

Curtis Huttenhower

List of Publications by Year in descending order

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Version: 2024-02-01

242
papers

98,927
citations

872

117
h-index

877

243
g-index

276
all docs

276
docs citations

276
times ranked

79257
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.	12.1	55
2	The oral microbiome in relation to pancreatic cancer risk in African Americans. <i>British Journal of Cancer</i> , 2022, 126, 287-296.	6.4	9
3	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. <i>Bioinformatics</i> , 2022, 38, 612-620.	4.1	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.	3.6	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.	28.9	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.	3.3	8
7	Human gut bacteria produce ß-17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	27.8	210
8	Association of midlife antibiotic use with subsequent cognitive function in women. <i>PLoS ONE</i> , 2022, 17, e0264649.	2.5	12
9	Strain Identification and Quantitative Analysis in Microbial Communities. <i>Journal of Molecular Biology</i> , 2022, 434, 167582.	4.2	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, .	5.0	17
11	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	4.1	18
12	Discovery of bioactive microbial gene products in inflammatory bowel disease. <i>Nature</i> , 2022, 606, 754-760.	27.8	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.	0.3	1
14	The human gut microbiota in people with amyotrophic lateral sclerosis. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2021, 22, 186-194.	1.7	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.	1.3	48
16	Microbiome Biomarkers: One Step Closer in NAFLD Cirrhosis. <i>Hepatology</i> , 2021, 73, 2063-2066.	7.3	4
17	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	11.0	20
18	Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. <i>Microbiome</i> , 2021, 9, 17.	11.1	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.	7.0	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.	30.7	179
21	The colorectal cancer-associated faecal microbiome of developing countries resembles that of developed countries. <i>Genome Medicine</i> , 2021, 13, 27.	8.2	25
22	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	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.	7.0	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.	12.0	7
25	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	30.7	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.	2.3	5
27	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	6.0	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.	8.2	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.	2.9	20
30	Statistical approaches for differential expression analysis in metatranscriptomics. <i>Bioinformatics</i> , 2021, 37, i34-i41.	4.1	26
31	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	6.5	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.	1.3	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.	2.5	7
34	A statistical model for describing and simulating microbial community profiles. <i>PLoS Computational Biology</i> , 2021, 17, e1008913.	3.2	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.	11.0	111
36	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 2021, 27, 321-332.	30.7	477

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37	Of mice and men and women: Sexual dimorphism of the gut microbiome. International Journal of Women's Dermatology, 2021, 7, 533-538.	2.0	10
38	Association Between the Sulfur Microbial Diet and Risk of Colorectal Cancer. JAMA Network Open, 2021, 4, e2134308.	5.9	28
39	Multivariable association discovery in population-scale meta-omics studies. PLoS Computational Biology, 2021, 17, e1009442.	3.2	691
40	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
41	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. Science, 2021, 374, 1632-1640.	12.6	369
42	Association of autophagy status with amount of <i>Fusobacterium nucleatum</i> in colorectal cancer. Journal of Pathology, 2020, 250, 397-408.	4.5	27
43	Strain-level epidemiology of microbial communities and the human microbiome. Genome Medicine, 2020, 12, 71.	8.2	75
44	Determinants of Staphylococcus aureus carriage in the developing infant nasal microbiome. Genome Biology, 2020, 21, 301.	8.8	11
45	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. Nature Communications, 2020, 11, 2500.	12.8	368
46	PICRUSt2 for prediction of metagenome functions. Nature Biotechnology, 2020, 38, 685-688.	17.5	2,621
47	The Gut Microbiome Modifies the Protective Effects of a Mediterranean Diet Against Cardiometabolic Disease Risk. Current Developments in Nutrition, 2020, 4, nzaa062_054.	0.3	1
48	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138.	8.8	72
49	Global chemical effects of the microbiome include new bile-acid conjugations. Nature, 2020, 579, 123-129.	27.8	316
50	Mobilizable antibiotic resistance genes are present in dust microbial communities. PLoS Pathogens, 2020, 16, e1008211.	4.7	25
51	Growth effects of N-acyl ethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. Nature Microbiology, 2020, 5, 486-497.	13.3	59
52	Association Between Sulfur-Metabolizing Bacterial Communities in Stool and Risk of Distal Colorectal Cancer in Men. Gastroenterology, 2020, 158, 1313-1325.	1.3	88
53	Structure of the Mucosal and Stool Microbiome in Lynch Syndrome. Cell Host and Microbe, 2020, 27, 585-600.e4.	11.0	40
54	Delivery Mode Affects Stability of Early Infant Gut Microbiota. Cell Reports Medicine, 2020, 1, 100156.	6.5	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.	2.8	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.	2.9	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.	11.0	274
58	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	12.8	176
59	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
60	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	11.0	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.	3.6	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.	1.3	0
63	Comparative genomics and genome biology of Campylobacter showae. <i>Emerging Microbes and Infections</i> , 2019, 8, 827-840.	6.5	8
64	Naturally acquired immunity against immature <i>Plasmodium falciparum</i> gametocytes. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	31
65	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	27.8	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.	11.0	274
67	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	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.	13.3	164
69	Ulcerative colitis mucosal transcriptomes reveal mitochondriopathy and personalized mechanisms underlying disease severity and treatment response. <i>Nature Communications</i> , 2019, 10, 38.	12.8	215
70	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 584-590.	2.5	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.	28.9	1,087
72	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. <i>American Journal of Epidemiology</i> , 2019, 188, 1023-1026.	3.4	30

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73	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	13.3	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.	2.9	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.	6.0	44
76	Long-term use of antibiotics and risk of colorectal adenoma. <i>Gut</i> , 2018, 67, gutjnl-2016-313413.	12.1	125
77	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	4.1	241
78	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	13.3	717
79	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	13.3	168
80	Stability of the human faecal microbiome in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 347-355.	13.3	203
81	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	13.3	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.	12.1	590
83	The Role of Gut Microbiome in the Pathogenesis of Prostate Cancer: A Prospective, Pilot Study. <i>Urology</i> , 2018, 111, 122-128.	1.0	138
84	Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. <i>MSystems</i> , 2018, 3, .	3.8	63
85	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. <i>Genome Biology</i> , 2018, 19, 142.	8.8	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.	3.8	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.	11.0	193
88	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	27.8	1,220
89	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	27.8	623
90	Daylight exposure modulates bacterial communities associated with household dust. <i>Microbiome</i> , 2018, 6, 175.	11.1	62

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91	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.0	1,125
92	Multimomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2018, 155, e1-e4.	1.3	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.	3.4	127
94	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
95	<i>Plasmodium</i> gametocytes display homing and vascular transmigration in the host bone marrow. <i>Science Advances</i> , 2018, 4, eaat3775.	10.3	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.	11.0	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.	11.0	311
98	Host genetic variation and its microbiome interactions within the Human Microbiome Project. <i>Genome Medicine</i> , 2018, 10, 6.	8.2	134
99	Bone Marrow Is a Major Parasite Reservoir in <i>Plasmodium vivax</i> Infection. <i>MBio</i> , 2018, 9, .	4.1	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.	0.5	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.	14.3	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.	13.7	482
103	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	5.5	540
104	A prominent glycol radical enzyme in human gut microbiomes metabolizes <i>trans</i> -4-hydroxy- <i>l</i> -proline. <i>Science</i> , 2017, 355, .	12.6	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.	1.6	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.	7.1	47
107	Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.	19.0	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.	17.5	400

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109	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	27.8	929
110	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. <i>Science</i> , 2017, 357, 1156-1160.	12.6	1,059
111	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017, 2, .	3.8	18
112	Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	11.0	523
113	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <i>Scientific Reports</i> , 2017, 7, 17686.	3.3	97
114	PWE-026â€¦Elucidating the pathogenic potential of the intestinal pathogen <i>campylobacter 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.	7.1	243
116	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	8.8	143
117	A novel <i>Ruminococcus gnavus</i> clade enriched in inflammatory bowel disease patients. <i>Genome Medicine</i> , 2017, 9, 103.	8.2	478
118	SchrÃ¶dingerâ€™s microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	11.1	347
119	A Bayesian method for detecting pairwise associations in compositional data. <i>PLoS Computational Biology</i> , 2017, 13, e1005852.	3.2	37
120	Paneth cell defects in Crohnâ€™s disease patients promote dysbiosis. <i>JCI Insight</i> , 2016, 1, e86907.	5.0	91
121	A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. <i>ELife</i> , 2016, 5, .	6.0	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.	12.1	0
123	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , 2016, 1, .	3.8	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.	3.1	9
125	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	28.9	968
126	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	12.6	1,398

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127	The healthy human microbiome. <i>Genome Medicine</i> , 2016, 8, 51.	8.2	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.	10.0	125
129	CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. <i>Genome Biology</i> , 2016, 17, 201.	8.8	24
130	Uncovering oral <i>Neisseria</i> tropism and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	13.3	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.	12.4	763
132	<i>Fusobacterium nucleatum</i> in Colorectal Carcinoma Tissue According to Tumor Location. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e200.	2.5	225
133	Infected erythrocyte-derived extracellular vesicles alter vascular function via regulatory Ago2-miRNA complexes in malaria. <i>Nature Communications</i> , 2016, 7, 12727.	12.8	205
134	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	28.9	806
135	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	8.2	219
136	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. <i>Nature Communications</i> , 2016, 7, 10391.	12.8	784
137	Fecal Microbiome in Epidemiologic Studies—Letter. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 869-869.	2.5	3
138	<i>Fusobacterium nucleatum</i> in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016, 65, 1973-1980.	12.1	718
139	Computational Reconstruction of NF- κ B Pathway Interaction Mechanisms during Prostate Cancer. <i>PLoS Computational Biology</i> , 2016, 12, e1004820.	3.2	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.	3.5	154
142	Cervicovaginal Bacteria Are a Major Modulator of Host Inflammatory Responses in the Female Genital Tract. <i>Immunity</i> , 2015, 42, 965-976.	14.3	554
143	<i>Fusobacterium nucleatum</i> and T Cells in Colorectal Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 653.	7.1	498
144	The microbiome quality control project: baseline study design and future directions. <i>Genome Biology</i> , 2015, 16, 276.	8.8	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.	11.0	1,008
146	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. <i>Genome Medicine</i> , 2015, 7, 19.	8.2	77
147	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	11.0	273
148	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	28.6	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.	7.1	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.	8.8	166
151	MetaPhlAn2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	19.0	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.	3.2	235
154	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. <i>PeerJ</i> , 2015, 3, e1029.	2.0	701
155	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015, 3, e791.	2.0	12
156	Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.	8.2	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.	9.8	182
158	Cross-study validation for the assessment of prediction algorithms. <i>Bioinformatics</i> , 2014, 30, i105-i112.	4.1	75
159	MÃs-o-menos: a simple sign averaging method for discrimination in genomic data analysis. <i>Bioinformatics</i> , 2014, 30, 3062-3069.	4.1	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.	3.8	83
161	Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	6.3	184
162	Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. <i>ISME Journal</i> , 2014, 8, 493-503.	9.8	40

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163	Functional and phylogenetic assembly of microbial communities in the human microbiome. Trends in Microbiology, 2014, 22, 261-266.	7.7	184
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