

Peter J Turnbaugh

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

124,339
citations

19608

61
h-index

23472

111
g-index

156
all docs

156
docs citations

156
times ranked

91924
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
3	An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> , 2006, 444, 1027-1031.	13.7	10,136
4	Human gut microbes associated with obesity. <i>Nature</i> , 2006, 444, 1022-1023.	13.7	7,595
5	Diet rapidly and reproducibly alters the human gut microbiome. <i>Nature</i> , 2014, 505, 559-563.	13.7	7,592
6	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, 4516-4522.	3.3	7,425
7	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009, 457, 480-484.	13.7	6,819
8	Obesity alters gut microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11070-11075.	3.3	5,247
9	The Human Microbiome Project. <i>Nature</i> , 2007, 449, 804-810.	13.7	4,750
10	Metagenomic Analysis of the Human Distal Gut Microbiome. <i>Science</i> , 2006, 312, 1355-1359.	6.0	3,964
11	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	3,171
12	Diet-Induced Obesity Is Linked to Marked but Reversible Alterations in the Mouse Distal Gut Microbiome. <i>Cell Host and Microbe</i> , 2008, 3, 213-223.	5.1	2,535
13	The Effect of Diet on the Human Gut Microbiome: A Metagenomic Analysis in Humanized Gnotobiotic Mice. <i>Science Translational Medicine</i> , 2009, 1, 6ra14.	5.8	2,492
14	Detecting Novel Associations in Large Data Sets. <i>Science</i> , 2011, 334, 1518-1524.	6.0	2,252
15	Removing Noise From Pyrosequenced Amplicons. <i>BMC Bioinformatics</i> , 2011, 12, 38.	1.2	1,320
16	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.	2.2	1,015
17	Diet Dominates Host Genotype in Shaping the Murine Gut Microbiota. <i>Cell Host and Microbe</i> , 2015, 17, 72-84.	5.1	941
18	The core gut microbiome, energy balance and obesity. <i>Journal of Physiology</i> , 2009, 587, 4153-4158.	1.3	846

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19	Conserved Shifts in the Gut Microbiota Due to Gastric Bypass Reduce Host Weight and Adiposity. <i>Science Translational Medicine</i> , 2013, 5, 178ra41.	5.8	824
20	Xenobiotics Shape the Physiology and Gene Expression of the Active Human Gut Microbiome. <i>Cell</i> , 2013, 152, 39-50.	13.5	705
21	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, 594-599.	3.3	699
22	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, 5859-5864.	3.3	612
23	The microbial pharmacists within us: a metagenomic view of xenobiotic metabolism. <i>Nature Reviews Microbiology</i> , 2016, 14, 273-287.	13.6	552
24	Predicting and Manipulating Cardiac Drug Inactivation by the Human Gut Bacterium <i>Eggerthella lenta</i> . <i>Science</i> , 2013, 341, 295-298.	6.0	536
25	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, 2847-2858.	0.3	526
26	Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. <i>Science</i> , 2019, 364, .	6.0	431
27	Rapid fucosylation of intestinal epithelium sustains host-commensal symbiosis in sickness. <i>Nature</i> , 2014, 514, 638-641.	13.7	428
28	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, 7503-7508.	3.3	414
29	A Metabolite-Triggered Tuft Cell-ILC2 Circuit Drives Small Intestinal Remodeling. <i>Cell</i> , 2018, 174, 271-284.e14.	13.5	320
30	Ketogenic Diets Alter the Gut Microbiome Resulting in Decreased Intestinal Th17 Cells. <i>Cell</i> , 2020, 181, 1263-1275.e16.	13.5	292
31	Marked seasonal variation in the wild mouse gut microbiota. <i>ISME Journal</i> , 2015, 9, 2423-2434.	4.4	282
32	An Invitation to the Marriage of Metagenomics and Metabolomics. <i>Cell</i> , 2008, 134, 708-713.	13.5	236
33	The Intestinal Metabolome: An Intersection Between Microbiota and Host. <i>Gastroenterology</i> , 2014, 146, 1470-1476.	0.6	227
34	Host-microbial interactions in the metabolism of therapeutic and diet-derived xenobiotics. <i>Journal of Clinical Investigation</i> , 2014, 124, 4173-4181.	3.9	211
35	Human gut bacteria produce β -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	13.7	210
36	Functional Characterization of Bacteria Isolated from Ancient Arctic Soil Exposes Diverse Resistance Mechanisms to Modern Antibiotics. <i>PLoS ONE</i> , 2015, 10, e0069533.	1.1	202

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37	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011, 8, 191-192.	9.0	198
38	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.	5.1	194
39	Characterization and Detection of a Widely Distributed Gene Cluster That Predicts Anaerobic Choline Utilization by Human Gut Bacteria. <i>MBio</i> , 2015, 6, .	1.8	173
40	Combining 16S rRNA gene variable regions enables high-resolution microbial community profiling. <i>Microbiome</i> , 2018, 6, 17.	4.9	171
41	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
42	Developing a metagenomic view of xenobiotic metabolism. <i>Pharmacological Research</i> , 2013, 69, 21-31.	3.1	159
43	Gut Microbial Succession Follows Acute Secretory Diarrhea in Humans. <i>MBio</i> , 2015, 6, e00381-15.	1.8	150
44	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
45	Mechanistic insight into digoxin inactivation by <i>Eggerthella lenta</i> augments our understanding of its pharmacokinetics. <i>Gut Microbes</i> , 2014, 5, 233-238.	4.3	139
46	Gut microbiota-specific IgA ⁺ B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020, 5, .	5.6	132
47	Is It Time for a Metagenomic Basis of Therapeutics?. <i>Science</i> , 2012, 336, 1253-1255.	6.0	121
48	Cooking shapes the structure and function of the gut microbiome. <i>Nature Microbiology</i> , 2019, 4, 2052-2063.	5.9	112
49	Dissecting the contribution of host genetics and the microbiome in complex behaviors. <i>Cell</i> , 2021, 184, 1740-1756.e16.	13.5	109
50	Caloric restriction disrupts the microbiota and colonization resistance. <i>Nature</i> , 2021, 595, 272-277.	13.7	109
51	The mind-body-microbial continuum. <i>Dialogues in Clinical Neuroscience</i> , 2011, 13, 55-62.	1.8	109
52	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 109-114.	2.8	104
53	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, .	2.8	93
54	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016, 1, .	1.7	89

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55	Human gut bacterial metabolism drives Th17 activation and colitis. <i>Cell Host and Microbe</i> , 2022, 30, 17-30.e9.	5.1	83
56	Functional genetics of human gut commensal <i>Bacteroides thetaiotaomicron</i> reveals metabolic requirements for growth across environments. <i>Cell Reports</i> , 2021, 34, 108789.	2.9	82
57	Effects of underfeeding and oral vancomycin on gut microbiome and nutrient absorption in humans. <i>Nature Medicine</i> , 2020, 26, 589-598.	15.2	81
58	Precision Medicine Goes Microscopic: Engineering the Microbiome to Improve Drug Outcomes. <i>Cell Host and Microbe</i> , 2019, 26, 22-34.	5.1	80
59	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.	2.9	78
60	Deconstructing Mechanisms of Diet-Microbiome-Immune Interactions. <i>Immunity</i> , 2020, 53, 264-276.	6.6	77
61	Pharmacomicrobiomics in inflammatory arthritis: gut microbiome as modulator of therapeutic response. <i>Nature Reviews Rheumatology</i> , 2020, 16, 282-292.	3.5	76
62	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.	1.9	72
63	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.	5.1	70
64	Phage-delivered CRISPR-Cas9 for strain-specific depletion and genomic deletions in the gut microbiome. <i>Cell Reports</i> , 2021, 37, 109930.	2.9	68
65	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.	5.9	63
66	Microbes and Diet-Induced Obesity: Fast, Cheap, and Out of Control. <i>Cell Host and Microbe</i> , 2017, 21, 278-281.	5.1	61
67	Pathways and mechanisms linking dietary components to cardiometabolic disease: thinking beyond calories. <i>Obesity Reviews</i> , 2018, 19, 1205-1235.	3.1	60
68	COMPANION ANIMALS SYMPOSIUM: Humanized animal models of the microbiome. <i>Journal of Animal Science</i> , 2011, 89, 1531-1537.	0.2	58
69	Taking a metagenomic view of human nutrition. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2012, 15, 448-454.	1.3	54
70	Microbial Determinants of Biochemical Individuality and Their Impact on Toxicology and Pharmacology. <i>Cell Metabolism</i> , 2014, 20, 761-768.	7.2	53
71	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.	5.1	53
72	Non-catalytic ubiquitin binding by A20 prevents psoriatic arthritis-like disease and inflammation. <i>Nature Immunology</i> , 2020, 21, 422-433.	7.0	49

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73	Sensing Living Bacteria <i>in Vivo</i> Using α -Alanine-Derived ^{11}C Radiotracers. ACS Central Science, 2020, 6, 155-165.	5.3	48
74	High-resolution microbial community reconstruction by integrating short reads from multiple 16S rRNA regions. Nucleic Acids Research, 2013, 41, e205-e205.	6.5	46
75	Investigating Ketone Bodies as Immunometabolic Countermeasures against Respiratory Viral Infections. Med, 2020, 1, 43-65.	2.2	40
76	A widely distributed metalloenzyme class enables gut microbial metabolism of host- and diet-derived catechols. ELife, 2020, 9, .	2.8	40
77	A Genomic Toolkit for the Mechanistic Dissection of Intractable Human Gut Bacteria. Cell Host and Microbe, 2020, 27, 1001-1013.e9.	5.1	39
78	Bacterial metabolism rescues the inhibition of intestinal drug absorption by food and drug additives. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16009-16018.	3.3	39
79	Effects of caloric restriction on the gut microbiome are linked with immune senescence. Microbiome, 2022, 10, 57.	4.9	38
80	Fat, bile and gut microbes. Nature, 2012, 487, 47-48.	13.7	36
81	How to Determine the Role of the Microbiome in Drug Disposition. Drug Metabolism and Disposition, 2018, 46, 1588-1595.	1.7	36
82	Discovery, validation, and genetic dissection of transcription factor binding sites by comparative and functional genomics. Genome Research, 2005, 15, 1145-1152.	2.4	31
83	Mirror, mirror on the wall: which microbiomes will help heal them all?. BMC Medicine, 2016, 14, 72.	2.3	31
84	Nutrient Sensing in CD11c Cells Alters the Gut Microbiota to Regulate Food Intake and Body Mass. Cell Metabolism, 2019, 30, 364-373.e7.	7.2	31
85	Translating the human microbiome. Nature Biotechnology, 2013, 31, 304-308.	9.4	30
86	Viewing the human microbiome through three-dimensional glasses: integrating structural and functional studies to better define the properties of myriad carbohydrate-active enzymes. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1261-1264.	0.7	26
87	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. Microbiome, 2014, 2, .	4.9	25
88	Probing the tumor micro(b)environment. Science, 2020, 368, 938-939.	6.0	25
89	The East Asian gut microbiome is distinct from colocalized White subjects and connected to metabolic health. ELife, 2021, 10, .	2.8	25
90	Synthetic glycans control gut microbiome structure and mitigate colitis in mice. Nature Communications, 2022, 13, 1244.	5.8	25

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91	Quantifying the metabolic activities of human-associated microbial communities across multiple ecological scales. <i>FEMS Microbiology Reviews</i> , 2013, 37, 830-848.	3.9	22
92	Human Health and Disease in a Microbial World. <i>Frontiers in Microbiology</i> , 2011, 2, 190.	1.5	20
93	Regulation of drug metabolism and toxicity by multiple factors of genetics, epigenetics, lncRNAs, gut microbiota, and diseases: a meeting report of the 21st International Symposium on Microsomes and Drug Oxidations (MDO). <i>Acta Pharmaceutica Sinica B</i> , 2017, 7, 241-248.	5.7	20
94	Gut Microbes Make for Fattier Fish. <i>Cell Host and Microbe</i> , 2012, 12, 259-261.	5.1	18
95	Using DNA Metabarcoding To Evaluate the Plant Component of Human Diets: a Proof of Concept. <i>MSystems</i> , 2019, 4, .	1.7	18
96	Microbial signals, MyD88, and lymphotoxin drive TNF-independent intestinal epithelial tissue damage. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	15
97	Quantifying and Identifying the Active and Damaged Subsets of Indigenous Microbial Communities. <i>Methods in Enzymology</i> , 2013, 531, 91-107.	0.4	13
98	Broad collateral damage of drugs against the gut microbiome. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018, 15, 457-458.	8.2	13
99	Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome. , 2018, , .		12
100	Antibiotic Exposure Promotes Fat Gain. <i>Cell Metabolism</i> , 2012, 16, 408-410.	7.2	10
101	Siri, What Should I Eat?. <i>Cell</i> , 2015, 163, 1051-1052.	13.5	10
102	Diet should be a tool for researchers, not a treatment. <i>Nature</i> , 2020, 577, S23-S23.	13.7	8
103	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.	3.3	7
104	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.	0.7	7
105	A Microbe-Dependent Viral Key to Crohn's Box. <i>Science Translational Medicine</i> , 2010, 2, 43ps39.	5.8	5
106	An acidic link. <i>Nature</i> , 2013, 499, 37-38.	13.7	5
107	Tiny Gatekeepers: Microbial Control of Host Drug Transporters. <i>Clinical Pharmacology and Therapeutics</i> , 2022, 112, 443-445.	2.3	5
108	Methotrexate Impacts Conserved Pathways in Diverse Human Gut Bacteria Leading to Decreased Host Immune Activation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3

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109	Making Millennial Medicine More Meta. MSystems, 2018, 3, .	1.7	2
110	Diet Induces Reproducible Alterations in the Mouse and Human Gut Microbiome. SSRN Electronic Journal, 0, , .	0.4	2
111	Stressed-out gut bacteria are pterin up gut inflammation. Nature Microbiology, 2020, 5, 1316-1318.	5.9	1
112	Announcement of 2019 Keystone Symposia Conference: "Microbiome: Chemical Mechanisms and Biological Consequences" MSystems, 2018, 3, .	1.7	0
113	The Metabolism of Fluoropyrimidine Anticancer Drugs by the Human Gut Microbiome. FASEB Journal, 2018, 32, 534.22.	0.2	0
114	CRISPR-Cas Immune System of a Prevalent Human Gut Bacterium Reveals Hypertargeting Against Gut Virome Phages. SSRN Electronic Journal, 0, , .	0.4	0
115	Fluoropyrimidine Bioactivation and Metabolism by the Gut Microbiome. FASEB Journal, 2022, 36, .	0.2	0
116	The tiny pharmacists within: How the microbiome impacts the treatment of human disease. FASEB Journal, 2022, 36, .	0.2	0
117	Designed secretion deters microbiome depletion. Nature Microbiology, 0, , .	5.9	0