

Ruth E Ley

List of Publications by Year in descending order

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146
papers

140,959
citations

7551

77
h-index

10708

138
g-index

187
all docs

187
docs citations

187
times ranked

97844
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
3	An obesity-associated gut microbiome with increased capacity for energy harvest. <i>Nature</i> , 2006, 444, 1027-1031.	13.7	10,136
4	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	13.7	9,614
5	Human gut microbes associated with obesity. <i>Nature</i> , 2006, 444, 1022-1023.	13.7	7,595
6	A core gut microbiome in obese and lean twins. <i>Nature</i> , 2009, 457, 480-484.	13.7	6,819
7	Obesity alters gut microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 11070-11075.	3.3	5,247
8	The Human Microbiome Project. <i>Nature</i> , 2007, 449, 804-810.	13.7	4,750
9	Host-Bacterial Mutualism in the Human Intestine. <i>Science</i> , 2005, 307, 1915-1920.	6.0	4,326
10	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	3,171
11	Ecological and Evolutionary Forces Shaping Microbial Diversity in the Human Intestine. <i>Cell</i> , 2006, 124, 837-848.	13.5	2,744
12	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
13	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	13.7	2,475
14	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	13.7	2,249
15	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> , 2011, 108, 4578-4585.	3.3	2,108
16	Metabolic Syndrome and Altered Gut Microbiota in Mice Lacking Toll-Like Receptor 5. <i>Science</i> , 2010, 328, 228-231.	6.0	1,804
17	Innate immunity and intestinal microbiota in the development of Type 1 diabetes. <i>Nature</i> , 2008, 455, 1109-1113.	13.7	1,745
18	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. <i>Cell</i> , 2012, 150, 470-480.	13.5	1,603

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19	Diversity and heritability of the maize rhizosphere microbiome under field conditions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6548-6553.	3.3	1,594
20	Dietary emulsifiers impact the mouse gut microbiota promoting colitis and metabolic syndrome. Nature, 2015, 519, 92-96.	13.7	1,457
21	Worlds within worlds: evolution of the vertebrate gut microbiota. Nature Reviews Microbiology, 2008, 6, 776-788.	13.6	1,342
22	Unravelling the effects of the environment and host genotype on the gut microbiome. Nature Reviews Microbiology, 2011, 9, 279-290.	13.6	1,305
23	The Antibacterial Lectin RegIII ^β Promotes the Spatial Segregation of Microbiota and Host in the Intestine. Science, 2011, 334, 255-258.	6.0	1,163
24	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.	3.3	943
25	Genetic Determinants of the Gut Microbiome in UK Twins. Cell Host and Microbe, 2016, 19, 731-743.	5.1	831
26	Reciprocal Gut Microbiota Transplants from Zebrafish and Mice to Germ-free Recipients Reveal Host Habitat Selection. Cell, 2006, 127, 423-433.	13.5	808
27	Enterotypes in the landscape of gut microbial community composition. Nature Microbiology, 2018, 3, 8-16.	5.9	717
28	Obesity and the human microbiome. Current Opinion in Gastroenterology, 2010, 26, 5-11.	1.0	688
29	Proton pump inhibitors alter the composition of the gut microbiota. Gut, 2016, 65, 749-756.	6.1	682
30	Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host and Microbe, 2015, 17, 603-616.	5.1	628
31	Conducting a Microbiome Study. Cell, 2014, 158, 250-262.	13.5	625
32	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	3.8	612
33	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608
34	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	1.7	604
35	The Human Gut Microbiome: Ecology and Recent Evolutionary Changes. Annual Review of Microbiology, 2011, 65, 411-429.	2.9	589
36	Selection on soil microbiomes reveals reproducible impacts on plant function. ISME Journal, 2015, 9, 980-989.	4.4	549

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37	Impact of training sets on classification of high-throughput bacterial 16s rRNA gene surveys. ISME Journal, 2012, 6, 94-103.	4.4	537
38	Evolution of Symbiotic Bacteria in the Distal Human Intestine. PLoS Biology, 2007, 5, e156.	2.6	490
39	Genomic features of bacterial adaptation to plants. Nature Genetics, 2018, 50, 138-150.	9.4	480
40	Transient Inability to Manage Proteobacteria Promotes Chronic Gut Inflammation in TLR5-Deficient Mice. Cell Host and Microbe, 2012, 12, 139-152.	5.1	459
41	A Guide to Enterotypes across the Human Body: Meta-Analysis of Microbial Community Structures in Human Microbiome Datasets. PLoS Computational Biology, 2013, 9, e1002863.	1.5	446
42	Unexpected Diversity and Complexity of the Guerrero Negro Hypersaline Microbial Mat. Applied and Environmental Microbiology, 2006, 72, 3685-3695.	1.4	435
43	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.	3.3	435
44	The human gut bacteria Christensenellaceae are widespread, heritable, and associated with health. BMC Biology, 2019, 17, 83.	1.7	406
45	Prevotella in the gut: choose carefully. Nature Reviews Gastroenterology and Hepatology, 2016, 13, 69-70.	8.2	394
46	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. ELife, 2013, 2, e01102.	2.8	355
47	Responses of Gut Microbiota to Diet Composition and Weight Loss in Lean and Obese Mice. Obesity, 2012, 20, 738-747.	1.5	352
48	Development of the Human Gastrointestinal Microbiota and Insights From High-Throughput Sequencing. Gastroenterology, 2011, 140, 1713-1719.	0.6	329
49	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. Gut, 2012, 61, 1124-1131.	6.1	321
50	Innate and Adaptive Immunity Interact to Quench Microbiome Flagellar Motility in the Gut. Cell Host and Microbe, 2013, 14, 571-581.	5.1	321
51	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. Nature Communications, 2019, 10, 2200.	5.8	317
52	Signatures of early frailty in the gut microbiota. Genome Medicine, 2016, 8, 8.	3.6	297
53	Microbiome and metabolic disease: revisiting the bacterial phylum Bacteroidetes. Journal of Molecular Medicine, 2017, 95, 1-8.	1.7	267
54	Reduced diversity and altered composition of the gut microbiome in individuals with myalgic encephalomyelitis/chronic fatigue syndrome. Microbiome, 2016, 4, 30.	4.9	263

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55	The Relationship Between the Human Genome and Microbiome Comes into View. <i>Annual Review of Genetics</i> , 2017, 51, 413-433.	3.2	237
56	Cross-species comparisons of host genetic associations with the microbiome. <i>Science</i> , 2016, 352, 532-535.	6.0	233
57	Intestinal Epithelial Cell Toll-like Receptor 5 Regulates the Intestinal Microbiota to Prevent Low-Grade Inflammation and Metabolic Syndrome in Mice. <i>Gastroenterology</i> , 2014, 147, 1363-1377.e17.	0.6	231
58	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019, 4, .	1.7	214
59	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
60	AIEC pathobiont instigates chronic colitis in susceptible hosts by altering microbiota composition. <i>Gut</i> , 2014, 63, 1069-1080.	6.1	182
61	TGR5 contributes to glucoregulatory improvements after vertical sleeve gastrectomy in mice. <i>Gut</i> , 2017, 66, 226-234.	6.1	182
62	The Earth Microbiome Project: Meeting report of the 1st EMP meeting on sample selection and acquisition at Argonne National Laboratory October 6th 2010.. <i>Standards in Genomic Sciences</i> , 2010, 3, 249-253.	1.5	176
63	Gut Microbiota as an Epigenetic Regulator: Pilot Study Based on Whole-Genome Methylation Analysis. <i>MBio</i> , 2014, 5, .	1.8	172
64	Sphingolipids produced by gut bacteria enter host metabolic pathways impacting ceramide levels. <i>Nature Communications</i> , 2020, 11, 2471.	5.8	172
65	Branched Chain Fatty Acids Reduce the Incidence of Necrotizing Enterocolitis and Alter Gastrointestinal Microbial Ecology in a Neonatal Rat Model. <i>PLoS ONE</i> , 2011, 6, e29032.	1.1	168
66	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , 2019, 25, 261-272.e5.	5.1	159
67	Sphingolipids in host-microbial interactions. <i>Current Opinion in Microbiology</i> , 2018, 43, 92-99.	2.3	144
68	Subfreezing Activity of Microorganisms and the Potential Habitability of Mars' Polar Regions. <i>Astrobiology</i> , 2003, 3, 343-350.	1.5	143
69	Direct sequencing of the human microbiome readily reveals community differences. <i>Genome Biology</i> , 2010, 11, 210.	13.9	134
70	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015, 10, e0134311.	1.1	134
71	Randomized Controlled-Feeding Study of Dietary Emulsifier Carboxymethylcellulose Reveals Detrimental Impacts on the Gut Microbiota and Metabolome. <i>Gastroenterology</i> , 2022, 162, 743-756.	0.6	111
72	Alterations to the Gut Microbiome Impair Bone Strength and Tissue Material Properties. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 1343-1353.	3.1	109

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73	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 109-114.	2.8	104
74	Human Salivary Amylase Gene Copy Number Impacts Oral and Gut Microbiomes. <i>Cell Host and Microbe</i> , 2019, 25, 553-564.e7.	5.1	102
75	Probiotics, prebiotics, and the host microbiome: the science of translation. <i>Annals of the New York Academy of Sciences</i> , 2013, 1306, 1-17.	1.8	98
76	Microbial population dynamics in an extreme environment: controlling factors in talus soils at 3750 m in the Colorado Rocky Mountains. <i>Biogeochemistry</i> , 2004, 68, 297-311.	1.7	81
77	Syntrophy via Interspecies H ₂ Transfer between <i>Christensenella</i> and <i>Methanobrevibacter</i> Underlies Their Global Cooccurrence in the Human Gut. <i>MBio</i> , 2020, 11, .	1.8	73
78	Eucaryotic Diversity in a Hypersaline Microbial Mat. <i>Applied and Environmental Microbiology</i> , 2008, 74, 329-332.	1.4	70
79	Interleukin-1 β (IL-1 β) promotes susceptibility of Toll-like receptor 5 (TLR5) deficient mice to colitis. <i>Gut</i> , 2012, 61, 373-384.	6.1	68
80	Exotic grass invasion alters potential rates of N fixation in Hawaiian woodlands. <i>Oecologia</i> , 1998, 113, 179-187.	0.9	67
81	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	13.5	64
82	Flagellin-elicited adaptive immunity suppresses flagellated microbiota and vaccinates against chronic inflammatory diseases. <i>Nature Communications</i> , 2019, 10, 5650.	5.8	64
83	Complexity in Natural Microbial Ecosystems: The Guerrero Negro Experience. <i>Biological Bulletin</i> , 2003, 204, 168-173.	0.7	63
84	Crossover Control Study of the Effect of Personal Care Products Containing Triclosan on the Microbiome. <i>MSphere</i> , 2016, 1, .	1.3	62
85	Bacterial Community in the Crop of the Hoatzin, a Neotropical Folivorous Flying Bird. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5905-5912.	1.4	61
86	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , 2016, 17, 941.	1.2	61
87	The role of the microbiota in human genetic adaptation. <i>Science</i> , 2020, 370, .	6.0	61
88	Soil Microbial Dynamics in Costa Rica: Seasonal and Biogeochemical Constraints. <i>Biotropica</i> , 2004, 36, 184-195.	0.8	58
89	The human microbiome: eliminating the biomedical/environmental dichotomy in microbial ecology. <i>Environmental Microbiology</i> , 2007, 9, 3-4.	1.8	58
90	Potential applications of next generation DNA sequencing of 16S rRNA gene amplicons in microbial water quality monitoring. <i>Water Science and Technology</i> , 2015, 72, 1962-1972.	1.2	53

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91	ALTERATION OF ECOSYSTEM NITROGEN DYNAMICS BY EXOTIC PLANTS: A CASE STUDY OF C4GRASSES IN HAWAII. , 2001, 11, 1323-1335.		51
92	Impacts of chronic nitrogen additions vary seasonally and by microbial functional group in tundra soils. <i>Biogeochemistry</i> , 2004, 69, 1-17.	1.7	49
93	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. <i>MSystems</i> , 2020, 5, .	1.7	47
94	Soil ecological interactions: comparisons between tropical and subalpine forests. <i>Oecologia</i> , 2001, 128, 549-556.	0.9	44
95	Discordance between changes in the gut microbiota and pathogenicity in a mouse model of spontaneous colitis. <i>Gut Microbes</i> , 2014, 5, 286-485.	4.3	44
96	Diet-Induced Alterations in Gut Microflora Contribute to Lethal Pulmonary Damage in TLR2/TLR4-Deficient Mice. <i>Cell Reports</i> , 2014, 8, 137-149.	2.9	43
97	Interactions between the Gut Microbiome and Mucosal Immunoglobulins A, M, and G in the Developing Infant Gut. <i>MSystems</i> , 2019, 4, .	1.7	43
98	Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , 2011, 5, 570-573.	4.4	42
99	Blowing Hot and Cold: Body Temperature and the Microbiome. <i>MSystems</i> , 2021, 6, e0070721.	1.7	40
100	Epithelial Sell1L is required for the maintenance of intestinal homeostasis. <i>Molecular Biology of the Cell</i> , 2016, 27, 483-490.	0.9	36
101	Fungal and bacterial responses to phenolic compounds and amino acids in high altitude barren soils. <i>Soil Biology and Biochemistry</i> , 2002, 34, 989-995.	4.2	35
102	Integrated and novel survey methods for rhinoceros populations confirm the extinction of <i>Rhinoceros sondaicus annamiticus</i> from Vietnam. <i>Biological Conservation</i> , 2012, 155, 59-67.	1.9	35
103	Vertebrate host phylogeny influences gut archaeal diversity. <i>Nature Microbiology</i> , 2021, 6, 1443-1454.	5.9	34
104	Exploring the maize rhizosphere microbiome in the field: A glimpse into a highly complex system. <i>Communicative and Integrative Biology</i> , 2013, 6, e25177.	0.6	31
105	Struo: a pipeline for building custom databases for common metagenome profilers. <i>Bioinformatics</i> , 2020, 36, 2314-2315.	1.8	30
106	Microbial Biomass Levels in Barren and Vegetated High Altitude Talus Soils. <i>Soil Science Society of America Journal</i> , 2001, 65, 111-117.	1.2	29
107	The developing infant gut microbiome: A strain-level view. <i>Cell Host and Microbe</i> , 2022, 30, 627-638.	5.1	29
108	Epidemiology and associated microbiota changes in deployed military personnel at high risk of traveler's diarrhea. <i>PLoS ONE</i> , 2020, 15, e0236703.	1.1	28

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109	Vertical sleeve gastrectomy reduces blood pressure and hypothalamic endoplasmic reticulum stress in mice. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 235-243.	1.2	27
110	DeepMAseD: evaluating the quality of metagenomic assemblies. <i>Bioinformatics</i> , 2020, 36, 3011-3017.	1.8	27
111	Linking genetic variation in human Toll-like receptor 5 genes to the gut microbiome's potential to cause inflammation. <i>Immunology Letters</i> , 2014, 162, 3-9.	1.1	26
112	Human microbiome science: vision for the future, Bethesda, MD, July 24 to 26, 2013. <i>Microbiome</i> , 2014, 2, .	4.9	25
113	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. <i>PeerJ</i> , 2021, 9, e12198.	0.9	24
114	Free-Living, Psychrotrophic Bacteria of the Genus <i>Psychrobacter</i> Are Descendants of Pathobionts. <i>MSystems</i> , 2021, 6, .	1.7	23
115	Genomic Insights into Adaptations of Trimethylamine-Utilizing Methanogens to Diverse Habitats, Including the Human Gut. <i>MSystems</i> , 2021, 6, .	1.7	21
116	Characterization of inositol lipid metabolism in gut-associated Bacteroidetes. <i>Nature Microbiology</i> , 2022, 7, 986-1000.	5.9	19
117	Harnessing Microbiota to Kill a Pathogen: The sweet tooth of <i>Clostridium difficile</i> . <i>Nature Medicine</i> , 2014, 20, 248-249.	15.2	18
118	Resilience of small intestinal beneficial bacteria to the toxicity of soybean oil fatty acids. <i>ELife</i> , 2018, 7, .	2.8	14
119	The Gene "Microbe Link. <i>Nature</i> , 2015, 518, S7-S7.	13.7	13
120	Novel Rhizosphere Soil Alleles for the Enzyme 1-Aminocyclopropane-1-Carboxylate Deaminase Queried for Function with an <i>In Vivo</i> Competition Assay. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1050-1059.	1.4	13
121	Methane Emission in a Specific Riparian-Zone Sediment Decreased with Bioelectrochemical Manipulation and Corresponded to the Microbial Community Dynamics. <i>Frontiers in Microbiology</i> , 2015, 6, 1523.	1.5	12
122	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> , 2019, 3, nzy070.	0.1	12
123	Strain-Level Analysis of <i>Bifidobacterium</i> spp. from Gut Microbiomes of Adults with Differing Lactase Persistence Genotypes. <i>MSystems</i> , 2020, 5, .	1.7	12
124	Reclassification of <i>Catabacter hongkongensis</i> as <i>Christensenella hongkongensis</i> comb. nov. based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
125	Corralling Colonic Flagellated Microbiota. <i>New England Journal of Medicine</i> , 2016, 375, 85-87.	13.9	10
126	Microbiome engineering: Taming the untractable. <i>Cell</i> , 2022, 185, 416-418.	13.5	9

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127	Alteration of Ecosystem Nitrogen Dynamics by Exotic Plants: A Case Study of C 4 Grasses in Hawaii. , 2001, 11, 1323.		6
128	The microbiome affects liver sphingolipids and plasma fatty acids in a murine model of the Western diet based on soybean oil. Journal of Nutritional Biochemistry, 2021, 97, 108808.	1.9	6
129	When guests turn hostile. Nature, 2013, 494, 437-438.	13.7	3
130	Iron Deficiency Causes Wrinkles in Host-Commensal Relationships. Cell Metabolism, 2020, 31, 8-10.	7.2	3
131	MicroRNAs and extracellular vesicles in the gut: new host modulators of the microbiome?. MicroLife, 2021, 2, .	1.0	3
132	Incorporating genomeâ€based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes. Environmental Microbiology, 2022, 24, 3966-3984.	1.8	2
133	Symbiosis research, technology, and education: Proceedings of the 6th International Symbiosis Society Congress held in Madison Wisconsin, USA, August 2009. Symbiosis, 2010, 51, 1-12.	1.2	1
134	Colitis in TLR5-deficiency Mice: Role of the Microbiota. Inflammatory Bowel Diseases, 2012, 18, S113-S114.	0.9	1
135	Expanding the scope and scale of microbiome research. Genome Biology, 2019, 20, 191.	3.8	1
136	Microbes set the (woodrat) menu: Host genetics control diet-specific gut microbes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
137	The human intestinal microbiota and its relationship to energy balance. Food Nutrition Research, 2006, 50, 121-123.	0.3	0
138	The Human Intestinal Microbiota and Microbiome. , 0, , 635-644.		0
139	The Gene-Microbe Link. Scientific American, 2015, 312, S7-S7.	1.0	0
140	Reply to â€Triclocarban and Health: the Jury Is Still Outâ€. MSphere, 2016, 1, .	1.3	0
141	Title is missing!. , 2020, 15, e0236703.		0
142	Title is missing!. , 2020, 15, e0236703.		0
143	Title is missing!. , 2020, 15, e0236703.		0
144	Title is missing!. , 2020, 15, e0236703.		0

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145	Title is missing!. , 2020, 15, e0236703.		0
146	Title is missing!. , 2020, 15, e0236703.		0