

Sara Vieira-Silva

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

58
papers

10,569
citations

29
h-index

65
g-index

65
ext. papers

14,873
ext. citations

18.8
avg, IF

6
L-index

#	Paper	IF	Citations
58	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 ,	19.2	5
57	Microbiome and metabolome features of the cardiometabolic disease spectrum.. <i>Nature Medicine</i> , 2022 ,	50.5	4
56	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	11.5	2
55	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021 ,	50.4	11
54	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> , 2021 , 56, 24-38	1.2	2
53	Specific contributions of segmental transit times to gut microbiota composition. <i>Gut</i> , 2021 ,	19.2	1
52	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	19.2	13
51	is a newly isolated human commensal bacterium preventing diet-induced obesity and metabolic disorders in mice. <i>Gut</i> , 2021 ,	19.2	17
50	Novel insights into the genetically obese (ob/ob) and diabetic (db/db) mice: two sides of the same coin. <i>Microbiome</i> , 2021 , 9, 147	16.6	15
49	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. <i>Nature Communications</i> , 2021 , 12, 3562	17.4	8
48	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
47	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	5.7	2
46	Successional Stages in Infant Gut Microbiota Maturation.. <i>MBio</i> , 2021 , e0185721	7.8	7
45	Variation and transmission of the human gut microbiota across multiple familial generations.. <i>Nature Microbiology</i> , 2021 ,	26.6	4
44	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020 , 581, 310-315	50.4	100
43	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020 , 5, 1079-1087	26.6	55
42	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020 , 7, 170	8.2	20

41	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	6.1	15
40	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020 , 11, 5881	17.4	29
39	The reproductive microbiome - clinical practice recommendations for fertility specialists. <i>Reproductive BioMedicine Online</i> , 2020 , 41, 443-453	4	14
38	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. <i>Nature Microbiology</i> , 2019 , 4, 1826-1831	26.6	71
37	The human microbiome in health and disease: hype or hope. <i>Acta Clinica Belgica</i> , 2019 , 74, 53-64	1.8	20
36	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	50.5	650
35	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019 , 4, 623-632	26.6	651
34	Population-level analysis of subtype prevalence and variation in the human gut microbiota. <i>Gut</i> , 2019 , 68, 1180-1189	19.2	79
33	Gut microbiota dynamics and uraemic toxins: one size does not fit all. <i>Gut</i> , 2019 , 68, 2257-2260	19.2	22
32	Richness and ecosystem development across faecal snapshots of the gut microbiota. <i>Nature Microbiology</i> , 2018 , 3, 526-528	26.6	48
31	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. <i>Frontiers in Microbiology</i> , 2018 , 9, 31	5.7	22
30	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. <i>Nature Communications</i> , 2018 , 9, 4630	17.4	69
29	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. <i>Gut</i> , 2017 , 66, 1968-1974	19.2	236
28	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. <i>Gastroenterology</i> , 2017 , 152, S1	13.3	3
27	Water activity does not shape the microbiota in the human colon. <i>Gut</i> , 2017 , 66, 1865-1866	19.2	8
26	Nlrp6- and ASC-Dependent Inflammasomes Do Not Shape the Commensal Gut Microbiota Composition. <i>Immunity</i> , 2017 , 47, 339-348.e4	32.3	108
25	Quantitative microbiome profiling links gut community variation to microbial load. <i>Nature</i> , 2017 , 551, 507-511	50.4	475
24	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. <i>Gut</i> , 2016 , 65, 57-62	19.2	488

23	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016 , 535, 376-81	50.4	977
22	Species-function relationships shape ecological properties of the human gut microbiome. <i>Nature Microbiology</i> , 2016 , 1, 16088	26.6	145
21	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. <i>Journal of Crohns and Colitis</i> , 2016 , 10, 735-46	1.5	23
20	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	3.7	59
19	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. <i>Gut</i> , 2016 , 65, 1681-9	19.2	212
18	Towards biome-specific analysis of meta-omics data. <i>ISME Journal</i> , 2016 , 10, 1025-8	11.9	40
17	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016 , 352, 565-9	33.3	929
16	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016 , 352, 560-4	33.3	1120
15	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016 , 17, 189	18.3	124
14	Microbiology Meets Big Data: The Case of Gut Microbiota-Derived Trimethylamine. <i>Annual Review of Microbiology</i> , 2015 , 69, 305-21	17.5	94
13	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015 , 528, 262-266	50.4	1107
12	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359	33.3	1261
11	How informative is the mouse for human gut microbiota research?. <i>DMM Disease Models and Mechanisms</i> , 2015 , 8, 1-16	4.1	691
10	A20 controls intestinal homeostasis through cell-specific activities. <i>Nature Communications</i> , 2014 , 5, 5103	17.4	78
9	Immune subversion and quorum-sensing shape the variation in infectious dose among bacterial pathogens. <i>PLoS Pathogens</i> , 2012 , 8, e1002503	7.6	29
8	Association of hemicellulose- and pectin-modifying gene expression with <i>Eucalyptus globulus</i> secondary growth. <i>Plant Physiology and Biochemistry</i> , 2011 , 49, 873-81	5.4	25
7	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, 20030-5	11.5	7
6	The systemic imprint of growth and its uses in ecological (meta)genomics. <i>PLoS Genetics</i> , 2010 , 6, e1000808	8.08	205

5	No evidence for elemental-based streamlining of prokaryotic genomes. <i>Trends in Ecology and Evolution</i> , 2010 , 25, 319-20; author reply 320-1	10.9	22
4	An assessment of the impacts of molecular oxygen on the evolution of proteomes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1931-42	8.3	31
3	Microbiome Determinants and Physiological Effects of the Benzoate-Hippurate Microbial-Host Co-Metabolic Pathway		1
2	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
1	Successional Stages in Infant Gut Microbiota Maturation		2