

Sara Vieira-Silva

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

18,271
citations

87888

38
h-index

144013

57
g-index

65
all docs

65
docs citations

65
times ranked

24476
citing authors

#	ARTICLE	IF	CITATIONS
1	<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.	12.1	95
2	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.	12.1	53
3	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.	0.7	26
4	Microbiome and metabolome features of the cardiometabolic disease spectrum. <i>Nature Medicine</i> , 2022, 28, 303-314.	30.7	102
5	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.	7.1	30
6	Variation and transmission of the human gut microbiota across multiple familial generations. <i>Nature Microbiology</i> , 2022, 7, 87-96.	13.3	32
7	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
8	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.	12.1	58
9	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.	11.1	92
10	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. <i>Nature Communications</i> , 2021, 12, 3562.	12.8	30
11	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.	4.3	16
12	Specific contributions of segmental transit times to gut microbiota composition. <i>Gut</i> , 2021, , gutjnl-2021-325916.	12.1	4
13	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	27.8	102
14	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	4.1	48
15	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.	3.7	36
16	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	12.8	122
17	The reproductive microbiome - clinical practice recommendations for fertility specialists. <i>Reproductive BioMedicine Online</i> , 2020, 41, 443-453.	2.4	30
18	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	27.8	283

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19	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020, 5, 1079-1087.	13.3	144
20	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020, 7, 170.	5.3	59
21	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.	30.7	1,281
22	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019, 4, 1826-1831.	13.3	149
23	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019, 74, 53-64.	1.2	34
24	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019, 4, 623-632.	13.3	1,206
25	Population-level analysis of <i>Blastocystis</i> subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019, 68, 1180-1189.	12.1	149
26	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , 2019, 68, 2257.1-2260.	12.1	37
27	Practical guidelines for gut microbiome analysis in microbiota-gut-brain axis research. <i>Behavioral and Brain Sciences</i> , 2019, 42, .	0.7	1
28	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018, 3, 526-528.	13.3	81
29	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , 2018, 9, 4630.	12.8	124
30	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018, 9, 31.	3.5	45
31	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017, 66, 1968-1974.	12.1	370
32	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. <i>Gastroenterology</i> , 2017, 152, S1.	1.3	5
33	Profiling of the Fecal Microbiota and Metabolome in Patients with Inflammatory Bowel Disease and their Unaffected Relatives. <i>Gastroenterology</i> , 2017, 152, S991.	1.3	0
34	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , 2017, 66, 1865-1866.	12.1	9
35	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017, 47, 339-348.e4.	14.3	141
36	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017, 551, 507-511.	27.8	791

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37	Faecal Metaproteomic Analysis Reveals a Personalized and Stable Functional Microbiome and Limited Effects of a Probiotic Intervention in Adults. PLoS ONE, 2016, 11, e0153294.	2.5	70
38	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. Gut, 2016, 65, 1681-1689.	12.1	312
39	Tu1713 Host-Microbiome Interactions in Primary Sclerosing Cholangitis. Gastroenterology, 2016, 150, S927-S928.	1.3	0
40	Su1909 Genetic Risk for Crohn's Disease has Little Impact on Intestinal Microbiota Composition. Gastroenterology, 2016, 150, S585-S586.	1.3	0
41	Towards biome-specific analysis of meta-omics data. ISME Journal, 2016, 10, 1025-1028.	9.8	72
42	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
43	Population-level analysis of gut microbiome variation. Science, 2016, 352, 560-564.	12.6	1,716
44	Heritable components of the human fecal microbiome are associated with visceral fat. Genome Biology, 2016, 17, 189.	8.8	183
45	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
46	Speciesâ€function relationships shape ecological properties of the human gut microbiome. Nature Microbiology, 2016, 1, 16088.	13.3	279
47	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. Journal of Crohn's and Colitis, 2016, 10, 735-746.	1.3	37
48	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. Gut, 2016, 65, 57-62.	12.1	737
49	Structure and function of the global ocean microbiome. Science, 2015, 348, 1261359.	12.6	2,137
50	How informative is the mouse for human gut microbiota research?. DMM Disease Models and Mechanisms, 2015, 8, 1-16.	2.4	990
51	Microbiology Meets Big Data: The Case of Gut Microbiotaâ€Derived Trimethylamine. Annual Review of Microbiology, 2015, 69, 305-321.	7.3	133
52	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	27.8	1,627
53	A20 controls intestinal homeostasis through cell-specific activities. Nature Communications, 2014, 5, 5103.	12.8	109
54	Immune Subversion and Quorum-Sensing Shape the Variation in Infectious Dose among Bacterial Pathogens. PLoS Pathogens, 2012, 8, e1002503.	4.7	36

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55	Association of hemicellulose- and pectin-modifying gene expression with Eucalyptus globulus secondary growth. <i>Plant Physiology and Biochemistry</i> , 2011, 49, 873-881.	5.8	40
56	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.	7.1	7
57	The Systemic Imprint of Growth and Its Uses in Ecological (Meta)Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000808.	3.5	286
58	No evidence for elemental-based streamlining of prokaryotic genomes. <i>Trends in Ecology and Evolution</i> , 2010, 25, 319-320.	8.7	25
59	An Assessment of the Impacts of Molecular Oxygen on the Evolution of Proteomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1931-1942.	8.9	37