

# Francesco Asnicar

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

20,456  
citations

172386

29  
h-index

233338

45  
g-index

58  
all docs

58  
docs citations

58  
times ranked

23244  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. <i>Cell</i> , 2019, 176, 649-662.e20.	13.5	1,087
3	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	5.1	822
4	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
5	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. <i>PeerJ</i> , 2015, 3, e1029.	0.9	701
6	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. <i>Nature Medicine</i> , 2019, 25, 667-678.	15.2	602
7	Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. <i>Nature Medicine</i> , 2021, 27, 321-332.	15.2	477
8	Human postprandial responses to food and potential for precision nutrition. <i>Nature Medicine</i> , 2020, 26, 964-973.	15.2	418
9	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
10	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. <i>MSystems</i> , 2017, 2, .	1.7	329
11	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
12	Strain-Level Analysis of Mother-to-Child Bacterial Transmission during the First Few Months of Life. <i>Cell Host and Microbe</i> , 2018, 24, 146-154.e4.	5.1	311
13	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019, 26, 666-679.e7.	5.1	274
14	Endogenous murine microbiota member <i>Faecalibaculum rodentium</i> and its human homologue protect from intestinal tumour growth. <i>Nature Microbiology</i> , 2020, 5, 511-524.	5.9	248
15	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
16	Gut vascular barrier impairment leads to intestinal bacteria dissemination and colorectal cancer metastasis to liver. <i>Cancer Cell</i> , 2021, 39, 708-724.e11.	7.7	175
17	Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 14.	2.9	159
18	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.	15.2	158

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19	Ketogenic diet and ketone bodies enhance the anticancer effects of PD-1 blockade. JCI Insight, 2021, 6, .	2.3	143
20	Blue poo: impact of gut transit time on the gut microbiome using a novel marker. Gut, 2021, 70, 1665-1674.	6.1	84
21	Faecal microbiota transplantation for the treatment of diarrhoea induced by tyrosine-kinase inhibitors in patients with metastatic renal cell carcinoma. Nature Communications, 2020, 11, 4333.	5.8	82
22	Analysis of 1321 Eubacterium rectale genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. Genome Biology, 2020, 21, 138.	3.8	72
23	Detecting contamination in viromes using ViromeQC. Nature Biotechnology, 2019, 37, 1408-1412.	9.4	69
24	Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. Nature Microbiology, 2016, 1, 16070.	5.9	68
25	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. Genome Biology, 2019, 20, 299.	3.8	58
26	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of Staphylococcus aureus strains in a paediatric hospital. Genome Medicine, 2018, 10, 82.	3.6	54
27	Genomic and metagenomic insights into the microbial community of a thermal spring. Microbiome, 2019, 7, 8.	4.9	40
28	High intake of vegetables is linked to lower white blood cell profile and the effect is mediated by the gut microbiome. BMC Medicine, 2021, 19, 37.	2.3	30
29	Profiling microbial strains in urban environments using metagenomic sequencing data. Biology Direct, 2018, 13, 9.	1.9	29
30	Gut microbiome diversity and composition is associated with hypertension in women. Journal of Hypertension, 2021, 39, 1810-1816.	0.3	22
31	Discovering Causal Relationships in Grapevine Expression Data to Expand Gene Networks. A Case Study: Four Networks Related to Climate Change. Frontiers in Plant Science, 2018, 9, 1385.	1.7	17
32	NES2RA. International Journal of High Performance Computing Applications, 2018, 32, 380-392.	2.4	13
33	Recent genetic exchanges and admixture shape the genome and population structure of the zoonotic pathogen <i>Cryptosporidium parvum</i> . Molecular Ecology, 2023, 32, 2633-2645.	2.0	9
34	Genes Encoding Microbial Acyl Coenzyme A Binding Protein/Diazepam-Binding Inhibitor Orthologs Are Rare in the Human Gut Microbiome and Show No Links to Obesity. Applied and Environmental Microbiology, 2021, 87, e0047121.	1.4	7
35	Draft Genome Sequence of the Planktic Cyanobacterium Tychonema bourrellyi, Isolated from Alpine Lentic Freshwater. Genome Announcements, 2017, 5, .	0.8	6
36	A Computing System for Discovering Causal Relationships Among Human Genes to Improve Drug Repositioning. IEEE Transactions on Emerging Topics in Computing, 2021, 9, 1667-1682.	3.2	5

#	ARTICLE	IF	CITATIONS
37	Discovering Candidates for Gene Network Expansion by Distributed Volunteer Computing. , 2015, , .		4
38	Draft Genome Sequences of Novel <i>Pseudomonas</i> , <i>Flavobacterium</i> , and <i>Sediminibacterium</i> Species Strains from a Freshwater Ecosystem. Genome Announcements, 2018, 6, .	0.8	4
39	OneGenE: Regulatory Gene Network Expansion via Distributed Volunteer Computing on BOINC. , 2019, , .		3
40	Integrating Metagenomic Information into Personalized Nutrition Tools: The PREDICT I Study (P20-005-19). Current Developments in Nutrition, 2019, 3, nzz040.P20-005-19.	0.1	3
41	Microbiome Signatures of Nutrients, Foods and Dietary Patterns: Potential for Personalized Nutrition from The PREDICT 1 Study. Current Developments in Nutrition, 2020, 4, nzaa062_044.	0.1	3
42	Impact of Postprandial Lipemia and Glycemia on Inflammatory Factors in over 1000 Individuals in the US and UK: Insights from the PREDICT 1 and InterCardio Studies. Current Developments in Nutrition, 2020, 4, nzaa068_003.	0.1	1
43	Influence of Gut Microbial Communities on Fasting and Postprandial Lipids and Circulating Metabolites: The PREDICT 1 Study. Current Developments in Nutrition, 2020, 4, nzaa062_004.	0.1	1