

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	BugSigDB captures patterns of differential abundance across a broad range of host-associated microbial signatures. <i>Nature Biotechnology</i> , 2024, 42, 790-802.	20.4	5
2	Integrated annotation prioritizes metabolites with bioactivity in inflammatory bowel disease. <i>Molecular Systems Biology</i> , 2024, 20, 338-361.	7.2	1
3	A host-microbiota interactome reveals extensive transkingdom connectivity. <i>Nature</i> , 2024, 628, 171-179.	35.3	3
4	Gut microbiome composition and metabolic activity in women with diverticulitis. <i>Nature Communications</i> , 2024, 15, .	12.8	0
5	Optimized model architectures for deep learning on genomic data. <i>Communications Biology</i> , 2024, 7, .	4.4	0
6	Dimensions of Individual, Occupational, and Organizational Characteristics on the Performance. <i>Jurnal Manajemen Pelayanan Publik</i> , 2024, 8, 144-156.	0.1	0
7	The Efficacy of Paraprobiotic Lozenges (<i>Lactobacillus helveticus</i> MIMLh5) for the Prevention of Acute and Chronic Nose and Throat Infections in Children. <i>Medicina (Lithuania)</i> , 2024, 60, 1235.	2.0	0
8	Microbiome epidemiology and association studies in human health. <i>Nature Reviews Genetics</i> , 2023, 24, 109-124.	16.4	31
9	Questioning the fetal microbiome illustrates pitfalls of low-biomass microbial studies. <i>Nature</i> , 2023, 613, 639-649.	35.3	151
10	Integrated molecular approaches for fermented food microbiome research. <i>FEMS Microbiology Reviews</i> , 2023, 47, .	8.7	9
11	Gut microbial metabolism of 5-ASA diminishes its clinical efficacy in inflammatory bowel disease. <i>Nature Medicine</i> , 2023, 29, 700-709.	29.5	43
12	Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlan 4. <i>Nature Biotechnology</i> , 2023, 41, 1633-1644.	20.4	250
13	Alterations in the gut microbiome implicate key taxa and metabolic pathways across inflammatory arthritis phenotypes. <i>Science Translational Medicine</i> , 2023, 15, .	13.2	10
14	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.	13.4	70
15	The oral microbiome in relation to pancreatic cancer risk in African Americans. <i>British Journal of Cancer</i> , 2022, 126, 287-296.	6.5	10
16	Density-based binning of gene clusters to infer function or evolutionary history using GeneGrouper. <i>Bioinformatics</i> , 2022, 38, 612-620.	4.2	4
17	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.	3.5	12
18	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.	27.3	45

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19	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	14
20	Human gut bacteria produce β -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	35.3	266
21	Association of midlife antibiotic use with subsequent cognitive function in women. <i>PLoS ONE</i> , 2022, 17, e0264649.	2.5	15
22	Strain Identification and Quantitative Analysis in Microbial Communities. <i>Journal of Molecular Biology</i> , 2022, 434, 167582.	4.2	17
23	Mucosal metabolites fuel the growth and virulence of <i>E. coli</i> linked to Crohn's disease. <i>Journal of Clinical Investigation</i> , 2022, 7, .	6.5	18
24	Discovery of bioactive microbial gene products in inflammatory bowel disease. <i>Nature</i> , 2022, 606, 754-760.	35.3	43
25	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
26	A biosynthetic pathway for the selective sulfonation of steroidal metabolites by human gut bacteria. <i>Nature Microbiology</i> , 2022, 7, 1404-1418.	12.7	34
27	Population structure discovery in meta-analyzed microbial communities and inflammatory bowel disease using MMUPHin. <i>Genome Biology</i> , 2022, 23, .	9.1	52
28	Human threat learning is associated with gut microbiota composition. <i>PNAS Nexus</i> , 2022, 1, .	2.5	1
29	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
30	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
31	Microbiome Biomarkers: One Step Closer in NAFLD Cirrhosis. <i>Hepatology</i> , 2021, 73, 2063-2066.	8.0	4
32	Thermochemistry and viscous heat dissipative effects on unsteady upper-convected Maxwell fluid flow past a stretching vertical plate with thermophysical variables. <i>Heat Transfer</i> , 2021, 50, 2950-2974.	3.0	5
33	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	10.8	20
34	Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. <i>Microbiome</i> , 2021, 9, 17.	11.4	41
35	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
36	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

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37	The colorectal cancer-associated faecal microbiome of developing countries resembles that of developed countries. <i>Genome Medicine</i> , 2021, 13, 27.	8.4	28
38	Triclosan Tolerance Is Driven by a Conserved Mechanism in Diverse <i>Pseudomonas</i> Species. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	10
39	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.	7.1	20
40	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.	12.2	9
41	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	29.5	53
42	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
43	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	5.8	1,002
44	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. <i>Genome Medicine</i> , 2021, 13, 102.	8.4	78
45	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.	2.7	24
46	Statistical approaches for differential expression analysis in metatranscriptomics. <i>Bioinformatics</i> , 2021, 37, i34-i41.	4.2	31
47	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	6.4	45
48	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
49	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	10
50	A statistical model for describing and simulating microbial community profiles. <i>PLoS Computational Biology</i> , 2021, 17, e1008913.	3.0	30
51	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
52	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
53	Of mice and men and women: Sexual dimorphism of the gut microbiome. <i>International Journal of Women's Dermatology</i> , 2021, 7, 533-538.	2.0	15
54	Association Between the Sulfur Microbial Diet and Risk of Colorectal Cancer. <i>JAMA Network Open</i> , 2021, 4, e2134308.	5.9	33

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55	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	3.0	917
56	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	29.5	210
57	The Survey on the development of Secure Multi-Party Computing in the blockchain. , 2021, , .		3
58	Association of autophagy status with amount of <i>Fusobacterium nucleatum</i> in colorectal cancer. <i>Journal of Pathology</i> , 2020, 250, 397-408.	4.4	28
59	Strain-level epidemiology of microbial communities and the human microbiome. <i>Genome Medicine</i> , 2020, 12, 71.	8.4	84
60	Determinants of <i>Staphylococcus aureus</i> carriage in the developing infant nasal microbiome. <i>Genome Biology</i> , 2020, 21, 301.	9.1	13
61	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	12.8	433
62	PICRUSt2 for prediction of metagenome functions. <i>Nature Biotechnology</i> , 2020, 38, 685-688.	20.4	3,120
63	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.	0.3	1
64	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.	9.1	85
65	Global chemical effects of the microbiome include new bile-acid conjugations. <i>Nature</i> , 2020, 579, 123-129.	35.3	375
66	Mobilizable antibiotic resistance genes are present in dust microbial communities. <i>PLoS Pathogens</i> , 2020, 16, e1008211.	4.0	27
67	Growth effects of N-acylethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. <i>Nature Microbiology</i> , 2020, 5, 486-497.	12.7	73
68	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
69	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
70	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. <i>Molecular Cell</i> , 2020, 78, 459-476.e13.	9.4	78
71	Delivery Mode Affects Stability of Early Infant Gut Microbiota. <i>Cell Reports Medicine</i> , 2020, 1, 100156.	5.8	119
72	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.	3.0	15

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73	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
74	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	12.8	197
75	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	20.4	12,956
76	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.	10.8	306
77	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	21
78	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.	1.2	0
79	Comparative genomics and genome biology of <i>Campylobacter showae</i> . <i>Emerging Microbes and Infections</i> , 2019, 8, 827-840.	6.4	9
80	Naturally acquired immunity against immature <i>Plasmodium falciparum</i> gametocytes. <i>Science Translational Medicine</i> , 2019, 11, .	13.2	34
81	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	35.3	1,829
82	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. <i>Cell Host and Microbe</i> , 2019, 25, 668-680.e7.	10.8	308
83	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	12.8	230
84	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
85	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
86	Low Tristetraprolin Expression Is Associated with Lethal Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 584-590.	1.9	8
87	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
88	HMP16SData: Efficient Access to the Human Microbiome Project Through Bioconductor. <i>American Journal of Epidemiology</i> , 2019, 188, 1023-1026.	3.6	32
89	Sense of Mission and Subsequent Health and Well-Being Among Young Adults: An Outcome-Wide Analysis. <i>American Journal of Epidemiology</i> , 2019, 188, 664-673.	3.6	43
90	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	12.7	1,225

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91	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
92	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
93	Long-term use of antibiotics and risk of colorectal adenoma. <i>Gut</i> , 2018, 67, gutjnl-2016-313413.	13.4	129
94	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	4.2	266
95	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	12.7	783
96	Metatranscriptome of human faecal microbial communities in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 356-366.	12.7	181
97	Stability of the human faecal microbiome in a cohort of adult men. <i>Nature Microbiology</i> , 2018, 3, 347-355.	12.7	223
98	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	12.7	432
99	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
100	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
101	Translating microbiome futures. <i>Nature Biotechnology</i> , 2018, 36, 1037-1042.	20.4	29
102	Antimicrobial Chemicals Associate with Microbial Function and Antibiotic Resistance Indoors. <i>MSystems</i> , 2018, 3, .	3.9	70
103	Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. <i>Genome Biology</i> , 2018, 19, 142.	9.1	22
104	Non-beta-amyloid/tau cerebrospinal fluid markers inform staging and progression in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2018, 10, 98.	6.3	25
105	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
106	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
107	Temporal development of the gut microbiome in early childhood from the TEDDY study. <i>Nature</i> , 2018, 562, 583-588.	35.3	1,322
108	The human gut microbiome in early-onset type 1 diabetes from the TEDDY study. <i>Nature</i> , 2018, 562, 589-594.	35.3	660

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109	Daylight exposure modulates bacterial communities associated with household dust. <i>Microbiome</i> , 2018, 6, 175.	11.4	68
110	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.2	1,193
111	Multimomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2018, 155, e1-e4.	1.3	25
112	<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
113	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.9	632
114	<i>Plasmodium</i> gametocytes display homing and vascular transmigration in the host bone marrow. <i>Science Advances</i> , 2018, 4, eaat3775.	10.7	77
115	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
116	Host genetic variation and its microbiome interactions within the Human Microbiome Project. <i>Genome Medicine</i> , 2018, 10, 6.	8.4	143
117	Bone Marrow Is a Major Parasite Reservoir in <i>Plasmodium vivax</i> Infection. <i>MBio</i> , 2018, 9, .	4.2	152
118	<i>Bifidobacterium</i> Genus in Colorectal Carcinoma Tissue in relation to Tumor Characteristics and Patient Survival. <i>FASEB Journal</i> , 2018, 32, 407.3.	0.4	0
119	<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.	13.8	512
120	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
121	Microbial strain-level population structure and genetic diversity from metagenomes. <i>Genome Research</i> , 2017, 27, 626-638.	5.5	585
122	A prominent glycol radical enzyme in human gut microbiomes metabolizes <i>trans</i> -4-hydroxy- <i>l</i> -proline. <i>Science</i> , 2017, 355, .	19.6	128
123	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	37
124	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
125	Accessible, curated metagenomic data through ExperimentHub. <i>Nature Methods</i> , 2017, 14, 1023-1024.	19.2	328
126	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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127	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	35.3	981
128	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017, 2, .	3.9	21
129	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
130	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
131	PWE-026â€¦Elucidating the pathogenic potential of the intestinal pathogen <i>Campylobacter showae</i> . <i>Gut</i> , 2017, , .	13.4	0
132	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
133	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	9.1	150
134	A novel <i>Ruminococcus gnavus</i> clade enriched in inflammatory bowel disease patients. <i>Genome Medicine</i> , 2017, 9, 103.	8.4	519
135	SchrÃ¶dingerâ€™s microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	11.4	364
136	A Bayesian method for detecting pairwise associations in compositional data. <i>PLoS Computational Biology</i> , 2017, 13, e1005852.	3.0	40
137	Paneth cell defects in Crohnâ€™s disease patients promote dysbiosis. <i>Journal of Clinical Investigation</i> , 2016, 1, e86907.	6.5	95
138	A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. <i>ELife</i> , 2016, 5, .	5.8	123
139	Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. <i>MSystems</i> , 2016, 1, .	3.9	115
140	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1897.	27.3	184
141	The <i>Chthonomonas calidirosea</i> Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's TaupÅ•Volcanic Zone. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3572-3581.	3.1	9
142	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	27.3	1,029
143	The healthy human microbiome. <i>Genome Medicine</i> , 2016, 8, 51.	8.4	1,296
144	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

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145	CellMapper: rapid and accurate inference of gene expression in difficult-to-isolate cell types. <i>Genome Biology</i> , 2016, 17, 201.	9.1	24
146	Uncovering oral <i>Neisseria</i> tropism and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	12.7	72
147	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
148	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
149	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	27.3	852
150	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 1551.	27.3	202
151	Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. <i>Genome Medicine</i> , 2016, 8, 17.	8.4	231
152	Intestinal microbiome analyses identify melanoma patients at risk for checkpoint-blockade-induced colitis. <i>Nature Communications</i> , 2016, 7, 10391.	12.8	810
153	Fecal Microbiome in Epidemiologic Studies—Letter. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 869-869.	1.9	3
154	<i>Fusobacterium nucleatum</i> in colorectal carcinoma tissue and patient prognosis. <i>Gut</i> , 2016, 65, 1973-1980.	13.4	763
155	Computational Reconstruction of NF κ B Pathway Interaction Mechanisms during Prostate Cancer. <i>PLoS Computational Biology</i> , 2016, 12, e1004820.	3.0	28
156	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
157	<i>Fusobacterium nucleatum</i> and T Cells in Colorectal Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 653.	7.2	523
158	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
159	Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. <i>Genome Medicine</i> , 2015, 7, 19.	8.4	78
160	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	10.8	277
161	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	28.6	569
162	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.	7.4	391

#	ARTICLE	IF	CITATIONS
163	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
164	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	19.2	1,936
165	American Diabetes Association and JDRF Research Symposium: Diabetes and the Microbiome. <i>Diabetes</i> , 2015, 64, 3967-3977.	0.9	33
166	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	3.0	259
167	Compact graphical representation of phylogenetic data and metadata with GraPhlan. <i>PeerJ</i> , 2015, 3, e1029.	2.0	726
168	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015, 3, e791.	2.0	12
169	Complex host genetics influence the microbiome in inflammatory bowel disease. <i>Genome Medicine</i> , 2014, 6, 107.	8.4	328
170	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
171	Cross-study validation for the assessment of prediction algorithms. <i>Bioinformatics</i> , 2014, 30, i105-i112.	4.2	78
172	MÃ¡s-o-menos: a simple sign averaging method for discrimination in genomic data analysis. <i>Bioinformatics</i> , 2014, 30, 3062-3069.	4.2	35
173	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
174	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	43
175	Functional and phylogenetic assembly of microbial communities in the human microbiome. <i>Trends in Microbiology</i> , 2014, 22, 261-266.	7.6	185
176	Meta'omic Analytic Techniques for Studying the Intestinal Microbiome. <i>Gastroenterology</i> , 2014, 146, 1437-1448.e1.	1.3	140
177	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	10.8	2,700
178	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
179	Simvastatin for the Prevention of Exacerbations in Moderate-to-Severe COPD. <i>New England Journal of Medicine</i> , 2014, 370, 2201-2210.	29.6	287
180	Analysis of CD4+ CD8+ double-positive T cells in blood, cerebrospinal fluid and multiple sclerosis lesions. <i>Clinical and Experimental Immunology</i> , 2014, 177, 404-411.	2.6	27

#	ARTICLE	IF	CITATIONS
181	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
182	Determining Microbial Products and Identifying Molecular Targets in the Human Microbiome. <i>Cell Metabolism</i> , 2014, 20, 731-741.	15.5	85
183	Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. <i>ISME Journal</i> , 2014, 8, 1403-1417.	9.8	359
184	Inflammatory Bowel Disease as a Model for Translating the Microbiome. <i>Immunity</i> , 2014, 40, 843-854.	13.8	293
185	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	27.3	64
186	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
187	MetaRef: a pan-genomic database for comparative and community microbial genomics. <i>Nucleic Acids Research</i> , 2014, 42, D617-D624.	13.8	52
188	Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature. <i>Journal of Clinical Investigation</i> , 2014, 124, 3617-3633.	6.5	446
189	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	20.4	8,414
190	PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. <i>Nature Communications</i> , 2013, 4, 2304.	12.8	818
191	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	8.4	63
192	Two-stage microbial community experimental design. <i>ISME Journal</i> , 2013, 7, 2330-2339.	9.8	36
193	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
194	Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants. <i>Microbiome</i> , 2013, 1, 13.	11.4	291
195	P698 Characterization of the tissue-associated microbiome in active and inactive IBD. <i>Journal of Crohn's and Colitis</i> , 2013, 7, S291.	1.2	0
196	Tryptophan Biosynthesis Protects Mycobacteria from CD4 T-Cell-Mediated Killing. <i>Cell</i> , 2013, 155, 1296-1308.	27.3	309
197	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	9.1	6
198	Biodiversity and functional genomics in the human microbiome. <i>Trends in Genetics</i> , 2013, 29, 51-58.	6.7	213

#	ARTICLE	IF	CITATIONS
199	P700 Evaluation of location-specific, tissue-associated microbiota in the ileal pouch, terminal ileum and colon in inflammatory bowel disease (IBD). <i>Journal of Crohn's and Colitis</i> , 2013, 7, S291-S292.	1.2	0
200	Translating the human microbiome. <i>Nature Biotechnology</i> , 2013, 31, 304-308.	20.4	30
201	Computational meta'omics for microbial community studies. <i>Molecular Systems Biology</i> , 2013, 9, 666.	7.2	268
202	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
203	Simultaneous Quantification of Multiple Bacteria by the BactoChip Microarray Designed to Target Species-Specific Marker Genes. <i>PLoS ONE</i> , 2013, 8, e55764.	2.5	18
204	Inferring Developmental Stage Composition from Gene Expression in Human Malaria. <i>PLoS Computational Biology</i> , 2013, 9, e1003392.	3.0	47
205	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
206	Expansion of intestinal <i>Prevotella copri</i> correlates with enhanced susceptibility to arthritis. <i>ELife</i> , 2013, 2, e01202.	5.8	1,575
207	Passing Messages between Biological Networks to Refine Predicted Interactions. <i>PLoS ONE</i> , 2013, 8, e64832.	2.5	190
208	Early intestinal colonization phenotypes predict necrotizing enterocolitis in preterm infants. <i>FASEB Journal</i> , 2013, 27, 357.1.	0.4	0
209	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002358.	3.0	965
210	Microbial Co-occurrence Relationships in the Human Microbiome. <i>PLoS Computational Biology</i> , 2012, 8, e1002606.	3.0	1,313
211	Chapter 12: Human Microbiome Analysis. <i>PLoS Computational Biology</i> , 2012, 8, e1002808.	3.0	418
212	Bioinformatics for the Human Microbiome Project. <i>PLoS Computational Biology</i> , 2012, 8, e1002779.	3.0	76
213	Global Assessment of Genomic Regions Required for Growth in <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002946.	4.0	222
214	Genomic analysis identifies association of <i>Fusobacterium</i> with colorectal carcinoma. <i>Genome Research</i> , 2012, 22, 292-298.	5.5	1,659
215	Expression Profiling of Archival Tumors for Long-term Health Studies. <i>Clinical Cancer Research</i> , 2012, 18, 6136-6146.	7.1	32
216	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

#	ARTICLE	IF	CITATIONS
217	Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. <i>Genome Biology</i> , 2012, 13, R79.	9.1	2,324
218	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
219	Report on emerging technologies for translational bioinformatics: a symposium on gene expression profiling for archival tissues. <i>BMC Cancer</i> , 2012, 12, 124.	2.6	20
220	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. <i>PLoS Biology</i> , 2012, 10, e1001377.	5.3	383
221	Metagenomic microbial community profiling using unique clade-specific marker genes. <i>Nature Methods</i> , 2012, 9, 811-814.	19.2	1,640
222	Colorectal cancer: a tale of two sides or a continuum?: Figure 1. <i>Gut</i> , 2012, 61, 794-797.	13.4	227
223	Integrative Approaches for Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2012, 802, 157-182.	0.7	4
224	A Case Study for Large-Scale Human Microbiome Analysis Using JCVI's Metagenomics Reports (METAREP). <i>PLoS ONE</i> , 2012, 7, e29044.	2.5	11
225	A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy. <i>PLoS ONE</i> , 2012, 7, e36466.	2.5	592
226	As we come to the end of 2011, several members of the Genome Biology Editorial Board give their views on the state of play in genomics. <i>Genome Biology</i> , 2011, 12, 137.	9.1	0
227	Metagenomic biomarker discovery and explanation. <i>Genome Biology</i> , 2011, 12, R60.	9.1	11,988
228	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
229	Toward an Efficient Method of Identifying Core Genes for Evolutionary and Functional Microbial Phylogenies. <i>PLoS ONE</i> , 2011, 6, e24704.	2.5	92
230	Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts. <i>Cellular Microbiology</i> , 2011, 13, 508-517.	2.2	25
231	Current Concepts of the Intestinal Microbiota and the Pathogenesis of Infection. <i>Current Infectious Disease Reports</i> , 2011, 13, 28-34.	3.1	90
232	Optimized application of penalized regression methods to diverse genomic data. <i>Bioinformatics</i> , 2011, 27, 3399-3406.	4.2	75
233	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
234	A Quick Guide to Large-Scale Genomic Data Mining. <i>PLoS Computational Biology</i> , 2010, 6, e1000779.	3.0	34

#	ARTICLE	IF	CITATIONS
235	Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components. <i>PLoS Computational Biology</i> , 2010, 6, e1001009.	3.0	20
236	Integrated functional networks of process, tissue, and developmental stage specific interactions in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2010, 4, 180.	2.9	21
237	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
238	The impact of incomplete knowledge on evaluation: an experimental benchmark for protein function prediction. <i>Bioinformatics</i> , 2009, 25, 2404-2410.	4.2	33
239	Detailing regulatory networks through large scale data integration. <i>Bioinformatics</i> , 2009, 25, 3267-3274.	4.2	80
240	Predicting Cellular Growth from Gene Expression Signatures. <i>PLoS Computational Biology</i> , 2009, 5, e1000257.	3.0	101
241	Computationally Driven, Quantitative Experiments Discover Genes Required for Mitochondrial Biogenesis. <i>PLoS Genetics</i> , 2009, 5, e1000407.	3.3	131
242	Directing Experimental Biology: A Case Study in Mitochondrial Biogenesis. <i>PLoS Computational Biology</i> , 2009, 5, e1000322.	3.0	35
243	Exploring the human genome with functional maps. <i>Genome Research</i> , 2009, 19, 1093-1106.	5.5	200
244	Graphle: Interactive exploration of large, dense graphs. <i>BMC Bioinformatics</i> , 2009, 10, 417.	2.6	15
245	Computational Analysis of the Yeast Proteome: Understanding and Exploiting Functional Specificity in Genomic Data. <i>Methods in Molecular Biology</i> , 2009, 548, 273-293.	0.7	1
246	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.	3.0	84
247	Assessing the functional structure of genomic data. <i>Bioinformatics</i> , 2008, 24, i330-i338.	4.2	15
248	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
249	The Sleipnir library for computational functional genomics. <i>Bioinformatics</i> , 2008, 24, 1559-1561.	4.2	68
250	Exploring the functional landscape of gene expression: directed search of large microarray compendia. <i>Bioinformatics</i> , 2007, 23, 2692-2699.	4.2	243
251	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
252	Nearest Neighbor Networks: clustering expression data based on gene neighborhoods. <i>BMC Bioinformatics</i> , 2007, 8, 250.	2.6	59

#	ARTICLE	IF	CITATIONS
253	A scalable method for integration and functional analysis of multiple microarray datasets. <i>Bioinformatics</i> , 2006, 22, 2890-2897.	4.2	128
254	BAYESIAN DATA INTEGRATION: A FUNCTIONAL PERSPECTIVE. , 2006, , .		12
255	Gender-Neutral Language in English and French Linguo-Cultures. , 0, , .		0
256	Strain-specific gut microbial signatures in type 2 diabetes identified in a cross-cohort analysis of 8,117 metagenomes. <i>Nature Medicine</i> , 0, , .	29.5	0