Yoshiki VÃ¡zquez-Baeza

List of Publications by Year
in descending order

58 papers	45,202 citations	101496 36 h-index	138417 58 g-index
76 all docs	76 docs citations	76 times ranked	57525 citing authors

#	Article	IF	Citations
1	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. Biometrics, 2022, 78, 1155-1167.	0.8	4
2	Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity. Nature Microbiology, 2022, 7, 262-276.	5.9	110
3	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. Nature Genetics, 2022, 54, 134-142.	9.4	164
4	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. Cell Metabolism, 2022, 34, 719-730.e4.	7.2	35
5	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. MSystems, 2022, 7, e0016722.	1.7	35
6	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. MSystems, 2022, 7, e0005022.	1.7	4
7	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. Inflammatory Bowel Diseases, 2021, 27, 603-616.	0.9	25
8	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. Nature Chemical Biology, 2021, 17, 146-151.	3.9	73
9	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. Brain, Behavior, and Immunity, 2021, 91, 245-256.	2.0	44
10	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. Nature Biotechnology, 2021, 39, 165-168.	9.4	61
11	Reply to: Examining microbe–metabolite correlations by linear methods. Nature Methods, 2021, 18, 40-41.	9.0	6
12	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. MSystems, 2021, 6, .	1.7	36
13	Challenges in benchmarking metagenomic profilers. Nature Methods, 2021, 18, 618-626.	9.0	63
14	Persons With Schizophrenia Exhibit Altered Gut Microbiome Functional Pathways Related to Immune Modulation and Cardiovascular Risk. Biological Psychiatry, 2021, 89, S101.	0.7	0
15	Candidate probiotic Lactiplantibacillus plantarum HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. Microbiome, 2021, 9, 151.	4.9	30
16	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. PLoS Computational Biology, 2021, 17, e1009056.	1.5	2
17	Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. ISME Journal, 2021, 15, 3399-3411.	4.4	30
18	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. Microbiome, 2021, 9, 132.	4.9	37

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19	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. Genome Research, 2021, 31, 2131-2137.	2.4	16
20	Links between gut microbiome composition and fatty liver disease in a large population sample. Gut Microbes, 2021, 13, 1-22.	4.3	41
21	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. MSystems, 2021, 6, e0069121.	1.7	27
22	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. MSystems, 2020, 5, .	1.7	47
23	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. MSystems, 2020, 5, .	1.7	80
24	SciPy 1.0: fundamental algorithms for scientific computing in Python. Nature Methods, 2020, 17, 261-272.	9.0	17,539
25	QIIME 2 Enables Comprehensive Endâ€toâ€End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. Current Protocols in Bioinformatics, 2020, 70, e100.	25.8	212
26	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
27	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology, 2019, 20, 219.	3.8	94
28	Learning representations of microbeâ€"metabolite interactions. Nature Methods, 2019, 16, 1306-1314.	9.0	184
29	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. MSystems, 2019, 4, .	1.7	23
30	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
31	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. Nature, 2019, 569, 655-662.	13.7	1,638
32	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. MSystems, 2019, 4, .	1.7	40
33	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. Clinical Gastroenterology and Hepatology, 2019, 17, 218-230.	2.4	187
34	Creating a 3D microbial and chemical snapshot of a human habitat. Scientific Reports, 2018, 8, 3669.	1.6	34
35	Guiding longitudinal sampling in IBD cohorts. Gut, 2018, 67, 1743-1745.	6.1	32
36	Impacts of the Human Gut Microbiome on Therapeutics. Annual Review of Pharmacology and Toxicology, 2018, 58, 253-270.	4.2	74

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37	Qiita: rapid, web-enabled microbiome meta-analysis. Nature Methods, 2018, 15, 796-798.	9.0	459
38	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	9.0	71
39	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	1.7	604
40	Are microbiome studies ready for hypothesis-driven research?. Current Opinion in Microbiology, 2018, 44, 61-69.	2.3	27
41	Balance Trees Reveal Microbial Niche Differentiation. MSystems, 2017, 2, .	1.7	284
42	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	5.1	95
43	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	4.9	1,434
44	Dynamics of the human gut microbiome in inflammatory bowel disease. Nature Microbiology, 2017, 2, 17004.	5.9	830
45	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
46	A communal catalogue reveals Earth's multiscale microbial diversity. Nature, 2017, 551, 457-463.	13.7	1,942
47	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. Journal of Microbiology and Biology Education, 2016, 17, 46-50.	0.5	42
48	From Sample to Multi-Omics Conclusions in under 48 Hours. MSystems, 2016, 1, .	1.7	53
49	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. Nature Microbiology, 2016, 1, 16177.	5.9	194
50	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. Genome Biology, 2016, 17, 217.	3.8	128
51	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
52	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. Cell Host and Microbe, 2014, 15, 382-392.	5.1	2,582
53	Longitudinal analysis of microbial interaction between humans and the indoor environment. Science, 2014, 345, 1048-1052.	6.0	751
54	SnapShot: The Human Microbiome. Cell, 2014, 158, 690-690.e1.	13.5	26

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55	Meta-analyses of studies of the human microbiota. Genome Research, 2013, 23, 1704-1714.	2.4	352
56	EMPeror: a tool for visualizing high-throughput microbial community data. GigaScience, 2013, 2, 16.	3.3	1,096
57	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	0.4	553
58	From molecules to dynamic biological communities. Biology and Philosophy, 2013, 28, 241-259.	0.7	12