

Leonardo Mancabelli

List of Publications by Year in descending order

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104
papers

7,423
citations

71102

41
h-index

60623

81
g-index

105
all docs

105
docs citations

105
times ranked

8231
citing authors

#	ARTICLE	IF	CITATIONS
1	The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. <i>Microbiology and Molecular Biology Reviews</i> , 2017, 81, .	6.6	1,118
2	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	11.0	822
3	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	11.1	240
4	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	3.3	233
5	Gut microbiota composition and <i>Clostridium difficile</i> infection in hospitalized elderly individuals: a metagenomic study. <i>Scientific Reports</i> , 2016, 6, 25945.	3.3	207
6	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	3.1	203
7	Exploring Vertical Transmission of <i>Bifidobacteria</i> from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	3.1	191
8	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	191
9	Genomics of the Genus <i>Bifidobacterium</i> Reveals Species-Specific Adaptation to the Glycan-Rich Gut Environment. <i>Applied and Environmental Microbiology</i> , 2016, 82, 980-991.	3.1	165
10	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	3.8	153
11	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	3.8	152
12	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	3.3	148
13	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	3.3	146
14	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. <i>ISME Journal</i> , 2016, 10, 1656-1668.	9.8	145
15	<i>Bifidobacterium adolescentis</i> as a key member of the human gut microbiota in the production of GABA. <i>Scientific Reports</i> , 2020, 10, 14112.	3.3	140
16	Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. <i>Gut</i> , 2018, 67, 2097-2106.	12.1	130
17	<i>Bifidobacteria</i> and the infant gut: an example of co-evolution and natural selection. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 103-118.	5.4	129
18	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	3.3	123

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19	Investigation of the Evolutionary Development of the Genus Bifidobacterium by Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6383-6394.	3.1	117
20	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, ffw191.	2.7	102
21	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , 2017, 18, 568.	2.8	98
22	Evaluation of genetic diversity among strains of the human gut commensal Bifidobacterium adolescentis. <i>Scientific Reports</i> , 2016, 6, 23971.	3.3	97
23	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	9.8	96
24	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw049.	1.8	94
25	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	88
26	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. <i>Frontiers in Microbiology</i> , 2017, 8, 1749.	3.5	86
27	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . <i>Environmental Microbiology</i> , 2015, 17, 2515-2531.	3.8	80
28	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. <i>Frontiers in Microbiology</i> , 2015, 6, 1030.	3.5	74
29	Evaluation of bifidobacterial community composition in the human gut by means of a targeted amplicon sequencing (ITS) protocol. <i>FEMS Microbiology Ecology</i> , 2014, 90, n/a-n/a.	2.7	71
30	Prophages of the genus <i>Bifidobacterium</i> as modulating agents of the infant gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 2196-2213.	3.8	66
31	Evidence for cholesterol-lowering activity by Bifidobacterium bifidum PRL2010 through gut microbiota modulation. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6813-6829.	3.6	64
32	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. <i>Environmental Microbiology</i> , 2019, 21, 1331-1343.	3.8	60
33	The Gut-Muscle Axis in Older Subjects with Low Muscle Mass and Performance: A Proof of Concept Study Exploring Fecal Microbiota Composition and Function with Shotgun Metagenomics Sequencing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8946.	4.1	59
34	Phylogenetic classification of six novel species belonging to the genus Bifidobacterium comprising Bifidobacterium anseris sp. nov., Bifidobacterium criceti sp. nov., Bifidobacterium imperatoris sp. nov., Bifidobacterium italicum sp. nov., Bifidobacterium margollesii sp. nov. and Bifidobacterium parmae sp. nov.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 173-183.	2.8	58
35	Tracking the Taxonomy of the Genus Bifidobacterium Based on a Phylogenomic Approach. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	58
36	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. <i>Microbiome</i> , 2018, 6, 145.	11.1	54

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37	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017, 19, 4771-4783.	3.8	49
38	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host co-evolution. <i>Environmental Microbiology</i> , 2019, 21, 3683-3695.	3.8	47
39	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019, 10, 1286.	12.8	46
40	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , 2015, 6, 1331.	3.5	45
41	Ancient bacteria of the <i>Ä-tzi</i> ™s microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	11.1	45
42	Fecal microbiota profile in a group of myasthenia gravis patients. <i>Scientific Reports</i> , 2018, 8, 14384.	3.3	45
43	Characterization of the phylogenetic diversity of five novel species belonging to the genus <i>Bifidobacterium</i> : <i>Bifidobacterium castoris</i> sp. nov., <i>Bifidobacterium callimiconis</i> sp. nov., <i>Bifidobacterium goeldii</i> sp. nov., <i>Bifidobacterium samirii</i> sp. nov. and <i>Bifidobacterium dolichotidis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1288-1298.	1.7	45
44	Modulation of the <i>eps</i> -ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv056.	2.7	44
45	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. <i>Genome Biology</i> , 2019, 20, 96.	8.8	44
46	Unveiling Genomic Diversity among Members of the Species <i>Bifidobacterium pseudolongum</i> , a Widely Distributed Gut Commensal of the Animal Kingdom. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	44
47	Microbiota and Derived Parameters in Fecal Samples of Infants with Non-IgE Cow's Milk Protein Allergy under a Restricted Diet. <i>Nutrients</i> , 2018, 10, 1481.	4.1	40
48	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	3.8	35
49	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	33
50	<i>Bifidobacterium vansinderenii</i> sp. nov., isolated from faeces of emperor tamarin (<i>Saguinus imperator</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3987-3995.	1.7	32
51	The Sortase-Dependent Fimbriome of the Genus <i>Bifidobacterium</i> : Extracellular Structures with Potential To Modulate Microbe-Host Dialogue. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	31
52	Vaginotypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	3.8	30
53	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	30
54	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	3.0	30

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55	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	29
56	In Vitro Evaluation of Different Prebiotics on the Modulation of Gut Microbiota Composition and Function in Morbid Obese and Normal-Weight Subjects. <i>International Journal of Molecular Sciences</i> , 2020, 21, 906.	4.1	29
57	Early-Life Development of the Bifidobacterial Community in the Infant Gut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3382.	4.1	28
58	Next generation sequencing-based multigene panel for high throughput detection of food-borne pathogens. <i>International Journal of Food Microbiology</i> , 2017, 256, 20-29.	4.7	27
59	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. <i>International Journal of Food Microbiology</i> , 2019, 294, 1-9.	4.7	26
60	Five novel bifidobacterial species isolated from faeces of primates in two Czech zoos: <i>Bifidobacterium erythrocebi</i> sp. nov., <i>Bifidobacterium moraviense</i> sp. nov., <i>Bifidobacterium oedipodis</i> sp. nov., <i>Bifidobacterium olomucense</i> sp. nov. and <i>Bifidobacterium panos</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	26
61	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. <i>Microorganisms</i> , 2020, 8, 131.	3.6	26
62	Multi-omics Approaches To Decipher the Impact of Diet and Host Physiology on the Mammalian Gut Microbiome. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	24
63	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5755.	3.3	22
64	Characterization of the phylogenetic diversity of two novel species belonging to the genus <i>Bifidobacterium</i> : <i>Bifidobacterium cebidarum</i> sp. nov. and <i>Bifidobacterium leontopithecii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2288-2297.	1.7	22
65	Multi-population cohort meta-analysis of human intestinal microbiota in early life reveals the existence of infant community state types (ICSTs). <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2480-2493.	4.1	19
66	Impact of Extreme Obesity and Diet-Induced Weight Loss on the Fecal Metabolome and Gut Microbiota. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2000030.	3.3	19
67	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	3.6	18
68	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	3.8	17
69	Phylotype-Level Profiling of Lactobacilli in Highly Complex Environments by Means of an Internal Transcribed Spacer-Based Metagenomic Approach. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	16
70	<i>Bifidobacterium bifidum</i> PRL2010 alleviates intestinal ischemia/reperfusion injury. <i>PLoS ONE</i> , 2018, 13, e0202670.	2.5	16
71	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	16
72	Insights into teichoic acid biosynthesis by <i>Bifidobacterium bifidum</i> PRL2010. <i>FEMS Microbiology Letters</i> , 2015, 362, fnv141.	1.8	15

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73	Interaction Between Diet and Microbiota in the Pathophysiology of Alzheimer's Disease: Focus on Polyphenols and Dietary Fibers. <i>Journal of Alzheimer's Disease</i> , 2022, 86, 961-982.	2.6	15
74	Evaluation of Modulatory Activities of <i>Lactobacillus crispatus</i> Strains in the Context of the Vaginal Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, e0273321.	3.0	14
75	The Influence of Fungicide Treatments on Mycobiota of Grapes and Its Evolution during Fermentation Evaluated by Metagenomic and Culture-Dependent Methods. <i>Microorganisms</i> , 2019, 7, 114.	3.6	13
76	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	3.8	13
77	Donated Human Milk as a Determinant Factor for the Gut Bifidobacterial Ecology in Premature Babies. <i>Microorganisms</i> , 2020, 8, 760.	3.6	13
78	Probiogenomics Analysis of 97 <i>Lactobacillus crispatus</i> Strains as a Tool for the Identification of Promising Next-Generation Probiotics. <i>Microorganisms</i> , 2021, 9, 73.	3.6	13
79	A genome-based identification approach for members of the genus <i>Bifidobacterium</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	12
80	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	11
81	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	3.5	11
82	Modulation of the Bifidobacterial Communities of the Dog Microbiota by Zeolite. <i>Frontiers in Microbiology</i> , 2016, 7, 1491.	3.5	10
83	A microbiome reality check: limitations of <i>in silico</i> -based metagenomic approaches to study complex bacterial communities. <i>Environmental Microbiology Reports</i> , 2019, 11, 840-847.	2.4	10
84	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. <i>Microorganisms</i> , 2019, 7, 535.	3.6	10
85	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. <i>Microorganisms</i> , 2019, 7, 293.	3.6	10
86	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	9
87	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
88	Investigation of the Ecological Link between Recurrent Microbial Human Gut Communities and Physical Activity. <i>Microbiology Spectrum</i> , 2022, 10, e0042022.	3.0	9
89	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. <i>Microorganisms</i> , 2019, 7, 599.	3.6	8
90	Assessing the Genomic Variability of <i>Gardnerella vaginalis</i> through Comparative Genomic Analyses: Evolutionary and Ecological Implications. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	8

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91	Comparative Genome Analyses of <i>Lactobacillus crispatus</i> Isolates from Different Ecological Niches Reveal an Adaptation of This Species to the Human Vaginal Environment. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	8
92	Effect of Intrapartum Antibiotics Prophylaxis on the Bifidobacterial Establishment within the Neonatal Gut. <i>Microorganisms</i> , 2021, 9, 1867.	3.6	8
93	Free DNA and Metagenomics Analyses: Evaluation of Free DNA Inactivation Protocols for Shotgun Metagenomics Analysis of Human Biological Matrices. <i>Frontiers in Microbiology</i> , 2021, 12, 749373.	3.5	7
94	Exploring the effects of COLOSTRONONI on the mammalian gut microbiota composition. <i>PLoS ONE</i> , 2019, 14, e0217609.	2.5	6
95	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	2.7	6
96	Genetic insights into the dark matter of the mammalian gut microbiota through targeted genome reconstruction. <i>Environmental Microbiology</i> , 2021, 23, 3294-3305.	3.8	5
97	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. <i>Environmental Microbiology</i> , 2022, , .	3.8	5
98	Exploring the Ecological Effects of Naturally Antibiotic-Insensitive Bifidobacteria in the Recovery of the Resilience of the Gut Microbiota during and after Antibiotic Treatment. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	3.1	4
99	Disclosing the Genomic Diversity among Members of the <i>Bifidobacterium</i> Genus of Canine and Feline Origin with Respect to Those from Human. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0203821.	3.1	3
100	Investigating the infant gut microbiota in developing countries: worldwide metagenomic meta-analysis involving infants living in sub-urban areas of CÔte d'Ivoire. <i>Environmental Microbiology Reports</i> , 2021, 13, 626-636.	2.4	2
101	Reply: "Letter to the editor Re: Diaz M., et al. <i>Nutrients</i> 2018, 10, 1481" <i>Nutrients</i> , 2019, 11, 476.	4.1	1
102	The Role of Bifidobacteria in Ulcerative Colitis: Preliminary Results. <i>American Journal of Gastroenterology</i> , 2016, 111, S325-S326.	0.4	0
103	OC.03.6 UNDERSTANDING THE GUT-KIDNEY AXIS IN NEPHROLITHIASIS: AN ANALYSIS OF THE GUT MICROBIOTA COMPOSITION AND FUNCTIONALITY OF STONE FORMERS. <i>Digestive and Liver Disease</i> , 2019, 51, e85-e86.	0.9	0
104	Interaction Between Diet and Microbiota in the Pathophysiology of Alzheimer's Disease: Focus on Polyphenols and Dietary Fibers. <i>Advances in Alzheimer's Disease</i> , 2022, , .	0.2	0