

Muriel Derrien

List of Publications by Year in descending order

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76
papers

22,837
citations

66250

44
h-index

97045

71
g-index

90
all docs

90
docs citations

90
times ranked

28158
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Gut Microbiota in all its States: From Disturbance to Resilience. , 2022, , 161-178.		4
2	A posteriori dietary patterns better explain variations of the gut microbiome than individual markers in the American Gut Project. American Journal of Clinical Nutrition, 2022, 115, 432-443.	2.2	28
3	Yoghurt consumption is associated with changes in the composition of the human gut microbiome and metabolome. BMC Microbiology, 2022, 22, 39.	1.3	31
4	Insights into endogenous Bifidobacterium species in the human gut microbiota during adulthood. Trends in Microbiology, 2022, 30, 940-947.	3.5	56
5	Akkermansia muciniphila: paradigm for next-generation beneficial microorganisms. Nature Reviews Gastroenterology and Hepatology, 2022, 19, 625-637.	8.2	239
6	A novel stepwise integrative analysis pipeline reveals distinct microbiota-host interactions and link to symptoms in irritable bowel syndrome. Scientific Reports, 2021, 11, 5521.	1.6	4
7	Diet and gut microbiome interactions of relevance for symptoms in irritable bowel syndrome. Microbiome, 2021, 9, 74.	4.9	25
8	A Randomised, Controlled Trial: Effect of a Multi-Strain Fermented Milk on the Gut Microbiota Recovery after Helicobacter pylori Therapy. Nutrients, 2021, 13, 3171.	1.7	20
9	A Fermented Milk Product Containing B. lactis CNCM I-2494 Improves the Tolerance of a Plant-Based Diet in Patients with Disorders of Gut-Brain Interactions. Nutrients, 2021, 13, 4542.	1.7	1
10	Safety and functional enrichment of gut microbiome in healthy subjects consuming a multi-strain fermented milk product: a randomised controlled trial. Scientific Reports, 2020, 10, 15974.	1.6	18
11	Metabolic Response of Faecalibacterium prausnitzii to Cell-Free Supernatants from Lactic Acid Bacteria. Microorganisms, 2020, 8, 1528.	1.6	16
12	Vitamin Biosynthesis by Human Gut Butyrate-Producing Bacteria and Cross-Feeding in Synthetic Microbial Communities. MBio, 2020, 11, .	1.8	103
13	Moving from probiotics to precision probiotics. Nature Microbiology, 2020, 5, 878-880.	5.9	110
14	Consumption of Fermented Plant Foods Is Associated with Systematic Differences in the Human Gut Microbiome and Metabolome. Current Developments in Nutrition, 2020, 4, nzaa062_030.	0.1	0
15	A Fermented Milk Product with B. lactis CNCM I-2494 and Lactic Acid Bacteria Improves Gastrointestinal Comfort in Response to a Challenge Diet Rich in Fermentable Residues in Healthy Subjects. Nutrients, 2020, 12, 320.	1.7	7
16	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. MSystems, 2020, 5, .	1.7	81
17	The Gut Microbiota in the First Decade of Life. Trends in Microbiology, 2019, 27, 997-1010.	3.5	368
18	Effects of the long-term storage of human fecal microbiota samples collected in RNAlater. Scientific Reports, 2019, 9, 601.	1.6	36

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19	Evidence for an association of gut microbial Clostridia with brain functional connectivity and gastrointestinal sensorimotor function in patients with irritable bowel syndrome, based on tripartite network analysis. <i>Microbiome</i> , 2019, 7, 45.	4.9	83
20	The potential probiotic <i>Lactobacillus rhamnosus</i> CNCM I-3690 strain protects the intestinal barrier by stimulating both mucus production and cytoprotective response. <i>Scientific Reports</i> , 2019, 9, 5398.	1.6	98
21	Fasting breath H ₂ and gut microbiota metabolic potential are associated with the response to a fermented milk product in irritable bowel syndrome. <i>PLoS ONE</i> , 2019, 14, e0214273.	1.1	12
22	In vitro Study of <i>Lactobacillus paracasei</i> CNCM I-1518 in Healthy and <i>Clostridioides difficile</i> Colonized Elderly Gut Microbiota. <i>Frontiers in Nutrition</i> , 2019, 6, 184.	1.6	12
23	<i>Lactobacillus paracasei</i> CNCM I-3689 reduces vancomycin-resistant <i>Enterococcus</i> persistence and promotes <i>Bacteroidetes</i> resilience in the gut following antibiotic challenge. <i>Scientific Reports</i> , 2018, 8, 5098.	1.6	37
24	Fecal chromogranins and secretogranins are linked to the fecal and mucosal intestinal bacterial composition of IBS patients and healthy subjects. <i>Scientific Reports</i> , 2018, 8, 16821.	1.6	10
25	Altered intestinal antibacterial gene expression response profile in irritable bowel syndrome is linked to bacterial composition and immune activation. <i>Neurogastroenterology and Motility</i> , 2018, 30, e13468.	1.6	15
26	Mo1942 - Association Between Dietary Habits and the Gut Metagenome in Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2018, 154, S-859.	0.6	0
27	<i>Akkermansia muciniphila</i> and its role in regulating host functions. <i>Microbial Pathogenesis</i> , 2017, 106, 171-181.	1.3	775
28	Homeostasis of the gut barrier and potential biomarkers. <i>American Journal of Physiology - Renal Physiology</i> , 2017, 312, G171-G193.	1.6	408
29	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017, 5, 43.	4.9	132
30	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
31	Clostridia from the Gut Microbiome are Associated with Brain Functional Connectivity and Evoked Symptoms in IBS. <i>Gastroenterology</i> , 2017, 152, S40.	0.6	6
32	Brain Structure and Response to Emotional Stimuli as Related to Gut Microbial Profiles in Healthy Women. <i>Psychosomatic Medicine</i> , 2017, 79, 905-913.	1.3	158
33	Rethinking Diet to Aid Human-Microbe Symbiosis. <i>Trends in Microbiology</i> , 2017, 25, 100-112.	3.5	99
34	Identification of an Intestinal Microbiota Signature Associated With Severity of Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2017, 152, 111-123.e8.	0.6	470
35	<i>Lactobacillus paracasei</i> feeding improves immune control of influenza infection in mice. <i>PLoS ONE</i> , 2017, 12, e0184976.	1.1	76
36	Reply. <i>Clinical Gastroenterology and Hepatology</i> , 2016, 14, 1222-1223.	2.4	0

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37	Clostridium difficile colonization and antibiotics response in PolyFermS continuous model mimicking elderly intestinal fermentation. Gut Pathogens, 2016, 8, 63.	1.6	13
38	Effect of a long-term high-protein diet on survival, obesity development, and gut microbiota in mice. American Journal of Physiology - Endocrinology and Metabolism, 2016, 310, E886-E899.	1.8	55
39	Ecological robustness of the gut microbiota in response to ingestion of transient food-borne microbes. ISME Journal, 2016, 10, 2235-2245.	4.4	187
40	Lactulose Challenge Determines Visceral Sensitivity and Severity of Symptoms in Patients With Irritable Bowel Syndrome. Clinical Gastroenterology and Hepatology, 2016, 14, 226-233.e3.	2.4	38
41	Design and Investigation of PolyFermS In Vitro Continuous Fermentation Models Inoculated with Immobilized Fecal Microbiota Mimicking the Elderly Colon. PLoS ONE, 2015, 10, e0142793.	1.1	59
42	753 Identification of a Gut Microbial Signature Linked to Severity of Irritable Bowel Syndrome. Gastroenterology, 2015, 148, S-142-S-143.	0.6	0
43	Fate, activity, and impact of ingested bacteria within the human gut microbiota. Trends in Microbiology, 2015, 23, 354-366.	3.5	474
44	Host lysozyme-mediated lysis of <i>Lactococcus lactis</i> facilitates delivery of colitis-attenuating superoxide dismutase to inflamed colons. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7803-7808.	3.3	99
45	Modulation of gut microbiota during probiotic-mediated attenuation of metabolic syndrome in high fat diet-fed mice. ISME Journal, 2015, 9, 1-15.	4.4	703
46	Fermented Dairy Products Modulate Citrobacter rodentium-Induced Colonic Hyperplasia. Journal of Infectious Diseases, 2014, 210, 1029-1041.	1.9	31
47	375 Human Gut Microbial Clusters Correlate With Anatomical Brain Signatures: A Pilot Study. Gastroenterology, 2014, 146, S-82.	0.6	0
48	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	9.4	909
49	375 Human gut microbial clusters correlate with anatomical brain signatures: a pilot study. Gastrointestinal Endoscopy, 2014, 79, AB402.	0.5	0
50	Transient inflammatory-like state and microbial dysbiosis are pivotal in establishment of mucosal homeostasis during colonisation of germ-free mice. Beneficial Microbes, 2014, 5, 67-77.	1.0	64
51	The gut microbiota elicits a profound metabolic reorientation in the mouse jejunal mucosa during conventionalisation. Gut, 2013, 62, 1306-1314.	6.1	118
52	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	13.7	3,641
53	Gut bacteria-host metabolic interplay during conventionalisation of the mouse germfree colon. ISME Journal, 2013, 7, 743-755.	4.4	84
54	Cross-talk between <i>Akkermansia muciniphila</i> and intestinal epithelium controls diet-induced obesity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9066-9071.	3.3	3,474

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55	Laxative treatment with polyethylene glycol decreases microbial primary bile salt dehydroxylation and lipid metabolism in the intestine of rats. <i>American Journal of Physiology - Renal Physiology</i> , 2013, 305, G474-G482.	1.6	10
56	Saturated fat stimulates obesity and hepatic steatosis and affects gut microbiota composition by an enhanced overflow of dietary fat to the distal intestine. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, G589-G599.	1.6	330
57	Epithelial-microbial crosstalk in polymeric Ig receptor deficient mice. <i>European Journal of Immunology</i> , 2012, 42, 2959-2970.	1.6	102
58	Transfer of Intestinal Microbiota From Lean Donors Increases Insulin Sensitivity in Individuals With Metabolic Syndrome. <i>Gastroenterology</i> , 2012, 143, 913-916.e7.	0.6	2,287
59	Temporal and spatial interplay of microbiota and intestinal mucosa drive establishment of immune homeostasis in conventionalized mice. <i>Mucosal Immunology</i> , 2012, 5, 567-579.	2.7	201
60	Dietary Heme Alters Microbiota and Mucosa of Mouse Colon without Functional Changes in Host-Microbe Cross-Talk. <i>PLoS ONE</i> , 2012, 7, e49868.	1.1	99
61	Arabinoxylans and inulin differentially modulate the mucosal and luminal gut microbiota and mucin-degradation in humanized rats. <i>Environmental Microbiology</i> , 2011, 13, 2667-2680.	1.8	215
62	Responses of Gut Microbiota and Glucose and Lipid Metabolism to Prebiotics in Genetic Obese and Diet-Induced Leptin-Resistant Mice. <i>Diabetes</i> , 2011, 60, 2775-2786.	0.3	881
63	Impact of microbial transformation of food on health—from fermented foods to fermentation in the gastro-intestinal tract. <i>Current Opinion in Biotechnology</i> , 2011, 22, 211-219.	3.3	104
64	Modulation of Mucosal Immune Response, Tolerance, and Proliferation in Mice Colonized by the Mucin-Degrader <i>Akkermansia muciniphila</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 166.	1.5	438
65	Altered Gut Microbiota and Endocannabinoid System Tone in Obese and Diabetic Leptin-Resistant Mice: Impact on Apelin Regulation in Adipose Tissue. <i>Frontiers in Microbiology</i> , 2011, 2, 149.	1.5	267
66	The Genome of <i>Akkermansia muciniphila</i> , a Dedicated Intestinal Mucin Degrader, and Its Use in Exploring Intestinal Metagenomes. <i>PLoS ONE</i> , 2011, 6, e16876.	1.1	328
67	Mucin-bacterial interactions in the human oral cavity and digestive tract. <i>Gut Microbes</i> , 2010, 1, 254-268.	4.3	421
68	Microbial Community Development in a Dynamic Gut Model Is Reproducible, Colon Region Specific, and Selective for <i>Bacteroidetes</i> and <i>Clostridium</i> Cluster IX. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5237-5246.	1.4	272
69	Phylum XXII. Lentisphaerae Cho, Vergin, Morris and Giovannoni 2004a, 1005VP (Effective publication:) Tj ETQq1 1 0.784314 µgBT /Over		
70	The Mucin Degrader <i>Akkermansia muciniphila</i> Is an Abundant Resident of the Human Intestinal Tract. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1646-1648.	1.4	517
71	Intestinal Integrity and <i>Akkermansia muciniphila</i> , a Mucin-Degrading Member of the Intestinal Microbiota Present in Infants, Adults, and the Elderly. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7767-7770.	1.4	540
72	Prebiotics and other microbial substrates for gut functionality. <i>Current Opinion in Biotechnology</i> , 2005, 16, 212-217.	3.3	148

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73	The intestinal mucosa as a habitat of the gut microbiota and a rational target for probiotic functionality and safety. <i>Microbial Ecology in Health and Disease</i> , 2004, 16, 137-144.	3.8	11
74	<i>Akkermansia muciniphila</i> gen. nov., sp. nov., a human intestinal mucin-degrading bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1469-1476.	0.8	1,566
75	Microbial Functionality in the Human Gastrointestinal Tract. <i>Microbes and Environments</i> , 2004, 19, 276-280.	0.7	3
76	The Intestinal Mucosa as a Habitat of the Gut Microbiota and a Rational Target for Probiotic Functionality and Safety. <i>Microbial Ecology in Health and Disease</i> , 2004, 16, .	3.8	1