 66, 101148.	1.2	10
115	Low production of 12 α -hydroxylated bile acids prevents hepatic steatosis in Cyp2c70 $^{-/-}$ mice by reducing fat absorption. Journal of Lipid Research, 2021, 62, 100134.	2.0	9
116	The role of the gut microbiome in graft fibrosis after pediatric liver transplantation. Human Genetics, 2021, 140, 709-724.	1.8	8
117	Inflammatory Protein Profiles in Plasma of Candidaemia Patients and the Contribution of Host Genetics to Their Variability. Frontiers in Immunology, 2021, 12, 662171.	2.2	6
118	Is gut microbiota a relevant and competitive dietary target for cardio-metabolic health? Proceedings of an expert workshop. Trends in Food Science and Technology, 2018, 81, 146-154.	7.8	4
119	Patient attitudes towards faecal sampling for gut microbiome studies and clinical care reveal positive engagement and room for improvement. PLoS ONE, 2021, 16, e0249405.	1.1	4
120	A combination of fecal calprotectin and human beta-defensin 2 facilitates diagnosis and monitoring of inflammatory bowel disease. Gut Microbes, 2021, 13, 1943288.	4.3	4
121	Optimal Design of Genetic Studies of Gene Expression With Two-Color Microarrays in Outbred Crosses. Genetics, 2008, 180, 1691-1698.	1.2	3
122	Hematopoietic Npc1 mutation shifts gut microbiota composition in Ldlr $^{-/-}$ mice on a high-fat, high-cholesterol diet. Scientific Reports, 2019, 9, 14956.	1.6	3
123	Systems genetics approach reveals cross-talk between bile acids and intestinal microbes. PLoS Genetics, 2019, 15, e1008307.	1.5	3
124	Microbial Impact on Plasma Metabolites is Linked to the Cardiovascular Risk and Phenotypes. Atherosclerosis Supplements, 2018, 32, 118-119.	1.2	2
125	The Long-Term Genetic Stability and Individual Specificity of the Human Gut Microbiome. SSRN Electronic Journal, 0, , .	0.4	2
126	Large HDL particles negatively associate with leukocyte counts independent of cholesterol efflux capacity: A cross sectional study in the population-based LifeLines DEEP cohort. Atherosclerosis, 2022, 343, 20-27.	0.4	2

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127	87 Gene-Microbiome Interactions Underlying the Onset and the Clinical Phenotypes of Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2016, 150, S22.	0.6	1
128	OP014 Analysis of 1792 gut metagenomes reveals microbial treatment targets for inflammatory bowel disease and irritable bowel syndrome. <i>Journal of Crohn's and Colitis</i> , 2018, 12, S010-S010.	0.6	1
129	Omeprazole-Induced Dysbiosis Impacts Bile Acid Metabolism In Mice And Humans. <i>Atherosclerosis</i> , 2019, 287, e120.	0.4	1
130	OP29 Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Journal of Crohn's and Colitis</i> , 2021, 15, S028-S029.	0.6	1
131	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.	0.0	0
132	PS13 - 7. Plasma cholesteryl ester transfer protein: a biomarker for hepatic macrophages. <i>Nederlands Tijdschrift Voor Diabetologie</i> , 2013, 11, 195-195.	0.0	0
133	Plasma CETP is derived from hepatic kupffer cells rather than adipose tissue. <i>Atherosclerosis</i> , 2016, 252, e244.	0.4	0
134	P102 Increased abundance of gut microbial virulence genes and pro-inflammatory pathways during Crohn's disease exacerbations. <i>Journal of Crohn's and Colitis</i> , 2018, 12, S145-S145.	0.6	0
135	149 " In-Depth Characterization of Host-Genetics and Gut Microbiome Unravels Novel Host-Microbiome Interactions in Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2019, 156, S-34.	0.6	0
136	OP01 In-depth characterisation of host genetics and gut microbiome unravels novel host-microbiome interactions in inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , 2019, 13, S001-S001.	0.6	0
137	Gut microbiome composition and its relation to joint pain and inflammation. <i>Osteoarthritis and Cartilage</i> , 2019, 27, S26.	0.6	0
138	Gut Microbial Structural Variations as Determinants of Human Bile Acid Metabolism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
139	Gut Microbial Structural Variations as Determinants of Human Bile Acid Metabolism. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
140	P006 Host-genetics, dysbiosis, and clinical history explains fecal metabolic alterations in patients with Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2021, 15, S128-S128.	0.6	0
141	The non-coding genome in cancer. <i>Non-coding RNA Investigation</i> , 0, 2, 4-4.	0.6	0
142	Stability of the Human Gut Virome and Effect of Gluten-Free Diet. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0