

Eric A Franzosa

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

17,223
citations

126708

33
h-index

233125

45
g-index

53
all docs

53
docs citations

53
times ranked

20518
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	13.5	36
2	Human gut bacteria produce β -17-modulating bile acid metabolites. <i>Nature</i> , 2022, 603, 907-912.	13.7	210
3	High-sensitivity pattern discovery in large, paired multiomic datasets. <i>Bioinformatics</i> , 2022, 38, i378-i385.	1.8	18
4	Discovery of bioactive microbial gene products in inflammatory bowel disease. <i>Nature</i> , 2022, 606, 754-760.	13.7	38
5	Identification of Natural CRISPR Systems and Targets in the Human Microbiome. <i>Cell Host and Microbe</i> , 2021, 29, 94-106.e4.	5.1	20
6	A framework for microbiome science in public health. <i>Nature Medicine</i> , 2021, 27, 766-774.	15.2	47
7	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
8	Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. <i>Genome Medicine</i> , 2021, 13, 102.	3.6	62
9	Statistical approaches for differential expression analysis in metatranscriptomics. <i>Bioinformatics</i> , 2021, 37, i34-i41.	1.8	26
10	Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 279-311.	2.8	36
11	A statistical model for describing and simulating microbial community profiles. <i>PLoS Computational Biology</i> , 2021, 17, e1008913.	1.5	21
12	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.	5.1	111
13	Multivariable association discovery in population-scale meta-omics studies. <i>PLoS Computational Biology</i> , 2021, 17, e1009442.	1.5	691
14	Strain-level epidemiology of microbial communities and the human microbiome. <i>Genome Medicine</i> , 2020, 12, 71.	3.6	75
15	Determinants of <i>Staphylococcus aureus</i> carriage in the developing infant nasal microbiome. <i>Genome Biology</i> , 2020, 21, 301.	3.8	11
16	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.	5.9	59
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.	5.1	274
18	Predictive metabolomic profiling of microbial communities using amplicon or metagenomic sequences. <i>Nature Communications</i> , 2019, 10, 3136.	5.8	176

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19	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
20	Bacteroides-Derived Sphingolipids Are Critical for Maintaining Intestinal Homeostasis and Symbiosis. <i>Cell Host and Microbe</i> , 2019, 25, 668-680.e7.	5.1	274
21	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019, 4, 293-305.	5.9	1,094
22	bioBakery: a meta-omic analysis environment. <i>Bioinformatics</i> , 2018, 34, 1235-1237.	1.8	241
23	Dynamics of metatranscription in the inflammatory bowel disease gut microbiome. <i>Nature Microbiology</i> , 2018, 3, 337-346.	5.9	408
24	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.	1.5	24
25	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.	5.1	193
26	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	9.0	1,125
27	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	13.7	929
28	Fluoride Depletes Acidogenic Taxa in Oral but Not Gut Microbial Communities in Mice. <i>MSystems</i> , 2017, 2, .	1.7	18
29	Indoleacrylic Acid Produced by Commensal <i>Peptostreptococcus</i> Species Suppresses Inflammation. <i>Cell Host and Microbe</i> , 2017, 22, 25-37.e6.	5.1	523
30	Alterations in oral bacterial communities are associated with risk factors for oral and oropharyngeal cancer. <i>Scientific Reports</i> , 2017, 7, 17686.	1.6	97
31	Experimental design and quantitative analysis of microbial community multiomics. <i>Genome Biology</i> , 2017, 18, 228.	3.8	143
32	Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. <i>Cell</i> , 2016, 165, 842-853.	13.5	968
33	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.	5.8	763
34	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016, 167, 1125-1136.e8.	13.5	806
35	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.	5.1	1,008
36	Biogeography of the Intestinal Mucosal and Lumenal Microbiome in the Rhesus Macaque. <i>Cell Host and Microbe</i> , 2015, 17, 385-391.	5.1	273

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37	Sequencing and beyond: integrating molecular 'omics' for microbial community profiling. <i>Nature Reviews Microbiology</i> , 2015, 13, 360-372.	13.6	544
38	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.	3.3	377
39	MetaPhlan2 for enhanced metagenomic taxonomic profiling. <i>Nature Methods</i> , 2015, 12, 902-903.	9.0	1,843
40	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	1.5	235
41	A reproducible approach to high-throughput biological data acquisition and integration. <i>PeerJ</i> , 2015, 3, e791.	0.9	12
42	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.	3.3	552
43	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	13.5	64
44	Functional profiling of the gut microbiome in disease-associated inflammation. <i>Genome Medicine</i> , 2013, 5, 65.	3.6	61