

Peter J Turnbaugh

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/2820266/peter-j-turnbaugh-publications-by-year.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Microbial signals, MyD88, and lymphotoxin drive TNF-independent intestinal epithelial tissue damage.. <i>Journal of Clinical Investigation</i> , 2022 ,	15.9	2
120	Synthetic glycans control gut microbiome structure and mitigate colitis in mice.. <i>Nature Communications</i> , 2022 , 13, 1244	17.4	3
119	Human gut bacteria produce γ -modulating bile acid metabolites.. <i>Nature</i> , 2022 ,	50.4	20
118	Effects of caloric restriction on the gut microbiome are linked with immune senescence.. <i>Microbiome</i> , 2022 , 10, 57	16.6	1
117	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
116	Human gut bacterial metabolism drives Th17 activation and colitis. <i>Cell Host and Microbe</i> , 2021 ,	23.4	9
115	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
114	The East Asian gut microbiome is distinct from colocalized White subjects and connected to metabolic health. <i>ELife</i> , 2021 , 10,	8.9	6
113	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
112	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
111	Dissecting the contribution of host genetics and the microbiome in complex behaviors. <i>Cell</i> , 2021 , 184, 1740-1756.e16	56.2	28
110	Caloric restriction disrupts the microbiota and colonization resistance. <i>Nature</i> , 2021 , 595, 272-277	50.4	32
109	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
108	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
107	Probing the tumor micro(b)environment. <i>Science</i> , 2020 , 368, 938-939	33.3	8
106	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
105	Non-catalytic ubiquitin binding by A20 prevents psoriatic arthritis-like disease and inflammation. <i>Nature Immunology</i> , 2020 , 21, 422-433	19.1	31

104	Pharmacomicrobiomics in inflammatory arthritis: gut microbiome as modulator of therapeutic response. <i>Nature Reviews Rheumatology</i> , 2020 , 16, 282-292	8.1	35
103	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
102	Sensing Living Bacteria Using d-Alanine-Derived C Radiotracers. <i>ACS Central Science</i> , 2020 , 6, 155-165	16.8	15
101	A widely distributed metalloenzyme class enables gut microbial metabolism of host- and diet-derived catechols. <i>ELife</i> , 2020 , 9,	8.9	14
100	Ketogenic Diets Alter the Gut Microbiome Resulting in Decreased Intestinal Th17 Cells. <i>Cell</i> , 2020 , 181, 1263-1275.e16	56.2	126
99	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
98	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
97	Deconstructing Mechanisms of Diet-Microbiome-Immune Interactions. <i>Immunity</i> , 2020 , 53, 264-276	32.3	24
96	Stressed-out gut bacteria are pterin up gut inflammation. <i>Nature Microbiology</i> , 2020 , 5, 1316-1318	26.6	1
95	Investigating Ketone Bodies as Immunometabolic Countermeasures against Respiratory Viral Infections. <i>Med</i> , 2020 , 1, 43-65	31.7	15
94	Gut microbiota-specific IgA B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020 , 5,	28	48
93	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
92	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019 , 4, 693-700	26.6	89
91	Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. <i>Science</i> , 2019 , 364,	33.3	217
90	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
89	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
88	Precision Medicine Goes Microscopic: Engineering the Microbiome to Improve Drug Outcomes. <i>Cell Host and Microbe</i> , 2019 , 26, 22-34	23.4	50
87	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050

86	Using DNA Metabarcoding To Evaluate the Plant Component of Human Diets: a Proof of Concept. <i>MSystems</i> , 2019 , 4,	7.6	7
85	Cooking shapes the structure and function of the gut microbiome. <i>Nature Microbiology</i> , 2019 , 4, 2052-2066	6.6	66
84	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
83	Making Millennial Medicine More Meta. <i>MSystems</i> , 2018 , 3,	7.6	2
82	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
81	Combining 16S rRNA gene variable regions enables high-resolution microbial community profiling. <i>Microbiome</i> , 2018 , 6, 17	16.6	91
80	Broad collateral damage of drugs against the gut microbiome. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 457-458	24.2	10
79	How to Determine the Role of the Microbiome in Drug Disposition. <i>Drug Metabolism and Disposition</i> , 2018 , 46, 1588-1595	4	21
78	A Metabolite-Triggered Tuft Cell-ILC2 Circuit Drives Small Intestinal Remodeling. <i>Cell</i> , 2018 , 174, 271-284	46.14	189
77	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
76	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
75	The Metabolism of Fluoropyrimidine Anticancer Drugs by the Human Gut Microbiome. <i>FASEB Journal</i> , 2018 , 32, 534.22	0.9	
74	Chemical reaction vector embeddings: towards predicting drug metabolism in the human gut microbiome 2018 ,		3
73	Pathways and mechanisms linking dietary components to cardiometabolic disease: thinking beyond calories. <i>Obesity Reviews</i> , 2018 , 19, 1205-1235	10.6	37
72	Microbes and Diet-Induced Obesity: Fast, Cheap, and Out of Control. <i>Cell Host and Microbe</i> , 2017 , 21, 278-281	23.4	46
71	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
70	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016 , 1,	7.6	55
69	The microbial pharmacists within us: a metagenomic view of xenobiotic metabolism. <i>Nature Reviews Microbiology</i> , 2016 , 14, 273-87	22.2	382

68	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
67	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
66	Siri, What Should I Eat?. <i>Cell</i> , 2015 , 163, 1051-1052	56.2	8
65	Diet dominates host genotype in shaping the murine gut microbiota. <i>Cell Host and Microbe</i> , 2015 , 17, 72-84	23.4	658
64	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
63	Marked seasonal variation in the wild mouse gut microbiota. <i>ISME Journal</i> , 2015 , 9, 2423-34	11.9	173
62	Gut microbial succession follows acute secretory diarrhea in humans. <i>MBio</i> , 2015 , 6, e00381-15	7.8	104
61	The intestinal metabolome: an intersection between microbiota and host. <i>Gastroenterology</i> , 2014 , 146, 1470-6	13.3	165
60	Diet rapidly and reproducibly alters the human gut microbiome. <i>Nature</i> , 2014 , 505, 559-63	50.4	5264
59	Rapid fucosylation of intestinal epithelium sustains host-commensal symbiosis in sickness. <i>Nature</i> , 2014 , 514, 638-41	50.4	343
58	Microbial determinants of biochemical individuality and their impact on toxicology and pharmacology. <i>Cell Metabolism</i> , 2014 , 20, 761-768	24.6	43
57	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014 , 2,	16.6	18
56	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
55	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
54	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
53	Developing a metagenomic view of xenobiotic metabolism. <i>Pharmacological Research</i> , 2013 , 69, 21-31	10.2	123
52	Quantifying and identifying the active and damaged subsets of indigenous microbial communities. <i>Methods in Enzymology</i> , 2013 , 531, 91-107	1.7	8
51	Xenobiotics shape the physiology and gene expression of the active human gut microbiome. <i>Cell</i> , 2013 , 152, 39-50	56.2	560

50	Translating the human microbiome. <i>Nature Biotechnology</i> , 2013 , 31, 304-8	44.5	25
49	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
48	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
47	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
46	Gut microbes make for fatter fish. <i>Cell Host and Microbe</i> , 2012 , 12, 259-61	23.4	14
45	Is it time for a metagenomic basis of therapeutics?. <i>Science</i> , 2012 , 336, 1253-5	33.3	99
44	Antibiotic exposure promotes fat gain. <i>Cell Metabolism</i> , 2012 , 16, 408-10	24.6	8
43	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
42	Microbiology: fat, bile and gut microbes. <i>Nature</i> , 2012 , 487, 47-8	50.4	29
41	Taking a metagenomic view of human nutrition. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2012 , 15, 448-54	3.8	43
40	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
39	Human health and disease in a microbial world. <i>Frontiers in Microbiology</i> , 2011 , 2, 190	5.7	11
38	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011 , 8, 191-2	21.6	161
37	Removing noise from pyrosequenced amplicons. <i>BMC Bioinformatics</i> , 2011 , 12, 38	3.6	1088
36	Detecting novel associations in large data sets. <i>Science</i> , 2011 , 334, 1518-24	33.3	1464
35	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
34	Companion animals symposium: humanized animal models of the microbiome. <i>Journal of Animal Science</i> , 2011 , 89, 1531-7	0.7	50
33	The mind-body-microbial continuum. <i>Dialogues in Clinical Neuroscience</i> , 2011 , 13, 55-62	5.7	85

32	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21.6	22879
31	A microbe-dependent viral key to Crohn's box. <i>Science Translational Medicine</i> , 2010 , 2, 43ps39	17.5	3
30	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
29	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
28	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
27	The core gut microbiome, energy balance and obesity. <i>Journal of Physiology</i> , 2009 , 587, 4153-8	3.9	673
26	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009 , 457, 480-4	50.4	5429
25	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
24	An invitation to the marriage of metagenomics and metabolomics. <i>Cell</i> , 2008 , 134, 708-13	56.2	194
23	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
22	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008 , 12, 109-14	9.7	87
21	Evolution of mammals and their gut microbes. <i>Science</i> , 2008 , 320, 1647-51	33.3	2355
20	The human microbiome project. <i>Nature</i> , 2007 , 449, 804-10	50.4	3576
19	Microbial ecology: human gut microbes associated with obesity. <i>Nature</i> , 2006 , 444, 1022-3	50.4	5833
18	An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> , 2006 , 444, 1027-31	50.4	7807
17	Metagenomic analysis of the human distal gut microbiome. <i>Science</i> , 2006 , 312, 1355-9	33.3	3163
16	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
15	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

14	Diet Induces Reproducible Alterations in the Mouse and Human Gut Microbiome. <i>SSRN Electronic Journal</i> ,	1	2
13	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
12	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
11	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
10	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
9	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		8
8	Phage-delivered CRISPR-Cas9 for strain-specific depletion and genomic deletions in the gut microbiome		3
7	Illuminating the microbiome's dark matter: a functional genomic toolkit for the study of human gut Actinobacteria		6
6	The Genetic Basis for the Cooperative Bioactivation of Plant Lignans by a Human Gut Bacterial Consortium		5
5	Diet induces reproducible alterations in the mouse and human gut microbiome		3
4	Perturbation of the human gut microbiome by a non-antibiotic drug contributes to the resolution of autoimmune disease		7
3	A diet-dependent enzyme from the human gut microbiome promotes Th17 cell accumulation and colitis		3
2	Drug resistant gut bacteria mimic a host mechanism for anticancer drug clearance		1
1	Human gut bacteria produce TH17-modulating bile acid metabolites		3