M Andrea Azcarate-Peril

List of Publications by Year
in descending order

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121 papers	7,515 citations	50276 46 h-index	56724 83 g-index
129 all docs	129 docs citations	129 times ranked	10055 citing authors

#	Article	IF	Citations
1	Complete genome sequence of the probiotic lactic acid bacteriumLactobacillus acidophilusNCFM. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3906-3912.	7.1	565
2	Fusobacterium Is Associated with Colorectal Adenomas. PLoS ONE, 2013, 8, e53653.	2.5	459
3	Infant Gut Microbiome Associated With CognitiveÂDevelopment. Biological Psychiatry, 2018, 83, 148-159.	1.3	362
4	Meta-analysis of effects of exclusive breastfeeding on infant gut microbiota across populations. Nature Communications, 2018, 9, 4169.	12.8	283
5	Shaping the Future of Probiotics and Prebiotics. Trends in Microbiology, 2021, 29, 667-685.	7.7	270
6	The intestinal microbiota, gastrointestinal environment and colorectal cancer: a putative role for probiotics in prevention of colorectal cancer?. American Journal of Physiology - Renal Physiology, 2011, 301, G401-G424.	3.4	201
7	A comparison of sequencing platforms and bioinformatics pipelines for compositional analysis of the gut microbiome. BMC Microbiology, 2017, 17, 194.	3.3	196
8	Impact of short-chain galactooligosaccharides on the gut microbiome of lactose-intolerant individuals. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E367-E375.	7.1	193
9	Global analysis of carbohydrate utilization by Lactobacillus acidophilus using cDNA microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3816-3821.	7.1	185
10	Genomic features of lactic acid bacteria effecting bioprocessing and health. FEMS Microbiology Reviews, 2005, 29, 393-409.	8.6	176
11	Milk- and solid-feeding practices and daycare attendance are associated with differences in bacterial diversity, predominant communities, and metabolic and immune function of the infant gut microbiome. Frontiers in Cellular and Infection Microbiology, 2015, 5, 3.	3.9	174
12	A High-Throughput Organoid Microinjection Platform to Study Gastrointestinal Microbiota and Luminal Physiology. Cellular and Molecular Gastroenterology and Hepatology, 2018, 6, 301-319.	4.5	168
13	Use of the second-generation antipsychotic, risperidone, and secondary weight gain are associated with an altered gut microbiota in children. Translational Psychiatry, 2015, 5, e652-e652.	4.8	154
14	Analysis of the Genome Sequence ofLactobacillus gasseriATCC 33323 Reveals the Molecular Basis of an Autochthonous Intestinal Organism. Applied and Environmental Microbiology, 2008, 74, 4610-4625.	3.1	152
15	Emerging Technologies for Gut Microbiome Research. Trends in Microbiology, 2016, 24, 887-901.	7.7	148
16	Identification and Inactivation of Genetic Loci Involved with Lactobacillus acidophilus Acid Tolerance. Applied and Environmental Microbiology, 2004, 70, 5315-5322.	3.1	144
17	Characterization of a Novel Bile-Inducible Operon Encoding a Two-Component Regulatory System inLactobacillus acidophilus. Journal of Bacteriology, 2007, 189, 4624-4634.	2.2	143
18	Development and Application of a upp -Based Counterselective Gene Replacement System for the Study of the S-Layer Protein SlpX of Lactobacillus acidophilus NCFM. Applied and Environmental Microbiology, 2009, 75, 3093-3105.	3.1	141

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19	Intestinal Epithelial Sirtuin 1 Regulates Intestinal Inflammation During Aging in Mice by Altering the Intestinal Microbiota. Gastroenterology, 2017, 153, 772-786.	1.3	123
20	Targeted inhibition of gut bacterial Î²-glucuronidase activity enhances anticancer drug efficacy. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7374-7381.	7.1	121
21	Microarray Analysis of a Two-Component Regulatory System Involved in Acid Resistance and Proteolytic Activity in Lactobacillus acidophilus. Applied and Environmental Microbiology, 2005, 71, 5794-5804.	3.1	120
22	A preliminary examination of gut microbiota, sleep, and cognitive flexibility in healthy older adults. Sleep Medicine, 2017, 38, 104-107.	1.6	116
23	Diet Complexity and Estrogen Receptor Î² Status Affect the Composition of the Murine Intestinal Microbiota. Applied and Environmental Microbiology, 2013, 79, 5763-5773.	3.1	115
24	Genomic features of lactic acid bacteria effecting bioprocessing and health. FEMS Microbiology Reviews, 2005, 29, 393-409.	8.6	101
25	Inter-niche and inter-individual variation in gut microbial community assessment using stool, rectal swab, and mucosal samples. Scientific Reports, 2018, 8, 4139.	3.3	100
26	Gut microbiome compositional and functional differences between tumor and non-tumor adjacent tissues from cohorts from the US and Spain. Gut Microbes, 2015, 6, 161-172.	9.8	98
27	Galacto-oligosaccharides and colorectal cancer: Feeding our intestinal probiome. Journal of Functional Foods, 2015, 12, 92-108.	3.4	92
28	Gut microbiome and brain functional connectivity in infants-a preliminary study focusing on the amygdala. Psychopharmacology, 2019, 236, 1641-1651.	3.1	91
29	Comparison of Bacterial Community Composition of Primary and Persistent Endodontic Infections Using Pyrosequencing. Journal of Endodontics, 2015, 41, 1226-1233.	3.1	86
30	High purity galacto-oligosaccharides enhance specific Bifidobacterium species and their metabolic activity in the mouse gut microbiome. Beneficial Microbes, 2016, 7, 247-264.	2.4	85
31	Preliminary Evidence for an Association Between the Composition of the Gut Microbiome and Cognitive Function in Neurologically Healthy Older Adults. Journal of the International Neuropsychological Society, 2017, 23, 700-705.	1.8	77
32	Transcriptional and Functional Analysis of Oxalyl-Coenzyme A (CoA) Decarboxylase and Formyl-CoA Transferase Genes from Lactobacillus acidophilus. Applied and Environmental Microbiology, 2006, 72, 1891-1899.	3.1	75
33	Role of Antioxidant Enzymes in Bacterial Resistance to Organic Acids. Applied and Environmental Microbiology, 2010, 76, 2747-2753.	3.1	75
34	Space Environmental Factor Impacts upon Murine Colon Microbiota and Mucosal Homeostasis. PLoS ONE, 2015, 10, e0125792.	2.5	73
35	Role of autoinducer-2 on the adhesion ability ofLactobacillus acidophilus. Journal of Applied Microbiology, 2009, 107, 269-279.	3.1	70
36	Gut microbiome of Moroccan colorectal cancer patients. Medical Microbiology and Immunology, 2018, 207, 211-225.	4.8	68

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37	Polyphenol-rich sorghum brans alter colon microbiota and impact species diversity and species richness after multiple bouts of dextran sodium sulfate-induced colitis. FEMS Microbiology Ecology, 2015, 91, .	2.7	66
38	Osteoarthritis induced by destabilization of the medial meniscus is reduced in germ-free mice. Osteoarthritis and Cartilage, 2018, 26, 1098-1109.	1.3	64
39	Acute necrotizing enterocolitis of preterm piglets is characterized by dysbiosis of ileal mucosa-associated bacteria. Gut Microbes, 2011, 2, 234-243.	9.8	61
40	Fusobacterium spp. and colorectal cancer: cause or consequence?. Trends in Microbiology, 2013, 21, 506-508.	7.7	59
41	An Attenuated Salmonella enterica Serovar Typhimurium Strain and Galacto-Oligosaccharides Accelerate Clearance of Salmonella Infections in Poultry through Modifications to the Gut Microbiome. Applied and Environmental Microbiology, 2018, 84, .	3.1	59
42	Modeling human enteric dysbiosis and rotavirus immunity in gnotobiotic pigs. Gut Pathogens, 2016, 8, 51.	3.4	56
43	The oral bacterial microbiome of occlusal surfaces in children and its association with diet and caries. PLoS ONE, 2017, 12, e0180621.	2.5	55
44	Impact of Ileocecal Resection and Concomitant Antibiotics on the Microbiome of the Murine Jejunum and Colon. PLoS ONE, 2013, 8, e73140.	2.5	54
45	Temporal gene expression and probiotic attributes of Lactobacillus acidophilus during growth in milk. Journal of Dairy Science, 2009, 92, 870-886.	3.4	53
46	Maternal Gut Microbiome Biodiversity in Pregnancy. American Journal of Perinatology, 2018, 35, 024-030.	1.4	51
47	Construction of vectors for inducible and constitutive gene expression in Lactobacillus. Microbial Biotechnology, 2011, 4, 357-367.	4.2	50
48	The Salivary Microbiome and Oral Cancer Risk: A Pilot Study in Fanconi Anemia. Journal of Dental Research, 2017, 96, 292-299.	5.2	50
49	Shaping functional gut microbiota using dietary bioactives to reduce colon cancer risk. Seminars in Cancer Biology, 2017, 46, 191-204.	9.6	45
50	Reassessment of the succession of lactic acid bacteria in commercial cucumber fermentations and physiological and genomic features associated with their dominance. Food Microbiology, 2017, 63, 217-227.	4.2	43
51	The pleiotropic effects of prebiotic galacto-oligosaccharides on the aging gut. Microbiome, 2021, 9, 31.	11.1	43
52	Bacterial Ecology of Fermented Cucumber Rising pH Spoilage as Determined by Nonculture€Based Methods. Journal of Food Science, 2016, 81, M121-9.	3.1	41
53	Oral colostrum priming shortens hospitalization without changing the immunomicrobial milieu. Journal of Perinatology, 2017, 37, 36-41.	2.0	37
54	Prebiotics for Lactose Intolerance: Variability in Galacto-Oligosaccharide Utilization by Intestinal Lactobacillus rhamnosus. Nutrients, 2018, 10, 1517.	4.1	36

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55	Infant gut microbiome composition is associated with non-social fear behavior in a pilot study. Nature Communications, 2021, 12, 3294.	12.8	36
56	Association between Gut Microbiome Composition and Rotavirus Vaccine Response among Nicaraguan Infants. American Journal of Tropical Medicine and Hygiene, 2020, 102, 213-219.	1.4	35
57	Genome Sequence and Characteristics of Lrm1, a Prophage from Industrial Lactobacillus rhamnosus Strain M1. Applied and Environmental Microbiology, 2008, 74, 4601-4609.	3.1	34
58	Assessment of the non-lactic acid bacteria microbiota in fresh cucumbers and commercially fermented cucumber pickles brined with 6% NaCl. Food Microbiology, 2019, 77, 10-20.	4.2	34
59	Randomized Clinical Trial Examining the Impact of Lactobacillus rhamnosus GG Probiotic Supplementation on Cognitive Functioning in Middle-aged and Older Adults . Neuropsychiatric Disease and Treatment, 2020, Volume 16, 2765-2777.	2.2	33
60	Gut Microbiome Composition in Young Nicaraguan Children During Diarrhea Episodes and Recovery. American Journal of Tropical Medicine and Hygiene, 2015, 93, 1187-1193.	1.4	30
61	Influence of the Dairy Environment on Gene Expression and Substrate Utilization in Lactic Acid Bacteria1, ,. Journal of Nutrition, 2007, 137, 748S-750S.	2.9	29
62	Marker-free chromosomal integration of the manganese superoxide dismutase gene (sodA) fromStreptococcus thermophilusintoLactobacillus gasseri. FEMS Microbiology Letters, 2005, 246, 91-101.	1.8	28
63	Highly diverse anaerobe-predominant vaginal microbiota among HIV-infected pregnant women in Zambia. PLoS ONE, 2019, 14, e0223128.	2.5	28
64	Intra-species Genomic and Physiological Variability Impact Stress Resistance in Strains of Probiotic Potential. Frontiers in Microbiology, 2018, 9, 242.	3.5	27
65	Fecal metabolomics reveals products of dysregulated proteolysis and altered microbial metabolism in obesity-related osteoarthritis. Osteoarthritis and Cartilage, 2022, 30, 81-91.	1.3	25
66	Exposures Related to House Dust Microbiota in a U.S. Farming Population. Environmental Health Perspectives, 2018, 126, 067001.	6.0	23
67	Maternal precarity and HPA axis functioning shape infant gut microbiota and HPA axis development in humans. PLoS ONE, 2021, 16, e0251782.	2.5	23
68	House dust microbiota in relation to adult asthma and atopy in a US farming population. Journal of Allergy and Clinical Immunology, 2021, 147, 910-920.	2.9	21
69	A preliminary study of gut microbiome variation and HPA axis reactivity in healthy infants. Psychoneuroendocrinology, 2021, 124, 105046.	2.7	21
70	Association of Increased Serum Lipopolysaccharide, But Not Microbial Dysbiosis, With <scp>Obesityâ€Related</scp> Osteoarthritis. Arthritis and Rheumatology, 2022, 74, 227-236.	5.6	21
71	Longitudinal changes during pregnancy in gut microbiota and methylmercury biomarkers, and reversal of microbe-exposure correlations. Environmental Research, 2019, 172, 700-712.	7.5	20
72	Cohort Profile: ZOE 2.0â€"A Community-Based Genetic Epidemiologic Study of Early Childhood Oral Health. International Journal of Environmental Research and Public Health, 2020, 17, 8056.	2.6	20

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73	Fecal IgA, Antigen Absorption, and Gut Microbiome Composition Are Associated With Food Antigen Sensitization in Genetically Susceptible Mice. Frontiers in Immunology, 2020, 11, 599637.	4.8	20
74	On the robustness of inference of association with the gut microbiota in stool, rectal swab and mucosal tissue samples. Scientific Reports, 2021, 11, 14828.	3.3	18
75	Comparative phenotypic analysis and genome sequence of Clostridium beijerinckii SA-1, an offspring of NCIMB 8052. Microbiology (United Kingdom), 2013, 159, 2558-2570.	1.8	17
76	A randomized clinical trial examining the impact of LGG probiotic supplementation on psychological status in middle-aged and older adults. Contemporary Clinical Trials Communications, 2018, 12, 192-197.	1.1	17
77	The Supragingival Biofilm in Early Childhood Caries: Clinical and Laboratory Protocols and Bioinformatics Pipelines Supporting Metagenomics, Metatranscriptomics, and Metabolomics Studies of the Oral Microbiome. Methods in Molecular Biology, 2019, 1922, 525-548.	0.9	17
78	Characterization of the microbial diversity in yacon spontaneous fermentation at 20Â°C. International Journal of Food Microbiology, 2015, 203, 35-40.	4.7	15
79	Enhanced GII.4 human norovirus infection in gnotobiotic pigs transplanted with a human gut microbiota. Journal of General Virology, 2019, 100, 1530-1540.	2.9	15
80	Use of high throughput amplicon sequencing and ethidium monoazide dye to track microbiota changes in an equol-producing menopausal woman receiving a long-term isoflavones treatment. AIMS Microbiology, 2019, 5, 102-116.	2.2	15
81	The bacterial microbiome and metabolome in caries progression and arrest. Journal of Oral Microbiology, 2021, 13, 1886748.	2.7	14
82	Heterologous Expression of a Bioactive Î²-Hexosyltransferase, an Enzyme Producer of Prebiotics, from Sporobolomyces singularis. Applied and Environmental Microbiology, 2013, 79, 1241-1249.	3.1	13
83	Lactobacillus rhamnosus GG and HbA1c in middle age and older adults without type 2 diabetes mellitus: A preliminary randomized study. Diabetes and Metabolic Syndrome: Clinical Research and Reviews, 2020, 14, 907-909.	3.6	13
84	A double-blind, 377-subject randomized study identifies Ruminococcus, Coprococcus, Christensenella, and Collinsella as long-term potential key players in the modulation of the gut microbiome of lactose intolerant individuals by galacto-oligosaccharides. Gut Microbes, 2021, 13, 1957536.	9.8	12
85	Genome Sequences of Potential Probiotic Lactobacillus rhamnosus Isolates from Human Infants. Genome Announcements, 2017, 5, .	0.8	9
86	Dysbiosis of fecal microbiota in cats with naturally occurring and experimentally induced Tritrichomonas foetus infection. PLoS ONE, 2021, 16, e0246957.	2.5	9
87	Safety and Modulatory Effects of Humanized Galacto-Oligosaccharides on the Gut Microbiome. Frontiers in Nutrition, 2021, 8, 640100.	3.7	9
88	Sequence analysis of pLBB1, a cryptic plasmid from Lactobacillus delbrueckii subsp. bulgaricus. Canadian Journal of Microbiology, 2002, 48, 105-112.	1.7	8
89	Galacto-Oligosaccharide RP-G28 Improves Multiple Clinical Outcomes in Lactose-Intolerant Patients. Nutrients, 2020, 12, 1058.	4.1	8
90	Methods for Plasmid and Genomic DNA Isolation from Lactobacilli. , 2001, , 135-139.		7

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91	Impact of Dietary Isoflavone Supplementation on the Fecal Microbiota and Its Metabolites in Postmenopausal Women. International Journal of Environmental Research and Public Health, 2021, 18, 7939.	2.6	7
92	Tu1967 Microbiome Alterations of Lactose Intolerant Individuals in Response to Dietary Intervention With Galacto-Oligosaccharides May Help Negate Symptoms of Lactose Intolerance. Gastroenterology, 2013, 144, S-893.	1.3	6
93	Magnesium and imidazole propionate. Clinical Nutrition ESPEN, 2021, 41, 436-438.	1.2	5
94	Deoxyribonuclease activities in Lactobacillus delbrueckii. Microbiological Research, 2000, 155, 101-106.	5.3	3
95	Genomic Perspectives on Probiotic Lactic Acid Bacteria. Bioscience and Microflora, 2005, 24, 31-33.	0.5	3
96	Is Fluorescence Technology a Promising Tool for Detecting Infected Dentin in Deep Carious Lesions?. Caries Research, 2020, 54, 205-217.	2.0	3
97	Genomics of Lactic Acid Bacteria: The Post-Genomics Challenge-From Sequence to Function. , 0, , 35-56.		3
98	427: Maternal antibiotic exposure, diet, and milk microbiome diversity. American Journal of Obstetrics and Gynecology, 2014, 210, S216.	1.3	2
99	The effects of medication adherence on study outcomes in randomized clinical trials: A role for cognitive dysfunction?. Applied Neuropsychology Adult, 2021, 28, 641-646.	1.2	2
100	Accelerated Biodegradation of the Agrochemical Ametoctradin by Soil-Derived Microbial Consortia. Frontiers in Microbiology, 2020, 11, 1898.	3.5	2
101	742. Gut Microbiome and Brain Functional Connectivity in Infants: A Preliminary Study Focusing on the Amygdala. Biological Psychiatry, 2017, 81, S300-S301.	1.3	1
102	Genome Sequence of Citrobacter freundii AMC0703, Isolated from the Intestinal Lumen of an 11-Year-Old Organ Donor. Microbiology Resource Announcements, 2020, 9, .	0.6	1
103	Hologenomics: The Interaction Between Host, Microbiome and Diet. , 2021, , 212-228.		1
104	Food antigen sensitization in genetically-susceptible mice is influenced by fecal IgA, antigen absorption, and gut microbiome composition. Journal of Allergy and Clinical Immunology, 2021, 147, AB142.	2.9	1
105	Beneficial Modulation of the Gut Microbiome: Probiotics and Prebiotics. , 2019, , 309-324.		1
106	Novel sorghum brans containing bioactive compounds alter colon microbiota in response to a DSSâ€induced chronic inflammatory state. FASEB Journal, 2013, 27, 247.2.	0.5	1
107	Lumen and mucosa-associatedLactobacillus rhamnosusfrom the intestinal tract of organ donors. Gut Microbiome, 2020, 1, .	3.2	1
108	Use of high throughput amplicon sequencing and ethidium monoazide dye to track microbiota changes in an equol-producing menopausal woman receiving a long-term isoflavones treatment. AIMS Microbiology, 2019, 5, 102-116.	2.2	1

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109	Problems with Genetically Modified Foods. , 2001, , 481-484.		0
110	W1839 Radiation Induces a Dysbiosis of the Murine Fecal Microbiota. Gastroenterology, 2010, 138, S-750-S-751.	1.3	0
111	21: Maternal gut microbiome, obesity and gestational weight gain. American Journal of Obstetrics and Gynecology, 2016, 215, S836.	1.3	0
112	Sa1986 Impact of Short-Chain Galactooligosaccharides on the Gut Microbiome of Lactose Intolerant Individuals. Gastroenterology, 2016, 150, S424.	1.3	0
113	Su1194 MODIFICATION OF THE INFLAMMATION-RELATED PHENOTYPE OF THE TRPM7 GENOTYPE THROUGH THE GUT MICROBIOTA. Gastroenterology, 2020, 158, S-538.	1.3	0
114	Maternal and Infant Autonomic Nervous System Dysfunction. Biological Psychiatry, 2021, 89, S335.	1.3	0
115	Untargeted Fecal Metabolomics to Investigate the Role of the Microbiome and Nutrients in Osteoarthritis. Current Developments in Nutrition, 2021, 5, 47.	0.3	0
116	Abstract 2580: Synergistic effect of magnesium with metformin for the prevention of liver and colorectal cancer. , 2021, , .		0
117	Abstract 3266: Measurement and comparison of the gut microbial communities in fecal, rectal swab, and mucosal samples. , 2018, , .		0
118	A Novel Galacto-Oligosaccharide (RP-G28) Promotes Beneficial Adaptations to the Human Gut Microbiome in Patients With Lactose Intolerance. American Journal of Gastroenterology, 2018, 113, S268.	0.4	0
119	Giving Good Bacteria to Chickens to Keep Humans From Getting Sick. Frontiers for Young Minds, 0, 9, .	0.8	0
120	Draft Genome Sequence of Lactobacillus rhamnosus NCB 441, Isolated from Egyptian White Domiati Cheese. Microbiology Resource Announcements, 2020, 9, .	0.6	0
121	Genome Sequence of Eubacterium callanderi AMC0717, Isolated from the Colonic Mucosa of an 11-Year-Old Organ Donor. Microbiology Resource Announcements, 2020, 9, .	0.6	0