

Antonio González

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

39,820
citations

31902

53
h-index

53109

85
g-index

108
all docs

108
docs citations

108
times ranked

41337
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	The Treatment-Naïve Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
3	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
4	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712
5	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
6	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. <i>Cell</i> , 2012, 150, 470-480.	13.5	1,603
7	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
8	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
9	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
10	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013, 2, 16.	3.3	1,096
11	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	13.9	934
12	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	830
13	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016, 22, 250-253.	15.2	736
14	Microbiota and Host Nutrition across Plant and Animal Kingdoms. <i>Cell Host and Microbe</i> , 2015, 17, 603-616.	5.1	628
15	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
16	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
17	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
18	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	0.9	535

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19	Transient Inability to Manage Proteobacteria Promotes Chronic Gut Inflammation in TLR5-Deficient Mice. <i>Cell Host and Microbe</i> , 2012, 12, 139-152.	5.1	459
20	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
21	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.	1.5	446
22	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	1.7	376
23	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	3.8	355
24	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	2.4	352
25	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	4.4	325
26	Rethinking "Enterotypes". <i>Cell Host and Microbe</i> , 2014, 16, 433-437.	5.1	321
27	Convergence of gut microbiomes in myrmecophagous mammals. <i>Molecular Ecology</i> , 2014, 23, 1301-1317.	2.0	311
28	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.	3.3	288
29	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	1.7	284
30	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.	4.9	218
31	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.	25.8	212
32	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. <i>MSystems</i> , 2018, 3, .	1.7	204
33	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	193
34	Antifungal isolates database of amphibian skin-associated bacteria and function against emerging fungal pathogens. <i>Ecology</i> , 2015, 96, 595-595.	1.5	192
35	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.	3.3	186
36	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6200-6209.	1.4	167

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37	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.	1.1	150
38	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. Genome Biology, 2016, 17, 217.	3.8	128
39	Bacterial Diversity in Two Neonatal Intensive Care Units (NICUs). PLoS ONE, 2013, 8, e54703.	1.1	120
40	Changes in microbial ecology after fecal microbiota transplantation for recurrent C. difficile infection affected by underlying inflammatory bowel disease. Microbiome, 2017, 5, 55.	4.9	118
41	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1Åmonth. Microbiome, 2019, 7, 34.	4.9	115
42	The mind-body-microbial continuum. Dialogues in Clinical Neuroscience, 2011, 13, 55-62.	1.8	109
43	Suppression of the gut microbiome ameliorates ageâ€related arterial dysfunction and oxidative stress in mice. Journal of Physiology, 2019, 597, 2361-2378.	1.3	106
44	Characterizing microbial communities through space and time. Current Opinion in Biotechnology, 2012, 23, 431-436.	3.3	98
45	VisualizingÂ™omic feature rankings and log-ratios using Qurro. NAR Genomics and Bioinformatics, 2020, 2, lqaa023.	1.5	97
46	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	5.1	95
47	Diversity of Rickettsiales in the Microbiome of the Lone Star Tick, Amblyomma americanum. Applied and Environmental Microbiology, 2014, 80, 354-359.	1.4	82
48	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. Nature Chemical Biology, 2021, 17, 146-151.	3.9	73
49	Our microbial selves: what ecology can teach us. EMBO Reports, 2011, 12, 775-784.	2.0	71
50	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	9.0	71
51	From Animalcules to an Ecosystem: Application of Ecological Concepts to the Human Microbiome. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 137-155.	3.8	68
52	Migraines Are Correlated with Higher Levels of Nitrate-, Nitrite-, and Nitric Oxide-Reducing Oral Microbes in the American Gut Project Cohort. MSystems, 2016, 1, .	1.7	63
53	Advancing analytical algorithms and pipelines for billions of microbial sequences. Current Opinion in Biotechnology, 2012, 23, 64-71.	3.3	57
54	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. PLoS ONE, 2020, 15, e0229001.	1.1	56

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55	Microbial Diversity in Clinical Microbiome Studies: Sample Size and Statistical Power Considerations. <i>Gastroenterology</i> , 2020, 158, 1524-1528.	0.6	55
56	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology</i> 2000, 2020, 82, 26-41.	6.3	50
57	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	1.7	47
58	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
59	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016, 5, 27.	3.3	35
60	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	1.7	35
61	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	1.7	35
62	<i>Ruminiclostridium 5</i> , <i>Parabacteroides distasonis</i> , 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.	2.0	34
63	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018, 67, 1743-1745.	6.1	32
64	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018, 9, .	1.8	28
65	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.	1.5	27
66	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	2.3	27
67	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021, 6, e0069121.	1.7	27
68	SnapShot: The Human Microbiome. <i>Cell</i> , 2014, 158, 690-690.e1.	13.5	26
69	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. <i>MSystems</i> , 2019, 4, .	1.7	24
70	SitePainter: a tool for exploring biogeographical patterns. <i>Bioinformatics</i> , 2012, 28, 436-438.	1.8	22
71	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. <i>ISME Journal</i> , 2013, 7, 461-464.	4.4	19
72	A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. <i>MBio</i> , 2020, 11, .	1.8	19

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73	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. <i>Frontiers in Psychiatry</i> , 2020, 11, 518.	1.3	19
74	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	1.7	16
75	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.	0.6	16
76	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
77	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	10
78	Effects of Immunization With the Soil-Derived Bacterium <i>Mycobacterium vaccae</i> on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. <i>Frontiers in Physiology</i> , 2020, 11, 524833.	1.3	9
79	Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians. <i>Molecular Ecology</i> , 2022, 31, 2140-2156.	2.0	7
80	A Prebiotic Diet Alters the Fecal Microbiome and Improves Sleep in Response to Sleep Disruption in Rats. <i>Frontiers in Neuroscience</i> , 2022, 16, .	1.4	6
81	Impact of Vaginal Estrogen on the Urobiome in Postmenopausal Women With Recurrent Urinary Tract Infection. <i>Female Pelvic Medicine and Reconstructive Surgery</i> , 2022, 28, 20-26.	0.6	5
82	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. <i>Springer Protocols</i> , 2015, , 89-113.	0.1	4
83	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	1.7	2
84	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	1.8	0
85	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
86	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
87	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0