

Marion c Leclerc

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

28,297
citations

125106

35
h-index

162838

57
g-index

65
all docs

65
docs citations

65
times ranked

33455
citing authors

#	ARTICLE	IF	CITATIONS
1	Interplay Between Exercise and Gut Microbiome in the Context of Human Health and Performance. <i>Frontiers in Nutrition</i> , 2021, 8, 637010.	1.6	109
2	Parasites and diet as main drivers of the Malagasy gut microbiome richness and function. <i>Scientific Reports</i> , 2021, 11, 17630.	1.6	3
3	Nitric Oxide Impacts Human Gut Microbiota Diversity and Functionalities. <i>MSystems</i> , 2021, 6, e0055821.	1.7	13
4	FiberGrowth Pipeline: A Framework Toward Predicting Fiber-Specific Growth From Human Gut Bacteroidetes Genomes. <i>Frontiers in Microbiology</i> , 2021, 12, 632567.	1.5	1
5	Comparison of fecal sample collection methods for microbial analysis embedded within colorectal cancer screening programs. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, , cebp.0188.2021.	1.1	10
6	Investigating host-microbiome interactions by droplet based microfluidics. <i>Microbiome</i> , 2020, 8, 141.	4.9	33
7	Elevated serum ceramides are linked with obesity-associated gut dysbiosis and impaired glucose metabolism. <i>Metabolomics</i> , 2019, 15, 140.	1.4	26
8	Investigating Host Microbiota Relationships Through Functional Metagenomics. <i>Frontiers in Microbiology</i> , 2019, 10, 1286.	1.5	13
9	Dietary Protein Intake Level Modulates Mucosal Healing and Mucosa-Adherent Microbiota in Mouse Model of Colitis. <i>Nutrients</i> , 2019, 11, 514.	1.7	25
10	Modulation of the microbiota by oral antibiotics treats immunoglobulin A nephropathy in humanized mice. <i>Nephrology Dialysis Transplantation</i> , 2019, 34, 1135-1144.	0.4	59
11	Mucosal healing progression after acute colitis in mice. <i>World Journal of Gastroenterology</i> , 2019, 25, 3572-3589.	1.4	21
12	Lipo-Protein Emulsion Structure in the Diet Affects Protein Digestion Kinetics, Intestinal Mucosa Parameters and Microbiota Composition. <i>Molecular Nutrition and Food Research</i> , 2018, 62, 1700570.	1.5	16
13	A Data Integration Multi-Omics Approach to Study Calorie Restriction-Induced Changes in Insulin Sensitivity. <i>Frontiers in Physiology</i> , 2018, 9, 1958.	1.3	39
14	A fibrolytic potential in the human ileum mucosal microbiota revealed by functional metagenomic. <i>Scientific Reports</i> , 2017, 7, 40248.	1.6	38
15	Structure of protein emulsion in food impacts intestinal microbiota, caecal luminal content composition and distal intestine characteristics in rats. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700078.	1.5	12
16	Human Gut Metagenomics: Success and Limits of the Activity-Based Approaches. , 2017, , 161-178.		0
17	Gut Microbiota Diversity and Human Diseases: Should We Reintroduce Key Predators in Our Ecosystem?. <i>Frontiers in Microbiology</i> , 2016, 7, 455.	1.5	438
18	Respective Roles of Hematopoietic and Nonhematopoietic Nod2 on the Gut Microbiota and Mucosal Homeostasis. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 763-773.	0.9	24

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19	A Constrained NMF Approach to Analyze Quantitative Metagenomic Data * *Sebastien Raguideau is funded by a PhD grant of the Meta-omics and Microbial Ecosystems (MME) program of INRA.. IFAC-PapersOnLine, 2016, 49, 71-76.	0.5	0
20	Structural robustness of the gut mucosal microbiota is associated with Crohn's disease remission after surgery. Gut, 2016, 65, 954-962.	6.1	106
21	<i>Akkermansia muciniphila</i> and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. Gut, 2016, 65, 426-436.	6.1	1,379
22	Inferring Aggregated Functional Traits from Metagenomic Data Using Constrained Non-negative Matrix Factorization: Application to Fiber Degradation in the Human Gut Microbiota. PLoS Computational Biology, 2016, 12, e1005252.	1.5	16
23	Gut microbiota richness promotes its stability upon increased dietary fibre intake in healthy adults. Environmental Microbiology, 2015, 17, 4954-4964.	1.8	279
24	Identification of Metabolic Signatures Linked to Anti-Inflammatory Effects of <i>Faecalibacterium prausnitzii</i> . MBio, 2015, 6, .	1.8	206
25	Tu1746 <i>Faecalibacterium prausnitzii</i> Provides Host Beneficial Metabolic Profile During Inflammation. Gastroenterology, 2014, 146, S-832.	0.6	0
26	Bacteriophages: an underestimated role in human and animal health?. Frontiers in Cellular and Infection Microbiology, 2014, 4, 39.	1.8	142
27	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	13.7	3,641
28	Dietary intervention impact on gut microbial gene richness. Nature, 2013, 500, 585-588.	13.7	1,485
29	A metagenomic insight into our gut's microbiome. Gut, 2013, 62, 146-158.	6.1	302
30	Functional Metagenomics Reveals Novel Pathways of Prebiotic Breakdown by Human Gut Bacteria. PLoS ONE, 2013, 8, e72766.	1.1	78
31	Altered gut microbiota composition in immune-impaired <i>Nod2</i> ^{-/-} mice. Gut, 2012, 61, 634-635.	6.1	80
32	Kinetic modelling of lactate utilization and butyrate production by key human colonic bacterial species. FEMS Microbiology Ecology, 2011, 76, 615-624.	1.3	129
33	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	13.7	5,800
34	Highlighting new phylogenetic specificities of Crohn's disease microbiota. Inflammatory Bowel Diseases, 2011, 17, 185-192.	0.9	235
35	A metagenomic β -glucuronidase uncovers a core adaptive function of the human intestinal microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4539-4546.	3.3	173
36	Dysbiosis of fecal microbiota in Crohn's disease patients as revealed by a custom phylogenetic microarray. Inflammatory Bowel Diseases, 2010, 16, 2034-2042.	0.9	314

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37	Mathematical modelling of carbohydrate degradation by human colonic microbiota. <i>Journal of Theoretical Biology</i> , 2010, 266, 189-201.	0.8	66
38	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
39	Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. <i>Genome Research</i> , 2010, 20, 1605-1612.	2.4	228
40	Potential role of the intestinal microbiota of the mother in neonatal immune education. <i>Proceedings of the Nutrition Society</i> , 2010, 69, 407-415.	0.4	158
41	Towards the human intestinal microbiota phylogenetic core. <i>Environmental Microbiology</i> , 2009, 11, 2574-2584.	1.8	773
42	Dysbiosis in inflammatory bowel disease: a role for bacteriophages?. <i>Gut</i> , 2008, 57, 424-425.	6.1	206
43	Modelling and identification of in vitro homoacetogenesis by human-colon bacteria. , 2008, , .		4
44	Mycolactone Diffuses from <i>Mycobacterium ulcerans</i> â€“Infected Tissues and Targets Mononuclear Cells in Peripheral Blood and Lymphoid Organs. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e325.	1.3	80
45	Bacterial Imprinting of the Neonatal Immune System: Lessons From Maternal Cells?. <i>Pediatrics</i> , 2007, 119, e724-e732.	1.0	542
46	Development of High-Throughput Phenotyping of Metagenomic Clones from the Human Gut Microbiome for Modulation of Eukaryotic Cell Growth. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3734-3737.	1.4	56
47	Characterization of the xylan-degrading microbial community from human faeces. <i>FEMS Microbiology Ecology</i> , 2007, 61, 121-131.	1.3	127
48	<i>Bacteroides</i> sp. Strain D8, the First Cholesterol-Reducing Bacterium Isolated from Human Feces. <i>Applied and Environmental Microbiology</i> , 2007, 73, 5742-5749.	1.4	104
49	¹³ C-NMR study of glucose and pyruvate catabolism in four acetogenic species isolated from the human colon. <i>FEMS Microbiology Letters</i> , 2006, 146, 199-204.	0.7	12
50	Diversity of the archaeal community in 44 anaerobic digesters as determined by single strand conformation polymorphism analysis and 16S rDNA sequencing. <i>Environmental Microbiology</i> , 2004, 6, 809-819.	1.8	168
51	A molecular method to study population and activity dynamics in anaerobic digestors. <i>Water Science and Technology</i> , 2001, 43, 51-57.	1.2	15
52	Single strand conformation polymorphism monitoring of 16S rDNA Archaea during start-up of an anaerobic digester. <i>FEMS Microbiology Ecology</i> , 2001, 34, 213-220.	1.3	68
53	Proteorhodopsin phototrophy in the ocean. <i>Nature</i> , 2001, 411, 786-789.	13.7	740
54	Effect of Yeast Extract on Growth and Metabolism of H ₂ -Utilizing Acetogenic Bacteria from the Human Colon. <i>Current Microbiology</i> , 1998, 37, 166-171.	1.0	15

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55	H ₂ /CO ₂ Metabolism in Acetogenic Bacteria Isolated From the Human Colon. <i>Anaerobe</i> , 1997, 3, 307-315.	1.0	47
56	Characteristics of H ₂ /CO ₂ metabolism in acetogenic bacteria from the human colon. <i>Reproduction, Nutrition, Development</i> , 1997, 37, 68-69.	1.9	0
57	<i>Ruminococcus hydrogenotrophicus</i> sp. nov., a new H ₂ /CO ₂ -utilizing acetogenic bacterium isolated from human feces. <i>Archives of Microbiology</i> , 1996, 166, 176-183.	1.0	140
58	Diversity of H ₂ /CO ₂ -Utilizing Acetogenic Bacteria from Feces of Non-Methane-Producing Humans. <i>Current Microbiology</i> , 1996, 33, 94-99.	1.0	35
59	Plasmids and phase variation in <i>Xenorhabdus</i> spp. <i>Applied and Environmental Microbiology</i> , 1991, 57, 2597-2601.	1.4	25
60	Single strand conformation polymorphism monitoring of 16S rDNA Archaea during start-up of an anaerobic digester. , 0, .		5