

Eric A Franzosa

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

17,223
citations

126907

33
h-index

233421

45
g-index

53
all docs

53
docs citations

53
times ranked

20518
citing authors

#	ARTICLE	IF	CITATIONS
1	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	19.0	1,843
2	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	27.8	1,638
3	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.0	1,125
4	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	13.3	1,094
5	The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes. <i>Cell Host and Microbe</i> , 2015, 17, 260-273.	11.0	1,008
6	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	28.9	968
7	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	27.8	929
8	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	6.0	808
9	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	28.9	806
10	Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. <i>Science Translational Medicine</i> , 2016, 8, 343ra81.	12.4	763
11	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	3.2	691
12	Relating the metatranscriptome and metagenome of the human gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2329-38.	7.1	552
13	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	28.6	544
14	Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	11.0	523
15	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	13.3	408
16	Identifying personal microbiomes using metagenomic codes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2930-8.	7.1	377
17	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. <i>Cell Host and Microbe</i> , 2019, 26, 252-264.e10.	11.0	274
18	<i>Bacteroides</i> -Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. <i>Cell Host and Microbe</i> , 2019, 25, 668-680.e7.	11.0	274

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19	Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	11.0	273
20	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	4.1	241
21	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	3.2	235
22	Human gut bacteria produce ω -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	27.8	210
23	Compositional and Temporal Changes in the Gut Microbiome of Pediatric Ulcerative Colitis Patients Are Linked to Disease Course. <i>Cell Host and Microbe</i> , 2018, 24, 600-610.e4.	11.0	193
24	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	12.8	176
25	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	8.8	143
26	A bacterial bile acid metabolite modulates Treg activity through the nuclear hormone receptor NR4A1. <i>Cell Host and Microbe</i> , 2021, 29, 1366-1377.e9.	11.0	111
27	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <i>Scientific Reports</i> , 2017, 7, 17686.	3.3	97
28	Strain-level epidemiology of microbial communities and the human microbiome. <i>Genome Medicine</i> , 2020, 12, 71.	8.2	75
29	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	28.9	64
30	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. <i>Genome Medicine</i> , 2021, 13, 102.	8.2	62
31	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	8.2	61
32	Growth effects of N-acyl ethanolamines on gut bacteria reflect altered bacterial abundances in inflammatory bowel disease. <i>Nature Microbiology</i> , 2020, 5, 486-497.	13.3	59
33	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	30.7	47
34	Discovery of bioactive microbial gene products in inflammatory bowel disease. <i>Nature</i> , 2022, 606, 754-760.	27.8	38
35	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	6.5	36
36	Strain-level fitness in the gut microbiome is an emergent property of glycans and a single metabolite. <i>Cell</i> , 2022, 185, 513-529.e21.	28.9	36

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37	Statistical approaches for differential expression analysis in metatranscriptomics. <i>Bioinformatics</i> , 2021, 37, i34-i41.	4.1	26
38	The classroom microbiome and asthma morbidity in children attending 3 inner-city schools. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2311-2313.	2.9	24
39	A statistical model for describing and simulating microbial community profiles. <i>PLoS Computational Biology</i> , 2021, 17, e1008913.	3.2	21
40	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	11.0	20
41	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017, 2, .	3.8	18
42	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	4.1	18
43	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015, 3, e791.	2.0	12
44	Determinants of <i>Staphylococcus aureus</i> carriage in the developing infant nasal microbiome. <i>Genome Biology</i> , 2020, 21, 301.	8.8	11