

# Peter J Turnbaugh

## List of Articles by Year in descending order

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106

PR articles

97,436

PR citations

20596

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37216

95

g-index

135

documents

115177

doc citations

18683

63

h-index

128521

citing authors

#	ARTICLE	IF	CITATIONS
1	Pharma[e]cology: How the Gut Microbiome Contributes to Variations in Drug Response. Annual Review of Pharmacology and Toxicology, 2025, 65, 355-373.	11.8	12
2	Expansion of a bacterial operon during cancer treatment ameliorates fluoropyrimidine toxicity. Science Translational Medicine, 2025, 17, .	12.5	8
3	Microbial vitamin biosynthesis links gut microbiota dynamics to chemotherapy toxicity. MBio, 2025, 16, .	4.4	4
4	Microbiome Single Cell Atlases Generated with a Commercial Instrument. Advanced Science, 2025, 12, .	12.6	2
5	Simvastatin induces human gut bacterial cell surface genes. Molecular Microbiology, 2024, 122, 372-386.	2.5	12
6	High fat intake sustains sorbitol intolerance after antibiotic-mediated Clostridia depletion from the gut microbiota. Cell, 2024, 187, 1191-1205.e15.	33.7	35
7	Gut bacteria convert glucocorticoids into progestins in the presence of hydrogen gas. Cell, 2024, 187, 2952-2968.e13.	33.7	66
8	Effects of high dose aspartame-based sweetener on the gut microbiota and bone strength in young and aged mice. JBMR Plus, 2024, 8, .	2.1	3
9	Human gut Actinobacteria boost drug absorption by secreting P-glycoprotein ATPase inhibitors. IScience, 2024, 27, 110122.	3.6	8
10	Digesting the complex metabolic effects of diet on the host and microbiome. Cell, 2024, 187, 3857-3876.	33.7	46
11	Effects of Early Life Exposures to the Aryl Hydrocarbon Receptor Ligand TCDF on Gut Microbiota and Host Metabolic Homeostasis in C57BL/6J Mice. Environmental Health Perspectives, 2024, 132, .	8.4	4
12	Metatranscriptomics-guided discovery and characterization of a polyphenol-metabolizing gut microbial enzyme. Cell Host and Microbe, 2024, 32, 1887-1896.e8.	15.1	21
13	A diet-dependent host metabolite shapes the gut microbiota to protect from autoimmunity. Cell Reports, 2024, 43, 114891.	6.3	20
14	Systems biology elucidates the distinctive metabolic niche filled by the human gut microbe Eggerthella lenta. PLoS Biology, 2023, 21, e3002125.	5.0	33
15	Variety of Fruit and Vegetables and Alcohol Intake are Associated with Gut Microbial Species and Gene Abundance in Colorectal Cancer Survivors. American Journal of Clinical Nutrition, 2023, 118, 518-529.	4.7	12
16	The global anaerobic metabolism regulator <i>fnr</i> is necessary for the degradation of food dyes and drugs by <i>Escherichia coli</i> . MBio, 2023, 14, .	4.4	5
17	Associations between the Gut Microbiota, Race, and Ethnicity of Patients with Colorectal Cancer: A Pilot and Feasibility Study. Cancers, 2023, 15, 4546.	3.8	15
18	Human gut bacterial metabolism drives Th17 activation and colitis. Cell Host and Microbe, 2022, 30, 17-30.e9.	15.1	213

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19	Synthetic glycans control gut microbiome structure and mitigate colitis in mice. <i>Nature Communications</i> , 2022, 13, .	13.7	58
20	Human gut bacteria produce $\beta$ -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	37.9	489
21	Effects of caloric restriction on the gut microbiome are linked with immune senescence. <i>Microbiome</i> , 2022, 10, .	11.5	92
22	Fluoropyrimidine Bioactivation and Metabolism by the Gut Microbiome. <i>FASEB Journal</i> , 2022, 36, .	0.6	1
23	The tiny pharmacists within: How the microbiome impacts the treatment of human disease. <i>FASEB Journal</i> , 2022, 36, .	0.6	0
24	Host and gut bacteria share metabolic pathways for anti-cancer drug metabolism. <i>Nature Microbiology</i> , 2022, 7, 1605-1620.	16.0	91
25	Genetic manipulation of the human gut bacterium <i>Eggerthella lenta</i> reveals a widespread family of transcriptional regulators. <i>Nature Communications</i> , 2022, 13, .	13.7	39
26	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.	6.2	130
27	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.	15.1	120
28	Functional genetics of human gut commensal <i>Bacteroides thetaiotaomicron</i> reveals metabolic requirements for growth across environments. <i>Cell Reports</i> , 2021, 34, 108789.	6.3	142
29	Dissecting the contribution of host genetics and the microbiome in complex behaviors. <i>Cell</i> , 2021, 184, 1740-1756.e16.	33.7	185
30	Caloric restriction disrupts the microbiota and colonization resistance. <i>Nature</i> , 2021, 595, 272-277.	37.9	187
31	Phage-delivered CRISPR-Cas9 for strain-specific depletion and genomic deletions in the gut microbiome. <i>Cell Reports</i> , 2021, 37, 109930.	6.3	132
32	Deconstructing Mechanisms of Diet-Microbiome-Immune Interactions. <i>Immunity</i> , 2020, 53, 264-276.	22.6	130
33	Gut microbiota-specific IgA + B cells traffic to the CNS in active multiple sclerosis. <i>Science Immunology</i> , 2020, 5, .	13.4	203
34	A Genomic Toolkit for the Mechanistic Dissection of Intractable Human Gut Bacteria. <i>Cell Host and Microbe</i> , 2020, 27, 1001-1013.e9.	15.1	60
35	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.	7.5	54
36	Non-catalytic ubiquitin binding by A20 prevents psoriatic arthritis-like disease and inflammation. <i>Nature Immunology</i> , 2020, 21, 422-433.	23.6	70

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37	Pharmacomicrobiomics in inflammatory arthritis: gut microbiome as modulator of therapeutic response. <i>Nature Reviews Rheumatology</i> , 2020, 16, 282-292.	25.5	104
38	Effects of underfeeding and oral vancomycin on gut microbiome and nutrient absorption in humans. <i>Nature Medicine</i> , 2020, 26, 589-598.	33.0	125
39	Sensing Living Bacteria in Vivo Using d-Alanine-Derived <sup>11</sup> C Radiotracers. <i>ACS Central Science</i> , 2020, 6, 155-165.	9.2	67
40	Ketogenic Diets Alter the Gut Microbiome Resulting in Decreased Intestinal Th17 Cells. <i>Cell</i> , 2020, 181, 1263-1275.e16.	33.7	493
41	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.	7.5	10
42	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.	15.1	297
43	Precision Medicine Goes Microscopic: Engineering the Microbiome to Improve Drug Outcomes. <i>Cell Host and Microbe</i> , 2019, 26, 22-34.	15.1	107
44	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	29.8	19,394
45	Using DNA Metabarcoding To Evaluate the Plant Component of Human Diets: a Proof of Concept. <i>MSystems</i> , 2019, 4, .	4.4	31
46	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.	15.1	65
47	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	16.0	197
48	Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism. <i>Science</i> , 2019, 364, .	36.2	633
49	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.	25.2	38
50	Cooking shapes the structure and function of the gut microbiome. <i>Nature Microbiology</i> , 2019, 4, 2052-2063.	16.0	141
51	Genetic basis for the cooperative bioactivation of plant lignans by <i>Eggerthella lenta</i> and other human gut bacteria. <i>Nature Microbiology</i> , 2019, 5, 56-66.	16.0	95
52	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.	4.9	85
53	Making Millennial Medicine More Meta. <i>MSystems</i> , 2018, 3, .	4.4	2
54	Pathways and mechanisms linking dietary components to cardiometabolic disease: thinking beyond calories. <i>Obesity Reviews</i> , 2018, 19, 1205-1235.	7.5	76

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55	Combining 16S rRNA gene variable regions enables high-resolution microbial community profiling. <i>Microbiome</i> , 2018, 6, .	11.5	226
56	How to Determine the Role of the Microbiome in Drug Disposition. <i>Drug Metabolism and Disposition</i> , 2018, 46, 1588-1595.	3.6	45
57	A Metabolite-Triggered Tuft Cell-ILC2 Circuit Drives Small Intestinal Remodeling. <i>Cell</i> , 2018, 174, 271-284.e14.	33.7	451
58	The Metabolism of Fluoropyrimidine Anticancer Drugs by the Human Gut Microbiome. <i>FASEB Journal</i> , 2018, 32, .	0.6	1
59	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.	12.6	26
60	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016, 1, .	4.4	102
61	The microbial pharmacists within us: a metagenomic view of xenobiotic metabolism. <i>Nature Reviews Microbiology</i> , 2016, 14, 273-287.	83.5	672
62	Functional Characterization of Bacteria Isolated from Ancient Arctic Soil Exposes Diverse Resistance Mechanisms to Modern Antibiotics. <i>PLoS ONE</i> , 2015, 10, e0069533.	2.3	241
63	Marked seasonal variation in the wild mouse gut microbiota. <i>ISME Journal</i> , 2015, 9, 2423-2434.	9.1	344
64	Gut Microbial Succession Follows Acute Secretory Diarrhea in Humans. <i>MBio</i> , 2015, 6, .	4.4	178
65	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.	4.2	611
66	Characterization and Detection of a Widely Distributed Gene Cluster That Predicts Anaerobic Choline Utilization by Human Gut Bacteria. <i>MBio</i> , 2015, 6, .	4.4	216
67	Diet Dominates Host Genotype in Shaping the Murine Gut Microbiota. <i>Cell Host and Microbe</i> , 2015, 17, 72-84.	15.1	1,064
68	The Intestinal Metabolome: An Intersection Between Microbiota and Host. <i>Gastroenterology</i> , 2014, 146, 1470-1476.	0.9	309
69	Rapid fucosylation of intestinal epithelium sustains host-commensal symbiosis in sickness. <i>Nature</i> , 2014, 514, 638-641.	37.9	490
70	Host-microbial interactions in the metabolism of therapeutic and diet-derived xenobiotics. <i>Journal of Clinical Investigation</i> , 2014, 124, 4173-4181.	10.6	236
71	Developing a metagenomic view of xenobiotic metabolism. <i>Pharmacological Research</i> , 2013, 69, 21-31.	9.1	181
72	Xenobiotics Shape the Physiology and Gene Expression of the Active Human Gut Microbiome. <i>Cell</i> , 2013, 152, 39-50.	33.7	786

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73	Quantifying the metabolic activities of human-associated microbial communities across multiple ecological scales. <i>FEMS Microbiology Reviews</i> , 2013, 37, 830-848.	10.6	23
74	Conserved Shifts in the Gut Microbiota Due to Gastric Bypass Reduce Host Weight and Adiposity. <i>Science Translational Medicine</i> , 2013, 5, .	12.5	893
75	High-resolution microbial community reconstruction by integrating short reads from multiple 16S rRNA regions. <i>Nucleic Acids Research</i> , 2013, 41, e205-e205.	15.5	51
76	Diet rapidly and reproducibly alters the human gut microbiome. <i>Nature</i> , 2013, 505, 559-563.	37.9	9,194
77	Taking a metagenomic view of human nutrition. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2012, 15, 448-454.	3.0	54
78	Is It Time for a Metagenomic Basis of Therapeutics?. <i>Science</i> , 2012, 336, 1253-1255.	36.2	131
79	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.	7.5	760
80	Taxonomic metagenome sequence assignment with structured output models. <i>Nature Methods</i> , 2011, 8, 191-192.	24.6	201
81	Wild immunology: converging on the real world. <i>Annals of the New York Academy of Sciences</i> , 2011, 1236, 17-29.	4.0	33
82	Removing Noise From Pyrosequenced Amplicons. <i>BMC Bioinformatics</i> , 2011, 12, .	3.0	1,443
83	Detecting Novel Associations in Large Data Sets. <i>Science</i> , 2011, 334, 1518-1524.	36.2	2,915
84	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.	4.7	1,138
85	COMPANION ANIMALS SYMPOSIUM: Microbes and health <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 1496-1497.	0.7	6
86	COMPANION ANIMALS SYMPOSIUM: Humanized animal models of the microbiome <sup>1</sup> . <i>Journal of Animal Science</i> , 2011, 89, 1531-1537.	0.7	58
87	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, 1261-1264.	0.7	28
88	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	24.6	35,161
89	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.	7.5	433
90	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.	7.5	679

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91	The core gut microbiome, energy balance and obesity. <i>Journal of Physiology</i> , 2009, 587, 4153-4158.	3.4	914
92	The Effect of Diet on the Human Gut Microbiome: A Metagenomic Analysis in Humanized Gnotobiotic Mice. <i>Science Translational Medicine</i> , 2009, 1, .	12.5	2,733
93	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 109-114.	5.8	105
94	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.	15.1	2,785
95	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2008, 457, 480-484.	37.9	7,427
96	Human gut microbes associated with obesity. <i>Nature</i> , 2006, 444, 1022-1023.	37.9	8,479
97	An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> , 2006, 444, 1027-1031.	37.9	11,436
98	Discovery, validation, and genetic dissection of transcription factor binding sites by comparative and functional genomics. <i>Genome Research</i> , 2005, 15, 1145-1152.	4.6	31
99	Obesity alters gut microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11070-11075.	7.5	5,756
100	Discovery and characterization of a prevalent human gut bacterial enzyme sufficient for the inactivation of a family of plant toxins. <i>ELife</i> , 0, 7, .	1.6	123
101	A widely distributed metalloenzyme class enables gut microbial metabolism of host- and diet-derived catechols. <i>ELife</i> , 0, 9, .	1.6	66
102	The East Asian gut microbiome is distinct from colocalized White subjects and connected to metabolic health. <i>ELife</i> , 0, 10, .	1.6	45
103	Mild SARS-CoV-2 infection results in long-lasting microbiota instability. <i>MBio</i> , 0, , .	4.4	24
104	SIMMER employs similarity algorithms to accurately identify human gut microbiome species and enzymes capable of known chemical transformations. <i>ELife</i> , 0, 12, .	1.6	19
105	Human xenobiotic metabolism proteins have full-length and split homologs in the gut microbiome. <i>G3: Genes, Genomes, Genetics</i> , 0, 15, .	1.9	0
106	Microbiota and kidney disease: the road ahead. <i>Nature Reviews Nephrology</i> , 0, 21, 702-716.	32.8	9