Antonio Gonzlez

List of Publications by Year in Descending Order

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	Predicting fungal infection rate and severity with skin-associated microbial communities on amphibians.. *Molecular Ecology*, **2022**,	5.7	2
91	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. *MSystems*, **2022**, e0016722	7.6	3
90	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. *MSystems*, **2021**, 6, e0069121	7.6	4
89	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. *MSystems*, **2021**, 6,	7.6	14
88	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. *Nature Chemical Biology*, **2021**, 17, 146-151	11.7	29
87	Sleep and Circadian Disruption and the Gut Microbiome-Possible Links to Dysregulated Metabolism. *Current Opinion in Endocrine and Metabolic Research*, **2021**, 17, 26-37	1.7	2
86	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. *Genome Research*, **2021**, 31, 2131-2137	9.7	3
85	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. *Brain, Behavior, and Immunity*, **2021**, 97, 150-166	16.6	6
84	Visualizing omic feature rankings and log-ratios using Qurro. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa023	3.7	48
83	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. *MSystems*, **2020**, 5,	7.6	24
82	Paroxetine Administration Affects Microbiota and Bile Acid Levels in Mice. *Frontiers in Psychiatry*, **2020**, 11, 518	5	5
81	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome. *PLoS ONE*, **2020**, 15, e0229001	3.7	20
80	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	24.2	63
79	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. *MSystems*, **2020**, 5,	7.6	12
78	Microbial biogeography and ecology of the mouth and implications for periodontal diseases. *Periodontology 2000*, **2020**, 82, 26-41	12.9	32
77	A Distinct Microbiome Signature in Posttreatment Lyme Disease Patients. *MBio*, **2020**, 11,	7.8	7
76	Effects of Immunization With the Soil-Derived Bacterium on Stress Coping Behaviors and Cognitive Performance in a "Two Hit" Stressor Model. *Frontiers in Physiology*, **2020**, 11, 524833	4.6	7

75	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome **2020**, 15, e0229001		
74	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome **2020**, 15, e0229001		
73	Repeated sleep disruption in mice leads to persistent shifts in the fecal microbiome and metabolome **2020**, 15, e0229001		
72	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. *Journal of Physiology*, **2019**, 597, 2361-2378	3.9	64
71	redbiom: a Rapid Sample Discovery and Feature Characterization System. *MSystems*, **2019**, 4,	7.6	17
70	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. *Nature*, **2019**, 569, 655-662	50.4	761
69	Intermittent Hypoxia and Hypercapnia Reproducibly Change the Gut Microbiome and Metabolome across Rodent Model Systems. *MSystems*, **2019**, 4,	7.6	13
68	Environmental toxicants in breast milk of Norwegian mothers and gut bacteria composition and metabolites in their infants at 1 month. *Microbiome*, **2019**, 7, 34	16.6	58
67	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
66	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. *MSystems*, **2018**, 3,	7.6	181
65	Gut Microbiota Offers Universal Biomarkers across Ethnicity in Inflammatory Bowel Disease Diagnosis and Infliximab Response Prediction. *MSystems*, **2018**, 3,	7.6	115
64	Guiding longitudinal sampling in IBD cohorts. *Gut*, **2018**, 67, 1743-1745	19.2	23
63	Are microbiome studies ready for hypothesis-driven research?. *Current Opinion in Microbiology*, **2018**, 44, 61-69	7.9	18
62	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science **2018**,		78
61	Identifying and Predicting Novelty in Microbiome Studies. *MBio*, **2018**, 9,	7.8	21
60	Qiita: rapid, web-enabled microbiome meta-analysis. *Nature Methods*, **2018**, 15, 796-798	21.6	231
59	Striped UniFrac: enabling microbiome analysis at unprecedented scale. *Nature Methods*, **2018**, 15, 847-848	21.6	40
58	American Gut: an Open Platform for Citizen Science Microbiome Research. *MSystems*, **2018**, 3,	7.6	336

57	Best practices for analysing microbiomes. *Nature Reviews Microbiology*, **2018**, 16, 410-422	22.2	668
56	Balance Trees Reveal Microbial Niche Differentiation. *MSystems*, **2017**, 2,	7.6	177
55	Bringing the Dynamic Microbiome to Life with Animations. *Cell Host and Microbe*, **2017**, 21, 7-10	23.4	44
54	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. *MSystems*, **2017**, 2,	7.6	763
53	Normalization and microbial differential abundance strategies depend upon data characteristics. *Microbiome*, **2017**, 5, 27	16.6	840
52	Dynamics of the human gut microbiome in inflammatory bowel disease. *Nature Microbiology*, **2017**, 2, 17004	26.6	533
51	Changes in microbial ecology after fecal microbiota transplantation for recurrent C. difficile infection affected by underlying inflammatory bowel disease. *Microbiome*, **2017**, 5, 55	16.6	74
50	A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, **2017**, 551, 457-463	50.4	1076
49	The sponge microbiome project. *GigaScience*, **2017**, 6, 1-7	7.6	101
48	Migraines Are Correlated with Higher Levels of Nitrate-, Nitrite-, and Nitric Oxide-Reducing Oral Microbes in the American Gut Project Cohort. *MSystems*, **2016**, 1,	7.6	29
47	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. *Genome Biology*, **2016**, 17, 217	18.3	86
46	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. *GigaScience*, **2016**, 5, 27	7.6	16
45	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. *Nature Medicine*, **2016**, 22, 250-3	50.5	536
44	Immunization with a heat-killed preparation of the environmental bacterium Mycobacterium vaccae promotes stress resilience in mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E3130-9	11.5	137
43	Antifungal isolates database of amphibian skin-associated bacteria and function against emerging fungal pathogens. *Ecology*, **2015**, 96, 595-595	4.6	107
42	Dynamic changes in short- and long-term bacterial composition following fecal microbiota transplantation for recurrent Clostridium difficile infection. *Microbiome*, **2015**, 3, 10	16.6	175
41	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	11.5	237
40	Variation in the Microbiota of Ixodes Ticks with Regard to Geography, Species, and Sex. *Applied and Environmental Microbiology*, **2015**, 81, 6200-9	4.8	110

39	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. *Springer Protocols*, **2015**, 89-113	0.3	1
38	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	3.7	106
37	Microbiota and Host Nutrition across Plant and Animal Kingdoms. *Cell Host and Microbe*, **2015**, 17, 603-16	23.4	373
36	Convergence of gut microbiomes in myrmecophagous mammals. *Molecular Ecology*, **2014**, 23, 1301-17	5.7	179
35	The treatment-naive microbiome in new-onset Crohn's disease. *Cell Host and Microbe*, **2014**, 15, 382-392	23.4	1836
34	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. *ISME Journal*, **2014**, 8, 1464-75	11.9	262
33	SnapShot: the human microbiome. *Cell*, **2014**, 158, 690-690.e1	56.2	20
32	Rethinking "enterotypes". *Cell Host and Microbe*, **2014**, 16, 433-7	23.4	234
31	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. *PeerJ*, **2014**, 2, e545	3.1	395
30	Diversity of Rickettsiales in the microbiome of the lone star tick, Amblyomma americanum. *Applied and Environmental Microbiology*, **2014**, 80, 354-9	4.8	62
29	Temporal variability is a personalized feature of the human microbiome. *Genome Biology*, **2014**, 15, 531	18.3	255
28	Meta-analyses of studies of the human microbiota. *Genome Research*, **2013**, 23, 1704-14	9.7	289
27	EMPeror: a tool for visualizing high-throughput microbial community data. *GigaScience*, **2013**, 2, 16	7.6	711
26	Advancing our understanding of the human microbiome using QIIME. *Methods in Enzymology*, **2013**, 531, 371-444	1.7	373
25	A guide to enterotypes across the human body: meta-analysis of microbial community structures in human microbiome datasets. *PLoS Computational Biology*, **2013**, 9, e1002863	5	359
24	Collaborative cloud-enabled tools allow rapid, reproducible biological insights. *ISME Journal*, **2013**, 7, 461-4	11.9	14
23	Bacterial diversity in two Neonatal Intensive Care Units (NICUs). *PLoS ONE*, **2013**, 8, e54703	3.7	97
22	Advancing analytical algorithms and pipelines for billions of microbial sequences. *Current Opinion in Biotechnology*, **2012**, 23, 64-71	11.4	46

21 Host remodeling of the gut microbiome and metabolic changes during pregnancy. *Cell*, **2012**, 150, 470-80 96.2 1117

20 Transient inability to manage proteobacteria promotes chronic gut inflammation in TLR5-deficient mice. *Cell Host and Microbe*, **2012**, 12, 139-52 23.4 325

19 Characterizing microbial communities through space and time. *Current Opinion in Biotechnology*, **2012**, 23, 431-6 11.4 73

18 From Animalcules to an Ecosystem: Application of Ecological Concepts to the Human Microbiome. *Annual Review of Ecology, Evolution, and Systematics*, **2012**, 43, 137-155 13.5 64

17 Carbon, metals, and grain size correlate with bacterial community structure in sediments of a high arsenic aquifer. *Frontiers in Microbiology*, **2012**, 3, 82 5.7 19

16 SitePainter: a tool for exploring biogeographical patterns. *Bioinformatics*, **2012**, 28, 436-8 7.2 18

15 Diet drives convergence in gut microbiome functions across mammalian phylogeny and within humans. *Science*, **2011**, 332, 970-4 33.3 1215

14 Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. *Nature Biotechnology*, **2011**, 29, 415-20 44.5 445

13 Moving pictures of the human microbiome. *Genome Biology*, **2011**, 12, R50 18.3 723

12 Our microbial selves: what ecology can teach us. *EMBO Reports*, **2011**, 12, 775-84 6.5 65

11 The mind-body-microbial continuum. *Dialogues in Clinical Neuroscience*, **2011**, 13, 55-62 5.7 85

10 Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data 5

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8 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 36

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