

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	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
2	Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians. <i>Molecular Ecology</i> , 2022, 31, 2140-2156.	2.0	7
3	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	10
4	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	1.7	35
5	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
6	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	1.7	2
7	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	3.9	73
8	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
9	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
10	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
11	<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
12	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
13	Microbial Diversity in Clinical Microbiome Studies: Sample Size and Statistical Power Considerations. <i>Gastroenterology</i> , 2020, 158, 1524-1528.	0.6	55
14	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. <i>Periodontology 2000</i> , 2020, 82, 26-41.	6.3	50
15	A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. <i>MBio</i> , 2020, 11, .	1.8	19
16	Visualizing ¹⁶ S rRNA gene feature rankings and log-ratios using Qurro. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa023.	1.5	97
17	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	1.7	47
18	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. <i>Frontiers in Psychiatry</i> , 2020, 11, 518.	1.3	19

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19	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. PLoS ONE, 2020, 15, e0229001.	1.1	56
20	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. Current Protocols in Bioinformatics, 2020, 70, e100.	25.8	212
21	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. MSystems, 2020, 5, .	1.7	16
22	Effects of Immunization With the Soil-Derived Bacterium Mycobacterium vaccae on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. Frontiers in Physiology, 2020, 11, 524833.	1.3	9
23	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
24	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
25	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. , 2020, 15, e0229001.		0
26	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy" MBio, 2019, 10, .	1.8	0
27	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
28	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. Journal of Physiology, 2019, 597, 2361-2378.	1.3	106
29	redbiom: a Rapid Sample Discovery and Feature Characterization System. MSystems, 2019, 4, .	1.7	35
30	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	13.7	1,638
31	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. MSystems, 2019, 4, .	1.7	24
32	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1 month. Microbiome, 2019, 7, 34.	4.9	115
33	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. MSystems, 2018, 3, .	1.7	376
34	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. MSystems, 2018, 3, .	1.7	204
35	Guiding longitudinal sampling in IBD cohorts. Gut, 2018, 67, 1743-1745.	6.1	32
36	Identifying and Predicting Novelty in Microbiome Studies. MBio, 2018, 9, .	1.8	28

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37	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
38	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	9.0	71
39	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
40	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
41	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	2.3	27
42	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	1.7	284
43	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017, 21, 7-10.	5.1	95
44	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
45	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
46	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	830
47	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.	4.9	118
48	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
49	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	193
50	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
51	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, .	1.7	63
52	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016, 17, 217.	3.8	128
53	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016, 5, 27.	3.3	35
54	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016, 22, 250-253.	15.2	736

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55	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. Springer Protocols, 2015, , 89-113.	0.1	4
56	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
57	Microbiota and Host Nutrition across Plant and Animal Kingdoms. Cell Host and Microbe, 2015, 17, 603-616.	5.1	628
58	Antifungal isolates database of amphibian skin-associated bacteria and function against emerging fungal pathogens. Ecology, 2015, 96, 595-595.	1.5	192
59	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection. Microbiome, 2015, 3, 10.	4.9	218
60	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.	3.3	288
61	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. Applied and Environmental Microbiology, 2015, 81, 6200-6209.	1.4	167
62	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. PeerJ, 2014, 2, e545.	0.9	535
63	Diversity of Rickettsiales in the Microbiome of the Lone Star Tick, Amblyomma americanum. Applied and Environmental Microbiology, 2014, 80, 354-359.	1.4	82
64	Temporal variability is a personalized feature of the human microbiome. Genome Biology, 2014, 15, 531.	3.8	355
65	Convergence of gut microbiomes in myrmecophagous mammals. Molecular Ecology, 2014, 23, 1301-1317.	2.0	311
66	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. Cell Host and Microbe, 2014, 15, 382-392.	5.1	2,582
67	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. ISME Journal, 2014, 8, 1464-1475.	4.4	325
68	SnapShot: The Human Microbiome. Cell, 2014, 158, 690-690.e1.	13.5	26
69	Rethinking "Enterotypes". Cell Host and Microbe, 2014, 16, 433-437.	5.1	321
70	Meta-analyses of studies of the human microbiota. Genome Research, 2013, 23, 1704-1714.	2.4	352
71	EMPeror: a tool for visualizing high-throughput microbial community data. GigaScience, 2013, 2, 16.	3.3	1,096
72	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553

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73	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
74	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. <i>ISME Journal</i> , 2013, 7, 461-464.	4.4	19
75	Bacterial Diversity in Two Neonatal Intensive Care Units (NICUs). <i>PLoS ONE</i> , 2013, 8, e54703.	1.1	120
76	SitePainter: a tool for exploring biogeographical patterns. <i>Bioinformatics</i> , 2012, 28, 436-438.	1.8	22
77	Host Remodeling of the Gut Microbiome and Metabolic Changes during Pregnancy. <i>Cell</i> , 2012, 150, 470-480.	13.5	1,603
78	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
79	Characterizing microbial communities through space and time. <i>Current Opinion in Biotechnology</i> , 2012, 23, 431-436.	3.3	98
80	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.	3.8	68
81	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
82	Advancing analytical algorithms and pipelines for billions of microbial sequences. <i>Current Opinion in Biotechnology</i> , 2012, 23, 64-71.	3.3	57
83	Diet Drives Convergence in Gut Microbiome Functions Across Mammalian Phylogeny and Within Humans. <i>Science</i> , 2011, 332, 970-974.	6.0	1,712
84	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
85	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	13.9	934
86	Our microbial selves: what ecology can teach us. <i>EMBO Reports</i> , 2011, 12, 775-784.	2.0	71
87	The mind-body-microbial continuum. <i>Dialogues in Clinical Neuroscience</i> , 2011, 13, 55-62.	1.8	109