

Sara Vieira-Silva

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

18,271
citations

87723

38
h-index

143772

57
g-index

65
all docs

65
docs citations

65
times ranked

24476
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
2	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016, 352, 560-564.	6.0	1,716
3	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
4	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
5	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016, 352, 565-569.	6.0	1,398
6	Supplementation with <i>Akkermansia muciniphila</i> in overweight and obese human volunteers: a proof-of-concept exploratory study. <i>Nature Medicine</i> , 2019, 25, 1096-1103.	15.2	1,281
7	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019, 4, 623-632.	5.9	1,206
8	How informative is the mouse for human gut microbiota research?. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 1-16.	1.2	990
9	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511.	13.7	791
10	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , 2016, 65, 57-62.	6.1	737
11	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
12	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974.	6.1	370
13	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. <i>Gut</i> , 2016, 65, 1681-1689.	6.1	312
14	The Systemic Imprint of Growth and Its Uses in Ecological (Meta)Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000808.	1.5	286
15	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
16	Speciesâ€function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16088.	5.9	279
17	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
18	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019, 4, 1826-1831.	5.9	149

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19	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	6.1	149
20	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020, 5, 1079-1087.	5.9	144
21	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017, 47, 339-348.e4.	6.6	141
22	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. <i>Annual Review of Microbiology</i> , 2015, 69, 305-321.	2.9	133
23	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , 2018, 9, 4630.	5.8	124
24	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	5.8	122
25	A20 controls intestinal homeostasis through cell-specific activities. <i>Nature Communications</i> , 2014, 5, 5103.	5.8	109
26	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	13.7	102
27	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	15.2	102
28	<i>Dysosmobacter welbionis</i> is a newly isolated human commensal bacterium preventing diet-induced obesity and metabolic disorders in mice. <i>Gut</i> , 2022, 71, 534-543.	6.1	95
29	Novel insights into the genetically obese (<i>ob/ob</i>) and diabetic (<i>db/db</i>) mice: two sides of the same coin. <i>Microbiome</i> , 2021, 9, 147.	4.9	92
30	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018, 3, 526-528.	5.9	81
31	Towards biome-specific analysis of meta-omics data. <i>ISME Journal</i> , 2016, 10, 1025-1028.	4.4	72
32	Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. <i>PLoS ONE</i> , 2016, 11, e0153294.	1.1	70
33	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	2.4	59
34	Human and preclinical studies of the host-gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. <i>Gut</i> , 2021, 70, 2105-2114.	6.1	58
35	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. <i>Gut</i> , 2022, 71, 2463-2480.	6.1	53
36	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	1.8	48

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37	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, 31.	1.5	45
38	Association of hemicellulose- and pectin-modifying gene expression with <i>Eucalyptus globulus</i> secondary growth. <i>Plant Physiology and Biochemistry</i> , 2011, 49, 873-881.	2.8	40
39	An Assessment of the Impacts of Molecular Oxygen on the Evolution of Proteomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1931-1942.	3.5	37
40	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 735-746.	0.6	37
41	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , 2019, 68, 2257.1-2260.	6.1	37
42	Immune Subversion and Quorum-Sensing Shape the Variation in Infectious Dose among Bacterial Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002503.	2.1	36
43	Review article: how the intestinal microbiota may reflect disease activity and influence therapeutic outcome in inflammatory bowel disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 52, 1453-1468.	1.9	36
44	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019, 74, 53-64.	0.5	34
45	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	5.9	32
46	The reproductive microbiome – clinical practice recommendations for fertility specialists. <i>Reproductive BioMedicine Online</i> , 2020, 41, 443-453.	1.1	30
47	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. <i>Nature Communications</i> , 2021, 12, 3562.	5.8	30
48	The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119.	3.3	30
49	Exploring the relationship between the gut microbiome and mental health outcomes in a posttraumatic stress disorder cohort relative to trauma-exposed controls. <i>European Neuropsychopharmacology</i> , 2022, 56, 24-38.	0.3	26
50	No evidence for elemental-based streamlining of prokaryotic genomes. <i>Trends in Ecology and Evolution</i> , 2010, 25, 319-320.	4.2	25
51	Effect of obesity on gastrointestinal transit, pressure and pH using a wireless motility capsule. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2021, 167, 1-8.	2.0	16
52	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , 2017, 66, 1865-1866.	6.1	9
53	Investment in rapid growth shapes the evolutionary rates of essential proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20030-20035.	3.3	7
54	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. <i>Gastroenterology</i> , 2017, 152, S1.	0.6	5

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55	Specific contributions of segmental transit times to gut microbiota composition. <i>Gut</i> , 2021, , gutjnl-2021-325916.	6.1	4
56	Practical guidelines for gut microbiome analysis in microbiota-gut-brain axis research. <i>Behavioral and Brain Sciences</i> , 2019, 42, .	0.4	1
57	Tu1713 Host-Microbiome Interactions in Primary Sclerosing Cholangitis. <i>Gastroenterology</i> , 2016, 150, S927-S928.	0.6	0
58	Su1909 Genetic Risk for Crohn's Disease has Little Impact on Intestinal Microbiota Composition. <i>Gastroenterology</i> , 2016, 150, S585-S586.	0.6	0
59	Profiling of the Fecal Microbiota and Metabolome in Patients with Inflammatory Bowel Disease and their Unaffected Relatives. <i>Gastroenterology</i> , 2017, 152, S991.	0.6	0