

Yoshiki Vazquez-Baeza

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68

papers

19,834

citations

32

h-index

76

g-index

76

ext. papers

33,189

ext. citations

16.3

avg, IF

6

L-index

#	Paper	IF	Citations
68	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity.. <i>Nature Microbiology</i> , 2022 ,	26.6	13
67	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	36.3	18
66	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting.. <i>Cell Metabolism</i> , 2022 ,	24.6	2
65	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , 2022 , e0016722	7.6	3
64	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype.. <i>MSystems</i> , 2022 , e0005022	7.6	0
63	Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data. <i>MSystems</i> , 2021 , 6, e0069121	7.6	4
62	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021 , 6,	7.6	14
61	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021 , 18, 618-626	21.6	15
60	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	16.6	5
59	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021 , 17, e1009056	5	0
58	Compositional and genetic alterations in GravesDisease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021 , 15, 3399-3411	11.9	7
57	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021 , 9, 132	16.6	15
56	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , 2021 , 27, 603-616	4.5	8
55	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021 , 17, 146-151	11.7	29
54	Gut microbiome in Schizophrenia: Altered functional pathways related to immune modulation and atherosclerotic risk. <i>Brain, Behavior, and Immunity</i> , 2021 , 91, 245-256	16.6	17
53	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021 , 39, 165-168	44.5	23
52	Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , 2021 , 18, 40-41	21.6	2

51	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021 , 31, 2131-2137	9.7	3
50	Links between gut microbiome composition and fatty liver disease in a large population sample. <i>Gut Microbes</i> , 2021 , 13, 1-22	8.8	12
49	High-Resolution Longitudinal Dynamics of the Cystic Fibrosis Sputum Microbiome and Metabolome through Antibiotic Therapy. <i>MSystems</i> , 2020 , 5,	7.6	24
48	Human Skin, Oral, and Gut Microbiomes Predict Chronological Age. <i>MSystems</i> , 2020 , 5,	7.6	33
47	SciPy 1.0: fundamental algorithms for scientific computing in Python. <i>Nature Methods</i> , 2020 , 17, 261-272	11.6	6244
46	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	24.2	63
45	Microbial context predicts SARS-CoV-2 prevalence in patients and the hospital built environment 2020 ,		10
44	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems</i> , 2019 , 4,	7.6	15
43	Suppression of the gut microbiome ameliorates age-related arterial dysfunction and oxidative stress in mice. <i>Journal of Physiology</i> , 2019 , 597, 2361-2378	3.9	64
42	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019 , 569, 655-662	50.4	761
41	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019 , 4,	7.6	24
40	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
39	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	18.3	41
38	Learning representations of microbe-metabolite interactions. <i>Nature Methods</i> , 2019 , 16, 1306-1314	21.6	79
37	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , 2019 , 17, 218-230	6.9	107
36	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018 , 8, 3669	4.9	23
35	Guiding longitudinal sampling in IBD cohorts. <i>Gut</i> , 2018 , 67, 1743-1745	19.2	23
34	Impacts of the Human Gut Microbiome on Therapeutics. <i>Annual Review of Pharmacology and Toxicology</i> , 2018 , 58, 253-270	17.9	51

33	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018 , 44, 61-69	7.9	18
32	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
31	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018 , 15, 796-798	21.6	231
30	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018 , 15, 847-848	21.6	40
29	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
28	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017 , 2,	7.6	177
27	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017 , 21, 7-10	23.4	44
26	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017 , 5, 27	16.6	840
25	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017 , 2, 17004	26.6	533
24	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	16.6	74
23	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
22	Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. <i>Nature Microbiology</i> , 2016 , 1, 16177	26.6	97
21	Tiny microbes, enormous impacts: what matters in gut microbiome studies?. <i>Genome Biology</i> , 2016 , 17, 217	18.3	86
20	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	1.3	28
19	From Sample to Multi-Omics Conclusions in under 48 Hours. <i>MSystems</i> , 2016 , 1,	7.6	45
18	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	16.6	175
17	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , 2014 , 15, 382-392	23.4	1836
16	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014 , 345, 1048-52	33.3	543

15	SnapShot: the human microbiome. <i>Cell</i> , 2014 , 158, 690-690.e1	56.2	20
14	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013 , 23, 1704-14	9.7	289
13	EMPeror: a tool for visualizing high-throughput microbial community data. <i>GigaScience</i> , 2013 , 2, 16	7.6	711
12	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.7	373
11	From molecules to dynamic biological communities. <i>Biology and Philosophy</i> , 2013 , 28, 241-259	1.7	12
10	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		5
9	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		23
8	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
7	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
6	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree		3
5	Early prediction of liver disease using conventional risk factors and gut microbiome-augmented gradient boosting		10
4	Links between gut microbiome composition and fatty liver disease in a large population sample		2
3	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort		4
2	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets		5
1	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures		7