

# Ruth E Ley

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

153 papers	99,426 citations	74 h-index	187 g-index
187 ext. papers	125,500 ext. citations	17.8 avg, IF	8.51 L-index

#	Paper	IF	Citations
153	The developing infant gut microbiome: A strain-level view.. <i>Cell Host and Microbe</i> , <b>2022</b> , 30, 627-638	23.4	3
152	Randomized controlled-feeding study of dietary emulsifier carboxymethylcellulose reveals detrimental impacts on the gut microbiota and metabolome. <i>Gastroenterology</i> , <b>2021</b> ,	13.3	15
151	Vertebrate host phylogeny influences gut archaeal diversity. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1443-1454	26.6	4
150	Reclassification of as comb. nov. based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2021</b> , 71,	2.2	1
149	Free-Living, Psychrotrophic Bacteria of the Genus Are Descendants of Pathobionts. <i>MSystems</i> , <b>2021</b> , 6,	7.6	4
148	Genomic Insights into Adaptations of Trimethylamine-Utilizing Methanogens to Diverse Habitats, Including the Human Gut. <i>MSystems</i> , <b>2021</b> , 6,	7.6	5
147	Blowing Hot and Cold: Body Temperature and the Microbiome. <i>MSystems</i> , <b>2021</b> , 6, e0070721	7.6	4
146	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. <i>PeerJ</i> , <b>2021</b> , 9, e12198	3.1	2
145	The microbiome affects liver sphingolipids and plasma fatty acids in a murine model of the Western diet based on soybean oil. <i>Journal of Nutritional Biochemistry</i> , <b>2021</b> , 97, 108808	6.3	3
144	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. <i>MSystems</i> , <b>2020</b> , 5,	7.6	21
143	Sphingolipids produced by gut bacteria enter host metabolic pathways impacting ceramide levels. <i>Nature Communications</i> , <b>2020</b> , 11, 2471	17.4	64
142	DeepMASeD: evaluating the quality of metagenomic assemblies. <i>Bioinformatics</i> , <b>2020</b> , 36, 3011-3017	7.2	16
141	Syntrophy via Interspecies H Transfer between and Underlies Their Global Cooccurrence in the Human Gut. <i>MBio</i> , <b>2020</b> , 11,	7.8	43
140	Iron Deficiency Causes Wrinkles in Host-Commensal Relationships. <i>Cell Metabolism</i> , <b>2020</b> , 31, 8-10	24.6	0
139	Struo: a pipeline for building custom databases for common metagenome profilers. <i>Bioinformatics</i> , <b>2020</b> , 36, 2314-2315	7.2	16
138	Strain-Level Analysis of spp. from Gut Microbiomes of Adults with Differing Lactase Persistence Genotypes. <i>MSystems</i> , <b>2020</b> , 5,	7.6	5
137	The role of the microbiota in human genetic adaptation. <i>Science</i> , <b>2020</b> , 370,	33.3	27

136	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea. <i>PLoS ONE</i> , <b>2020</b> , 15, e0236703	3.7	9
135	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea <b>2020</b> , 15, e0236703		
134	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea <b>2020</b> , 15, e0236703		
133	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea <b>2020</b> , 15, e0236703		
132	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea <b>2020</b> , 15, e0236703		
131	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea <b>2020</b> , 15, e0236703		
130	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea <b>2020</b> , 15, e0236703		
129	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , <b>2019</b> , 4,	7.6	110
128	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. <i>Nature Communications</i> , <b>2019</b> , 10, 2200	17.4	151
127	Human Salivary Amylase Gene Copy Number Impacts Oral and Gut Microbiomes. <i>Cell Host and Microbe</i> , <b>2019</b> , 25, 553-564.e7	23.4	62
126	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 852-857	44.5	4050
125	The human gut bacteria Christensenellaceae are widespread, heritable, and associated with health. <i>BMC Biology</i> , <b>2019</b> , 17, 83	7.3	145
124	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , <b>2019</b> , 25, 261-272.e5	23.4	89
123	Interactions between the Gut Microbiome and Mucosal Immunoglobulins A, M, and G in the Developing Infant Gut. <i>MSystems</i> , <b>2019</b> , 4,	7.6	22
122	Flagellin-elicited adaptive immunity suppresses flagellated microbiota and vaccinates against chronic inflammatory diseases. <i>Nature Communications</i> , <b>2019</b> , 10, 5650	17.4	41
121	Murine Methyl Donor Deficiency Impairs Early Growth in Association with Dysmorphic Small Intestinal Crypts and Reduced Gut Microbial Community Diversity. <i>Current Developments in Nutrition</i> , <b>2019</b> , 3,	0.4	4
120	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , <b>2018</b> , 3, 8-16	26.6	387
119	Sphingolipids in host-microbial interactions. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 43, 92-99	7.9	84

118	Resilience of small intestinal beneficial bacteria to the toxicity of soybean oil fatty acids. <i>ELife</i> , <b>2018</b> , 7,	8.9	10
117	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science <b>2018</b> ,		78
116	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , <b>2018</b> , 3,	7.6	336
115	Large-scale replicated field study of maize rhizosphere identifies heritable microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 7368-7373	11.5	230
114	TGR5 contributes to glucoregulatory improvements after vertical sleeve gastrectomy in mice. <i>Gut</i> , <b>2017</b> , 66, 226-234	19.2	138
113	Vertical sleeve gastrectomy reduces blood pressure and hypothalamic endoplasmic reticulum stress in mice. <i>DMM Disease Models and Mechanisms</i> , <b>2017</b> , 10, 235-243	4.1	22
112	Alterations to the Gut Microbiome Impair Bone Strength and Tissue Material Properties. <i>Journal of Bone and Mineral Research</i> , <b>2017</b> , 32, 1343-1353	6.3	74
111	Microbiome and metabolic disease: revisiting the bacterial phylum Bacteroidetes. <i>Journal of Molecular Medicine</i> , <b>2017</b> , 95, 1-8	5.5	159
110	Genomic features of bacterial adaptation to plants. <i>Nature Genetics</i> , <b>2017</b> , 50, 138-150	36.3	253
109	The Relationship Between the Human Genome and Microbiome Comes into View. <i>Annual Review of Genetics</i> , <b>2017</b> , 51, 413-433	14.5	158
108	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , <b>2016</b> , 17, 941	4.5	49
107	Reduced diversity and altered composition of the gut microbiome in individuals with myalgic encephalomyelitis/chronic fatigue syndrome. <i>Microbiome</i> , <b>2016</b> , 4, 30	16.6	166
106	Crossover Control Study of the Effect of Personal Care Products Containing Triclosan on the Microbiome. <i>MSphere</i> , <b>2016</b> , 1,	5	40
105	Epithelial Sel1L is required for the maintenance of intestinal homeostasis. <i>Molecular Biology of the Cell</i> , <b>2016</b> , 27, 483-90	3.5	23
104	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , <b>2016</b> , 8, 8	14.4	200
103	Gut microbiota in 2015: Prevotella in the gut: choose carefully. <i>Nature Reviews Gastroenterology and Hepatology</i> , <b>2016</b> , 13, 69-70	24.2	225
102	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , <b>2016</b> , 65, 749-56	19.2	454
101	Novel Rhizosphere Soil Alleles for the Enzyme 1-Aminocyclopropane-1-Carboxylate Deaminase Queried for Function with an In Vivo Competition Assay. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 1050-9	4.8	11

100	Corralling Colonic Flagellated Microbiota. <i>New England Journal of Medicine</i> , <b>2016</b> , 375, 85-7	59.2	7
99	Cross-species comparisons of host genetic associations with the microbiome. <i>Science</i> , <b>2016</b> , 352, 532-5	33.3	168
98	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , <b>2016</b> , 19, 731-43	23.4	547
97	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , <b>2016</b> , 17, 189	18.3	124
96	Dietary emulsifiers impact the mouse gut microbiota promoting colitis and metabolic syndrome. <i>Nature</i> , <b>2015</b> , 519, 92-6	50.4	1016
95	The gene-microbe link. <i>Nature</i> , <b>2015</b> , 518, S7	50.4	12
94	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , <b>2015</b> , 16, 191	18.3	428
93	Selection on soil microbiomes reveals reproducible impacts on plant function. <i>ISME Journal</i> , <b>2015</b> , 9, 980-9	11.9	368
92	The Human Intestinal Microbiota and Microbiome <b>2015</b> , 617-625		
91	Potential applications of next generation DNA sequencing of 16S rRNA gene amplicons in microbial water quality monitoring. <i>Water Science and Technology</i> , <b>2015</b> , 72, 1962-72	2.2	40
90	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134311	3.7	85
89	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , <b>2015</b> , 17, 603-16	3.4	373
88	Methane Emission in a Specific Riparian-Zone Sediment Decreased with Bioelectrochemical Manipulation and Corresponded to the Microbial Community Dynamics. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1523	5.7	9
87	Harnessing microbiota to kill a pathogen: the sweet tooth of <i>Clostridium difficile</i> . <i>Nature Medicine</i> , <b>2014</b> , 20, 248-9	50.5	16
86	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. <i>Gut</i> , <b>2014</b> , 63, 1069-80	19.2	149
85	Human genetics shape the gut microbiome. <i>Cell</i> , <b>2014</b> , 159, 789-99	56.2	1750
84	Linking genetic variation in human Toll-like receptor 5 genes to the gut microbiome's potential to cause inflammation. <i>Immunology Letters</i> , <b>2014</b> , 162, 3-9	4.1	21
83	Diet-induced alterations in gut microflora contribute to lethal pulmonary damage in TLR2/TLR4-deficient mice. <i>Cell Reports</i> , <b>2014</b> , 8, 137-49	10.6	35

82	Conducting a microbiome study. <i>Cell</i> , <b>2014</b> , 158, 250-262	56.2	428
81	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , <b>2014</b> , 2,	16.6	18
80	Advancing the microbiome research community. <i>Cell</i> , <b>2014</b> , 159, 227-30	56.2	50
79	Discordance between changes in the gut microbiota and pathogenicity in a mouse model of spontaneous colitis. <i>Gut Microbes</i> , <b>2014</b> , 5, 286-95	8.8	34
78	Gut microbiota as an epigenetic regulator: pilot study based on whole-genome methylation analysis. <i>MBio</i> , <b>2014</b> , 5,	7.8	120
77	Intestinal epithelial cell toll-like receptor 5 regulates the intestinal microbiota to prevent low-grade inflammation and metabolic syndrome in mice. <i>Gastroenterology</i> , <b>2014</b> , 147, 1363-77.e17	13.3	161
76	Probiotics, prebiotics, and the host microbiome: the science of translation. <i>Annals of the New York Academy of Sciences</i> , <b>2013</b> , 1306, 1-17	6.5	80
75	Diversity and heritability of the maize rhizosphere microbiome under field conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 6548-53	11.5	1067
74	Innate and adaptive immunity interact to quench microbiome flagellar motility in the gut. <i>Cell Host and Microbe</i> , <b>2013</b> , 14, 571-81	23.4	236
73	A guide to enterotypes across the human body: meta-analysis of microbial community structures in human microbiome datasets. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002863	5	359
72	Exploring the maize rhizosphere microbiome in the field: A glimpse into a highly complex system. <i>Communicative and Integrative Biology</i> , <b>2013</b> , 6, e25177	1.7	21
71	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. <i>ELife</i> , <b>2013</b> , 2, e01102	8.9	247
70	Host remodeling of the gut microbiome and metabolic changes during pregnancy. <i>Cell</i> , <b>2012</b> , 150, 470-80	56.2	1117
69	Transient inability to manage proteobacteria promotes chronic gut inflammation in TLR5-deficient mice. <i>Cell Host and Microbe</i> , <b>2012</b> , 12, 139-52	23.4	325
68	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , <b>2012</b> , 486, 207-14	50.4	6938
67	A framework for human microbiome research. <i>Nature</i> , <b>2012</b> , 486, 215-21	50.4	1722
66	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , <b>2012</b> , 488, 86-90	50.4	1613
65	Integrated and novel survey methods for rhinoceros populations confirm the extinction of <i>Rhinoceros sondaicus annamiticus</i> from Vietnam. <i>Biological Conservation</i> , <b>2012</b> , 155, 59-67	6.2	31

64	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. <i>Gut</i> , <b>2012</b> , 61, 1124-31	19.2	261
63	Responses of gut microbiota to diet composition and weight loss in lean and obese mice. <i>Obesity</i> , <b>2012</b> , 20, 738-47	8	287
62	Interleukin-1 $\beta$ promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. <i>Gut</i> , <b>2012</b> , 61, 373-84	19.2	59
61	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. <i>ISME Journal</i> , <b>2012</b> , 6, 94-103	11.9	385
60	Colitis in TLR5-deficiency Mice: Role of the Microbiota. <i>Inflammatory Bowel Diseases</i> , <b>2012</b> , 18, S113-S114.5		
59	Development of the human gastrointestinal microbiota and insights from high-throughput sequencing. <i>Gastroenterology</i> , <b>2011</b> , 140, 1713-9	13.3	283
58	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 415-20	44.5	445
57	Branched chain fatty acids reduce the incidence of necrotizing enterocolitis and alter gastrointestinal microbial ecology in a neonatal rat model. <i>PLoS ONE</i> , <b>2011</b> , 6, e29032	3.7	113
56	Unravelling the effects of the environment and host genotype on the gut microbiome. <i>Nature Reviews Microbiology</i> , <b>2011</b> , 9, 279-90	22.2	973
55	Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , <b>2011</b> , 5, 570-3	11.9	36
54	The human gut microbiome: ecology and recent evolutionary changes. <i>Annual Review of Microbiology</i> , <b>2011</b> , 65, 411-29	17.5	460
53	The antibacterial lectin RegIII $\gamma$ promotes the spatial segregation of microbiota and host in the intestine. <i>Science</i> , <b>2011</b> , 334, 255-8	33.3	948
52	Human oral, gut, and plaque microbiota in patients with atherosclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108 Suppl 1, 4592-6	11.5	679
51	Succession of microbial consortia in the developing infant gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108 Suppl 1, 4578-85	11.5	1674
50	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , <b>2010</b> , 7, 335-6	21.6	22879
49	Obesity and the human microbiome. <i>Current Opinion in Gastroenterology</i> , <b>2010</b> , 26, 5-11	3	555
48	Metabolic syndrome and altered gut microbiota in mice lacking Toll-like receptor 5. <i>Science</i> , <b>2010</b> , 328, 228-31	33.3	1513
47	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , <b>2010</b> , 11, 210	18.3	125

46	The Earth Microbiome Project: Meeting report of the "1 EMP meeting on sample selection and acquisition" at Argonne National Laboratory October 6 2010. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 249-53		146
45	Symbiosis research, technology, and education: Proceedings of the 6th International Symbiosis Society Congress held in Madison Wisconsin, USA, August 2009. <i>Symbiosis</i> , <b>2010</b> , 51, 1-12	3	1
44	A core gut microbiome in obese and lean twins. <i>Nature</i> , <b>2009</b> , 457, 480-4	50.4	5429
43	Innate immunity and intestinal microbiota in the development of Type 1 diabetes. <i>Nature</i> , <b>2008</b> , 455, 1109-13	50.4	1476
42	Worlds within worlds: evolution of the vertebrate gut microbiota. <i>Nature Reviews Microbiology</i> , <b>2008</b> , 6, 776-88	22.2	1042
41	Eucaryotic diversity in a hypersaline microbial mat. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 329-32	4.8	51
40	Bacterial community in the crop of the hoatzin, a neotropical folivorous flying bird. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 5905-12	4.8	53
39	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , <b>2008</b> , 12, 109-14	9.7	87
38	Evolution of mammals and their gut microbes. <i>Science</i> , <b>2008</b> , 320, 1647-51	33.3	2355
37	Evolution of symbiotic bacteria in the distal human intestine. <i>PLoS Biology</i> , <b>2007</b> , 5, e156	9.7	401
36	The human microbiome project. <i>Nature</i> , <b>2007</b> , 449, 804-10	50.4	3576
35	The human microbiome: eliminating the biomedical/environmental dichotomy in microbial ecology. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 3-4	5.2	52
34	The human intestinal microbiota and its relationship to energy balance. <i>Food Nutrition Research</i> , <b>2006</b> , 50, 121-123		
33	Unexpected diversity and complexity of the Guerrero Negro hypersaline microbial mat. <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 3685-95	4.8	364
32	Ecological and evolutionary forces shaping microbial diversity in the human intestine. <i>Cell</i> , <b>2006</b> , 124, 837-48	56.2	2212
31	Reciprocal gut microbiota transplants from zebrafish and mice to germ-free recipients reveal host habitat selection. <i>Cell</i> , <b>2006</b> , 127, 423-33	56.2	664
30	Microbial ecology: human gut microbes associated with obesity. <i>Nature</i> , <b>2006</b> , 444, 1022-3	50.4	5833
29	An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> , <b>2006</b> , 444, 1027-31	50.4	7807



28	Obesity alters gut microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 11070-5	11.5	4146
27	Host-bacterial mutualism in the human intestine. <i>Science</i> , <b>2005</b> , 307, 1915-20	33.3	3448
26	Soil Microbial Dynamics in Costa Rica: Seasonal and Biogeochemical Constraints. <i>Biotropica</i> , <b>2004</b> , 36, 184-195	2.3	52
25	Impacts of chronic nitrogen additions vary seasonally and by microbial functional group in tundra soils. <i>Biogeochemistry</i> , <b>2004</b> , 69, 1-17	3.8	42
24	Microbial population dynamics in an extreme environment: controlling factors in talus soils at 3750 m in the Colorado Rocky Mountains. <i>Biogeochemistry</i> , <b>2004</b> , 68, 297-311	3.8	66
23	Complexity in natural microbial ecosystems: the Guerrero Negro experience. <i>Biological Bulletin</i> , <b>2003</b> , 204, 168-73	1.5	58
22	Subfreezing activity of microorganisms and the potential habitability of MarsSpolar regions. <i>Astrobiology</i> , <b>2003</b> , 3, 343-50	3.7	115
21	Fungal and bacterial responses to phenolic compounds and amino acids in high altitude barren soils. <i>Soil Biology and Biochemistry</i> , <b>2002</b> , 34, 989-995	7.5	31
20	Alteration of Ecosystem Nitrogen Dynamics by Exotic Plants: A Case Study of C 4 Grasses in Hawaii <b>2001</b> , 11, 1323		6
19	Soil ecological interactions: comparisons between tropical and subalpine forests. <i>Oecologia</i> , <b>2001</b> , 128, 549-556	2.9	34
18	ALTERATION OF ECOSYSTEM NITROGEN DYNAMICS BY EXOTIC PLANTS: A CASE STUDY OF C4 GRASSES IN HAWAII <b>2001</b> , 11, 1323-1335		19
17	Microbial Biomass Levels in Barren and Vegetated High Altitude Talus Soils. <i>Soil Science Society of America Journal</i> , <b>2001</b> , 65, 111-117	2.5	22
16	Exotic grass invasion alters potential rates of N fixation in Hawaiian woodlands. <i>Oecologia</i> , <b>1998</b> , 113, 179-187	2.9	57
15	The Human Intestinal Microbiota and Microbiome635-644		
14	Incorporating genome-based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes		1
13	Genomic insights into adaptations of TMA-utilizing methanogens to diverse habitats including the human gut		2
12	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
11	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138

10	Codiversification of gut microbiota with humans	2
9	SynTracker: a synteny based tool for tracking microbial strains	3
8	Large scale metagenome assembly reveals novel animal-associated microbial genomes, biosynthetic gene clusters, and other genetic diversity	2
7	Strong influence of vertebrate host phylogeny on gut archaeal diversity	2
6	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades	3
5	GeNet: Deep Representations for Metagenomics	5
4	Age and sex-dependent patterns of gut microbial diversity in human adults	1
3	Sphingolipid production by gut Bacteroidetes regulates glucose homeostasis	2
2	High-resolution QTL mapping with Diversity Outbred mice identifies genetic variants that impact gut microbiome composition	1
1	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets	2