

Yoshiki Vázquez-Baeza

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

45,202
citations

101543

36
h-index

138484

58
g-index

76
all docs

76
docs citations

76
times ranked

57525
citing authors

#	ARTICLE	IF	CITATIONS
1	SciPy 1.0: fundamental algorithms for scientific computing in Python. <i>Nature Methods</i> , 2020, 17, 261-272.	19.0	17,539
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
3	The Treatment-Naive Microbiome in New-Onset Crohnâ€™s Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.0	2,582
4	A communal catalogue reveals Earthâ€™s multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
5	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	27.8	1,638
6	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	11.1	1,434
7	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013, 2, 16.	6.4	1,096
8	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	13.3	830
9	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	12.6	751
10	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	3.8	604
11	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	1.0	553
12	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	19.0	459
13	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013, 23, 1704-1714.	5.5	352
14	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	3.8	284
15	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.	11.1	218
16	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
17	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. <i>Nature Microbiology</i> , 2016, 1, 16177.	13.3	194
18	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 218-230.	4.4	187

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19	Learning representations of microbial metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314.	19.0	184
20	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. <i>Nature Genetics</i> , 2022, 54, 134-142.	21.4	164
21	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016, 17, 217.	8.8	128
22	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.	11.1	118
23	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity. <i>Nature Microbiology</i> , 2022, 7, 262-276.	13.3	110
24	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. <i>Journal of Physiology</i> , 2019, 597, 2361-2378.	2.9	106
25	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017, 21, 7-10.	11.0	95
26	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. <i>Genome Biology</i> , 2019, 20, 219.	8.8	94
27	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , 2020, 5, .	3.8	80
28	Impacts of the Human Gut Microbiome on Therapeutics. <i>Annual Review of Pharmacology and Toxicology</i> , 2018, 58, 253-270.	9.4	74
29	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	8.0	73
30	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	19.0	71
31	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	19.0	63
32	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	17.5	61
33	From Sample to Multi-Omics Conclusions in under 48 Hours. <i>MSystems</i> , 2016, 1, .	3.8	53
34	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020, 5, .	3.8	47
35	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. <i>Brain, Behavior, and Immunity</i> , 2021, 91, 245-256.	4.1	44
36	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. <i>Journal of Microbiology and Biology Education</i> , 2016, 17, 46-50.	1.0	42

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37	Links between gut microbiome composition and fatty liver disease in a large population sample. <i>Gut Microbes</i> , 2021, 13, 1-22.	9.8	41
38	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019, 4, .	3.8	40
39	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	11.1	37
40	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	3.8	36
41	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. <i>Cell Metabolism</i> , 2022, 34, 719-730.e4.	16.2	35
42	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	3.8	35
43	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, 3669.	3.3	34
44	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018, 67, 1743-1745.	12.1	32
45	Candidate probiotic <i>Lactiplantibacillus plantarum</i> HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. <i>Microbiome</i> , 2021, 9, 151.	11.1	30
46	Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021, 15, 3399-3411.	9.8	30
47	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	5.1	27
48	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021, 6, e0069121.	3.8	27
49	SnapShot: The Human Microbiome. <i>Cell</i> , 2014, 158, 690-690.e1.	28.9	26
50	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 603-616.	1.9	25
51	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems</i> , 2019, 4, .	3.8	23
52	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.5	16
53	From molecules to dynamic biological communities. <i>Biology and Philosophy</i> , 2013, 28, 241-259.	1.4	12
54	Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	19.0	6

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55	Utilizing stability criteria in choosing feature selection methods yields reproducible results in microbiome data. <i>Biometrics</i> , 2022, 78, 1155-1167.	1.4	4
56	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. <i>MSystems</i> , 2022, 7, e0005022.	3.8	4
57	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	3.2	2
58	Persons With Schizophrenia Exhibit Altered Gut Microbiome Functional Pathways Related to Immune Modulation and Cardiovascular Risk. <i>Biological Psychiatry</i> , 2021, 89, S101.	1.3	0