List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2862336/publications.pdf

Version: 2024-02-01

763	314,925	12 208	2 528
papers	citations	h-index	g-index

890	890	890	143432
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic Mutations Within the Host Microbiome: Adaptive Evolution or Purifying Selection. Engineering, 2023, 20, 96-102.	6.7	5
2	Impact of exclusive enteral nutrition on the gut microbiome of children with medical complexity. Journal of Parenteral and Enteral Nutrition, 2023, 47, 77-86.	2.6	2
3	Severe acute respiratory coronavirus virus 2 (SARS-CoV-2) screening among symptom-free healthcare workers. Infection Control and Hospital Epidemiology, 2022, 43, 657-660.	1.8	9
4	A semiparametric model for betweenâ€subject attributes: Applications to betaâ€diversity of microbiome data. Biometrics, 2022, 78, 950-962.	1.4	5
5	Impact of Vaginal Estrogen on the Urobiome in Postmenopausal Women With Recurrent Urinary Tract Infection. Female Pelvic Medicine and Reconstructive Surgery, 2022, 28, 20-26.	1.1	5
6	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. Biometrics, 2022, 78, 1155-1167.	1.4	4
7	Host and gut microbial tryptophan metabolism and type 2 diabetes: an integrative analysis of host genetics, diet, gut microbiome and circulating metabolites in cohort studies. Gut, 2022, 71, 1095-1105.	12.1	98
8	The microbiome and prostate cancer. Prostate Cancer and Prostatic Diseases, 2022, 25, 159-164.	3.9	21
9	Reduced Gut Microbiome Diversity in People With HIV Who Have Distal Neuropathic Pain. Journal of Pain, 2022, 23, 318-325.	1.4	9
10	Vitamin B-12 and the Gastrointestinal Microbiome: A Systematic Review. Advances in Nutrition, 2022, 13, 530-558.	6.4	20
11	A posteriori dietary patterns better explain variations of the gut microbiome than individual markers in the American Gut Project. American Journal of Clinical Nutrition, 2022, 115, 432-443.	4.7	28
12	The Gut Microbiome Modifies the Association Between a Mediterranean Diet and Diabetes in USA Hispanic/ Latino Population. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e924-e934.	3.6	9
13	Redrawing therapeutic boundaries: microbiota and cancer. Trends in Cancer, 2022, 8, 87-97.	7.4	11
14	Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity. Nature Microbiology, 2022, 7, 262-276.	13.3	110
15	Using all our genomes: Bloodâ€based liquid biopsies for the early detection of cancer. View, 2022, 3, .	5.3	21
16	Predicting fungal infection rate and severity with skinâ€associated microbial communities on amphibians. Molecular Ecology, 2022, 31, 2140-2156.	3.9	7
17	Gut Microbiome Composition Is Predictive of Incident Type 2 Diabetes in a Population Cohort of 5,572 Finnish Adults. Diabetes Care, 2022, 45, 811-818.	8.6	47
18	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. Nature Genetics, 2022, 54, 134-142.	21.4	164

#	Article	IF	Citations
19	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. Frontiers in Bioinformatics, 2022, 2, .	2.1	10
20	A gut-derived metabolite alters brain activity and anxiety behaviour in mice. Nature, 2022, 602, 647-653.	27.8	179
21	Cancer's second genome: Microbial cancer diagnostics and redefining clonal evolution as a multispecies process. BioEssays, 2022, 44, e2100252.	2.5	12
22	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. Cell Metabolism, 2022, 34, 719-730.e4.	16.2	35
23	Salivary bacterial signatures in depression-obesity comorbidity are associated with neurotransmitters and neuroactive dipeptides. BMC Microbiology, 2022, 22, 75.	3.3	8
24	The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction. Scientific Reports, 2022, 12, 5077.	3.3	12
25	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. MSystems, 2022, 7, e0137821.	3.8	3
26	Unlocking capacities of genomics for the COVID-19 response and future pandemics. Nature Methods, 2022, 19, 374-380.	19.0	35
27	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. MSystems, 2022, 7, e0016722.	3.8	35
28	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. Cellular and Molecular Gastroenterology and Hepatology, 2022, 14, 35-53.	4.5	10
29	Menopause Is Associated with an Altered Gut Microbiome and Estrobolome, with Implications for Adverse Cardiometabolic Risk in the Hispanic Community Health Study/Study of Latinos. MSystems, 2022, 7, .	3.8	16
30	Early microbial markers of periodontal and cardiometabolic diseases in ORIGINS. Npj Biofilms and Microbiomes, 2022, 8, 30.	6.4	7
31	The impact of maternal asthma on the preterm infants' gut metabolome and microbiome (MAP study). Scientific Reports, 2022, 12, 6437.	3.3	3
32	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. MSystems, 2022, 7, e0005022.	3.8	4
33	Nitrite Generating and Depleting Capacity of the Oral Microbiome and Cardiometabolic Risk: Results from ORIGINS. Journal of the American Heart Association, 2022, 11, e023038.	3.7	10
34	SARS-CoV-2 Distribution in Residential Housing Suggests Contact Deposition and Correlates with Rothia sp.. MSystems, 2022, 7, e0141121.	3.8	5
35	A Prebiotic Diet Alters the Fecal Microbiome and Improves Sleep in Response to Sleep Disruption in Rats. Frontiers in Neuroscience, 2022, 16, .	2.8	6
36	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. MSystems, 2022, 7, .	3.8	2

#	Article	IF	Citations
37	Multiomic Analyses of Nascent Preterm Infant Microbiomes Differentiation Suggest Opportunities for Targeted Intervention. Advanced Biology, 2022, 6, .	2.5	4
38	A comparison of six DNA extraction protocols for 16S, ITSÂand shotgun metagenomic sequencing of microbial communities. BioTechniques, 2022, 73, 34-46.	1.8	25
39	Sentinel Cards Provide Practical SARS-CoV-2 Monitoring in School Settings. MSystems, 2022, 7, .	3.8	1
40	Diurnal and eating-associated microbial patterns revealed via high-frequency saliva sampling. Genome Research, 2022, 32, 1112-1123.	5.5	3
41	The molecular impact of life in an indoor environment. Science Advances, 2022, 8, .	10.3	3
42	Implementation of Practical Surface SARS-CoV-2 Surveillance in School Settings. MSystems, 2022, 7, .	3.8	4
43	Context-aware deconvolution of cellâ€“cell communication with Tensor-cell2cell. Nature Communications, 2022, 13, .	12.8	32
44	Diet and feeding pattern modulate diurnal dynamics of the ileal microbiome and transcriptome. Cell Reports, 2022, 40, 111008.	6.4	32
45	Enhancing untargeted metabolomics using metadata-based source annotation. Nature Biotechnology, 2022, 40, 1774-1779.	17.5	25
46	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. Nature, 2022, 609, 101-108.	27.8	200
47	Gut microbiome in serious mental illnesses: A systematic review and critical evaluation. Schizophrenia Research, 2021, 234, 24-40.	2.0	47
48	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. Multiple Sclerosis Journal, 2021, 27, 366-379.	3.0	24
49	Auto-deconvolution and molecular networking of gas chromatographyâ€“mass spectrometry data. Nature Biotechnology, 2021, 39, 169-173.	17.5	78
50	Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. Gastroenterology, 2021, 160, 183-192.e3.	1.3	113
51	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. Inflammatory Bowel Diseases, 2021, 27, 603-616.	1.9	25
52	Deep metagenomics examines the oral microbiome during dental caries, revealing novel taxa and co-occurrences with host molecules. Genome Research, 2021, 31, 64-74.	5.5	59
53	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. Nature Chemical Biology, 2021, 17, 146-151.	8.0	73
54	Current Concepts, Opportunities, and Challenges of Gut Microbiome-Based Personalized Medicine in Nonalcoholic Fatty Liver Disease. Cell Metabolism, 2021, 33, 21-32.	16.2	98

#	Article	IF	Citations
55	Coinfection and infection duration shape how pathogens affect the African buffalo gut microbiota. ISME Journal, 2021, 15, 1359-1371.	9.8	17
56	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	19.0	198
57	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. Brain, Behavior, and Immunity, 2021, 91, 245-256.	4.1	44
58	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. Nature Biotechnology, 2021, 39, 165-168.	17.5	61
59	Identifying the effect of vancomycin on health careâ€“associated methicillin-resistant Staphylococcus aureus strains using bacteriological and physiological media. GigaScience, 2021, 10, .	6.4	5
60	Host DNA Depletion in Saliva Samples for Improved Shotgun Metagenomics. Methods in Molecular Biology, 2021, 2327, 87-92.	0.9	1
61	Nonalcoholic Steatohepatitis and HCC in a Hyperphagic Mouse Accelerated by Western Diet. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 891-920.	4.5	17
62	Reply to: Examining microbeâ€“metabolite correlations by linear methods. Nature Methods, 2021, 18, 40-41.	19.0	6
63	Early life gut microbiota is associated with rapid infant growth in Hispanics from Southern California. Gut Microbes, 2021, 13, 1961203.	9.8	32
64	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. Microbiome, 2021, 9, 25.	11.1	13
65	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. Marine Drugs, 2021, 19, 20.	4.6	19
66	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
67	Absence of <scp>CCR2</scp> reduces spontaneous intestinal tumorigenesis in the <scp>Apc^{Min}</scp>^{/+} mouse model. International Journal of Cancer, 2021, 148, 2594-2607.	5.1	7
68	Quantifying Live Microbial Load in Human Saliva Samples over Time Reveals Stable Composition and Dynamic Load. MSystems, 2021, 6, .	3.8	19
69	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. International Journal of Cancer, 2021, 148, 2712-2723.	5.1	33
70	The microbiome and human cancer. Science, 2021, 371, .	12.6	506
71	A comparison of DNA/RNA extraction protocols for high-throughput sequencing of microbial communities. BioTechniques, 2021, 70, 149-159.	1.8	17
72	Association of Loneliness and Wisdom With Gut Microbial Diversity and Composition: An Exploratory Study. Frontiers in Psychiatry, 2021, 12, 648475.	2.6	17

#	Article	IF	Citations
73	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. Environmental Science & Technology, 2021, 55, 4899-4913.	10.0	71
74	Dietary factors, gut microbiota, and serum trimethylamine-N-oxide associated with cardiovascular disease in the Hispanic Community Health Study/Study of Latinos. American Journal of Clinical Nutrition, 2021, 113, 1503-1514.	4.7	32
75	High-Throughput Wastewater SARS-CoV-2 Detection Enables Forecasting of Community Infection Dynamics in San Diego County. MSystems, 2021, 6, .	3.8	106
76	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. MSystems, 2021, 6, .	3.8	22
77	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. Microbiome, 2021, 9, 92.	11.1	40
78	Influence of Intermittent Hypoxia/Hypercapnia on Atherosclerosis, Gut Microbiome, and Metabolome. Frontiers in Physiology, 2021, 12, 663950.	2.8	20
79	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. MSystems, 2021, 6, .	3.8	36
80	Challenges in benchmarking metagenomic profilers. Nature Methods, 2021, 18, 618-626.	19.0	63
81	Associations of healthy food choices with gut microbiota profiles. American Journal of Clinical Nutrition, 2021, 114, 605-616.	4.7	42
82	Intratumoral bacteria generate a new class of therapeutically relevant tumor antigens in melanoma. Cancer Cell, 2021, 39, 601-603.	16.8	9
83	METTL3 regulates viral m6A RNA modification and host cell innate immune responses during SARS-CoV-2 infection. Cell Reports, 2021, 35, 109091.	6.4	124
84	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. Cell, 2021, 184, 2587-2594.e7.	28.9	285
85	Insight into the function and evolution of the Woodâ€“Ljungdahl pathway in Actinobacteria. ISME Journal, 2021, 15, 3005-3018.	9.8	55
86	Structure-based protein function prediction using graph convolutional networks. Nature Communications, 2021, 12, 3168.	12.8	300
87	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. Nature Communications, 2021, 12, 2671.	12.8	55
88	Impacts of the Marine Hatchery Built Environment, Water and Feed on Mucosal Microbiome Colonization Across Ontogeny in Yellowtail Kingfish, Seriola lalandi. Frontiers in Marine Science, 2021, 8, .	2.5	13
89	Candidate probiotic Lactiplantibacillus plantarum HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. Microbiome, 2021, 9, 151.	11.1	30
90	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. PLoS Computational Biology, 2021, 17, e1009056.	3.2	2

#	Article	IF	Citations
91	Intermittent Hypoxia and Hypercapnia Alter Diurnal Rhythms of Luminal Gut Microbiome and Metabolome. MSystems, 2021, 6, e0011621.	3.8	27
92	Effects of processed meat and drinking water nitrate on oral and fecal microbial populations in a controlled feeding study. Environmental Research, 2021, 197, 111084.	7.5	16
93	Compositional and genetic alterations in Gravesâ€™ disease gut microbiome reveal specific diagnostic biomarkers. ISME Journal, 2021, 15, 3399-3411.	9.8	30
94	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. Microbiome, 2021, 9, 132.	11.1	37
95	Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access. , 2021, , .		0
96	Nutritional Interventions and the Gut Microbiome in Children. Annual Review of Nutrition, 2021, 41, 479-510.	10.1	18
97	A Scale-Free, Fully Connected Global Transition Network Underlies Known Microbiome Diversity. MSystems, 2021, 6, e0039421.	3.8	5
98	Rapid, Large-Scale Wastewater Surveillance and Automated Reporting System Enable Early Detection of Nearly 85% of COVID-19 Cases on a University Campus. MSystems, 2021, 6, e0079321.	3.8	94
99	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. Med, 2021, 2, 951-964.e5.	4.4	37
100	Individuals with substance use disorders have a distinct oral microbiome pattern. Brain, Behavior, & Immunity - Health, 2021, 15, 100271.	2.5	11
101	A Pilot Study of Microbial Succession in Human Rib Skeletal Remains during Terrestrial Decomposition. MSphere, 2021, 6, e0045521.	2.9	12
102	Markers of Gut Barrier Function and Microbial Translocation Associate with Lower Gut Microbial Diversity in People with HIV. Viruses, 2021, 13, 1891.	3.3	17
103	Challenges in Determining the Role of Microbiome Evolution in Barrettâ€™s Esophagus and Progression to Esophageal Adenocarcinoma. Microorganisms, 2021, 9, 2003.	3.6	4
104	Emergence of an early SARS-CoV-2 epidemic in the United States. Cell, 2021, 184, 4939-4952.e15.	28.9	31
105	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. Genome Research, 2021, 31, 2131-2137.	5.5	16
106	Ruminiclostridium 5, Parabacteroides distasonis, and bile acid profile are modulated by prebiotic diet and associate with facilitated sleep/clock realignment after chronic disruption of rhythms. Brain, Behavior, and Immunity, 2021, 97, 150-166.	4.1	34
107	Links between gut microbiome composition and fatty liver disease in a large population sample. Gut Microbes, 2021, 13, 1-22.	9.8	41
108	Enabling microbiome research on personal devices. , 2021, , .		1

#	Article	IF	Citations
109	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. MSystems, 2021, 6, e0069121.	3.8	27
110	Fecal Microbiome Composition Does Not Predict Dietâ€Induced TMAO Production in Healthy Adults. Journal of the American Heart Association, 2021, 10, e021934.	3.7	14
111	Development of a Rapid and Sensitive CasRx-Based Diagnostic Assay for SARS-CoV-2. ACS Sensors, 2021, 6, 3957-3966.	7.8	35
112	Skin inflammation activates intestinal stromal fibroblasts and promotes colitis. Journal of Clinical Investigation, 2021, 131, .	8.2	12
113	Analysis of SARS-CoV-2 RNA Persistence across Indoor Surface Materials Reveals Best Practices for Environmental Monitoring Programs. MSystems, 2021, 6, e0113621.	3.8	14
114	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. MSystems, 2021, 6, e0100621.	3.8	8
115	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	30.7	170
116	Comparison of fecal and oral collection methods for studies of the human microbiota in two Iranian cohorts. BMC Microbiology, 2021, 21, 324.	3.3	4
117	Clean room microbiome complexity impacts planetary protection bioburden. Microbiome, 2021, 9, 238.	11.1	11
118	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. Genome Biology, 2021, 22, 336.	8.8	18
119	IL-4RÎ± Blockade by Dupilumab Decreases Staphylococcus aureus Colonization and Increases Microbial Diversity in Atopic Dermatitis. Journal of Investigative Dermatology, 2020, 140, 191-202.e7.	0.7	130
120	Microbial Diversity in Clinical Microbiome Studies: Sample Size and Statistical Power Considerations. Gastroenterology, 2020, 158, 1524-1528.	1.3	55
121	Effects of the microalgae Chlamydomonas on gastrointestinal health. Journal of Functional Foods, 2020, 65, 103738.	3.4	66
122	Mass spectrometry searches using MASST. Nature Biotechnology, 2020, 38, 23-26.	17.5	160
123	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. Periodontology 2000, 2020, 82, 26-41.	13.4	50
124	Using microbiome tools for estimating the postmortem interval. , 2020, , 171-191.		7
125	The emergence of microbiome centres. Nature Microbiology, 2020, 5, 2-3.	13.3	13
126	Threeâ€dimensional culture of oral progenitor cells: Effects on small extracellular vesicles production and proliferative function. Journal of Oral Pathology and Medicine, 2020, 49, 342-349.	2.7	17

#	Article	IF	Citations
127	Home chemical and microbial transitions across urbanization. Nature Microbiology, 2020, 5, 108-115.	13.3	83
128	Altered Gut Microbiota and Host Metabolite Profiles in Women With Human Immunodeficiency Virus. Clinical Infectious Diseases, 2020, 71, 2345-2353.	5.8	38
129	48: Oral probiotic versus placebo and the maternal microbiome during pregnancy: A randomized controlled trial. American Journal of Obstetrics and Gynecology, 2020, 222, S41-S42.	1.3	0
130	Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. Cell, 2020, 183, 666-683.e17.	28.9	211
131	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. MSphere, 2020, 5, .	2.9	20
132	A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. MBio, 2020, 11, .	4.1	19
133	Evaluating Organism-Wide Changes in the Metabolome and Microbiome following a Single Dose of Antibiotic. MSystems, 2020, 5, .	3.8	6
134	Early-life gut dysbiosis linked to juvenile mortality in ostriches. Microbiome, 2020, 8, 147.	11.1	30
135	Leveling up citizen science. Nature Biotechnology, 2020, 38, 1124-1126.	17.5	20
136	The Urinary Tract Microbiome in Older Women Exhibits Host Genetic and Environmental Influences. Cell Host and Microbe, 2020, 28, 298-305.e3.	11.0	45
137	Vitamin D metabolites and the gut microbiome in older men. Nature Communications, 2020, 11, 5997.	12.8	88
138	Triclosan leads to dysregulation of the metabolic regulator FGF21 exacerbating high fat diet-induced nonalcoholic fatty liver disease. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31259-31266.	7.1	43
139	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. MSystems, 2020, 5, .	3.8	9
140	Reduced Independence in Daily Living Is Associated with the Gut Microbiome in People with HIV and HCV. MSystems, 2020, 5, .	3.8	1
141	Handwashing and Detergent Treatment Greatly Reduce SARS-CoV-2 Viral Load on Halloween Candy Handled by COVID-19 Patients. MSystems, 2020, 5, .	3.8	11
142	The Gut Microbiome, Aging, and Longevity: A Systematic Review. Nutrients, 2020, 12, 3759.	4.1	207
143	Association Between the Gut Microbiota and Blood Pressure in a Population Cohort of 6953 Individuals. Journal of the American Heart Association, 2020, 9, e016641.	3.7	67
144	Microbiome and Metagenome Analyses of a Closed Habitat during Human Occupation. MSystems, 2020, 5, .	3.8	4

#	Article	IF	Citations
145	Expanding magnetic organelle biogenesis in the domain Bacteria. Microbiome, 2020, 8, 152.	11.1	44
146	Type I IFNs and CD8 T cells increase intestinal barrier permeability after chronic viral infection. Journal of Experimental Medicine, 2020, 217, .	8.5	28
147	Two hundred and fifty-four metagenome-assembled bacterial genomes from the bank vole gut microbiota. Scientific Data, 2020, 7, 312.	5.3	13
148	CD8 T cells drive anorexia, dysbiosis, and blooms of a commensal with immunosuppressive potential after viral infection. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24998-25007.	7.1	10
149	Fructose stimulated de novo lipogenesis is promoted by inflammation. Nature Metabolism, 2020, 2, 1034-1045.	11.9	174
150	Association of Body Mass Index with Fecal Microbial Diversity and Metabolites in the Northern Finland Birth Cohort. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2289-2299.	2.5	20
151	Mortality Risk Profiling of Staphylococcus aureus Bacteremia by Multi-omic Serum Analysis Reveals Early Predictive and Pathogenic Signatures. Cell, 2020, 182, 1311-1327.e14.	28.9	58
152	ReDU: a framework to find and reanalyze public mass spectrometry data. Nature Methods, 2020, 17, 901-904.	19.0	79
153	Effects of Diet versus Gastric Bypass on Metabolic Function in Diabetes. New England Journal of Medicine, 2020, 383, 721-732.	27.0	164
154	Microbe-Metabolite Associations Linked to the Rebounding Murine Gut Microbiome Postcolonization with Vancomycin-Resistant Enterococcus faecium. MSystems, 2020, 5, .	3.8	3
155	Host variables confound gut microbiota studies of human disease. Nature, 2020, 587, 448-454.	27.8	324
156	The Southern Bluefin Tuna Mucosal Microbiome Is Influenced by Husbandry Method, Net Pen Location, and Anti-parasite Treatment. Frontiers in Microbiology, 2020, 11, 2015.	3.5	12
157	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. Bioinformatics, 2020, 36, 4088-4090.	4.1	42
158	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. Nature Communications, 2020, 11, 2500.	12.8	368
159	VisualizingÂâ€™omic feature rankings and log-ratios using Qurro. NAR Genomics and Bioinformatics, 2020, 2, lqaa023.	3.2	97
160	Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information. Genome Research, 2020, 30, 898-909.	5.5	68
161	Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, Scomber japonicus. MSphere, 2020, 5, .	2.9	49
162	Earth microbial co-occurrence network reveals interconnection pattern across microbiomes. Microbiome, 2020, 8, 82.	11.1	239

#	Article	IF	Citations
163	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. Nature, 2020, 579, 567-574.	27.8	691
164	Enhanced Characterization of Drug Metabolism and the Influence of the Intestinal Microbiome: A Pharmacokinetic, Microbiome, and Untargeted Metabolomics Study. Clinical and Translational Science, 2020, 13, 972-984.	3.1	16
165	Longitudinal survey of microbiome associated with particulate matter in a megacity. Genome Biology, 2020, 21, 55.	8.8	59
166	Air pollution exposure is associated with the gut microbiome as revealed by shotgun metagenomic sequencing. Environment International, 2020, 138, 105604.	10.0	97
167	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. MSystems, 2020, 5, .	3.8	47
168	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. Frontiers in Psychiatry, 2020, 11, 518.	2.6	19
169	Patterns of Oral Microbiota Diversity in Adults and Children: A Crowdsourced Population Study. Scientific Reports, 2020, 10, 2133.	3.3	82
170	Global chemical effects of the microbiome include new bile-acid conjugations. Nature, 2020, 579, 123-129.	27.8	316
171	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. PLoS ONE, 2020, 15, e0229001.	2.5	56
172	OP31 Metaâ€“omics reveals microbiome-driven proteolysis as a contributing factor to the severity of ulcerative colitis disease activity. Journal of Crohn's and Colitis, 2020, 14, S030-S031.	1.3	2
173	Organ-level protein networks as a reference for the host effects of the microbiome. Genome Research, 2020, 30, 276-286.	5.5	6
174	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. MSystems, 2020, 5, .	3.8	80
175	Differing salivary microbiome diversity, community and diurnal rhythmicity in association with affective state and peripheral inflammation in adults. Brain, Behavior, and Immunity, 2020, 87, 591-602.	4.1	11
176	The effect of legume supplementation on the gut microbiota in rural Malawian infants aged 6 to 12 months. American Journal of Clinical Nutrition, 2020, 111, 884-892.	4.7	10
177	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. MBio, 2020, 11, .	4.1	204
178	QIIME 2 Enables Comprehensive Endâ€toâ€End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. Current Protocols in Bioinformatics, 2020, 70, e100.	25.8	212
179	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. MSystems, 2020, 5, .	3.8	81
180	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. MSystems, 2020, 5, .	3.8	16

#	Article	IF	Citations
181	Microbial Ecology of Atlantic Salmon (Salmo salar) Hatcheries: Impacts of the Built Environment on Fish Mucosal Microbiota. Applied and Environmental Microbiology, 2020, 86, .	3.1	71
182	Metabolome-Informed Microbiome Analysis Refines Metadata Classifications and Reveals Unexpected Medication Transfer in Captive Cheetahs. MSystems, 2020, 5, .	3.8	12
183	Effects of Immunization With the Soil-Derived Bacterium Mycobacterium vaccae on Stress Coping Behaviors and Cognitive Performance in a â€œTwo Hitâ€•Stressor Model. Frontiers in Physiology, 2020, 11, 524833.	2.8	9
184	A gut bacterial amyloid promotes Î±-synuclein aggregation and motor impairment in mice. ELife, 2020, 9, .	6.0	251
185	Porting and optimizing UniFrac for GPUs. , 2020, , .		3
186	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
187	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
188	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
189	Links between environment, diet, and the hunter-gatherer microbiome. Gut Microbes, 2019, 10, 216-227.	9.8	105
190	Evolutionary trends in host physiology outweigh dietary niche in structuring primate gut microbiomes. ISME Journal, 2019, 13, 576-587.	9.8	236
191	Reply to Sun et al., â€œIdentifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracyâ€• MBio, 2019, 10, .	4.1	0
192	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
193	Ten simple rules for writing and sharing computational analyses in Jupyter Notebooks. PLoS Computational Biology, 2019, 15, e1007007.	3.2	86
194	Associations of the Fecal Microbial Proteome Composition and Proneness to Diet-induced Obesity. Molecular and Cellular Proteomics, 2019, 18, 1864-1879.	3.8	19
195	Subgingival Microbiota and Longitudinal Glucose Change: The Oral Infections, Glucose Intolerance and Insulin Resistance Study (ORIGINS). Journal of Dental Research, 2019, 98, 1488-1496.	5.2	21
196	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. Cell Systems, 2019, 9, 600-608.e4.	6.2	46
197	Convergence of human and Old World monkey gut microbiomes demonstrates the importance of human ecology over phylogeny. Genome Biology, 2019, 20, 201.	8.8	57
198	Species abundance information improves sequence taxonomy classification accuracy. Nature Communications, 2019, 10, 4643.	12.8	86

#	Article	IF	Citations
199	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology, 2019, 20, 219.	8.8	94
200	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. Genome Biology, 2019, 20, 226.	8.8	47
201	Learning representations of microbeâ€“metabolite interactions. Nature Methods, 2019, 16, 1306-1314.	19.0	184
202	Neighborhoods to Nucleotidesâ€”Advances and Gaps for an Obesity Disparities Systems Epidemiology Model. Current Epidemiology Reports, 2019, 6, 476-485.	2.4	1
203	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. MSystems, 2019, 4, .	3.8	23
204	A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. MSystems, 2019, 4, .	3.8	22
205	Expanding the scope and scale of microbiome research. Genome Biology, 2019, 20, 191.	8.8	1
206	Challenges in the construction of knowledge bases for human microbiome-disease associations. Microbiome, 2019, 7, 129.	11.1	36
207	Benchmarking urine storage and collection conditions for evaluating the female urinary microbiome. Scientific Reports, 2019, 9, 13409.	3.3	33
208	Role of the microbiome in human development. Gut, 2019, 68, 1108-1114.	12.1	496
209	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	12.6	45
210	Suppression of the gut microbiome ameliorates ageâ€related arterial dysfunction and oxidative stress in mice. Journal of Physiology, 2019, 597, 2361-2378.	2.9	106
211	Farm-like indoor microbiota in non-farm homes protects children from asthma development. Nature Medicine, 2019, 25, 1089-1095.	30.7	219
212	Establishing microbial composition measurement standards with reference frames. Nature Communications, 2019, 10, 2719.	12.8	428
213	Diet and the Gut Microbiome in 10â€“18-Month-Old Children Living in Urban Slums of Mumbai, India (OR01-08-19). Current Developments in Nutrition, 2019, 3, nzz040.OR01-08-19.	0.3	0
214	redbiom: a Rapid Sample Discovery and Feature Characterization System. MSystems, 2019, 4, .	3.8	35
215	Quantifying and Understanding Well-to-Well Contamination in Microbiome Research. MSystems, 2019, 4, .	3.8	132
216	Ground beef microbiome changes with antimicrobial decontamination interventions and product storage. PLoS ONE, 2019, 14, e0217947.	2.5	30

#	Article	IF	Citations
217	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	27.8	1,638
218	Triplicate PCR reactions for 16S rRNA gene amplicon sequencing are unnecessary. BioTechniques, 2019, 67, 29-32.	1.8	48
219	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. Cell, 2019, 177, 1600-1618.e17.	28.9	701
220	Is there convergence of gut microbes in blood-feeding vertebrates?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180249.	4.0	21
221	The impact of skin care products on skin chemistry and microbiome dynamics. BMC Biology, 2019, 17, 47.	3.8	101
222	Gut microbiota in wild and captive Guizhou snubâ€nosed monkeys, Rhinopithecus brelichi. American Journal of Primatology, 2019, 81, e22989.	1.7	55
223	Trait-like vulnerability of higher-order cognition and ability to maintain wakefulness during combined sleep restriction and circadian misalignment. Sleep, 2019, 42, .	1.1	12
224	Early-Career Scientists Shaping the World. MSystems, 2019, 4, .	3.8	0
225	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. MSystems, 2019, 4, .	3.8	214
226	Consent insufficient for data releaseâ€"Response. Science, 2019, 364, 446-446.	12.6	5
227	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. MSystems, 2019, 4, .	3.8	24
228	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. Scientific Data, 2019, 6, 43.	5.3	14
229	Red Sea SAR11 and Prochlorococcus Single-Cell Genomes Reflect Globally Distributed Pangenomes. Applied and Environmental Microbiology, 2019, 85, .	3.1	11
230	Calour: an Interactive, Microbe-Centric Analysis Tool. MSystems, 2019, 4, .	3.8	28
231	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1Âmonth. Microbiome, 2019, 7, 34.	11.1	115
232	The genetic basis for adaptation of model-designed syntrophic co-cultures. PLoS Computational Biology, 2019, 15, e1006213.	3.2	17
233	Major shifts in gut microbiota during development and its relationship to growth in ostriches. Molecular Ecology, 2019, 28, 2653-2667.	3.9	53
234	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. Microbiome, 2019, 7, 50.	11.1	158

#	Article	IF	Citations
235	A gut microbiome signature for cirrhosis due to nonalcoholic fatty liver disease. Nature Communications, 2019, 10, 1406.	12.8	218
236	Neutrophilic proteolysis in the cystic fibrosis lung correlates with a pathogenic microbiome. Microbiome, 2019, 7, 23.	11.1	53
237	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. MSystems, 2019, 4, .	3.8	40
238	A Novel Sparse Compositional Technique Reveals Microbial Perturbations. MSystems, 2019, 4, .	3.8	295
239	Engineering the microbiome for animal health and conservation. Experimental Biology and Medicine, 2019, 244, 494-504.	2.4	65
240	FXR Regulates Intestinal Cancer Stem Cell Proliferation. Cell, 2019, 176, 1098-1112.e18.	28.9	291
241	Reply to Moossavi and Azad, â€œQuantifying and Interpreting the Association between Early-Life Gut Microbiota Composition and Childhood Obesityâ€• MBio, 2019, 10, .	4.1	0
242	Voices in methods development. Nature Methods, 2019, 16, 945-951.	19.0	5
243	Single-Cell Transcriptomics Reveal a Correlation between Genome Architecture and Gene Family Evolution in Ciliates. MBio, 2019, 10, .	4.1	37
244	Reproducibility, stability, and accuracy of microbial profiles by fecal sample collection method in three distinct populations. PLoS ONE, 2019, 14, e0224757.	2.5	19
245	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. Scientific Data, 2019, 6, 322.	5.3	8
246	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	12.8	197
247	The Microbiome and Its Potential for Pharmacology. Handbook of Experimental Pharmacology, 2019, 260, 301-326.	1.8	14
248	Disease-modifying therapies alter gut microbial composition in MS. Neurology: Neuroimmunology and NeuroInflammation, 2019, 6, e517.	6.0	75
249	Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. Trends in Microbiology, 2019, 27, 105-117.	7.7	652
250	Trace Evidence Potential in Postmortem Skin Microbiomes: From Death Scene to Morgue. Journal of Forensic Sciences, 2019, 64, 791-798.	1.6	40
251	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. Clinical Gastroenterology and Hepatology, 2019, 17, 218-230.	4.4	187
252	GABA-modulating bacteria of the human gut microbiota. Nature Microbiology, 2019, 4, 396-403.	13.3	590

#	Article	IF	Citations
253	Comparison of Oral Collection Methods for Studies of Microbiota. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 137-143.	2.5	28
254	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. Schizophrenia Research, 2019, 204, 23-29.	2.0	157
255	Creating a 3D microbial and chemical snapshot of a human habitat. Scientific Reports, 2018, 8, 3669.	3.3	34
256	Bacterial community changes in an industrial algae production system. Algal Research, 2018, 31, 147-156.	4.6	55
257	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. MSystems, 2018, 3, .	3.8	376
258	Hopanoid-producing bacteria in the Red Sea include the major marine nitrite oxidizers. FEMS Microbiology Ecology, 2018, 94, .	2.7	8
259	Integrated Approaches to Analyze Big Data in the Perinatal/Neonatal Space. Breastfeeding Medicine, 2018, 13, S-5-S-6.	1.7	1
260	Current understanding of the human microbiome. Nature Medicine, 2018, 24, 392-400.	30.7	1,593
261	Bacterial density rather than diversity correlates with hatching success across different avian species. FEMS Microbiology Ecology, 2018, 94, .	2.7	21
262	Overview and systematic review of studies of microbiome in schizophrenia and bipolar disorder. Journal of Psychiatric Research, 2018, 99, 50-61.	3.1	151
263	Coprolites reveal ecological interactions lost with the extinction of New Zealand birds. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1546-1551.	7.1	54
264	Exploration of the Germline Genome of the Ciliate Chilodonella uncinata through Single-Cell Omics (Transcriptomics and Genomics). MBio, 2018, 9, .	4.1	24
265	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	13.3	717
266	Gut microbiota utilize immunoglobulin A for mucosal colonization. Science, 2018, 360, 795-800.	12.6	447
267	0213 Trait-like Vulnerability Of Higher-order Cognition To Sleep Loss And Circadian Misalignment. Sleep, 2018, 41, A83-A84.	1.1	0
268	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. MSystems, 2018, 3, .	3.8	204
269	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. MSystems, 2018, 3, .	3.8	123
270	Diet Versus Phylogeny: a Comparison of Gut Microbiota in Captive Colobine Monkey Species. Microbial Ecology, 2018, 75, 515-527.	2.8	106

#	Article	IF	Citations
271	Guiding longitudinal sampling in IBD cohorts. Gut, 2018, 67, 1743-1745.	12.1	32
272	Impacts of the Human Gut Microbiome on Therapeutics. Annual Review of Pharmacology and Toxicology, 2018, 58, 253-270.	9.4	74
273	Social behaviour and gut microbiota in redâ€bellied lemurs (<scp>E</scp>ulemur rubriventer): In search of the role of immunity in the evolution of sociality. Journal of Animal Ecology, 2018, 87, 388-399.	2.8	57
274	Wildlife-microbiome interactions and disease: exploring opportunities for disease mitigation across ecological scales. Drug Discovery Today: Disease Models, 2018, 28, 105-115.	1.2	25
275	Plant Selenium Hyperaccumulation Affects Rhizosphere: Enhanced Species Richness and Altered Species Composition. Phytobiomes Journal, 2018, 2, 82-91.	2.7	9
276	The murine vaginal microbiota and its perturbation by the human pathogen group B Streptococcus. BMC Microbiology, 2018, 18, 197.	3.3	52
277	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, .	3.8	293
278	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. MSystems, 2018, 3, .	3.8	56
279	Identifying and Predicting Novelty in Microbiome Studies. MBio, 2018, 9, .	4.1	28
280	Metagenomics-Based, Strain-Level Analysis of Escherichia coli From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. Frontiers in Microbiology, 2018, 9, 2559.	3.5	37
281	High-Throughput Miniaturized 16S rRNA Amplicon Library Preparation Reduces Costs while Preserving Microbiome Integrity. MSystems, 2018, 3, .	3.8	58
282	Niche partitioning of a pathogenic microbiome driven by chemical gradients. Science Advances, 2018, 4, eaau1908.	10.3	40
283	Qiita: rapid, web-enabled microbiome meta-analysis. Nature Methods, 2018, 15, 796-798.	19.0	459
284	Preserving microbial diversity. Science, 2018, 362, 33-34.	12.6	133
285	Gut Microbiota in the First 2 Years of Life and the Association with Body Mass Index at Age 12 in a Norwegian Birth Cohort. MBio, 2018, 9, .	4.1	121
286	Differential Activation of Hepatic Invariant NKT Cell Subsets Plays a Key Role in Progression of Nonalcoholic Steatohepatitis. Journal of Immunology, 2018, 201, 3017-3035.	0.8	69
287	Species-level functional profiling of metagenomes and metatranscriptomes. Nature Methods, 2018, 15, 962-968.	19.0	1,125
288	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	19.0	71

#	Article	IF	Citations
289	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (Oreochromis shiranus) and North African catfish (Clarias gariepinus). MicrobiologyOpen, 2018, 7, e00716.	3.0	23
290	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	3.8	604
291	Earth Microbiome Project and Global Systems Biology. MSystems, 2018, 3, .	3.8	65
292	Best practices for analysing microbiomes. Nature Reviews Microbiology, 2018, 16, 410-422.	28.6	1,138
293	Methods for phylogenetic analysis of microbiome data. Nature Microbiology, 2018, 3, 652-661.	13.3	68
294	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. Nature Communications, 2018, 9, 2017.	12.8	103
295	Defining Host Responses during Systemic Bacterial Infection through Construction of a Murine Organ Proteome Atlas. Cell Systems, 2018, 6, 579-592.e4.	6.2	23
296	Large-scale replicated field study of maize rhizosphere identifies heritable microbes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7368-7373.	7.1	435
297	Twisted Tales: Insights into Genome Diversity of Ciliates Using Single-Cell â€˜Omics. Genome Biology and Evolution, 2018, 10, 1927-1938.	2.5	36
298	Docent. , 2018, , .		11
299	Microbiome Data Accurately Predicts the Postmortem Interval Using Random Forest Regression Models. Genes, 2018, 9, 104.	2.4	80
300	Are microbiome studies ready for hypothesis-driven research?. Current Opinion in Microbiology, 2018, 44, 61-69.	5.1	27
301	Environmental radiation alters the gut microbiome of the bank vole Myodes glareolus. ISME Journal, 2018, 12, 2801-2806.	9.8	44
302	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2â€™s q2-feature-classifier plugin. Microbiome, 2018, 6, 90.	11.1	3,159
303	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. Nature Communications, 2018, 9, 2832.	12.8	108
304	Antibiotic-induced microbiome depletion alters metabolic homeostasis by affecting gut signaling and colonic metabolism. Nature Communications, 2018, 9, 2872.	12.8	343
305	The gutâ€“liver axis and the intersection with the microbiome. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 397-411.	17.8	905
306	Improving saliva shotgun metagenomics by chemical host DNA depletion. Microbiome, 2018, 6, 42.	11.1	218

#	Article	IF	Citations
307	Exposure to toxic metals triggers unique responses from the rat gut microbiota. Scientific Reports, 2018, 8, 6578.	3.3	95
308	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. Nature Medicine, 2018, 24, 1532-1535.	30.7	629
309	Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. European Psychiatry, 2018, 53, 37-45.	0.2	88
310	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. MSystems, 2018, 3, .	3.8	96
311	Microbiota as in farm homes protect children from asthma. , 2018, , .		1
312	Experimental Chagas disease-induced perturbations of the fecal microbiome and metabolome. PLoS Neglected Tropical Diseases, 2018, 12, e0006344.	3.0	39
313	Ancient Diet: Gut Microbiota, Immunity, and Health. Yale Journal of Biology and Medicine, 2018, 91, 177-184.	0.2	11
314	Balance Trees Reveal Microbial Niche Differentiation. MSystems, 2017, 2, .	3.8	284
315	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	11.0	95
316	Patterns in Gut Microbiota Similarity Associated with Degree of Sociality among Sex Classes of a Neotropical Primate. Microbial Ecology, 2017, 74, 250-258.	2.8	70
317	A Microbiome Foundation for the Study of Crohnâ€™s Disease. Cell Host and Microbe, 2017, 21, 301-304.	11.0	46
318	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. MSystems, 2017, 2, .	3.8	1,339
319	Transcriptional characterization of Vibrio fischeri during colonization of juvenile Euprymna scolopes. Environmental Microbiology, 2017, 19, 1845-1856.	3.8	24
320	Comparison of Fecal Collection Methods for Microbiota Studies in Bangladesh. Applied and Environmental Microbiology, 2017, 83, .	3.1	50
321	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	11.1	1,434
322	Uncovering the Horseshoe Effect in Microbial Analyses. MSystems, 2017, 2, .	3.8	67
323	Dynamics of the human gut microbiome in inflammatory bowel disease. Nature Microbiology, 2017, 2, 17004.	13.3	830
324	Origin of microbial biomineralization and magnetotaxis during the Archean. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2171-2176.	7.1	98

#	Article	IF	Citations
325	Parkinson's disease and Parkinson's disease medications have distinct signatures of the gut microbiome. Movement Disorders, 2017, 32, 739-749.	3.9	649
326	An Elegan(t) Screen for Drug-Microbe Interactions. Cell Host and Microbe, 2017, 21, 555-556.	11.0	2
327	Coupling Targeted and Untargeted Mass Spectrometry for Metabolome-Microbiome-Wide Association Studies of Human Fecal Samples. Analytical Chemistry, 2017, 89, 7549-7559.	6.5	62
328	Changes in microbial ecology after fecal microbiota transplantation for recurrent C. difficile infection affected by underlying inflammatory bowel disease. Microbiome, 2017, 5, 55.	11.1	118
329	Bacterial colonization and succession in a newly opened hospital. Science Translational Medicine, 2017, 9, .	12.4	248
330	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. MSystems, 2017, 2, .	3.8	141
331	Reply to Wang and Chen: An ancient origin of magnetotactic bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5019-E5020.	7.1	3
332	The Microbiome and Human Biology. Annual Review of Genomics and Human Genetics, 2017, 18, 65-86.	6.2	266
333	Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. Engineering, 2017, 3, 66-70.	6.7	30
334	Microbiome Tools for Forensic Science. Trends in Biotechnology, 2017, 35, 814-823.	9.3	93
335	Intestinal adaptation in proximal and distal segments: Two epithelial responses diverge after intestinal separation. Surgery, 2017, 161, 1016-1027.	1.9	6
336	Comparison of Collection Methods for Fecal Samples in Microbiome Studies. American Journal of Epidemiology, 2017, 185, 115-123.	3.4	112
337	Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. Nature Biotechnology, 2017, 35, 1077-1086.	17.5	400
338	A communal catalogue reveals Earthâ€™s multiscale microbial diversity. Nature, 2017, 551, 457-463.	27.8	1,942
339	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. MSystems, 2017, 2, .	3.8	116
340	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. MSystems, 2017, 2, .	3.8	75
341	Three-Dimensional Microbiome and Metabolome Cartography of a Diseased Human Lung. Cell Host and Microbe, 2017, 22, 705-716.e4.	11.0	111
342	Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. MBio, 2017, 8, .	4.1	219

#	Article	IF	Citations
343	Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. Science, 2017, 357, 802-806.	12.6	694
344	The sponge microbiome project. GigaScience, 2017, 6, 1-7.	6.4	193
345	Strains, functions and dynamics in the expanded Human Microbiome Project. Nature, 2017, 550, 61-66.	27.8	929
346	Gut bacteria from multiple sclerosis patients modulate human T cells and exacerbate symptoms in mouse models. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10713-10718.	7.1	709
347	Mass Spectrometry-Based Chemical Cartography of a Cardiac Parasitic Infection. Analytical Chemistry, 2017, 89, 10414-10421.	6.5	35
348	Dramatic Differences in Gut Bacterial Densities Correlate with Diet and Habitat in Rainforest Ants. Integrative and Comparative Biology, 2017, 57, 705-722.	2.0	77
349	The Effects of Captivity on the Mammalian Gut Microbiome. Integrative and Comparative Biology, 2017, 57, 690-704.	2.0	301
350	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	17.5	1,512
351	Evaluating the impact of domestication and captivity on the horse gut microbiome. Scientific Reports, 2017, 7, 15497.	3.3	112
352	Inflammation-induced IgA+ cells dismantle anti-liver cancer immunity. Nature, 2017, 551, 340-345.	27.8	396
353	The Microbiome in Posttraumatic Stress Disorder and Trauma-Exposed Controls: An Exploratory Study. Psychosomatic Medicine, 2017, 79, 936-946.	2.0	153
354	Global chemical analysis of biology by mass spectrometry. Nature Reviews Chemistry, 2017, 1, .	30.2	146
355	Intermittent Hypoxia and Hypercapnia Accelerate Atherosclerosis, Partially via Trimethylamine-Oxide. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 581-588.	2.9	62
356	Bacterial Community Composition and Dynamics Spanning Five Years in Freshwater Bog Lakes. MSphere, 2017, 2, .	2.9	84
357	Multiplex growth rate phenotyping of synthetic mutants in selection to engineer glucose and xylose coâ€utilization in Escherichia coli. Biotechnology and Bioengineering, 2017, 114, 885-893.	3.3	4
358	Metagenomic covariation along densely sampled environmental gradients in the Red Sea. ISME Journal, 2017, 11, 138-151.	9.8	40
359	Expanding our Understanding of the Role of the Microbiome in Health and Disease. Archives of Medical Research, 2017, 48, 663-665.	3.3	6
360	Tracking Human Gut Microbiome Changes Resulting from a Colonoscopy. Methods of Information in Medicine, 2017, 56, 442-447.	1.2	6

#	Article	IF	Citations
361	DNA extraction for streamlined metagenomics of diverse environmental samples. BioTechniques, 2017, 62, 290-293.	1.8	178
362	Mass Spectrometry Based Molecular 3D-Cartography of Plant Metabolites. Frontiers in Plant Science, 2017, 8, 429.	3.6	24
363	Mosquito Microbiome Dynamics, a Background for Prevalence and Seasonality of West Nile Virus. Frontiers in Microbiology, 2017, 8, 526.	3.5	114
364	Gut microbiome of mothers delivering prematurely shows reduced diversity and lower relative abundance of Bifidobacterium and Streptococcus. PLoS ONE, 2017, 12, e0184336.	2.5	53
365	The human microbiome in evolution. BMC Biology, 2017, 15, 127.	3.8	243
366	Discrete False-Discovery Rate Improves Identification of Differentially Abundant Microbes. MSystems, 2017, 2, .	3.8	73
367	Pigs, Unlike Mice, Have Two Distinct Colonic Stem Cell Populations Similar to Humans That Respond to High-Calorie Diet prior to Insulin Resistance. Cancer Prevention Research, 2017, 10, 442-450.	1.5	10
368	Environmental reservoirs of pathogenic mycobacteria across the Ethiopian biogeographical landscape. PLoS ONE, 2017, 12, e0173811.	2.5	34
369	Digitizing mass spectrometry data to explore the chemical diversity and distribution of marine cyanobacteria and algae. ELife, 2017, 6, .	6.0	33
370	Vertebrate Hosts as Islands: Dynamics of Selection, Immigration, Loss, Persistence, and Potential Function of Bacteria on Salamander Skin. Frontiers in Microbiology, 2016, 7, 333.	3.5	65
371	Parallel Mapping of Antibiotic Resistance Alleles in Escherichia coli. PLoS ONE, 2016, 11, e0146916.	2.5	15
372	Let researchers try new paths. Nature, 2016, 538, 451-453.	27.8	4
373	Stress response, gut microbial diversity and sexual signals correlate with social interactions. Biology Letters, 2016, 12, 20160352.	2.3	47
374	Microbiome-wide association studies link dynamic microbial consortia to disease. Nature, 2016, 535, 94-103.	27.8	595
375	Avoiding Pandemic Fears in the Subway and Conquering the Platypus. MSystems, 2016, 1, .	3.8	27
376	Gut Microbiota Regulate Motor Deficits and Neuroinflammation in a Model of Parkinsonâ€™s Disease. Cell, 2016, 167, 1469-1480.e12.	28.9	2,399
377	Using machine learning to identify major shifts in human gut microbiome protein family abundance in disease. , 2016, , .		21
378	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. Journal of Microbiology and Biology Education, 2016, 17, 46-50.	1.0	42

#	Article	IF	Citations
379	Antibiotic discovery is a walk in the park. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14477-14479.	7.1	24
380	Diets high in resistant starch increase plasma levels of trimethylamine-N-oxide, a gut microbiome metabolite associated with CVD risk. British Journal of Nutrition, 2016, 116, 2020-2029.	2.3	86
381	Role of the microbiome, probiotics, and â€˜dysbiosis therapyâ€™ in critical illness. Current Opinion in Critical Care, 2016, 22, 347-353.	3.2	128
382	Precision medicine in alcoholic and nonalcoholic fatty liver disease via modulating the gut microbiota. American Journal of Physiology - Renal Physiology, 2016, 311, G1018-G1036.	3.4	64
383	Toward a Predictive Understanding of Earthâ€™s Microbiomes to Address 21st Century Challenges. MBio, 2016, 7, .	4.1	124
384	Immunization with a heat-killed preparation of the environmental bacterium Mycobacterium vaccae promotes stress resilience in mice. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3130-9.	7.1	186
385	Preservation Methods Differ in Fecal Microbiome Stability, Affecting Suitability for Field Studies. MSystems, 2016, 1, .	3.8	367
386	From Sample to Multi-Omics Conclusions in under 48 Hours. MSystems, 2016, 1, .	3.8	53
387	Microbial Skin Inhabitants: Friends Forever. Cell, 2016, 165, 771-772.	28.9	17
388	Genetic Determinants of the Gut Microbiome in UK Twins. Cell Host and Microbe, 2016, 19, 731-743.	11.0	831
389	Fecal Microbiome in Epidemiologic Studiesâ€”Response. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 870-871.	2.5	4
390	Comparison of Collection Methods for Fecal Samples for Discovery Metabolomics in Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1483-1490.	2.5	63
391	Mass Spectrometry-Based Visualization of Molecules Associated with Human Habitats. Analytical Chemistry, 2016, 88, 10775-10784.	6.5	44
392	Probiotic treatment restores protection against lethal fungal infection lost during amphibian captivity. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20161553.	2.6	144
393	Heritable components of the human fecal microbiome are associated with visceral fat. Genome Biology, 2016, 17, 189.	8.8	183
394	Effects of field conditions on fecal microbiota. Journal of Microbiological Methods, 2016, 130, 180-188.	1.6	28
395	The Oral and Skin Microbiomes of Captive Komodo Dragons Are Significantly Shared with Their Habitat. MSystems, 2016, 1, .	3.8	61
396	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	17.5	2,802

#	Article	IF	Citations
397	Using the gut microbiota as a novel tool for examining colobine primate GI health. Global Ecology and Conservation, 2016, 7, 225-237.	2.1	76
398	Extreme Dysbiosis of the Microbiome in Critical Illness. MSphere, 2016, 1, .	2.9	283
399	Prevalence and genetic diversity of Blastocystis in family units living in the United States. Infection, Genetics and Evolution, 2016, 45, 95-97.	2.3	40
400	Fat and vitamin intakes during pregnancy have stronger relations with a pro-inflammatory maternal microbiota than does carbohydrate intake. Microbiome, 2016, 4, 55.	11.1	101
401	Diversity, structure and convergent evolution of the global sponge microbiome. Nature Communications, 2016, 7, 11870.	12.8	594
402	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. MSystems, 2016, 1, .	3.8	89
403	The Microbiota, Immunoregulation, and Mental Health: Implications for Public Health. Current Environmental Health Reports, 2016, 3, 270-286.	6.7	150
404	Microbiology of death. Current Biology, 2016, 26, R561-R563.	3.9	50
405	Culturing: Looking it up in our gut. Nature Microbiology, 2016, 1, 16169.	13.3	1
406	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. Nature Microbiology, 2016, 1, 16177.	13.3	194
407	Lifestyle chemistries from phones for individual profiling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7645-E7654.	7.1	55
408	Migraines Are Correlated with Higher Levels of Nitrate-, Nitrite-, and Nitric Oxide-Reducing Oral Microbes in the American Gut Project Cohort. MSystems, 2016, 1, .	3.8	63
409	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. Genome Biology, 2016, 17, 217.	8.8	128
410	Host age, social group, and habitat type influence the gut microbiota of wild ringâ€tailed lemurs (Lemur catta). American Journal of Primatology, 2016, 78, 883-892.	1.7	98
411	Geography and Location Are the Primary Drivers of Office Microbiome Composition. MSystems, 2016, 1, .	3.8	110
412	The pediatric intestinal mucosal microbiome remains altered after clinical resolution of inflammatory and ischemic disease. Surgery, 2016, 160, 350-358.	1.9	8
413	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. GigaScience, 2016, 5, 27.	6.4	35
414	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. Microbiome, 2016, 4, 11.	11.1	51

#	Article	IF	Citations
415	Inhibitory bacteria reduce fungi on early life stages of endangered Colorado boreal toads (Anaxyrus boreas). ISME Journal, 2016, 10, 934-944.	9.8	111
416	Microbial community assembly and metabolic function during mammalian corpse decomposition. Science, 2016, 351, 158-162.	12.6	381
417	Walls talk: Microbial biogeography of homes spanning urbanization. Science Advances, 2016, 2, e1501061.	10.3	72
418	Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. MSystems, 2016, 1, .	3.8	1,364
419	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	9.8	593
420	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. Nature Medicine, 2016, 22, 250-253.	30.7	736
421	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
422	Phylogenetic and ecological factors impact the gut microbiota of two Neotropical primate species. Oecologia, 2016, 180, 717-733.	2.0	91
423	Tools for the Microbiome: Nano and Beyond. ACS Nano, 2016, 10, 6-37.	14.6	137
424	Collecting Fecal Samples for Microbiome Analyses in Epidemiology Studies. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 407-416.	2.5	154
425	Carcass mass has little influence on the structure of gravesoil microbial communities. International Journal of Legal Medicine, 2016, 130, 253-263.	2.2	49
426	Dietary Prebiotics and Bioactive Milk Fractions Improve NREM Sleep, Enhance REM Sleep Rebound and Attenuate the Stress-Induced Decrease in Diurnal Temperature and Gut Microbial Alpha Diversity. Frontiers in Behavioral Neuroscience, 2016, 10, 240.	2.0	67
427	Analysis of composition of microbiomes: a novel method for studying microbial composition. Microbial Ecology in Health and Disease, 2015, 26, 27663.	3.5	1,283
428	Changes in vaginal microbiota following antimicrobial and probiotic therapy. Microbial Ecology in Health and Disease, 2015, 26, 27799.	3.5	71
429	Short Course in the Microbiome. Journal of Circulating Biomarkers, 2015, 4, 8.	1.3	9
430	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. Microbiome, 2015, 3, 20.	11.1	115
431	Context and the human microbiome. Microbiome, 2015, 3, 52.	11.1	81
432	Variable responses of human and non-human primate gut microbiomes to a Western diet. Microbiome, 2015, 3, 53.	11.1	108

#	Article	IF	Citations
433	Towards large-cohort comparative studies to define the factors influencing the gut microbial community structure of ASD patients. Microbial Ecology in Health and Disease, 2015, 26, 26555.	3.5	16
434	Cross-biome comparison of microbial association networks. Frontiers in Microbiology, 2015, 6, 1200.	3.5	154
435	A population of Pax7-expressing muscle progenitor cells show differential responses to muscle injury dependent on developmental stage and injury extent. Frontiers in Aging Neuroscience, 2015, 7, 161.	3.4	33
436	Exercise Is More Effective at Altering Gut Microbial Composition and Producing Stable Changes in Lean Mass in Juvenile versus Adult Male F344 Rats. PLoS ONE, 2015, 10, e0125889.	2.5	150
437	Authors' reply to Mawer and Wilcox and Mullish and Williams. BMJ, The, 2015, 351, h6132-h6132.	6.0	2
438	Skin bacteria provide early protection for newly metamorphosed southern leopard frogs (Rana) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54 Conservation, 2015, 187, 91-102.	4.1	54
439	Microbiota at Multiple Body Sites during Pregnancy in a Rural Tanzanian Population and Effects of Moringa-Supplemented Probiotic Yogurt. Applied and Environmental Microbiology, 2015, 81, 4965-4975.	3.1	85
440	Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host and Microbe, 2015, 17, 603-616.	11.0	628
441	Can Your Microbiome Tell You What to Eat?. Cell Metabolism, 2015, 22, 960-961.	16.2	19
442	Euphorbia plant latex is inhabited by diverse microbial communities. American Journal of Botany, 2015, 102, 1966-1977.	1.7	13
443	The microbiome quality control project: baseline study design and future directions. Genome Biology, 2015, 16, 276.	8.8	196
444	Satellite remote sensing data can be used to model marine microbial metabolite turnover. ISME Journal, 2015, 9, 166-179.	9.8	17
445	Microbial endocrinology: the interplay between the microbiota and the endocrine system. FEMS Microbiology Reviews, 2015, 39, 509-521.	8.6	439
446	Why Microbiome Treatments Could Pay Off Soon. Nature, 2015, 518, S5-S5.	27.8	8
447	Antifungal isolates database of amphibian skinâ€associated bacteria and function against emerging fungal pathogens. Ecology, 2015, 96, 595-595.	3.2	192
448	Dietary effects on human gut microbiome diversity. British Journal of Nutrition, 2015, 113, S1-S5.	2.3	350
449	The gut microbiota in human energy homeostasis and obesity. Trends in Endocrinology and Metabolism, 2015, 26, 493-501.	7.1	350
450	Ribosomal RNA, the lens into life. Rna, 2015, 21, 692-694.	3.5	3

#	Article	IF	Citations
451	Dietary input of microbes and host genetic variation shape among-population differences in stickleback gut microbiota. ISME Journal, 2015, 9, 2515-2526.	9.8	291
452	The microbiome of uncontacted Amerindians. Science Advances, 2015, 1, .	10.3	721
453	Seasonal variation of postmortem microbial communities. Forensic Science, Medicine, and Pathology, 2015, 11, 202-207.	1.4	88
454	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection. Microbiome, 2015, 3, 10.	11.1	218
455	Subsistence strategies in traditional societies distinguish gut microbiomes. Nature Communications, 2015, 6, 6505.	12.8	449
456	Effect of preservation method on spider monkey (Ateles geoffroyi) fecal microbiota over 8weeks. Journal of Microbiological Methods, 2015, 113, 16-26.	1.6	118
457	Molecular cartography of the human skin surface in 3D. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2120-9.	7.1	288
458	Associations between human milk oligosaccharides and infant body composition in the first 6 mo of life. American Journal of Clinical Nutrition, 2015, 102, 1381-1388.	4.7	169
459	A unified initiative to harness Earth's microbiomes. Science, 2015, 350, 507-508.	12.6	195
460	Faecal transplants. BMJ, The, 2015, 351, h5149.	6.0	8
461	Genome-Wide Tuning of Protein Expression Levels to Rapidly Engineer Microbial Traits. ACS Synthetic Biology, 2015, 4, 1244-1253.	3.8	22
462	Genetic and environmental control of host-gut microbiota interactions. Genome Research, 2015, 25, 1558-1569.	5.5	288
463	The unifrac significance test is sensitive to tree topology. BMC Bioinformatics, 2015, 16, 211.	2.6	22
464	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. Applied and Environmental Microbiology, 2015, 81, 6200-6209.	3.1	167
465	Prediction of Early Childhood Caries via Spatial-Temporal Variations of Oral Microbiota. Cell Host and Microbe, 2015, 18, 296-306.	11.0	204
466	ConStrains identifies microbial strains in metagenomic datasets. Nature Biotechnology, 2015, 33, 1045-1052.	17.5	235
467	Why Microbiome Treatments Could Pay Off Soon. Scientific American, 2015, 312, S5-S5.	1.0	0
468	Changes in bacterial and eukaryotic communities during sewage decomposition in Mississippi river water. Water Research, 2015, 69, 30-39.	11.3	49

#	Article	IF	Citations
469	Identifying qualitative effects of different grazing types on belowâ€ground communities and function in a longâ€term field experiment. Environmental Microbiology, 2015, 17, 841-854.	3.8	21
470	Microbiome/Metabolic Syndrome/Diabetes and CVD. FASEB Journal, 2015, 29, 222.3.	0.5	0
471	HLA-B27 and Human Î²2-Microglobulin Affect the Gut Microbiota of Transgenic Rats. PLoS ONE, 2014, 9, e105684.	2.5	209
472	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. PeerJ, 2014, 2, e545.	2.0	535
473	Multilevel Research Strategies and Biological Systems. Philosophy of Science, 2014, 81, 811-828.	1.0	56
474	Glycan Degradation (GlyDeR) Analysis Predicts Mammalian Gut Microbiota Abundance and Host Diet-Specific Adaptations. MBio, 2014, 5, .	4.1	35
475	Metaâ€analyses of human gut microbes associated with obesity and IBD. FEBS Letters, 2014, 588, 4223-4233.	2.8	697
476	Diversity of Rickettsiales in the Microbiome of the Lone Star Tick, Amblyomma americanum. Applied and Environmental Microbiology, 2014, 80, 354-359.	3.1	82
477	Improved HF183 Quantitative Real-Time PCR Assay for Characterization of Human Fecal Pollution in Ambient Surface Water Samples. Applied and Environmental Microbiology, 2014, 80, 3086-3094.	3.1	221
478	Structural basis for diversity in the SAM clan of riboswitches. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6624-6629.	7.1	57
479	Impact of fire on active layer and permafrost microbial communities and metagenomes in an upland Alaskan boreal forest. ISME Journal, 2014, 8, 1904-1919.	9.8	150
480	MIxS-BE: a MIxS extension defining a minimum information standard for sequence data from the built environment. ISME Journal, 2014, 8, 1-3.	9.8	127
481	Communities of microbial eukaryotes in the mammalian gut within the context of environmental eukaryotic diversity. Frontiers in Microbiology, 2014, 5, 298.	3.5	130
482	Anal gas evacuation and colonic microbiota in patients with flatulence: effect of diet. Gut, 2014, 63, 401-408.	12.1	104
483	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
484	Individuals' diet diversity influences gut microbial diversity in two freshwater fish (threespine) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142	6.4	288
485	Ancient human oral plaque preserves a wealth of biological data. Nature Genetics, 2014, 46, 321-323.	21.4	20
486	The founding charter of the Genomic Observatories Network. GigaScience, 2014, 3, 2.	6.4	51

#	Article	IF	Citations
487	Temporal variability is a personalized feature of the human microbiome. Genome Biology, 2014, 15, 531.	8.8	355
488	Tracking down the sources of experimental contamination in microbiome studies. Genome Biology, 2014, 15, 564.	8.8	164
489	Conditionally Rare Taxa Disproportionately Contribute to Temporal Changes in Microbial Diversity. MBio, 2014, 5, e01371-14.	4.1	549
490	The amphibian skinâ€associated microbiome across species, space and life history stages. Molecular Ecology, 2014, 23, 1238-1250.	3.9	360
491	Convergence of gut microbiomes in myrmecophagous mammals. Molecular Ecology, 2014, 23, 1301-1317.	3.9	311
492	Eggshell Bacterial Load Is Related to Antimicrobial Properties of Feathers Lining Barn Swallow Nests. Microbial Ecology, 2014, 67, 480-487.	2.8	25
493	The Intestinal Metabolome: An Intersection Between Microbiota and Host. Gastroenterology, 2014, 146, 1470-1476.	1.3	227
494	The Treatment-Naive Microbiome in New-Onset Crohnâ€™s Disease. Cell Host and Microbe, 2014, 15, 382-392.	11.0	2,582
495	Bacterial phylogeny structures soil resistomes across habitats. Nature, 2014, 509, 612-616.	27.8	973
496	Microbial community dynamics and effect of environmental microbial reservoirs on red-backed salamanders (Plethodon cinereus). ISME Journal, 2014, 8, 830-840.	9.8	316
497	Human Genetics Shape the Gut Microbiome. Cell, 2014, 159, 789-799.	28.9	2,523
498	Specialized Metabolites from the Microbiome in Health and Disease. Cell Metabolism, 2014, 20, 719-730.	16.2	454
499	Gut Microbes and the Brain: Paradigm Shift in Neuroscience. Journal of Neuroscience, 2014, 34, 15490-15496.	3.6	719
500	Technology and Techniques for Microbial Ecology via DNA Sequencing. Annals of the American Thoracic Society, 2014, 11, S16-S20.	3.2	8
501	Vertebrate Decomposition Is Accelerated by Soil Microbes. Applied and Environmental Microbiology, 2014, 80, 4920-4929.	3.1	84
502	Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. Cell, 2014, 159, 253-266.	28.9	324
503	Longitudinal analysis of microbial interaction between humans and the indoor environment. Science, 2014, 345, 1048-1052.	12.6	751
504	Major <scp>H</scp>istocompatibility <scp>C</scp>omplex class <scp>II</scp>b polymorphism influences gut microbiota composition and diversity. Molecular Ecology, 2014, 23, 4831-4845.	3.9	174

#	Article	IF	Citations
505	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. ISME Journal, 2014, 8, 1464-1475.	9.8	325
506	Finding the Missing Links among Metabolites, Microbes, and the Host. Immunity, 2014, 40, 824-832.	14.3	256
507	Conducting a Microbiome Study. Cell, 2014, 158, 250-262.	28.9	625
508	SnapShot: The Human Microbiome. Cell, 2014, 158, 690-690.e1.	28.9	26
509	Which is more important for classifying microbial communities: whoâ€™s there or what they can do?. ISME Journal, 2014, 8, 2357-2359.	9.8	82
510	Individual diet has sex-dependent effects on vertebrate gut microbiota. Nature Communications, 2014, 5, 4500.	12.8	464
511	The Earth Microbiome project: successes and aspirations. BMC Biology, 2014, 12, 69.	3.8	723
512	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	28.9	64
513	pH is a good predictor of the distribution of anoxygenic purple phototrophic bacteria in Arctic soils. Soil Biology and Biochemistry, 2014, 74, 193-200.	8.8	55
514	Rethinking â€œEnterotypesâ€• Cell Host and Microbe, 2014, 16, 433-437.	11.0	321
515	Predictive modeling of gingivitis severity and susceptibility via oral microbiota. ISME Journal, 2014, 8, 1768-1780.	9.8	118
516	What Is the Value of a Food and Drug Administration Investigational New Drug Application for Fecal Microbiota Transplantation to Treat Clostridium difficile Infection?. Clinical Gastroenterology and Hepatology, 2014, 12, 289-291.	4.4	18
517	Comparison of the vaginal microbial communities in women with recurrent genital HSV receiving acyclovir intravaginal rings. Antiviral Research, 2014, 102, 87-94.	4.1	19
518	Meeting report for the 1st skin microbiota workshop, boulder, CO October 15-16 2012. Standards in Genomic Sciences, 2014, 9, .	1.5	0
519	Genomic Standards Consortium Projects. Standards in Genomic Sciences, 2014, 9, 599-601.	1.5	26
520	Interacting Symbionts and Immunity in the Amphibian Skin Mucosome Predict Disease Risk and Probiotic Effectiveness. PLoS ONE, 2014, 9, e96375.	2.5	191
521	Replenishing our defensive microbes. BioEssays, 2013, 35, 810-817.	2.5	39
522	Diversity, distribution and sources of bacteria in residential kitchens. Environmental Microbiology, 2013, 15, 588-596.	3.8	170

#	Article	IF	Citations
523	Baseline survey of the anatomical microbial ecology of an important food plant: Solanum lycopersicum (tomato). BMC Microbiology, 2013, 13, 114.	3.3	221
524	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	17.5	8,049
525	The Long-Term Stability of the Human Gut Microbiota. Science, 2013, 341, 1237439.	12.6	1,696
526	Genetically dictated change in host mucus carbohydrate landscape exerts a diet-dependent effect on the gut microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17059-17064.	7.1	237
527	Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. Science, 2013, 342, 621-624.	12.6	480
528	Gut Microbiota from Twins Discordant for Obesity Modulate Metabolism in Mice. Science, 2013, 341, 1241214.	12.6	3,006
529	Toward Effective Probiotics for Autism and Other Neurodevelopmental Disorders. Cell, 2013, 155, 1446-1448.	28.9	97
530	Meta-analyses of studies of the human microbiota. Genome Research, 2013, 23, 1704-1714.	5.5	352
531	EMPeror: a tool for visualizing high-throughput microbial community data. GigaScience, 2013, 2, 16.	6.4	1,096
532	Alterations in the Gut Microbiota Associated with HIV-1 Infection. Cell Host and Microbe, 2013, 14, 329-339.	11.0	387
533	A meta-analysis of changes in bacterial and archaeal communities with time. ISME Journal, 2013, 7, 1493-1506.	9.8	322
534	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553
535	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nature Methods, 2013, 10, 57-59.	19.0	3,402
536	Global biogeography of highly diverse protistan communities in soil. ISME Journal, 2013, 7, 652-659.	9.8	412
537	Distinct cutaneous bacterial assemblages in a sampling of South American Amerindians and US residents. ISME Journal, 2013, 7, 85-95.	9.8	101
538	The microbiome explored: recent insights and future challenges. Nature Reviews Microbiology, 2013, 11, 213-217.	28.6	162
539	How delivery mode and feeding can shape the bacterial community in the infant gut. Cmaj, 2013, 185, 373-374.	2.0	54
540	Crystal ball â€“ 2013. Microbial Biotechnology, 2013, 6, 3-16.	4.2	6

#	Article	IF	Citations
541	Xenobiotics and the Human Gut Microbiome: Metatranscriptomics Reveal the Active Players. Cell Metabolism, 2013, 17, 317-318.	16.2	35
542	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. Cell Metabolism, 2013, 17, 141-152.	16.2	464
543	Complex Interactions Among Diet, Gastrointestinal Transit, and Gut Microbiota in Humanized Mice. Gastroenterology, 2013, 144, 967-977.	1.3	387
544	Translating the human microbiome. Nature Biotechnology, 2013, 31, 304-308.	17.5	30
545	Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. ISME Journal, 2013, 7, 50-60.	9.8	198
546	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. PLoS Computational Biology, 2013, 9, e1002863.	3.2	446
547	Nucleotides Adjacent to the Ligand-Binding Pocket are Linked to Activity Tuning in the Purine Riboswitch. Journal of Molecular Biology, 2013, 425, 1596-1611.	4.2	50
548	From molecules to dynamic biological communities. Biology and Philosophy, 2013, 28, 241-259.	1.4	12
549	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. Science, 2013, 339, 548-554.	12.6	1,012
550	Widespread Colonization of the Lung by Tropheryma whipplei in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	5.6	175
551	Seasonal restructuring of the ground squirrel gut microbiota over the annual hibernation cycle. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2013, 304, R33-R42.	1.8	159
552	Simultaneous Amplicon Sequencing to Explore Co-Occurrence Patterns of Bacterial, Archaeal and Eukaryotic Microorganisms in Rumen Microbial Communities. PLoS ONE, 2013, 8, e47879.	2.5	304
553	Biphasic assembly of the murine intestinal microbiota during early development. ISME Journal, 2013, 7, 1112-1115.	9.8	142
554	Evidence for a persistent microbial seed bank throughout the global ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4651-4655.	7.1	200
555	The Hospital Microbiome Project: Meeting Report for the 1st Hospital Microbiome Project Workshop on sampling design and building science measurements, Chicago, USA, June 7th-8th 2012. Standards in Genomic Sciences, 2013, 8, 112-117.	1.5	18
556	Meeting Report: Fungal ITS Workshop (October 2012). Standards in Genomic Sciences, 2013, 8, 118-123.	1.5	34
557	A microbial clock provides an accurate estimate of the postmortem interval in a mouse model system. ELife, 2013, 2, e01104.	6.0	270
558	Bacterial Diversity in Two Neonatal Intensive Care Units (NICUs). PLoS ONE, 2013, 8, e54703.	2.5	120

#	Article	IF	Citations
559	The Ecology of Microbial Communities Associated with Macrocystis pyrifera. PLoS ONE, 2013, 8, e67480.	2.5	100
560	Co-Enriching Microflora Associated with Culture Based Methods to Detect Salmonella from Tomato Phyllosphere. PLoS ONE, 2013, 8, e73079.	2.5	49
561	Impact of Ileocecal Resection and Concomitant Antibiotics on the Microbiome of the Murine Jejunum and Colon. PLoS ONE, 2013, 8, e73140.	2.5	54
562	Cohabiting family members share microbiota with one another and with their dogs. ELife, 2013, 2, e00458.	6.0	801
563	A Modular Organization of the Human Intestinal Mucosal Microbiota and Its Association with Inflammatory Bowel Disease. PLoS ONE, 2013, 8, e80702.	2.5	147
564	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. Genome Research, 2012, 22, 1974-1984.	5.5	120
565	Nurture trumps nature in a longitudinal survey of salivary bacterial communities in twins from early adolescence to early adulthood. Genome Research, 2012, 22, 2146-2152.	5.5	167
566	Human Immunodeficiency VirusnefSignature Sequences Are Associated with Pulmonary Hypertension. AIDS Research and Human Retroviruses, 2012, 28, 607-618.	1.1	50
567	Interleukin-1Î² (IL-1Î²) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. Gut, 2012, 61, 373-384.	12.1	68
568	Lake microbial communities are resilient after a whole-ecosystem disturbance. ISME Journal, 2012, 6, 2153-2167.	9.8	198
569	Co-habiting amphibian species harbor unique skin bacterial communities in wild populations. ISME Journal, 2012, 6, 588-596.	9.8	282
570	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. ISME Journal, 2012, 6, 94-103.	9.8	537
571	SitePainter: a tool for exploring biogeographical patterns. Bioinformatics, 2012, 28, 436-438.	4.1	22
572	RNASTAR: An RNA STructural Alignment Repository that provides insight into the evolution of natural and artificial RNAs. Rna, 2012, 18, 1319-1327.	3.5	30
573	Conceptualizing a Genomics Software Institute (GSI). Standards in Genomic Sciences, 2012, 6, 136-144.	1.5	1
574	Defining the human microbiome. Nutrition Reviews, 2012, 70, S38-S44.	5.8	789
575	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. Cell, 2012, 150, 470-480.	28.9	1,603
576	Transient Inability to Manage Proteobacteria Promotes Chronic Gut Inflammation in TLR5-Deficient Mice. Cell Host and Microbe, 2012, 12, 139-152.	11.0	459

#	Article	IF	Citations
577	Microbiota Regulate Intestinal Absorption and Metabolism of Fatty Acids in the Zebrafish. Cell Host and Microbe, 2012, 12, 277-288.	11.0	717
578	The Western English Channel contains a persistent microbial seed bank. ISME Journal, 2012, 6, 1089-1093.	9.8	170
579	Spatial and temporal variability of the human microbiota. Clinical Microbiology and Infection, 2012, 18, 5-7.	6.0	61
580	The Impact of the Gut Microbiota on Human Health: An Integrative View. Cell, 2012, 148, 1258-1270.	28.9	2,920
581	Sequencing our way towards understanding global eukaryotic biodiversity. Trends in Ecology and Evolution, 2012, 27, 233-243.	8.7	395
582	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. GigaScience, 2012, 1, 7.	6.4	671
583	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. Current Protocols in Microbiology, 2012, 27, Unit 1E.5..	6.5	486
584	The interpersonal and intrapersonal diversity of human-associated microbiota in key body sites. Journal of Allergy and Clinical Immunology, 2012, 129, 1204-1208.	2.9	266
585	Characterizing microbial communities through space and time. Current Opinion in Biotechnology, 2012, 23, 431-436.	6.6	98
586	The Human Microbiome Project: A Community Resource for the Healthy Human Microbiome. PLoS Biology, 2012, 10, e1001377.	5.6	369
587	Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. ISME Journal, 2012, 6, 1007-1017.	9.8	1,405
588	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. ISME Journal, 2012, 6, 610-618.	9.8	4,581
589	A large-scale benchmark study of existing algorithms for taxonomy-independent microbial community analysis. Briefings in Bioinformatics, 2012, 13, 107-121.	6.5	133
590	Diversity, stability and resilience of the human gut microbiota. Nature, 2012, 489, 220-230.	27.8	4,114
591	Defining seasonal marine microbial community dynamics. ISME Journal, 2012, 6, 298-308.	9.8	928
592	Selection of primers for optimal taxonomic classification of environmental 16S rRNA gene sequences. ISME Journal, 2012, 6, 1440-1444.	9.8	326
593	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME Journal, 2012, 6, 1621-1624.	9.8	7,430
594	Analysis of the Gut Microbiota in the Old Order Amish and Its Relation to the Metabolic Syndrome. PLoS ONE, 2012, 7, e43052.	2.5	183

#	Article	IF	Citations
595	Commensal Bacteria and MAMPs Are Necessary for Stress-Induced Increases in IL-1Î² and IL-18 but Not IL-6, IL-10 or MCP-1. PLoS ONE, 2012, 7, e50636.	2.5	71
596	Insights from Characterizing Extinct Human Gut Microbiomes. PLoS ONE, 2012, 7, e51146.	2.5	178
597	Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227.	27.8	6,247
598	Secondary structure information does not improve OTU assignment for partial 16s rRNA sequences. ISME Journal, 2012, 6, 1277-1280.	9.8	24
599	Spatial and temporal dynamics of the microbial community in the Hanford unconfined aquifer. ISME Journal, 2012, 6, 1665-1676.	9.8	109
600	Unlocking the potential of metagenomics through replicated experimental design. Nature Biotechnology, 2012, 30, 513-520.	17.5	250
601	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. ISME Journal, 2012, 6, 1273-1276.	9.8	102
602	A preliminary survey of lichen associated eukaryotes using pyrosequencing. Lichenologist, 2012, 44, 137-146.	0.8	67
603	Experimental and analytical tools for studying the human microbiome. Nature Reviews Genetics, 2012, 13, 47-58.	16.3	601
604	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. Obesity, 2012, 20, 738-747.	3.0	352
605	Advancing analytical algorithms and pipelines for billions of microbial sequences. Current Opinion in Biotechnology, 2012, 23, 64-71.	6.6	57
606	Environmental and ecological factors that shape the gut bacterial communities of fish: a metaâ€analysis. Molecular Ecology, 2012, 21, 3363-3378.	3.9	814
607	Geographic distance and pH drive bacterial distribution in alkaline lake sediments across Tibetan Plateau. Environmental Microbiology, 2012, 14, 2457-2466.	3.8	484
608	Hibernation alters the gut microbial community in ground squirrels. FASEB Journal, 2012, 26, 1155.6.	0.5	0
609	Microbes do not follow the elevational diversity patterns of plants and animals. Ecology, 2011, 92, 797-804.	3.2	351
610	UCHIME improves sensitivity and speed of chimera detection. Bioinformatics, 2011, 27, 2194-2200.	4.1	13,241
611	Development of the Human Gastrointestinal Microbiota and Insights From High-Throughput Sequencing. Gastroenterology, 2011, 140, 1713-1719.	1.3	329
612	Using QIIME to Analyze 16S rRNA Gene Sequences from Microbial Communities. Current Protocols in Bioinformatics, 2011, 36, Unit 10.7..	25.8	507

#	Article	IF	Citations
613	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. Science, 2011, 332, 970-974.	12.6	1,712
614	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4516-4522.	7.1	7,425
615	Chimeric 16S rRNA sequence formation and detection in Sanger and 454-pyrosequenced PCR amplicons. Genome Research, 2011, 21, 494-504.	5.5	3,015
616	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	17.5	608
617	The Impact of a Consortium of Fermented Milk Strains on the Gut Microbiome of Gnotobiotic Mice and Monozygotic Twins. Science Translational Medicine, 2011, 3, 106ra106.	12.4	456
618	Moving pictures of the human microbiome. Genome Biology, 2011, 12, R50.	9.6	934
619	Human-Associated Microbial Signatures: Examining Their Predictive Value. Cell Host and Microbe, 2011, 10, 292-296.	11.0	134
620	Bacterial Communities Associated with the Lichen Symbiosis. Applied and Environmental Microbiology, 2011, 77, 1309-1314.	3.1	302
621	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. Trends in Microbiology, 2011, 19, 472-482.	7.7	23
622	Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. Science, 2011, 334, 105-108.	12.6	5,253
623	Microbial Eukaryotes in the Human Microbiome: Ecology, Evolution, and Future Directions. Frontiers in Microbiology, 2011, 2, 153.	3.5	186
624	Meeting report of the RNA Ontology Consortium January 8-9, 2011. Standards in Genomic Sciences, 2011, 4, 252-256.	1.5	1
625	The Earth Microbiome Project: The Meeting Report for the 1st International Earth Microbiome Project Conference, Shenzhen, China, June 13th-15th 2011. Standards in Genomic Sciences, 2011, 5, 243-247.	1.5	18
626	Global patterns in the biogeography of bacterial taxa. Environmental Microbiology, 2011, 13, 135-144.	3.8	362
627	Supervised classification of human microbiota. FEMS Microbiology Reviews, 2011, 35, 343-359.	8.6	377
628	Microbiota restoration: natural and supplemented recovery of human microbial communities. Nature Reviews Microbiology, 2011, 9, 27-38.	28.6	461
629	UniFrac: an effective distance metric for microbial community comparison. ISME Journal, 2011, 5, 169-172.	9.8	2,280
630	Supervised classification of microbiota mitigates mislabeling errors. ISME Journal, 2011, 5, 570-573.	9.8	42

#	Article	IF	Citations
631	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. ISME Journal, 2011, 5, 601-612.	9.8	385
632	Examining the global distribution of dominant archaeal populations in soil. ISME Journal, 2011, 5, 908-917.	9.8	1,112
633	The genomic standards consortium: bringing standards to life for microbial ecology. ISME Journal, 2011, 5, 1565-1567.	9.8	59
634	The under-recognized dominance of Verrucomicrobia in soil bacterial communities. Soil Biology and Biochemistry, 2011, 43, 1450-1455.	8.8	613
635	Our microbial selves: what ecology can teach us. EMBO Reports, 2011, 12, 775-784.	4.5	71
636	Bayesian community-wide culture-independent microbial source tracking. Nature Methods, 2011, 8, 761-763.	19.0	1,284
637	Human oral, gut, and plaque microbiota in patients with atherosclerosis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4592-4598.	7.1	943
638	Sources of Bacteria in Outdoor Air across Cities in the Midwestern United States. Applied and Environmental Microbiology, 2011, 77, 6350-6356.	3.1	237
639	Pan-genome of the dominant human gut-associated archaeon, Methanobrevibacter smithii , studied in twins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4599-4606.	7.1	221
640	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Applied Ontology, 2011, 6, 53-89.	2.0	23
641	Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition. PLoS ONE, 2011, 6, e16900.	2.5	43
642	Boulder ALignment Editor (ALE): a web-based RNA alignment tool. Bioinformatics, 2011, 27, 1706-1707.	4.1	8
643	Sharing and archiving nucleic acid structure mapping data. Rna, 2011, 17, 1204-1212.	3.5	28
644	TopiaryExplorer: visualizing large phylogenetic trees with environmental metadata. Bioinformatics, 2011, 27, 3067-3069.	4.1	15
645	Bacterial community structures are unique and resilient in full-scale bioenergy systems. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4158-4163.	7.1	412
646	New Insight into the Diversity of Life's Building Blocks: Evenness, Not Variance. Astrobiology, 2011, 11, 197-198.	3.0	1
647	Succession of microbial consortia in the developing infant gut microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4578-4585.	7.1	2,108
648	The Genomic Standards Consortium. PLoS Biology, 2011, 9, e1001088.	5.6	180

#	Article	IF	Citations
649	PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. Bioinformatics, 2011, 27, 1159-1161.	4.1	351
650	Microbial Biogeography of Public Restroom Surfaces. PLoS ONE, 2011, 6, e28132.	2.5	222
651	Composition of Human Skin Microbiota Affects Attractiveness to Malaria Mosquitoes. PLoS ONE, 2011, 6, e28991.	2.5	208
652	Natural and artificial RNAs occupy the same restricted region of sequence space. Rna, 2010, 16, 280-289.	3.5	21
653	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. Standards in Genomic Sciences, 2010, 3, 243-248.	1.5	228
654	The Earth Microbiome Project: Meeting report of the â€œ1st EMP meeting on sample selection and acquisitionâ€•at Argonne National Laboratory October 6th 2010.. Standards in Genomic Sciences, 2010, 3, 249-253.	1.5	176
655	Meeting report: GSC M5 roundtable at the 13th International Society for Microbial Ecology meeting in Seattle, WA, USA August 22-27, 2010. Standards in Genomic Sciences, 2010, 3, 235-239.	1.5	7
656	Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil. Soil Biology and Biochemistry, 2010, 42, 896-903.	8.8	436
657	Sampling and pyrosequencing methods for characterizing bacterial communities in the human gut using 16S sequence tags. BMC Microbiology, 2010, 10, 206.	3.3	335
658	Effect of storage conditions on the assessment of bacterial community structure in soil and human-associated samples. FEMS Microbiology Letters, 2010, 307, 80-86.	1.8	341
659	Bacterial communities of disease vectors sampled across time, space, and species. ISME Journal, 2010, 4, 223-231.	9.8	43
660	Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. ISME Journal, 2010, 4, 17-27.	9.8	1,025
661	Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME Journal, 2010, 4, 1340-1351.	9.8	3,154
662	Postprandial remodeling of the gut microbiota in Burmese pythons. ISME Journal, 2010, 4, 1375-1385.	9.8	229
663	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. Nature Methods, 2010, 7, 813-819.	19.0	249
664	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	19.0	31,818
665	Rapidly denoising pyrosequencing amplicon reads by exploiting rank-abundance distributions. Nature Methods, 2010, 7, 668-669.	19.0	647
666	Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. Environmental Microbiology, 2010, 12, 2998-3006.	3.8	551

#	Article	IF	Citations
667	Forensic identification using skin bacterial communities. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6477-6481.	7.1	507
668	Reply to Putignani et al.: Vagina as a major source of natural inoculum for the newborn. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, .	7.1	1
669	Stable tRNA-based phylogenies using only 76 nucleotides. Rna, 2010, 16, 1469-1477.	3.5	36
670	Simple, recurring RNA binding sites for L-arginine. Rna, 2010, 16, 805-816.	3.5	35
671	The bacterial microbiota in the oral mucosa of rural Amerindians. Microbiology (United Kingdom), 2010, 156, 3282-3287.	1.8	65
672	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. Genome Research, 2010, 20, 1411-1419.	5.5	284
673	Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. Nucleic Acids Research, 2010, 38, 3869-3879.	14.5	85
674	Nucleotides that are essential but not conserved; a sufficient L-tryptophan site in RNA. Rna, 2010, 16, 1915-1924.	3.5	11
675	Biogeography and habitat modelling of high-alpine bacteria. Nature Communications, 2010, 1, 53.	12.8	141
676	Metabolic Syndrome and Altered Gut Microbiota in Mice Lacking Toll-Like Receptor 5. Science, 2010, 328, 228-231.	12.6	1,804
677	Estimate of the abundance of cardiomyopathic mutations in the Î²-myosin gene. International Journal of Cardiology, 2010, 144, 124-126.	1.7	6
678	Changes through time: integrating microorganisms into the study of succession. Research in Microbiology, 2010, 161, 635-642.	2.1	334
679	Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11971-11975.	7.1	3,738
680	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. Environmental Microbiology, 2010, 12, 2885-2893.	3.8	574
681	PyNAST: a flexible tool for aligning sequences to a template alignment. Bioinformatics, 2010, 26, 266-267.	4.1	3,400
682	Consistent effects of nitrogen fertilization on soil bacterial communities in contrasting systems. Ecology, 2010, 91, 3463-3470.	3.2	475
683	Organismal, genetic, and transcriptional variation in the deeply sequenced gut microbiomes of identical twins. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7503-7508.	7.1	414
684	Direct sequencing of the human microbiome readily reveals community differences. Genome Biology, 2010, 11, 210.	9.6	134

#	Article	IF	Citations
685	The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. Nature Precedings, 2009, , .	0.1	3
686	Regulation of myocardial ketone body metabolism by the gut microbiota during nutrient deprivation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11276-11281.	7.1	224
687	Systems Biology: Understanding Function from Genes to Networks. Current Proteomics, 2009, 6, 93-103.	0.3	1
688	RNA structure prediction from evolutionary patterns of nucleotide composition. Nucleic Acids Research, 2009, 37, 1378-1386.	14.5	13
689	Ensemble dispatching on an IBM Blue Gene/L for a bioinformatics knowledge environment. , 2009, , .		3
690	The RNA structure alignment ontology. Rna, 2009, 15, 1623-1631.	3.5	34
691	CodonExplorer: an online tool for analyzing codon usage and sequence composition, scaling from genes to genomes. Bioinformatics, 2009, 25, 1331-1332.	4.1	3
692	The Cladistic Basis for the Phylogenetic Diversity (PD) Measure Links Evolutionary Features to Environmental Gradients and Supports Broad Applications of Microbial Ecologyâ€™s â€œPhylogenetic Beta Diversityâ€•Framework. International Journal of Molecular Sciences, 2009, 10, 4723-4741.	4.1	80
693	A Simulated MS/MS Library for Spectrum-to-spectrum Searching in Large Scale Identification of Proteins. Molecular and Cellular Proteomics, 2009, 8, 857-869.	3.8	49
694	Life Through A Microbial Lens. Metascience, 2009, 18, 179-205.	0.3	1
695	RNAâ€“Amino Acid Binding: A Stereochemical Era for the Genetic Code. Journal of Molecular Evolution, 2009, 69, 406-429.	1.8	166
696	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. ISME Journal, 2009, 3, 442-453.	9.8	984
697	A core gut microbiome in obese and lean twins. Nature, 2009, 457, 480-484.	27.8	6,819
698	The 'rare biosphere': a reality check. Nature Methods, 2009, 6, 636-637.	19.0	231
699	The Effect of Diet on the Human Gut Microbiome: A Metagenomic Analysis in Humanized Gnotobiotic Mice. Science Translational Medicine, 2009, 1, 6ra14.	12.4	2,492
700	Pyrosequencing-Based Assessment of Soil pH as a Predictor of Soil Bacterial Community Structure at the Continental Scale. Applied and Environmental Microbiology, 2009, 75, 5111-5120.	3.1	3,268
701	Identifying Genetic Determinants Needed to Establish a Human Gut Symbiont in Its Habitat. Cell Host and Microbe, 2009, 6, 279-289.	11.0	612
702	Characterization of Airborne Microbial Communities at a High-Elevation Site and Their Potential To Act as Atmospheric Ice Nuclei. Applied and Environmental Microbiology, 2009, 75, 5121-5130.	3.1	273

#	Article	IF	Citations
703	Bacterial Community Variation in Human Body Habitats Across Space and Time. Science, 2009, 326, 1694-1697.	12.6	2,713
704	Microbial community profiling for human microbiome projects: Tools, techniques, and challenges. Genome Research, 2009, 19, 1141-1152.	5.5	805
705	High-Fat Diet Determines the Composition of the Murine Gut Microbiome Independently of Obesity. Gastroenterology, 2009, 137, 1716-1724.e2.	1.3	1,344
706	CodonExplorer: An Interactive Online Database for the Analysis of Codon Usage and Sequence Composition. Methods in Molecular Biology, 2009, 537, 207-232.	0.9	2
707	Host-bacterial coevolution and the search for new drug targets. Current Opinion in Chemical Biology, 2008, 12, 109-114.	6.1	104
708	Evolution of Mammals and Their Gut Microbes. Science, 2008, 320, 1647-1651.	12.6	3,171
709	The influence of sex, handedness, and washing on the diversity of hand surface bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17994-17999.	7.1	980
710	Species divergence and the measurement of microbial diversity. FEMS Microbiology Reviews, 2008, 32, 557-578.	8.6	400
711	Error-correcting barcoded primers for pyrosequencing hundreds of samples in multiplex. Nature Methods, 2008, 5, 235-237.	19.0	1,190
712	Worlds within worlds: evolution of the vertebrate gut microbiota. Nature Reviews Microbiology, 2008, 6, 776-788.	28.6	1,342
713	Comparison of methods for estimating the nucleotide substitution matrix. BMC Bioinformatics, 2008, 9, 511.	2.6	8
714	Pathological rate matrices: from primates to pathogens. BMC Bioinformatics, 2008, 9, 550.	2.6	6
715	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. BMC Evolutionary Biology, 2008, 8, 327.	3.2	25
716	Insights and inferences about integron evolution from genomic data. BMC Genomics, 2008, 9, 261.	2.8	51
717	Bioinformatics Assessment of Î²-Myosin Mutations Reveals Myosin's High Sensitivity to Mutations. Trends in Cardiovascular Medicine, 2008, 18, 141-149.	4.9	46
718	Activating and inhibiting connections in biological network dynamics. Biology Direct, 2008, 3, 49.	4.6	11
719	MotifCluster: an interactive online tool for clustering and visualizing sequences using shared motifs. Genome Biology, 2008, 9, R128.	9.6	3
720	Short-Term Temporal Variability in Airborne Bacterial and Fungal Populations. Applied and Environmental Microbiology, 2008, 74, 200-207.	3.1	250

#	Article	IF	Citations
721	Accurate taxonomy assignments from 16S rRNA sequences produced by highly parallel pyrosequencers. Nucleic Acids Research, 2008, 36, e120-e120.	14.5	508
722	The convergence of carbohydrate active gene repertoires in human gut microbes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15076-15081.	7.1	120
723	The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis. PLoS Pathogens, 2008, 4, e20.	4.7	371
724	From knotted to nested RNA structures: A variety of computational methods for pseudoknot removal. Rna, 2008, 14, 410-416.	3.5	65
725	Are all horizontal gene transfers created equal? Prospects for mechanism-based studies of HGT patterns. Microbiology (United Kingdom), 2008, 154, 1-15.	1.8	88
726	Evolutionary rates vary among rRNA structural elements. Nucleic Acids Research, 2007, 35, 3339-3354.	14.5	87
727	Short pyrosequencing reads suffice for accurate microbial community analysis. Nucleic Acids Research, 2007, 35, e120-e120.	14.5	638
728	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	9.6	170
729	Quantitative and Qualitative Î² Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 1576-1585.	3.1	2,418
730	Tfap2 transcription factors in zebrafish neural crest development and ectodermal evolution. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 679-691.	1.3	110
731	The Human Microbiome Project. Nature, 2007, 449, 804-810.	27.8	4,750
732	The human microbiome: eliminating the biomedical/environmental dichotomy in microbial ecology. Environmental Microbiology, 2007, 9, 3-4.	3.8	58
733	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. Applied and Environmental Microbiology, 2007, 73, 7059-7066.	3.1	480
734	Global patterns in bacterial diversity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11436-11440.	7.1	1,461
735	Multiple pattern matching: a Markov chain approach. Journal of Mathematical Biology, 2007, 56, 51-92.	1.9	27
736	Reports of the death of the gene are greatly exaggerated. Biology and Philosophy, 2007, 22, 293-306.	1.4	11
737	Nematode contamination in sandpits of registered pre-school facilities in Bloemfontein. The Southern African Journal of Epidemiology & Infection: Official Journal of the Sexually Transmitted Diseases, Infectious Diseases and Epidemiological Societies of Southern Africa, 2006, 21, 173-177.	0.2	2
738	Fast-Find: a novel computational approach to analyzing combinatorial motifs. BMC Bioinformatics, 2006, 7, 1.	2.6	467

#	Article	IF	Citations
739	UniFrac--an online tool for comparing microbial community diversity in a phylogenetic context. BMC Bioinformatics, 2006, 7, 371.	2.6	1,321
740	Using the nucleotide substitution rate matrix to detect horizontal gene transfer. BMC Bioinformatics, 2006, 7, 476.	2.6	18
741	DivergentSet, a Tool for Picking Non-redundant Sequences from Large Sequence Collections. Molecular and Cellular Proteomics, 2006, 5, 1520-1532.	3.8	13
742	Natural selection is not required to explain universal compositional patterns in rRNA secondary structure categories. Rna, 2006, 12, 1-14.	3.5	72
743	Abundance of correctly folded RNA motifs in sequence space, calculated on computational grids. Nucleic Acids Research, 2005, 33, 5924-5935.	14.5	60
744	Key challenges in proteomics and proteoinformatics. IEEE Engineering in Medicine and Biology Magazine, 2005, 24, 34-40.	0.8	14
745	Does protein structure influence trypsin miscleavage?. IEEE Engineering in Medicine and Biology Magazine, 2005, 24, 58-66.	0.8	9
746	Error Minimization and Coding Triplet/Binding Site Associations Are Independent Features of the Canonical Genetic Code. Journal of Molecular Evolution, 2005, 61, 597-607.	1.8	32
747	tRNA Creation by Hairpin Duplication. Journal of Molecular Evolution, 2005, 61, 524-530.	1.8	75
748	Size, constant sequences, and optimal selection. Rna, 2005, 11, 1701-1709.	3.5	55
749	Occurrence of the aminoacyl-tRNA synthetases in high-molecular weight complexes correlates with the size of substrate amino acids. FEBS Letters, 2005, 579, 3467-3472.	2.8	9
750	ORIGINS OF THE GENETIC CODE: The Escaped Triplet Theory. Annual Review of Biochemistry, 2005, 74, 179-198.	11.1	155
751	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. Applied and Environmental Microbiology, 2005, 71, 8228-8235.	3.1	7,007
752	BayesFold: Rational 2Â folds that combine thermodynamic, covariation, and chemical data for aligned RNA sequences. Rna, 2004, 10, 1323-1336.	3.5	39
753	How biologists conceptualize genes: an empirical study. Studies in History and Philosophy of Science Part C:Studies in History and Philosophy of Biological and Biomedical Sciences, 2004, 35, 647-673.	1.3	92
754	Finding specific RNA motifs: Function in a zeptomole world?. Rna, 2003, 9, 218-230.	3.5	52
755	Contribution of human hippocampal region to novelty detection. Nature, 1996, 383, 256-259.	27.8	743
756	Artificial Selection: Finding Function amongst Randomized Sequences. , 0, , 783-806.		1

#	Article	IF	Citations
757	A Lightweight, Scalable Grid Computing Framework for Parallel Bioinformatics Applications. , 0, , .		4
758	Database-Driven Grid Computing and Distributed Web Applications: A Comparison. , 0, , 247-266.		1
759	Reference Data Based Insights Expand Understanding of Human Metabolomes. SSRN Electronic Journal, 0, , .	0.4	3
760	TaskSpaces: A Software Framework for Parallel Bioinformatics on Computational Grids. , 0, , 651-670.		3
761	Three Dimensional Cartography of Microbiome and Metabolome Data onto Radiological Images of the Human Lung. SSRN Electronic Journal, 0, , .	0.4	0
762	Targeted Activation of Enteric Neurons Shapes the Gut Environment of Mice. SSRN Electronic Journal, 0, , .	0.4	0
763	The oral microbiome and breast cancer and nonâ€malignant breast disease, and its relationship with the fecal microbiome in the Ghana Breast Health Study. International Journal of Cancer, 0, , .	5.1	13