

Antonio Gonzalez

List of Publications by Citations

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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.

92
papers

22,165
citations

50
h-index

108
g-index

108
ext. papers

32,422
ext. citations

13.6
avg, IF

6.35
L-index

#	Paper	IF	Citations
92	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
91	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , 2014 , 15, 382-392	23.4	1836
90	Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. <i>Science</i> , 2011 , 332, 970-4	33.3	1215
89	Host remodeling of the gut microbiome and metabolic changes during pregnancy. <i>Cell</i> , 2012 , 150, 470-80	16.2	1117
88	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
87	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017 , 5, 27	16.6	840
86	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2,	7.6	763
85	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019 , 569, 655-662	50.4	761
84	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011 , 12, R50	18.3	723
83	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013 , 2, 16	7.6	711
82	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018 , 16, 410-422	22.2	668
81	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016 , 22, 250-3	50.5	536
80	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017 , 2, 17004	26.6	533
79	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011 , 29, 415-20	44.5	445
78	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014 , 2, e545	3.1	395
77	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.7	373
76	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015 , 17, 603-16	13.4	373

75	A guide to enterotypes across the human body: meta-analysis of microbial community structures in human microbiome datasets. <i>PLoS Computational Biology</i> , 2013 , 9, e1002863	5	359
74	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
73	Transient inability to manage proteobacteria promotes chronic gut inflammation in TLR5-deficient mice. <i>Cell Host and Microbe</i> , 2012 , 12, 139-52	23.4	325
72	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013 , 23, 1704-14	9.7	289
71	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014 , 8, 1464-75	11.9	262
70	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014 , 15, 531	18.3	255
69	Molecular cartography of the human skin surface in 3D. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E2120-9	11.5	237
68	Rethinking "enterotypes". <i>Cell Host and Microbe</i> , 2014 , 16, 433-7	23.4	234
67	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018 , 15, 796-798	21.6	231
66	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018 , 3,	7.6	181
65	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014 , 23, 1301-17	5.7	179
64	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017 , 2,	7.6	177
63	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection. <i>Microbiome</i> , 2015 , 3, 10	16.6	175
62	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
61	Immunization with a heat-killed preparation of the environmental bacterium <i>Mycobacterium vaccae</i> promotes stress resilience in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3130-9	11.5	137
60	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <i>MSystems</i> , 2018 , 3,	7.6	115
59	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 6200-9	4.8	110
58	Antifungal isolates database of amphibian skin-associated bacteria and function against emerging fungal pathogens. <i>Ecology</i> , 2015 , 96, 595-595	4.6	107

57	Exercise is More Effective at Altering Gut Microbial Composition and Producing Stable Changes in Lean Mass in Juvenile versus Adult Male F344 Rats. <i>PLoS ONE</i> , 2015 , 10, e0125889	3.7	106
56	The sponge microbiome project. <i>GigaScience</i> , 2017 , 6, 1-7	7.6	101
55	Bacterial diversity in two Neonatal Intensive Care Units (NICUs). <i>PLoS ONE</i> , 2013 , 8, e54703	3.7	97
54	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016 , 17, 217	18.3	86
53	The mind-body-microbial continuum. <i>Dialogues in Clinical Neuroscience</i> , 2011 , 13, 55-62	5.7	85
52	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
51	Changes in microbial ecology after fecal microbiota transplantation for recurrent <i>C. difficile</i> infection affected by underlying inflammatory bowel disease. <i>Microbiome</i> , 2017 , 5, 55	16.6	74
50	Characterizing microbial communities through space and time. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 431-6	11.4	73
49	Our microbial selves: what ecology can teach us. <i>EMBO Reports</i> , 2011 , 12, 775-84	6.5	65
48	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. <i>Journal of Physiology</i> , 2019 , 597, 2361-2378	3.9	64
47	From Animalcules to an Ecosystem: Application of Ecological Concepts to the Human Microbiome. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2012 , 43, 137-155	13.5	64
46	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020 , 70, e100	24.2	63
45	Diversity of Rickettsiales in the microbiome of the lone star tick, <i>Amblyomma americanum</i> . <i>Applied and Environmental Microbiology</i> , 2014 , 80, 354-9	4.8	62
44	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1 month. <i>Microbiome</i> , 2019 , 7, 34	16.6	58
43	Visualizing genomic feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa023	3.7	48
42	Advancing analytical algorithms and pipelines for billions of microbial sequences. <i>Current Opinion in Biotechnology</i> , 2012 , 23, 64-71	11.4	46
41	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017 , 21, 7-10	23.4	44
40	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018 , 15, 847-848	11.6	40

39	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
38	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020 , 82, 26-41	12.9	32
37	Migraines Are Correlated with Higher Levels of Nitrate-, Nitrite-, and Nitric Oxide-Reducing Oral Microbes in the American Gut Project Cohort. <i>MSystems</i> , 2016 , 1,	7.6	29
36	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021 , 17, 146-151	11.7	29
35	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020 , 5,	7.6	24
34	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018 , 67, 1743-1745	19.2	23
33	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		23
32	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018 , 9,	7.8	21
31	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. <i>PLoS ONE</i> , 2020 , 15, e0229001	3.7	20
30	SnapShot: the human microbiome. <i>Cell</i> , 2014 , 158, 690-690.e1	56.2	20
29	Carbon, metals, and grain size correlate with bacterial community structure in sediments of a high arsenic aquifer. <i>Frontiers in Microbiology</i> , 2012 , 3, 82	5.7	19
28	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018 , 44, 61-69	7.9	18
27	SitePainter: a tool for exploring biogeographical patterns. <i>Bioinformatics</i> , 2012 , 28, 436-8	7.2	18
26	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019 , 4,	7.6	17
25	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016 , 5, 27	7.6	16
24	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. <i>ISME Journal</i> , 2013 , 7, 461-4	11.9	14
23	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021 , 6,	7.6	14
22	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. <i>MSystems</i> , 2019 , 4,	7.6	13

21	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020 , 5,	7.6	12
20	American Gut: an Open Platform for Citizen-Science Microbiome Research		11
19	A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. <i>MBio</i> , 2020 , 11,	7.8	7
18	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures		7
17	Effects of Immunization With the Soil-Derived Bacterium on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. <i>Frontiers in Physiology</i> , 2020 , 11, 524833	4.6	7
16	Visualizing β mic feature rankings and log-ratios using Qurro		6
15	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. <i>Brain, Behavior, and Immunity</i> , 2021 , 97, 150-166	16.6	6
14	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. <i>Frontiers in Psychiatry</i> , 2020 , 11, 518	5	5
13	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		5
12	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets		5
11	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021 , 6, e0069121	7.6	4
10	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree		3
9	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		3
8	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021 , 31, 2131-2137	9.7	3
7	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , 2022 , e0016722	7.6	3
6	Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians.. <i>Molecular Ecology</i> , 2022 ,	5.7	2
5	Sleep and Circadian Disruption and the Gut Microbiome-Possible Links to Dysregulated Metabolism. <i>Current Opinion in Endocrine and Metabolic Research</i> , 2021 , 17, 26-37	1.7	2
4	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. <i>Springer Protocols</i> , 2015 , 89-113	0.3	1

- 3 Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome **2020**, 15, e0229001
- 2 Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome **2020**, 15, e0229001
- 1 Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome **2020**, 15, e0229001