

# Curtis Huttenhower

## List of Publications by Year in descending order

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Version: 2024-02-01

242  
papers

98,927  
citations

870

117  
h-index

872

243  
g-index

276  
all docs

276  
docs citations

276  
times ranked

79257  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.	13.9	11,192
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	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
4	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	9.4	2,621
5	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
6	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , 2012, 13, R79.	13.9	2,258
7	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	9.0	1,843
8	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
9	Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.	9.0	1,591
10	Genomic analysis identifies association of <i>Fusobacterium</i> with colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 292-298.	2.4	1,587
11	Expansion of intestinal <i>Prevotella copri</i> correlates with enhanced susceptibility to arthritis. <i>ELife</i> , 2013, 2, e01202.	2.8	1,507
12	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398
13	Microbial Co-occurrence Relationships in the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002606.	1.5	1,268
14	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	13.7	1,220
15	The healthy human microbiome. <i>Genome Medicine</i> , 2016, 8, 51.	3.6	1,214
16	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	9.0	1,125
17	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	5.9	1,094
18	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019, 176, 649-662.e20.	13.5	1,087

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19	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. <i>Science</i> , 2017, 357, 1156-1160.	6.0	1,059
20	The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes. <i>Cell Host and Microbe</i> , 2015, 17, 260-273.	5.1	1,008
21	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	13.5	968
22	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002358.	1.5	939
23	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	13.7	929
24	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	5.1	822
25	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
26	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	13.5	806
27	Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. <i>Genome Biology</i> , 2012, 13, R42.	13.9	797
28	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013, 4, 2304.	5.8	797
29	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. <i>Nature Communications</i> , 2016, 7, 10391.	5.8	784
30	Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. <i>Science Translational Medicine</i> , 2016, 8, 343ra81.	5.8	763
31	<i>Fusobacterium nucleatum</i> in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016, 65, 1973-1980.	6.1	718
32	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
33	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. <i>PeerJ</i> , 2015, 3, e1029.	0.9	701
34	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	1.5	691
35	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	13.7	623
36	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604

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37	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
38	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. <i>PLoS ONE</i> , 2012, 7, e36466.	1.1	572
39	Cervicovaginal Bacteria Are a Major Modulator of Host Inflammatory Responses in the Female Genital Tract. <i>Immunity</i> , 2015, 42, 965-976.	6.6	554
40	Relating the metatranscriptome and metagenome of the human gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2329-38.	3.3	552
41	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	13.6	544
42	Analysis of phosphorylation sites on proteins from <i>Saccharomyces cerevisiae</i> by electron transfer dissociation (ETD) mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2193-2198.	3.3	541
43	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	2.4	540
44	Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 352-367.	0.9	524
45	Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	5.1	523
46	Assessment of colorectal cancer molecular features along bowel subsites challenges the conception of distinct dichotomy of proximal versus distal colorectum. <i>Gut</i> , 2012, 61, 847-854.	6.1	518
47	<i>Fusobacterium nucleatum</i> and T Cells in Colorectal Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 653.	3.4	498
48	Lactobacillus-Deficient Cervicovaginal Bacterial Communities Are Associated with Increased HIV Acquisition in Young South African Women. <i>Immunity</i> , 2017, 46, 29-37.	6.6	488
49	Prediction of complicated disease course for children newly diagnosed with Crohn's disease: a multicentre inception cohort study. <i>Lancet, The</i> , 2017, 389, 1710-1718.	6.3	482
50	A novel <i>Ruminococcus gnavus</i> clade enriched in inflammatory bowel disease patients. <i>Genome Medicine</i> , 2017, 9, 103.	3.6	478
51	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 2021, 27, 321-332.	15.2	477
52	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. <i>PLoS Computational Biology</i> , 2013, 9, e1002863.	1.5	446
53	Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature. <i>Journal of Clinical Investigation</i> , 2014, 124, 3617-3633.	3.9	431
54	Chapter 12: Human Microbiome Analysis. <i>PLoS Computational Biology</i> , 2012, 8, e1002808.	1.5	408

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55	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	5.9	408
56	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , 2017, 35, 1077-1086.	9.4	400
57	Identifying personal microbiomes using metagenomic codes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2930-8.	3.3	377
58	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. <i>PLoS Biology</i> , 2012, 10, e1001377.	2.6	369
59	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	6.0	369
60	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
61	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. <i>ISME Journal</i> , 2014, 8, 1403-1417.	4.4	352
62	Schrödinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	4.9	347
63	Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.	3.6	322
64	Global chemical effects of the microbiome include new bile-acid conjugations. <i>Nature</i> , 2020, 579, 123-129.	13.7	316
65	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. <i>Cell Host and Microbe</i> , 2018, 24, 146-154.e4.	5.1	311
66	Tryptophan Biosynthesis Protects Mycobacteria from CD4 T-Cell-Mediated Killing. <i>Cell</i> , 2013, 155, 1296-1308.	13.5	296
67	Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.	9.0	292
68	Inflammatory Bowel Disease as a Model for Translating the Microbiome. <i>Immunity</i> , 2014, 40, 843-854.	6.6	284
69	Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants. <i>Microbiome</i> , 2013, 1, 13.	4.9	281
70	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. <i>Cell Host and Microbe</i> , 2019, 26, 252-264.e10.	5.1	274
71	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	5.1	274
72	<i>Bacteroides</i> -Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. <i>Cell Host and Microbe</i> , 2019, 25, 668-680.e7.	5.1	274

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73	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	5.1	273
74	Integrative analysis of the microbiome and metabolome of the human intestinal mucosal surface reveals exquisite inter-relationships. <i>Microbiome</i> , 2013, 1, 17.	4.9	256
75	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	3.2	253
76	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007, 23, 2692-2699.	1.8	243
77	Association of Dietary Patterns With Risk of Colorectal Cancer Subtypes Classified by <i>Fusobacterium nucleatum</i> in Tumor Tissue. <i>JAMA Oncology</i> , 2017, 3, 921.	3.4	243
78	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	1.8	241
79	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	1.5	235
80	<i>Fusobacterium nucleatum</i> in Colorectal Carcinoma Tissue According to Tumor Location. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e200.	1.3	225
81	Colorectal cancer: a tale of two sides or a continuum?: Figure 1. <i>Gut</i> , 2012, 61, 794-797.	6.1	224
82	Global Assessment of Genomic Regions Required for Growth in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002946.	2.1	220
83	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	3.6	219
84	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019, 10, 38.	5.8	215
85	Human gut bacteria produce $\beta$ -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	13.7	210
86	Biodiversity and functional genomics in the human microbiome. <i>Trends in Genetics</i> , 2013, 29, 51-58.	2.9	207
87	Infected erythrocyte-derived extracellular vesicles alter vascular function via regulatory Ago2-miRNA complexes in malaria. <i>Nature Communications</i> , 2016, 7, 12727.	5.8	205
88	Stability of the human faecal microbiome in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 347-355.	5.9	203
89	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
90	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009, 19, 1093-1106.	2.4	196

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91	The microbiome quality control project: baseline study design and future directions. <i>Genome Biology</i> , 2015, 16, 276.	3.8	196
92	Compositional and Temporal Changes in the Gut Microbiome of Pediatric Ulcerative Colitis Patients Are Linked to Disease Course. <i>Cell Host and Microbe</i> , 2018, 24, 600-610.e4.	5.1	193
93	Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	3.0	184
94	Functional and phylogenetic assembly of microbial communities in the human microbiome. <i>Trends in Microbiology</i> , 2014, 22, 261-266.	3.5	184
95	Passing Messages between Biological Networks to Refine Predicted Interactions. <i>PLoS ONE</i> , 2013, 8, e64832.	1.1	183
96	Reprogramming of gut microbiome energy metabolism by the <i>FUT2</i> Crohn's disease risk polymorphism. <i>ISME Journal</i> , 2014, 8, 2193-2206.	4.4	182
97	The gut microbiome modulates the protective association between a Mediterranean diet and cardiometabolic disease risk. <i>Nature Medicine</i> , 2021, 27, 333-343.	15.2	179
98	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	5.8	176
99	The Genome of Th17 Cell-Inducing Segmented Filamentous Bacteria Reveals Extensive Auxotrophy and Adaptations to the Intestinal Environment. <i>Cell Host and Microbe</i> , 2011, 10, 260-272.	5.1	175
100	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
101	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	5.9	168
102	Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. <i>Genome Biology</i> , 2015, 16, 67.	3.8	166
103	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat013.	1.4	165
104	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. <i>Nature Microbiology</i> , 2019, 4, 470-479.	5.9	164
105	Establishing What Constitutes a Healthy Human Gut Microbiome: State of the Science, Regulatory Considerations, and Future Directions. <i>Journal of Nutrition</i> , 2019, 149, 1882-1895.	1.3	163
106	STAT3 Expression, Molecular Features, Inflammation Patterns, and Prognosis in a Database of 724 Colorectal Cancers. <i>Clinical Cancer Research</i> , 2011, 17, 1452-1462.	3.2	162
107	Cross-biome comparison of microbial association networks. <i>Frontiers in Microbiology</i> , 2015, 6, 1200.	1.5	154
108	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	3.8	143

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109	Bone Marrow Is a Major Parasite Reservoir in Plasmodium vivax Infection. MBio, 2018, 9, .	1.8	141
110	The Role of Gut Microbiome in the Pathogenesis of Prostate Cancer: A Prospective, Pilot Study. Urology, 2018, 111, 122-128.	0.5	138
111	Meta'omic Analytic Techniques for Studying the Intestinal Microbiome. Gastroenterology, 2014, 146, 1437-1448.e1.	0.6	137
112	Host genetic variation and its microbiome interactions within the Human Microbiome Project. Genome Medicine, 2018, 10, 6.	3.6	134
113	Epigenomic diversity of colorectal cancer indicated by LINE-1 methylation in a database of 869 tumors. Molecular Cancer, 2010, 9, 125.	7.9	131
114	Computationally Driven, Quantitative Experiments Discover Genes Required for Mitochondrial Biogenesis. PLoS Genetics, 2009, 5, e1000407.	1.5	129
115	A scalable method for integration and functional analysis of multiple microarray datasets. Bioinformatics, 2006, 22, 2890-2897.	1.8	127
116	<i>Fusobacterium nucleatum</i> in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. Cancer Immunology Research, 2018, 6, 1327-1336.	1.6	127
117	A prominent glycy radical enzyme in human gut microbiomes metabolizes <i>trans</i> -4-hydroxy- <sc>l</sc> -proline. Science, 2017, 355, .	6.0	126
118	Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. Environmental Science & Technology, 2016, 50, 9807-9815.	4.6	125
119	Long-term use of antibiotics and risk of colorectal adenoma. Gut, 2018, 67, gutjnl-2016-313413.	6.1	125
120	A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. ELife, 2016, 5, .	2.8	117
121	A bacterial bile acid metabolite modulates Treg activity through the nuclear hormone receptor NR4A1. Cell Host and Microbe, 2021, 29, 1366-1377.e9.	5.1	111
122	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	3.0	110
123	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. MSystems, 2016, 1, .	1.7	107
124	Predicting Cellular Growth from Gene Expression Signatures. PLoS Computational Biology, 2009, 5, e1000257.	1.5	97
125	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. Scientific Reports, 2017, 7, 17686.	1.6	97
126	Delivery Mode Affects Stability of Early Infant Gut Microbiota. Cell Reports Medicine, 2020, 1, 100156.	3.3	97



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127	Paneth cell defects in Crohn's disease patients promote dysbiosis. <i>JCI Insight</i> , 2016, 1, e86907.	2.3	91
128	Microbial community function and biomarker discovery in the human microbiome. <i>Genome Biology</i> , 2011, 12, .	13.9	89
129	Current Concepts of the Intestinal Microbiota and the Pathogenesis of Infection. <i>Current Infectious Disease Reports</i> , 2011, 13, 28-34.	1.3	89
130	Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. <i>Gastroenterology</i> , 2020, 158, 1313-1325.	0.6	88
131	Toward an Efficient Method of Identifying Core Genes for Evolutionary and Functional Microbial Phylogenies. <i>PLoS ONE</i> , 2011, 6, e24704.	1.1	86
132	Global Prediction of Tissue-Specific Gene Expression and Context-Dependent Gene Networks in <i>Caenorhabditis elegans</i> . <i>PLoS Computational Biology</i> , 2009, 5, e1000417.	1.5	84
133	Skin Microbiome Imbalance in Patients with STAT1/STAT3 Defects Impairs Innate Host Defense Responses. <i>Journal of Innate Immunity</i> , 2014, 6, 253-262.	1.8	83
134	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. <i>Cell Metabolism</i> , 2014, 20, 731-741.	7.2	82
135	Detailing regulatory networks through large scale data integration. <i>Bioinformatics</i> , 2009, 25, 3267-3274.	1.8	79
136	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. <i>Genome Medicine</i> , 2015, 7, 19.	3.6	77
137	Cross-study validation for the assessment of prediction algorithms. <i>Bioinformatics</i> , 2014, 30, i105-i112.	1.8	75
138	Strain-level epidemiology of microbial communities and the human microbiome. <i>Genome Medicine</i> , 2020, 12, 71.	3.6	75
139	Optimized application of penalized regression methods to diverse genomic data. <i>Bioinformatics</i> , 2011, 27, 3399-3406.	1.8	73
140	Bioinformatics for the Human Microbiome Project. <i>PLoS Computational Biology</i> , 2012, 8, e1002779.	1.5	73
141	<i>Plasmodium</i> gametocytes display homing and vascular transmigration in the host bone marrow. <i>Science Advances</i> , 2018, 4, eaat3775.	4.7	72
142	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	3.8	72
143	The Sleipnir library for computational functional genomics. <i>Bioinformatics</i> , 2008, 24, 1559-1561.	1.8	68
144	Uncovering oral <i>Neisseria</i> tropism and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	5.9	68

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145	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	13.5	64
146	Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. <i>MSystems</i> , 2018, 3, .	1.7	63
147	Daylight exposure modulates bacterial communities associated with household dust. <i>Microbiome</i> , 2018, 6, 175.	4.9	62
148	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. <i>Genome Medicine</i> , 2021, 13, 102.	3.6	62
149	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	3.6	61
150	Nearest Neighbor Networks: clustering expression data based on gene neighborhoods. <i>BMC Bioinformatics</i> , 2007, 8, 250.	1.2	59
151	Growth effects of N-acylethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. <i>Nature Microbiology</i> , 2020, 5, 486-497.	5.9	59
152	Interplay between diet and gut microbiome, and circulating concentrations of trimethylamine N-oxide: findings from a longitudinal cohort of US men. <i>Gut</i> , 2022, 71, 724-733.	6.1	55
153	MetaRef: a pan-genomic database for comparative and community microbial genomics. <i>Nucleic Acids Research</i> , 2014, 42, D617-D624.	6.5	51
154	The Amount of Bifidobacterium Genus in Colorectal Carcinoma Tissue in Relation to Tumor Characteristics and Clinical Outcome. <i>American Journal of Pathology</i> , 2018, 188, 2839-2852.	1.9	51
155	Sex Differences in Pulmonary Responses to Ozone in Mice. <i>Role of the Microbiome. American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 60, 198-208.	1.4	49
156	The human gut microbiota in people with amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2021, 22, 186-194.	1.1	49
157	A Phase 1b Safety Study of SER-287, a Spore-Based Microbiome Therapeutic, for Active Mild to Moderate Ulcerative Colitis. <i>Gastroenterology</i> , 2021, 160, 115-127.e30.	0.6	48
158	QseC inhibition as an antivirulence approach for colitis-associated bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 142-147.	3.3	47
159	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	15.2	47
160	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. <i>PLoS Computational Biology</i> , 2013, 9, e1003392.	1.5	45
161	The Sulfur Microbial Diet Is Associated With Increased Risk of Early-Onset Colorectal Cancer Precursors. <i>Gastroenterology</i> , 2021, 161, 1423-1432.e4.	0.6	45
162	A screen of Crohn's disease-associated microbial metabolites identifies ascorbate as a novel metabolic inhibitor of activated human T cells. <i>Mucosal Immunology</i> , 2019, 12, 457-467.	2.7	44

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163	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. ISME Journal, 2014, 8, 493-503.	4.4	40
164	Structure of the Mucosal and Stool Microbiome in Lynch Syndrome. Cell Host and Microbe, 2020, 27, 585-600.e4.	5.1	40
165	Discovery of bioactive microbial gene products in inflammatory bowel disease. Nature, 2022, 606, 754-760.	13.7	38
166	A Bayesian method for detecting pairwise associations in compositional data. PLoS Computational Biology, 2017, 13, e1005852.	1.5	37
167	ASpirin Intervention for the REDuction of colorectal cancer risk (ASPIRED): a study protocol for a randomized controlled trial. Trials, 2017, 18, 50.	0.7	36
168	Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. Microbiome, 2021, 9, 17.	4.9	36
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