

Peter J Turnbaugh

List of Publications by Citations

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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.

121
papers

86,333
citations

52
h-index

156
g-index

156
ext. papers

110,031
ext. citations

21
avg, IF

7.79
L-index

#	Paper	IF	Citations
121	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21.6	22879
120	An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> , 2006 , 444, 1027-31	50.4	7807
119	Microbial ecology: human gut microbes associated with obesity. <i>Nature</i> , 2006 , 444, 1022-3	50.4	5833
118	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009 , 457, 480-4	50.4	5429
117	Diet rapidly and reproducibly alters the human gut microbiome. <i>Nature</i> , 2014 , 505, 559-63	50.4	5264
116	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4516-22	11.5	4742
115	Obesity alters gut microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 11070-5	11.5	4146
114	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
113	The human microbiome project. <i>Nature</i> , 2007 , 449, 804-10	50.4	3576
112	Metagenomic analysis of the human distal gut microbiome. <i>Science</i> , 2006 , 312, 1355-9	33.3	3163
111	Evolution of mammals and their gut microbes. <i>Science</i> , 2008 , 320, 1647-51	33.3	2355
110	Diet-induced obesity is linked to marked but reversible alterations in the mouse distal gut microbiome. <i>Cell Host and Microbe</i> , 2008 , 3, 213-23	23.4	2003
109	The effect of diet on the human gut microbiome: a metagenomic analysis in humanized gnotobiotic mice. <i>Science Translational Medicine</i> , 2009 , 1, 6ra14	17.5	1977
108	Detecting novel associations in large data sets. <i>Science</i> , 2011 , 334, 1518-24	33.3	1464
107	Removing noise from pyrosequenced amplicons. <i>BMC Bioinformatics</i> , 2011 , 12, 38	3.6	1088
106	Energy-balance studies reveal associations between gut microbes, caloric load, and nutrient absorption in humans. <i>American Journal of Clinical Nutrition</i> , 2011 , 94, 58-65	7	755
105	Conserved shifts in the gut microbiota due to gastric bypass reduce host weight and adiposity. <i>Science Translational Medicine</i> , 2013 , 5, 178ra41	17.5	686

104	The core gut microbiome, energy balance and obesity. <i>Journal of Physiology</i> , 2009 , 587, 4153-8	3.9	673
103	Diet dominates host genotype in shaping the murine gut microbiota. <i>Cell Host and Microbe</i> , 2015 , 17, 72-84	23.4	658
102	Metagenomic systems biology of the human gut microbiome reveals topological shifts associated with obesity and inflammatory bowel disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 594-9	11.5	592
101	Xenobiotics shape the physiology and gene expression of the active human gut microbiome. <i>Cell</i> , 2013 , 152, 39-50	56.2	560
100	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 5859-64	11.5	478
99	Dietary Polyphenols Promote Growth of the Gut Bacterium <i>Akkermansia muciniphila</i> and Attenuate High-Fat Diet-Induced Metabolic Syndrome. <i>Diabetes</i> , 2015 , 64, 2847-58	0.9	393
98	The microbial pharmacists within us: a metagenomic view of xenobiotic metabolism. <i>Nature Reviews Microbiology</i> , 2016 , 14, 273-87	22.2	382
97	Predicting and manipulating cardiac drug inactivation by the human gut bacterium <i>Eggerthella lenta</i> . <i>Science</i> , 2013 , 341, 295-8	33.3	368
96	Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7503-8	11.5	364
95	Rapid fucosylation of intestinal epithelium sustains host-commensal symbiosis in sickness. <i>Nature</i> , 2014 , 514, 638-41	50.4	343
94	Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. <i>Science</i> , 2019 , 364,	33.3	217
93	An invitation to the marriage of metagenomics and metabolomics. <i>Cell</i> , 2008 , 134, 708-13	56.2	194
92	A Metabolite-Triggered Tuft Cell-ILC2 Circuit Drives Small Intestinal Remodeling. <i>Cell</i> , 2018 , 174, 271-284	6.14	189
91	Marked seasonal variation in the wild mouse gut microbiota. <i>ISME Journal</i> , 2015 , 9, 2423-34	11.9	173
90	Host-microbial interactions in the metabolism of therapeutic and diet-derived xenobiotics. <i>Journal of Clinical Investigation</i> , 2014 , 124, 4173-81	15.9	170
89	The intestinal metabolome: an intersection between microbiota and host. <i>Gastroenterology</i> , 2014 , 146, 1470-6	13.3	165
88	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011 , 8, 191-2	21.6	161
87	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138

86	Functional characterization of bacteria isolated from ancient arctic soil exposes diverse resistance mechanisms to modern antibiotics. <i>PLoS ONE</i> , 2015 , 10, e0069533	3.7	128
85	Ketogenic Diets Alter the Gut Microbiome Resulting in Decreased Intestinal Th17 Cells. <i>Cell</i> , 2020 , 181, 1263-1275.e16	56.2	126
84	Developing a metagenomic view of xenobiotic metabolism. <i>Pharmacological Research</i> , 2013 , 69, 21-31	10.2	123
83	Characterization and detection of a widely distributed gene cluster that predicts anaerobic choline utilization by human gut bacteria. <i>MBio</i> , 2015 , 6,	7.8	114
82	Gut microbial succession follows acute secretory diarrhea in humans. <i>MBio</i> , 2015 , 6, e00381-15	7.8	104
81	Is it time for a metagenomic basis of therapeutics?. <i>Science</i> , 2012 , 336, 1253-5	33.3	99
80	Mechanistic insight into digoxin inactivation by <i>Eggerthella lenta</i> augments our understanding of its pharmacokinetics. <i>Gut Microbes</i> , 2014 , 5, 233-8	8.8	97
79	Meta-Analysis Reveals Reproducible Gut Microbiome Alterations in Response to a High-Fat Diet. <i>Cell Host and Microbe</i> , 2019 , 26, 265-272.e4	23.4	92
78	Combining 16S rRNA gene variable regions enables high-resolution microbial community profiling. <i>Microbiome</i> , 2018 , 6, 17	16.6	91
77	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019 , 4, 693-700	26.6	89
76	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008 , 12, 109-14	9.7	87
75	The mind-body-microbial continuum. <i>Dialogues in Clinical Neuroscience</i> , 2011 , 13, 55-62	5.7	85
74	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
73	Cooking shapes the structure and function of the gut microbiome. <i>Nature Microbiology</i> , 2019 , 4, 2052-2066	26.6	66
72	Discovery and characterization of a prevalent human gut bacterial enzyme sufficient for the inactivation of a family of plant toxins. <i>ELife</i> , 2018 , 7,	8.9	60
71	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016 , 1,	7.6	55
70	Precision Medicine Goes Microscopic: Engineering the Microbiome to Improve Drug Outcomes. <i>Cell Host and Microbe</i> , 2019 , 26, 22-34	23.4	50
69	Companion animals symposium: humanized animal models of the microbiome. <i>Journal of Animal Science</i> , 2011 , 89, 1531-7	0.7	50

68	Gut microbiota-specific IgA B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020 , 5,	28	48
67	Microbes and Diet-Induced Obesity: Fast, Cheap, and Out of Control. <i>Cell Host and Microbe</i> , 2017 , 21, 278-281	23.4	46
66	Microbial determinants of biochemical individuality and their impact on toxicology and pharmacology. <i>Cell Metabolism</i> , 2014 , 20, 761-768	24.6	43
65	Taking a metagenomic view of human nutrition. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2012 , 15, 448-54	3.8	43
64	Grape proanthocyanidin-induced intestinal bloom of <i>Akkermansia muciniphila</i> is dependent on its baseline abundance and precedes activation of host genes related to metabolic health. <i>Journal of Nutritional Biochemistry</i> , 2018 , 56, 142-151	6.3	41
63	High-resolution microbial community reconstruction by integrating short reads from multiple 16S rRNA regions. <i>Nucleic Acids Research</i> , 2013 , 41, e205	20.1	40
62	Pathways and mechanisms linking dietary components to cardiometabolic disease: thinking beyond calories. <i>Obesity Reviews</i> , 2018 , 19, 1205-1235	10.6	37
61	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
60	Pharmacomicrobiomics in inflammatory arthritis: gut microbiome as modulator of therapeutic response. <i>Nature Reviews Rheumatology</i> , 2020 , 16, 282-292	8.1	35
59	Effects of underfeeding and oral vancomycin on gut microbiome and nutrient absorption in humans. <i>Nature Medicine</i> , 2020 , 26, 589-598	50.5	34
58	Caloric restriction disrupts the microbiota and colonization resistance. <i>Nature</i> , 2021 , 595, 272-277	50.4	32
57	Non-catalytic ubiquitin binding by A20 prevents psoriatic arthritis-like disease and inflammation. <i>Nature Immunology</i> , 2020 , 21, 422-433	19.1	31
56	Microbiology: fat, bile and gut microbes. <i>Nature</i> , 2012 , 487, 47-8	50.4	29
55	Genetic basis for the cooperative bioactivation of plant lignans by <i>Eggerthella lenta</i> and other human gut bacteria. <i>Nature Microbiology</i> , 2020 , 5, 56-66	26.6	29
54	Dissecting the contribution of host genetics and the microbiome in complex behaviors. <i>Cell</i> , 2021 , 184, 1740-1756.e16	56.2	28
53	The Pretreatment Gut Microbiome Is Associated With Lack of Response to Methotrexate in New-Onset Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2021 , 73, 931-942	9.5	28
52	CRISPR-Cas System of a Prevalent Human Gut Bacterium Reveals Hyper-targeting against Phages in a Human Virome Catalog. <i>Cell Host and Microbe</i> , 2019 , 26, 325-335.e5	23.4	25
51	Translating the human microbiome. <i>Nature Biotechnology</i> , 2013 , 31, 304-8	44.5	25

50	Deconstructing Mechanisms of Diet-Microbiome-Immune Interactions. <i>Immunity</i> , 2020 , 53, 264-276	32.3	24
49	Methotrexate impacts conserved pathways in diverse human gut bacteria leading to decreased host immune activation. <i>Cell Host and Microbe</i> , 2021 , 29, 362-377.e11	23.4	24
48	Viewing the human microbiome through three-dimensional glasses: integrating structural and functional studies to better define the properties of myriad carbohydrate-active enzymes. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1261-4		23
47	Discovery, validation, and genetic dissection of transcription factor binding sites by comparative and functional genomics. <i>Genome Research</i> , 2005 , 15, 1145-52	9.7	23
46	How to Determine the Role of the Microbiome in Drug Disposition. <i>Drug Metabolism and Disposition</i> , 2018 , 46, 1588-1595	4	21
45	Human gut bacteria produce γ -modulating bile acid metabolites.. <i>Nature</i> , 2022 ,	50.4	20
44	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
43	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014 , 2,	16.6	18
42	Regulation of drug metabolism and toxicity by multiple factors of genetics, epigenetics, lncRNAs, gut microbiota, and diseases: a meeting report of the 21 International Symposium on Microsomes and Drug Oxidations (MDO). <i>Acta Pharmaceutica Sinica B</i> , 2017 , 7, 241-248	15.5	17
41	Nutrient Sensing in CD11c Cells Alters the Gut Microbiota to Regulate Food Intake and Body Mass. <i>Cell Metabolism</i> , 2019 , 30, 364-373.e7	24.6	17
40	Quantifying the metabolic activities of human-associated microbial communities across multiple ecological scales. <i>FEMS Microbiology Reviews</i> , 2013 , 37, 830-48	15.1	17
39	A Genomic Toolkit for the Mechanistic Dissection of Intractable Human Gut Bacteria. <i>Cell Host and Microbe</i> , 2020 , 27, 1001-1013.e9	23.4	16
38	Functional genetics of human gut commensal <i>Bacteroides thetaiotaomicron</i> reveals metabolic requirements for growth across environments. <i>Cell Reports</i> , 2021 , 34, 108789	10.6	16
37	Bacterial metabolism rescues the inhibition of intestinal drug absorption by food and drug additives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16009-16018	11.5	15
36	Sensing Living Bacteria Using d-Alanine-Derived C Radiotracers. <i>ACS Central Science</i> , 2020 , 6, 155-165	16.8	15
35	Investigating Ketone Bodies as Immunometabolic Countermeasures against Respiratory Viral Infections. <i>Med</i> , 2020 , 1, 43-65	31.7	15
34	Gut microbes make for fattier fish. <i>Cell Host and Microbe</i> , 2012 , 12, 259-61	23.4	14
33	Phage-delivered CRISPR-Cas9 for strain-specific depletion and genomic deletions in the gut microbiome. <i>Cell Reports</i> , 2021 , 37, 109930	10.6	14

32	A widely distributed metalloenzyme class enables gut microbial metabolism of host- and diet-derived catechols. <i>ELife</i> , 2020 , 9,	8.9	14
31	Human health and disease in a microbial world. <i>Frontiers in Microbiology</i> , 2011 , 2, 190	5.7	11
30	Broad collateral damage of drugs against the gut microbiome. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 457-458	24.2	10
29	Human gut bacterial metabolism drives Th17 activation and colitis. <i>Cell Host and Microbe</i> , 2021 ,	23.4	9
28	Siri, What Should I Eat?. <i>Cell</i> , 2015 , 163, 1051-1052	56.2	8
27	Probing the tumor micro(b)environment. <i>Science</i> , 2020 , 368, 938-939	33.3	8
26	Quantifying and identifying the active and damaged subsets of indigenous microbial communities. <i>Methods in Enzymology</i> , 2013 , 531, 91-107	1.7	8
25	Antibiotic exposure promotes fat gain. <i>Cell Metabolism</i> , 2012 , 16, 408-10	24.6	8
24	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		8
23	Illuminating the microbiome's dark matter: a functional genomic toolkit for the study of human gut Actinobacteria		8
22	Using DNA Metabarcoding To Evaluate the Plant Component of Human Diets: a Proof of Concept. <i>MSystems</i> , 2019 , 4,	7.6	7
21	Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2018 , 23, 56-67	1.3	7
20	Perturbation of the human gut microbiome by a non-antibiotic drug contributes to the resolution of autoimmune disease		7
19	The East Asian gut microbiome is distinct from colocalized White subjects and connected to metabolic health. <i>ELife</i> , 2021 , 10,	8.9	6
18	The Genetic Basis for the Cooperative Bioactivation of Plant Lignans by a Human Gut Bacterial Consortium		5
17	A microbe-dependent viral key to Crohn's box. <i>Science Translational Medicine</i> , 2010 , 2, 43ps39	17.5	3
16	Phage-delivered CRISPR-Cas9 for strain-specific depletion and genomic deletions in the gut microbiome		3
15	Diet induces reproducible alterations in the mouse and human gut microbiome		3

14	A diet-dependent enzyme from the human gut microbiome promotes Th17 cell accumulation and colitis	3
13	Human gut bacteria produce TH17-modulating bile acid metabolites	3
12	Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome 2018 ,	3
11	Synthetic glycans control gut microbiome structure and mitigate colitis in mice.. <i>Nature Communications</i> , 2022 , 13, 1244	17.4 3
10	Making Millennial Medicine More Meta. <i>MSystems</i> , 2018 , 3,	7.6 2
9	Microbial signals, MyD88, and lymphotoxin drive TNF-independent intestinal epithelial tissue damage.. <i>Journal of Clinical Investigation</i> , 2022 ,	15.9 2
8	Diet Induces Reproducible Alterations in the Mouse and Human Gut Microbiome. <i>SSRN Electronic Journal</i> ,	1 2
7	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments	2
6	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments	2
5	A thermogenic fat-epithelium cell axis regulates intestinal disease tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 32029-32037	11.5 2
4	Drug resistant gut bacteria mimic a host mechanism for anticancer drug clearance	1
3	Stressed-out gut bacteria are pterin up gut inflammation. <i>Nature Microbiology</i> , 2020 , 5, 1316-1318	26.6 1
2	Effects of caloric restriction on the gut microbiome are linked with immune senescence.. <i>Microbiome</i> , 2022 , 10, 57	16.6 1
1	The Metabolism of Fluoropyrimidine Anticancer Drugs by the Human Gut Microbiome. <i>FASEB Journal</i> , 2018 , 32, 534.22	0.9