

# 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	Recent genetic exchanges and admixture shape the genome and population structure of the zoonotic pathogen <i>Cryptosporidium parvum</i> . <i>Molecular Ecology</i> , 2023, 32, 2633-2645.	2.0	9
2	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. <i>Nature Medicine</i> , 2022, 28, 535-544.	15.2	158
3	A Computing System for Discovering Causal Relationships Among Human Genes to Improve Drug Repositioning. <i>IEEE Transactions on Emerging Topics in Computing</i> , 2021, 9, 1667-1682.	3.2	5
4	Ketogenic diet and ketone bodies enhance the anticancer effects of PD-1 blockade. <i>JCI Insight</i> , 2021, 6, .	2.3	143
5	High intake of vegetables is linked to lower white blood cell profile and the effect is mediated by the gut microbiome. <i>BMC Medicine</i> , 2021, 19, 37.	2.3	30
6	Blue poo: impact of gut transit time on the gut microbiome using a novel marker. <i>Gut</i> , 2021, 70, 1665-1674.	6.1	84
7	Gut microbiome diversity and composition is associated with hypertension in women. <i>Journal of Hypertension</i> , 2021, 39, 1810-1816.	0.3	22
8	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. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0047121.	1.4	7
9	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
10	Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bioBakery 3. <i>ELife</i> , 2021, 10, .	2.8	808
11	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
12	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. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa068_003.	0.1	1
13	Faecal microbiota transplantation for the treatment of diarrhoea induced by tyrosine-kinase inhibitors in patients with metastatic renal cell carcinoma. <i>Nature Communications</i> , 2020, 11, 4333.	5.8	82
14	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
15	Human postprandial responses to food and potential for precision nutrition. <i>Nature Medicine</i> , 2020, 26, 964-973.	15.2	418
16	Microbiome Signatures of Nutrients, Foods and Dietary Patterns: Potential for Personalized Nutrition from The PREDICT 1 Study. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa062_044.	0.1	3
17	Influence of Gut Microbial Communities on Fasting and Postprandial Lipids and Circulating Metabolites: The PREDICT 1 Study. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa062_004.	0.1	1
18	Analysis of 1321 <i>Eubacterium rectale</i> genomes from metagenomes uncovers complex phylogeographic population structure and subspecies functional adaptations. <i>Genome Biology</i> , 2020, 21, 138.	3.8	72

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19	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
20	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
21	OneGenE: Regulatory Gene Network Expansion via Distributed Volunteer Computing on BOINC. , 2019, , .		3
22	Integrating Metagenomic Information into Personalized Nutrition Tools: The PREDICT I Study (P20-005-19). <i>Current Developments in Nutrition</i> , 2019, 3, nzz040.P20-005-19.	0.1	3
23	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
24	Genomic and metagenomic insights into the microbial community of a thermal spring. <i>Microbiome</i> , 2019, 7, 8.	4.9	40
25	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
26	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
27	Detecting contamination in viromes using ViromeQC. <i>Nature Biotechnology</i> , 2019, 37, 1408-1412.	9.4	69
28	Microbial genomes from non-human primate gut metagenomes expand the primate-associated bacterial tree of life with over 1000 novel species. <i>Genome Biology</i> , 2019, 20, 299.	3.8	58
29	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
30	Draft Genome Sequences of Novel <i>Pseudomonas</i> , <i>Flavobacterium</i> , and <i>Sediminibacterium</i> Species Strains from a Freshwater Ecosystem. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
31	NES2RA. <i>International Journal of High Performance Computing Applications</i> , 2018, 32, 380-392.	2.4	13
32	Whole-genome epidemiology, characterisation, and phylogenetic reconstruction of <i>Staphylococcus aureus</i> strains in a paediatric hospital. <i>Genome Medicine</i> , 2018, 10, 82.	3.6	54
33	Discovering Causal Relationships in Grapevine Expression Data to Expand Gene Networks. A Case Study: Four Networks Related to Climate Change. <i>Frontiers in Plant Science</i> , 2018, 9, 1385.	1.7	17
34	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
35	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
36	Profiling microbial strains in urban environments using metagenomic sequencing data. <i>Biology Direct</i> , 2018, 13, 9.	1.9	29

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37	Studying Vertical Microbiome Transmission from Mothers to Infants by Strain-Level Metagenomic Profiling. <i>MSystems</i> , 2017, 2, .	1.7	329
38	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
39	Draft Genome Sequence of the Planktic Cyanobacterium <i>Tychonema bourrellyi</i> , Isolated from Alpine Lentic Freshwater. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
40	Uncovering oral <i>Neisseria</i> tropism and persistence using metagenomic sequencing. <i>Nature Microbiology</i> , 2016, 1, 16070.	5.9	68
41	Strain-level microbial epidemiology and population genomics from shotgun metagenomics. <i>Nature Methods</i> , 2016, 13, 435-438.	9.0	328
42	Discovering Candidates for Gene Network Expansion by Distributed Volunteer Computing. , 2015, , .		4
43	Compact graphical representation of phylogenetic data and metadata with GraPhlAn. <i>PeerJ</i> , 2015, 3, e1029.	0.9	701