

Curtis Huttenhower

List of Publications by Year in descending order

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256
papers

106,895
citations

684

118
h-index

569

256
g-index

312
all docs

312
docs citations

312
times ranked

83258
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	20.4	12,956
2	Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.	9.1	11,988
3	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	20.4	8,414
4	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	20.4	3,120
5	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	10.8	2,700
6	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , 2012, 13, R79.	9.1	2,324
7	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	19.2	1,936
8	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	35.3	1,829
9	Genomic analysis identifies association of <i>Fusobacterium</i> with colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 292-298.	5.5	1,659
10	Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.	19.2	1,640
11	Expansion of intestinal <i>Prevotella copri</i> correlates with enhanced susceptibility to arthritis. <i>ELife</i> , 2013, 2, e01202.	5.8	1,575
12	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	35.3	1,322
13	Microbial Co-occurrence Relationships in the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002606.	3.0	1,313
14	The healthy human microbiome. <i>Genome Medicine</i> , 2016, 8, 51.	8.4	1,296
15	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	12.7	1,225
16	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.2	1,193
17	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.	27.3	1,168
18	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.	10.8	1,042

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19	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	27.3	1,029
20	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	5.8	1,002
21	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	35.3	981
22	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002358.	3.0	965
23	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	3.0	917
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.	10.8	887
25	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	27.3	852
26	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.	9.1	841
27	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013, 4, 2304.	12.8	818
28	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.	13.2	814
29	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. <i>Nature Communications</i> , 2016, 7, 10391.	12.8	810
30	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	12.7	783
31	<i>Fusobacterium nucleatum</i> in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016, 65, 1973-1980.	13.4	763
32	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. <i>PeerJ</i> , 2015, 3, e1029.	2.0	726
33	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	35.3	660
34	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.9	632
35	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. <i>Gut</i> , 2018, 67, 108-119.	13.4	628
36	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. <i>PLoS ONE</i> , 2012, 7, e36466.	2.5	592

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37	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	5.5	585
38	Cervicovaginal Bacteria Are a Major Modulator of Host Inflammatory Responses in the Female Genital Tract. <i>Immunity</i> , 2015, 42, 965-976.	13.8	582
39	Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	10.8	580
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.	7.4	573
41	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	28.6	569
42	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 2021, 27, 321-332.	29.5	550
43	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.	7.4	545
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.	2.3	529
45	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.	13.4	529
46	<i>Fusobacterium nucleatum</i> and T Cells in Colorectal Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 653.	7.2	523
47	A novel <i>Ruminococcus gnavus</i> clade enriched in inflammatory bowel disease patients. <i>Genome Medicine</i> , 2017, 9, 103.	8.4	519
48	Lactobacillus-Deficient Cervicovaginal Bacterial Communities Are Associated with Increased HIV Acquisition in Young South African Women. <i>Immunity</i> , 2017, 46, 29-37.	13.8	512
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.	11.9	512
50	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.	3.0	455
51	Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature. <i>Journal of Clinical Investigation</i> , 2014, 124, 3617-3633.	6.5	446
52	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	12.8	433
53	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	12.7	432
54	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. <i>Nature Biotechnology</i> , 2017, 35, 1077-1086.	20.4	423

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55	Chapter 12: Human Microbiome Analysis. PLoS Computational Biology, 2012, 8, e1002808.	3.0	418
56	Identifying personal microbiomes using metagenomic codes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2930-8.	7.4	391
57	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. PLoS Biology, 2012, 10, e1001377.	5.3	383
58	Global chemical effects of the microbiome include new bile-acid conjugations. Nature, 2020, 579, 123-129.	35.3	375
59	Schrödinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. Microbiome, 2017, 5, 86.	11.4	364
60	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. ISME Journal, 2014, 8, 1403-1417.	9.8	359
61	Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Medicine, 2014, 6, 107.	8.4	328
62	Accessible, curated metagenomic data through ExperimentHub. Nature Methods, 2017, 14, 1023-1024.	19.2	328
63	Tryptophan Biosynthesis Protects Mycobacteria from CD4 T-Cell-Mediated Killing. Cell, 2013, 155, 1296-1308.	27.3	309
64	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. Cell Host and Microbe, 2019, 25, 668-680.e7.	10.8	308
65	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. Cell Host and Microbe, 2019, 26, 666-679.e7.	10.8	306
66	Inflammatory Bowel Disease as a Model for Translating the Microbiome. Immunity, 2014, 40, 843-854.	13.8	293
67	Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants. Microbiome, 2013, 1, 13.	11.4	291
68	Simvastatin for the Prevention of Exacerbations in Moderate-to-Severe COPD. New England Journal of Medicine, 2014, 370, 2201-2210.	29.6	287
69	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. Cell Host and Microbe, 2015, 17, 385-391.	10.8	277
70	Computational meta'omics for microbial community studies. Molecular Systems Biology, 2013, 9, 666.	7.2	268
71	bioBakery: a meta-omic analysis environment. Bioinformatics, 2018, 34, 1235-1237.	4.2	266
72	Human gut bacteria produce ω -17-modulating bile acid metabolites. Nature, 2022, 603, 907-912.	35.3	266

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73	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	3.0	259
74	Integrative analysis of the microbiome and metabolome of the human intestinal mucosal surface reveals exquisite inter-relationships. <i>Microbiome</i> , 2013, 1, 17.	11.4	258
75	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.	7.2	255
76	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlan 4. <i>Nature Biotechnology</i> , 2023, 41, 1633-1644.	20.4	250
77	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007, 23, 2692-2699.	4.2	243
78	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019, 10, 38.	12.8	236
79	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	8.4	231
80	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	230
81	Colorectal cancer: a tale of two sides or a continuum?: Figure 1. <i>Gut</i> , 2012, 61, 794-797.	13.4	227
82	Stability of the human faecal microbiome in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 347-355.	12.7	223
83	Global Assessment of Genomic Regions Required for Growth in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002946.	4.0	222
84	Biodiversity and functional genomics in the human microbiome. <i>Trends in Genetics</i> , 2013, 29, 51-58.	6.7	213
85	Infected erythrocyte-derived extracellular vesicles alter vascular function via regulatory Ago2-miRNA complexes in malaria. <i>Nature Communications</i> , 2016, 7, 12727.	12.8	212
86	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.	10.8	211
87	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	29.5	210
88	The gut microbiome modulates the protective association between a Mediterranean diet and cardiometabolic disease risk. <i>Nature Medicine</i> , 2021, 27, 333-343.	29.5	206
89	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 1551.	27.3	202
90	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009, 19, 1093-1106.	5.5	200

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91	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	12.8	197
92	Passing Messages between Biological Networks to Refine Predicted Interactions. <i>PLoS ONE</i> , 2013, 8, e64832.	2.5	190
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, .	6.2	187
94	Functional and phylogenetic assembly of microbial communities in the human microbiome. <i>Trends in Microbiology</i> , 2014, 22, 261-266.	7.6	185
95	Reprogramming of gut microbiome energy metabolism by the <i>FUT2</i> Crohn's disease risk polymorphism. <i>ISME Journal</i> , 2014, 8, 2193-2206.	9.8	184
96	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1897.	27.3	184
97	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	12.7	181
98	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.	10.8	178
99	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.	2.7	178
100	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.	8.5	176
101	Genomic variation and strain-specific functional adaptation in the human gut microbiome during early life. <i>Nature Microbiology</i> , 2019, 4, 470-479.	12.7	176
102	curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat013.	3.1	171
103	STAT3 Expression, Molecular Features, Inflammation Patterns, and Prognosis in a Database of 724 Colorectal Cancers. <i>Clinical Cancer Research</i> , 2011, 17, 1452-1462.	7.1	167
104	Bone Marrow Is a Major Parasite Reservoir in <i>Plasmodium vivax</i> Infection. <i>MBio</i> , 2018, 9, .	4.2	152
105	The Role of Gut Microbiome in the Pathogenesis of Prostate Cancer: A Prospective, Pilot Study. <i>Urology</i> , 2018, 111, 122-128.	1.4	151
106	Questioning the fetal microbiome illustrates pitfalls of low-biomass microbial studies. <i>Nature</i> , 2023, 613, 639-649.	35.3	151
107	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	9.1	150
108	Host genetic variation and its microbiome interactions within the Human Microbiome Project. <i>Genome Medicine</i> , 2018, 10, 6.	8.4	143

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109	Meta'omic Analytic Techniques for Studying the Intestinal Microbiome. <i>Gastroenterology</i> , 2014, 146, 1437-1448.e1.	1.3	140
110	<i>Fusobacterium nucleatum</i> in Colorectal Cancer Relates to Immune Response Differentially by Tumor Microsatellite Instability Status. <i>Cancer Immunology Research</i> , 2018, 6, 1327-1336.	3.2	138
111	A bacterial bile acid metabolite modulates Treg activity through the nuclear hormone receptor NR4A1. <i>Cell Host and Microbe</i> , 2021, 29, 1366-1377.e9.	10.8	137
112	Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. <i>Environmental Science & Technology</i> , 2016, 50, 9807-9815.	10.2	136
113	Epigenomic diversity of colorectal cancer indicated by LINE-1 methylation in a database of 869 tumors. <i>Molecular Cancer</i> , 2010, 9, 125.	19.8	132
114	Computationally Driven, Quantitative Experiments Discover Genes Required for Mitochondrial Biogenesis. <i>PLoS Genetics</i> , 2009, 5, e1000407.	3.3	131
115	Long-term use of antibiotics and risk of colorectal adenoma. <i>Gut</i> , 2018, 67, gutjnl-2016-313413.	13.4	129
116	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006, 22, 2890-2897.	4.2	128
117	A prominent glycy radical enzyme in human gut microbiomes metabolizes <i>trans</i> -4-hydroxy- <i>l</i> -proline. <i>Science</i> , 2017, 355, .	19.6	128
118	A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. <i>ELife</i> , 2016, 5, .	5.8	123
119	Delivery Mode Affects Stability of Early Infant Gut Microbiota. <i>Cell Reports Medicine</i> , 2020, 1, 100156.	5.8	119
120	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , 2016, 1, .	3.9	115
121	Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.2	112
122	Predicting Cellular Growth from Gene Expression Signatures. <i>PLoS Computational Biology</i> , 2009, 5, e1000257.	3.0	101
123	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <i>Scientific Reports</i> , 2017, 7, 17686.	3.4	100
124	Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. <i>Gastroenterology</i> , 2020, 158, 1313-1325.	1.3	100
125	Shotgun glycomics of pig lung identifies natural endogenous receptors for influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2241-50.	7.4	98
126	Paneth cell defects in Crohn's disease patients promote dysbiosis. <i>Journal of Clinical Investigation</i> , 2016, 1, e86907.	6.5	95

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127	Toward an Efficient Method of Identifying Core Genes for Evolutionary and Functional Microbial Phylogenies. PLoS ONE, 2011, 6, e24704.	2.5	92
128	Current Concepts of the Intestinal Microbiota and the Pathogenesis of Infection. Current Infectious Disease Reports, 2011, 13, 28-34.	3.1	90
129	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. Cell Metabolism, 2014, 20, 731-741.	15.5	85
130	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138.	9.1	85
131	Strain-level epidemiology of microbial communities and the human microbiome. Genome Medicine, 2020, 12, 71.	8.4	84
132	Global Prediction of Tissue-Specific Gene Expression and Context-Dependent Gene Networks in Caenorhabditis elegans. PLoS Computational Biology, 2009, 5, e1000417.	3.0	84
133	Detailing regulatory networks through large scale data integration. Bioinformatics, 2009, 25, 3267-3274.	4.2	80
134	Cross-study validation for the assessment of prediction algorithms. Bioinformatics, 2014, 30, i105-i112.	4.2	78
135	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. Genome Medicine, 2015, 7, 19.	8.4	78
136	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. Molecular Cell, 2020, 78, 459-476.e13.	9.4	78
137	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. Genome Medicine, 2021, 13, 102.	8.4	78
138	<i>Plasmodium</i> gametocytes display homing and vascular transmigration in the host bone marrow. Science Advances, 2018, 4, eaat3775.	10.7	77
139	Bioinformatics for the Human Microbiome Project. PLoS Computational Biology, 2012, 8, e1002779.	3.0	76
140	Optimized application of penalized regression methods to diverse genomic data. Bioinformatics, 2011, 27, 3399-3406.	4.2	75
141	Growth effects of N-acyl ethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. Nature Microbiology, 2020, 5, 486-497.	12.7	73
142	Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. Nature Microbiology, 2016, 1, 16070.	12.7	72
143	Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. MSys, 2018, 3, .	3.9	70
144	Interplay between diet and gut microbiome, and circulating concentrations of trimethylamine N-oxide: findings from a longitudinal cohort of US men. Gut, 2022, 71, 724-733.	13.4	70

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145	The Sleipnir library for computational functional genomics. <i>Bioinformatics</i> , 2008, 24, 1559-1561.	4.2	68
146	Daylight exposure modulates bacterial communities associated with household dust. <i>Microbiome</i> , 2018, 6, 175.	11.4	68
147	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	27.3	64
148	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	8.4	63
149	Nearest Neighbor Networks: clustering expression data based on gene neighborhoods. <i>BMC Bioinformatics</i> , 2007, 8, 250.	2.6	59
150	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.	4.0	57
151	The human gut microbiota in people with amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2021, 22, 186-194.	2.1	57
152	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.	1.3	57
153	Phosphorylation-Regulated Activation of the Arabidopsis RRS1-R/RPS4 Immune Receptor Complex Reveals Two Distinct Effector Recognition Mechanisms. <i>Cell Host and Microbe</i> , 2020, 27, 769-781.e6.	10.8	53
154	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	29.5	53
155	MetaRef: a pan-genomic database for comparative and community microbial genomics. <i>Nucleic Acids Research</i> , 2014, 42, D617-D624.	13.8	52
156	The Sulfur Microbial Diet Is Associated With Increased Risk of Early-Onset Colorectal Cancer Precursors. <i>Gastroenterology</i> , 2021, 161, 1423-1432.e4.	1.3	52
157	Population structure discovery in meta-analyzed microbial communities and inflammatory bowel disease using MMUPHin. <i>Genome Biology</i> , 2022, 23, .	9.1	52
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.	7.4	50
159	Sex Differences in Pulmonary Responses to Ozone in Mice. Role of the Microbiome. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 60, 198-208.	3.2	49
160	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. <i>PLoS Computational Biology</i> , 2013, 9, e1003392.	3.0	47
161	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.	6.0	47
162	Association of <i>Fusobacterium nucleatum</i> with Specific T-cell Subsets in the Colorectal Carcinoma Microenvironment. <i>Clinical Cancer Research</i> , 2021, 27, 2816-2826.	7.1	46

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163	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. Annual Review of Biomedical Data Science, 2021, 4, 279-311.	6.4	45
164	Strain-level fitness in the gut microbiome is an emergent property of glycans and a single metabolite. Cell, 2022, 185, 513-529.e21.	27.3	45
165	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. ISME Journal, 2014, 8, 493-503.	9.8	43
166	Sense of Mission and Subsequent Health and Well-Being Among Young Adults: An Outcome-Wide Analysis. American Journal of Epidemiology, 2019, 188, 664-673.	3.6	43
167	Discovery of bioactive microbial gene products in inflammatory bowel disease. Nature, 2022, 606, 754-760.	35.3	43
168	Gut microbial metabolism of 5-ASA diminishes its clinical efficacy in inflammatory bowel disease. Nature Medicine, 2023, 29, 700-709.	29.5	43
169	Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. Microbiome, 2021, 9, 17.	11.4	41
170	A Bayesian method for detecting pairwise associations in compositional data. PLoS Computational Biology, 2017, 13, e1005852.	3.0	40
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