

Curtis Huttenhower

List of Publications by Year in descending order

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Version: 2024-02-01

242
papers

98,927
citations

1027

117
h-index

1013

243
g-index

276
all docs

276
docs citations

276
times ranked

85781
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	The oral microbiome in relation to pancreatic cancer risk in African Americans. <i>British Journal of Cancer</i> , 2022, 126, 287-296.	2.9	9
3	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. <i>Bioinformatics</i> , 2022, 38, 612-620.	1.8	4
4	The Gut Microbiome Modifies the Association Between a Mediterranean Diet and Diabetes in USA Hispanic/ Latino Population. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e924-e934.	1.8	9
5	Strain-level fitness in the gut microbiome is an emergent property of glycans and a single metabolite. <i>Cell</i> , 2022, 185, 513-529.e21.	13.5	36
6	Dietary lignans, plasma enterolactone levels, and metabolic risk in men: exploring the role of the gut microbiome. <i>BMC Microbiology</i> , 2022, 22, 82.	1.3	8
7	Human gut bacteria produce β -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	13.7	210
8	Association of midlife antibiotic use with subsequent cognitive function in women. <i>PLoS ONE</i> , 2022, 17, e0264649.	1.1	12
9	Strain Identification and Quantitative Analysis in Microbial Communities. <i>Journal of Molecular Biology</i> , 2022, 434, 167582.	2.0	15
10	Mucosal metabolites fuel the growth and virulence of <i>E. coli</i> linked to Crohn's disease. <i>JCI Insight</i> , 2022, 7, .	2.3	17
11	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	1.8	18
12	Discovery of bioactive microbial gene products in inflammatory bowel disease. <i>Nature</i> , 2022, 606, 754-760.	13.7	38
13	Histidine Intake, Human Gut Microbiome, Plasma Levels of Imidazole Propionate, and Coronary Heart Disease Risk in US Adults. <i>Current Developments in Nutrition</i> , 2022, 6, 1041.	0.1	1
14	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
15	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
16	Microbiome Biomarkers: One Step Closer in NAFLD Cirrhosis. <i>Hepatology</i> , 2021, 73, 2063-2066.	3.6	4
17	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	5.1	20
18	Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. <i>Microbiome</i> , 2021, 9, 17.	4.9	36

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19	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.	3.2	36
20	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
21	The colorectal cancer-associated faecal microbiome of developing countries resembles that of developed countries. <i>Genome Medicine</i> , 2021, 13, 27.	3.6	25
22	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
23	Microbiome Analysis of More Than 2,000 NHS Bowel Cancer Screening Programme Samples Shows the Potential to Improve Screening Accuracy. <i>Clinical Cancer Research</i> , 2021, 27, 2246-2254.	3.2	18
24	Overview of the Microbiome Among Nurses study (Micro-N) as an example of prospective characterization of the microbiome within cohort studies. <i>Nature Protocols</i> , 2021, 16, 2724-2731.	5.5	7
25	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	15.2	47
26	A polymorphism in the promoter of FRAS1 is a candidate SNP associated with metastatic prostate cancer. <i>Prostate</i> , 2021, 81, 683-693.	1.2	5
27	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
28	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
29	Plant-Based Diet Index and Metabolic Risk in Men: Exploring the Role of the Gut Microbiome. <i>Journal of Nutrition</i> , 2021, 151, 2780-2789.	1.3	20
30	Statistical approaches for differential expression analysis in metatranscriptomics. <i>Bioinformatics</i> , 2021, 37, i34-i41.	1.8	26
31	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	2.8	36
32	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
33	The Sulfur Microbial Diet and Risk of Colorectal Cancer by Molecular Subtypes and Intratumoral Microbial Species in Adult Men. <i>Clinical and Translational Gastroenterology</i> , 2021, 12, e00338.	1.3	7
34	A statistical model for describing and simulating microbial community profiles. <i>PLoS Computational Biology</i> , 2021, 17, e1008913.	1.5	21
35	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.	5.1	111
36	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

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37	Of mice and men and women: Sexual dimorphism of the gut microbiome. <i>International Journal of Women's Dermatology</i> , 2021, 7, 533-538.	1.1	10
38	Association Between the Sulfur Microbial Diet and Risk of Colorectal Cancer. <i>JAMA Network Open</i> , 2021, 4, e2134308.	2.8	28
39	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	1.5	691
40	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
41	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	6.0	369
42	Association of autophagy status with amount of <i>Fusobacterium nucleatum</i> in colorectal cancer. <i>Journal of Pathology</i> , 2020, 250, 397-408.	2.1	27
43	Strain-level epidemiology of microbial communities and the human microbiome. <i>Genome Medicine</i> , 2020, 12, 71.	3.6	75
44	Determinants of <i>Staphylococcus aureus</i> carriage in the developing infant nasal microbiome. <i>Genome Biology</i> , 2020, 21, 301.	3.8	11
45	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
46	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	9.4	2,621
47	The Gut Microbiome Modifies the Protective Effects of a Mediterranean Diet Against Cardiometabolic Disease Risk. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa062_054.	0.1	1
48	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
49	Global chemical effects of the microbiome include new bile-acid conjugations. <i>Nature</i> , 2020, 579, 123-129.	13.7	316
50	Mobilizable antibiotic resistance genes are present in dust microbial communities. <i>PLoS Pathogens</i> , 2020, 16, e1008211.	2.1	25
51	Growth effects of N-acyl ethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. <i>Nature Microbiology</i> , 2020, 5, 486-497.	5.9	59
52	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
53	Structure of the Mucosal and Stool Microbiome in Lynch Syndrome. <i>Cell Host and Microbe</i> , 2020, 27, 585-600.e4.	5.1	40
54	Delivery Mode Affects Stability of Early Infant Gut Microbiota. <i>Cell Reports Medicine</i> , 2020, 1, 100156.	3.3	97

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55	Analysis of the Associations Between the Human Fecal Microbiome and Bone Density, Structure, and Strength: The Osteoporotic Fractures in Men (MrOS) Cohort. <i>Journal of Bone and Mineral Research</i> , 2020, 37, 597-607.	3.1	13
56	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
57	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
58	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	5.8	176
59	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
60	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
61	The interleukin-33 receptor contributes to pulmonary responses to ozone in male mice: role of the microbiome. <i>Respiratory Research</i> , 2019, 20, 197.	1.4	19
62	OP19 Corticosteroid response rectal gene signature and associated microbial variation in treatment naïve ulcerative colitis. <i>Journal of Crohn's and Colitis</i> , 2019, 13, S013-S014.	0.6	0
63	Comparative genomics and genome biology of <i>Campylobacter showae</i> . <i>Emerging Microbes and Infections</i> , 2019, 8, 827-840.	3.0	8
64	Naturally acquired immunity against immature <i>Plasmodium falciparum</i> gametocytes. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	31
65	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
66	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. <i>Cell Host and Microbe</i> , 2019, 25, 668-680.e7.	5.1	274
67	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
68	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
69	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
70	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 584-590.	1.1	8
71	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
72	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. <i>American Journal of Epidemiology</i> , 2019, 188, 1023-1026.	1.6	30

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73	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	5.9	1,094
74	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.	1.4	49
75	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
76	Long-term use of antibiotics and risk of colorectal adenoma. <i>Gut</i> , 2018, 67, gutjnl-2016-313413.	6.1	125
77	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	1.8	241
78	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
79	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	5.9	168
80	Stability of the human faecal microbiome in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 347-355.	5.9	203
81	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	5.9	408
82	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
83	The Role of Gut Microbiome in the Pathogenesis of Prostate Cancer: A Prospective, Pilot Study. <i>Urology</i> , 2018, 111, 122-128.	0.5	138
84	Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. <i>MSystems</i> , 2018, 3, .	1.7	63
85	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. <i>Genome Biology</i> , 2018, 19, 142.	3.8	20
86	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
87	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
88	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	13.7	1,220
89	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	13.7	623
90	Daylight exposure modulates bacterial communities associated with household dust. <i>Microbiome</i> , 2018, 6, 175.	4.9	62

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91	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	9.0	1,125
92	Multimiomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2018, 155, e1-e4.	0.6	24
93	<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.	1.6	127
94	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
95	<i>Plasmodium</i> gametocytes display homing and vascular transmigration in the host bone marrow. <i>Science Advances</i> , 2018, 4, eaat3775.	4.7	72
96	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
97	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
98	Host genetic variation and its microbiome interactions within the Human Microbiome Project. <i>Genome Medicine</i> , 2018, 10, 6.	3.6	134
99	Bone Marrow Is a Major Parasite Reservoir in <i>Plasmodium vivax</i> Infection. <i>MBio</i> , 2018, 9, .	1.8	141
100	<i>Bifidobacterium</i> Genus in Colorectal Carcinoma Tissue in relation to Tumor Characteristics and Patient Survival. <i>FASEB Journal</i> , 2018, 32, 407.3.	0.2	0
101	<i>Lactobacillus</i> -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
102	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
103	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	2.4	540
104	A prominent glyxyl radical enzyme in human gut microbiomes metabolizes <i>trans</i> -4-hydroxy- <i>l</i> -proline. <i>Science</i> , 2017, 355, .	6.0	126
105	ASpirin Intervention for the REDuction of colorectal cancer risk (ASPIRED): a study protocol for a randomized controlled trial. <i>Trials</i> , 2017, 18, 50.	0.7	36
106	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
107	Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.	9.0	292
108	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

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109	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	13.7	929
110	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
111	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017, 2, .	1.7	18
112	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
113	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <i>Scientific Reports</i> , 2017, 7, 17686.	1.6	97
114	PWE-026â€¦Elucidating the pathogenic potential of the intestinal pathogen <i>Campylobacter</i> <i>showae</i> . , 2017, , .		0
115	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
116	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	3.8	143
117	A novel <i>Ruminococcus gnavus</i> clade enriched in inflammatory bowel disease patients. <i>Genome Medicine</i> , 2017, 9, 103.	3.6	478
118	SchrÃ¶dingerâ€™s microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	4.9	347
119	A Bayesian method for detecting pairwise associations in compositional data. <i>PLoS Computational Biology</i> , 2017, 13, e1005852.	1.5	37
120	Paneth cell defects in Crohnâ€™s disease patients promote dysbiosis. <i>JCI Insight</i> , 2016, 1, e86907.	2.3	91
121	A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. <i>ELife</i> , 2016, 5, .	2.8	117
122	PWE-102â€¦Elucidating The Role of Non JEJUNI/Coli-Campylobacter in The Development of Colorectal Cancer Utilising Comparative Genomics to Study Their Pathogenic Potential. <i>Gut</i> , 2016, 65, A188.2-A189.	6.1	0
123	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , 2016, 1, .	1.7	107
124	The <i>Chthonomonas calidirosea</i> Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's TaupÃ¶ Volcanic Zone. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3572-3581.	1.4	9
125	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	13.5	968
126	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398

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127	The healthy human microbiome. <i>Genome Medicine</i> , 2016, 8, 51.	3.6	1,214
128	Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. <i>Environmental Science & Technology</i> , 2016, 50, 9807-9815.	4.6	125
129	CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. <i>Genome Biology</i> , 2016, 17, 201.	3.8	24
130	Uncovering oral <i>Neisseria</i> tropism and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	5.9	68
131	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
132	<i>Fusobacterium nucleatum</i> in Colorectal Carcinoma Tissue According to Tumor Location. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e200.	1.3	225
133	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
134	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	13.5	806
135	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	3.6	219
136	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. <i>Nature Communications</i> , 2016, 7, 10391.	5.8	784
137	Fecal Microbiome in Epidemiologic Studies—Letter. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 869-869.	1.1	3
138	<i>Fusobacterium nucleatum</i> in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016, 65, 1973-1980.	6.1	718
139	Computational Reconstruction of NF- κ B Pathway Interaction Mechanisms during Prostate Cancer. <i>PLoS Computational Biology</i> , 2016, 12, e1004820.	1.5	27
140	Complete genome sequence of the thermophilic Acidobacteria, <i>Pyrinomonas methylaliphatogenes</i> type strain K22T. <i>Standards in Genomic Sciences</i> , 2015, 10, 101.	1.5	17
141	Cross-biome comparison of microbial association networks. <i>Frontiers in Microbiology</i> , 2015, 6, 1200.	1.5	154
142	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
143	<i>Fusobacterium nucleatum</i> and T Cells in Colorectal Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 653.	3.4	498
144	The microbiome quality control project: baseline study design and future directions. <i>Genome Biology</i> , 2015, 16, 276.	3.8	196

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145	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
146	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. <i>Genome Medicine</i> , 2015, 7, 19.	3.6	77
147	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
148	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	13.6	544
149	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
150	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
151	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	9.0	1,843
152	Genomic Sequencing and Other Tools for Studying Microbial Communities. <i>Microbe Magazine</i> , 2015, 10, 419-425.	0.4	4
153	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	1.5	235
154	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. <i>PeerJ</i> , 2015, 3, e1029.	0.9	701
155	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015, 3, e791.	0.9	12
156	Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.	3.6	322
157	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
158	Cross-study validation for the assessment of prediction algorithms. <i>Bioinformatics</i> , 2014, 30, i105-i112.	1.8	75
159	MÃ¡s-o-menos: a simple sign averaging method for discrimination in genomic data analysis. <i>Bioinformatics</i> , 2014, 30, 3062-3069.	1.8	34
160	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
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