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List of Publications by Year
in descending order

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71 papers	24,757 citations	61984 43 h-index	95266 68 g-index
79 all docs	79 docs citations	79 times ranked	27723 citing authors

#	Article	IF	Citations
1	A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature, 2012, 490, 55-60.	27.8	5,345
2	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
3	Population-level analysis of gut microbiome variation. Science, 2016, 352, 560-564.	12.6	1,716
4	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	27.8	1,627
5	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	27.8	1,506
6	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
7	Supplementation with Akkermansia muciniphila in overweight and obese human volunteers: a proof-of-concept exploratory study. Nature Medicine, 2019, 25, 1096-1103.	30.7	1,281
8	The neuroactive potential of the human gut microbiota in quality of life and depression. Nature Microbiology, 2019, 4, 623-632.	13.3	1,206
9	Quantitative microbiome profiling links gut community variation to microbial load. Nature, 2017, 551, 507-511.	27.8	791
10	Stool consistency is strongly associated with gut microbiota richness and composition, enterotypes and bacterial growth rates. Gut, 2016, 65, 57-62.	12.1	737
11	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
12	Prebiotic inulin-type fructans induce specific changes in the human gut microbiota. Gut, 2017, 66, 1968-1974.	12.1	370
13	Primary sclerosing cholangitis is characterised by intestinal dysbiosis independent from IBD. Gut, 2016, 65, 1681-1689.	12.1	312
14	Cross-Feeding between Bifidobacterium longum BB536 and Acetate-Converting, Butyrate-Producing Colon Bacteria during Growth on Oligofructose. Applied and Environmental Microbiology, 2006, 72, 7835-7841.	3.1	296
15	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	27.8	283
16	Speciesâ€“function relationships shape ecological properties of the human gut microbiome. Nature Microbiology, 2016, 1, 16088.	13.3	279
17	Quantitative microbiome profiling disentangles inflammation- and bile duct obstruction-associated microbiota alterations across PSC/IBD diagnoses. Nature Microbiology, 2019, 4, 1826-1831.	13.3	149
18	Population-level analysis of Blastocystis subtype prevalence and variation in the human gut microbiota. Gut, 2019, 68, 1180-1189.	12.1	149

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19	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. Nature Microbiology, 2020, 5, 1079-1087.	13.3	144
20	Practical considerations for large-scale gut microbiome studies. FEMS Microbiology Reviews, 2017, 41, S154-S167.	8.6	142
21	Probiotics in fermented sausages. Meat Science, 2008, 80, 75-78.	5.5	141
22	Microbiology Meets Big Data: The Case of Gut Microbiotaâ€“Derived Trimethylamine. Annual Review of Microbiology, 2015, 69, 305-321.	7.3	133
23	Species Diversity, Community Dynamics, and Metabolite Kinetics of the Microbiota Associated with Traditional Ecuadorian Spontaneous Cocoa Bean Fermentations. Applied and Environmental Microbiology, 2011, 77, 7698-7714.	3.1	128
24	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. Nature Communications, 2018, 9, 4630.	12.8	124
25	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. Nature Communications, 2020, 11, 5881.	12.8	122
26	In Vitro Kinetic Analysis of Fermentation of Prebiotic Inulin-Type Fructans by Bifidobacterium Species Reveals Four Different Phenotypes. Applied and Environmental Microbiology, 2009, 75, 454-461.	3.1	106
27	Combinatorial, additive and dose-dependent drugâ€“microbiome associations. Nature, 2021, 600, 500-505.	27.8	102
28	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	30.7	102
29	Coculture Fermentations ofBifidobacteriumSpecies andBacteroides thetaiotaomicronReveal a Mechanistic Insight into the Prebiotic Effect of Inulin-Type Fructans. Applied and Environmental Microbiology, 2009, 75, 2312-2319.	3.1	99
30	The Probiotic Butyricicoccus pullicaecorum Reduces Feed Conversion and Protects from Potentially Harmful Intestinal Microorganisms and Necrotic Enteritis in Broilers. Frontiers in Microbiology, 2016, 7, 1416.	3.5	99
31	Butyrate Producers as Potential Next-Generation Probiotics: Safety Assessment of the Administration of Butyricicoccus pullicaecorum to Healthy Volunteers. MSystems, 2018, 3, .	3.8	99
32	Dysosmobacter welbionis is a newly isolated human commensal bacterium preventing diet-induced obesity and metabolic disorders in mice. Gut, 2022, 71, 534-543.	12.1	95
33	Comparison of the bacterial species diversity of spontaneous cocoa bean fermentations carried out at selected farms in Ivory Coast and Brazil. Food Microbiology, 2011, 28, 964-973.	4.2	93
34	Novel insights into the genetically obese (ob/ob) and diabetic (db/db) mice: two sides of the same coin. Microbiome, 2021, 9, 147.	11.1	92
35	Richness and ecosystem development across faecal snapshots of the gut microbiota. Nature Microbiology, 2018, 3, 526-528.	13.3	81
36	Volatile analysis of spoiled, artisan-type, modified-atmosphere-packaged cooked ham stored under different temperatures. Food Microbiology, 2009, 26, 94-102.	4.2	76

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37	In Vitro Kinetics of Prebiotic Inulin-Type Fructan Fermentation by Butyrate-Producing Colon Bacteria: Implementation of Online Gas Chromatography for Quantitative Analysis of Carbon Dioxide and Hydrogen Gas Production. Applied and Environmental Microbiology, 2009, 75, 5884-5892.	3.1	73
38	Towards biome-specific analysis of meta-omics data. ISME Journal, 2016, 10, 1025-1028.	9.8	72
39	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
40	Integrated culturing, modeling and transcriptomics uncovers complex interactions and emergent behavior in a three-species synthetic gut community. ELife, 2018, 7, .	6.0	62
41	Human and preclinical studies of the hostâ€“gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. Gut, 2021, 70, 2105-2114.	12.1	58
42	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. Gut, 2022, 71, 2463-2480.	12.1	53
43	Effect of Erythritol and Xylitol on Dental Caries Prevention in Children. Caries Research, 2014, 48, 482-490.	2.0	51
44	Interindividual differences in response to treatment with butyrate-producing Butyricicoccus pullicaecorum 25â€“3T studied in an in vitro gut model. FEMS Microbiology Ecology, 2015, 91, .	2.7	50
45	Successional Stages in Infant Gut Microbiota Maturation. MBio, 2021, 12, e0185721.	4.1	48
46	Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. Frontiers in Microbiology, 2018, 9, 31.	3.5	45
47	The prebiotic, oligofructoseâ€enriched inulin modulates the faecal metabolite profile: Anin vitroanalysis. Molecular Nutrition and Food Research, 2010, 54, 1791-1801.	3.3	44
48	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. Journal of Crohn's and Colitis, 2016, 10, 735-746.	1.3	37
49	Gut microbiota dynamics and uraemic toxins: one size does not fit all. Gut, 2019, 68, 2257.1-2260.	12.1	37
50	Long-Term Effect of Erythritol on Dental Caries Development during Childhood: A Posttreatment Survival Analysis. Caries Research, 2016, 50, 579-588.	2.0	35
51	The human microbiome in health and disease: hype or hope. Acta Clinica Belgica, 2019, 74, 53-64.	1.2	34
52	Variation and transmission of the human gut microbiota across multiple familial generations. Nature Microbiology, 2022, 7, 87-96.	13.3	32
53	Benchmarking microbiome transformations favors experimental quantitative approaches to address compositionality and sampling depth biases. Nature Communications, 2021, 12, 3562.	12.8	30
54	The virota and its transkingdom interactions in the healthy infant gut. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114619119.	7.1	30

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55	Effect of obesity on gastrointestinal transit, pressure and pH using a wireless motility capsule. European Journal of Pharmaceutics and Biopharmaceutics, 2021, 167, 1-8.	4.3	16
56	Latest Developments in Probiotics. , 2008, , 217-229.		12
57	Water activity does not shape the microbiota in the human colon. Gut, 2017, 66, 1865-1866.	12.1	9
58	Letter to the Editor. Journal of Applied Microbiology, 2006, 100, 1388-1389.	3.1	8
59	FLEXiGUT: Rationale for exposomics associations with chronic low-grade gut inflammation. Environment International, 2022, 158, 106906.	10.0	7
60	Ecological Interactions of Bacteria in the Human Gut. , 2009, , 639-679.		6
61	Effect of cryopreservation medium conditions on growth and isolation of gut anaerobes from human faecal samples. Microbiome, 2022, 10, .	11.1	6
62	Therapeutic Manipulation of the Gut Microbiota Through Diet to Reduce Intestinal Inflammation: Results from the FIT Trial. Gastroenterology, 2017, 152, S1.	1.3	5
63	Beyond Oxalobacter: the gut microbiota and kidney stone formation. Gut, 2018, 67, 2078-2079.	12.1	5
64	Specific contributions of segmental transit times to gut microbiota composition. Gut, 2021, , gutjnl-2021-325916.	12.1	4
65	Perspectives and pitfalls of microbiome research through home based fecal sampling: the Flemish Gut Flora Project experience. Archives of Public Health, 2015, 73, .	2.4	1
66	P774 Metagenomics and metabolomics of patients with inflammatory bowel disease and their unaffected relatives. Journal of Crohn's and Colitis, 2017, 11, S476-S477.	1.3	1
67	P767 The FIT trial: anti-inflammatory dietary intervention effects on the intestinal microbiota. Journal of Crohn's and Colitis, 2017, 11, S473-S473.	1.3	1
68	Practical guidelines for gut microbiome analysis in microbiota-gut-brain axis research. Behavioral and Brain Sciences, 2019, 42, .	0.7	1
69	Tu1713 Host-Microbiome Interactions in Primary Sclerosing Cholangitis. Gastroenterology, 2016, 150, S927-S928.	1.3	0
70	Su1909 Genetic Risk for Crohn's Disease has Little Impact on Intestinal Microbiota Composition. Gastroenterology, 2016, 150, S585-S586.	1.3	0
71	Profiling of the Fecal Microbiota and Metabolome in Patients with Inflammatory Bowel Disease and their Unaffected Relatives. Gastroenterology, 2017, 152, S991.	1.3	0