

Leonardo Mancabelli

List of Publications by Year in descending order

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104
papers

7,423
citations

70961

41
h-index

60497

81
g-index

105
all docs

105
docs citations

105
times ranked

8231
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.2	15
2	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.	1.4	3
3	Evaluation of Modulatory Activities of <i>Lactobacillus crispatus</i> Strains in the Context of the Vaginal Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, e0273321.	1.2	14
4	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	1.2	6
5	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. <i>Environmental Microbiology</i> , 2022, , .	1.8	5
6	Investigation of the Ecological Link between Recurrent Microbial Human Gut Communities and Physical Activity. <i>Microbiology Spectrum</i> , 2022, 10, e0042022.	1.2	9
7	Exploring the Ecological Effects of Naturally Antibiotic-Insensitive <i>Bifidobacteria</i> in the Recovery of the Resilience of the Gut Microbiota during and after Antibiotic Treatment. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	4
8	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
9	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.	1.5	19
10	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, .	0.8	26
11	Vaginitypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
12	Early-Life Development of the Bifidobacterial Community in the Infant Gut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3382.	1.8	28
13	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
14	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, .	1.4	8
15	Genetic insights into the dark matter of the mammalian gut microbiota through targeted genome reconstruction. <i>Environmental Microbiology</i> , 2021, 23, 3294-3305.	1.8	5
16	Investigating the infant gut microbiota in developing countries: worldwide metagenomic meta-analysis involving infants living in suburban areas of Cote d'Ivoire. <i>Environmental Microbiology Reports</i> , 2021, 13, 626-636.	1.0	2
17	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35
18	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9

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19	Effect of Intrapartum Antibiotics Prophylaxis on the Bifidobacterial Establishment within the Neonatal Gut. <i>Microorganisms</i> , 2021, 9, 1867.	1.6	8
20	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.	1.5	7
21	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
22	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.	1.6	13
23	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	1.5	11
24	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.	1.8	59
25	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	1.7	13
26	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, .	1.4	8
27	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.	1.9	19
28	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, .	1.4	24
29	<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.	1.6	140
30	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
31	Evolutionary development and phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	1.8	17
32	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
33	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.	1.8	29
34	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
35	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.	0.8	22
36	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	30

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37	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. <i>Microorganisms</i> , 2020, 8, 131.	1.6	26
38	Donated Human Milk as a Determinant Factor for the Gut Bifidobacterial Ecology in Premature Babies. <i>Microorganisms</i> , 2020, 8, 760.	1.6	13
39	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	29
40	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.	1.0	10
41	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. <i>Microorganisms</i> , 2019, 7, 535.	1.6	10
42	Exploring the effects of COLOSTRONONI on the mammalian gut microbiota composition. <i>PLoS ONE</i> , 2019, 14, e0217609.	1.1	6
43	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. <i>Microorganisms</i> , 2019, 7, 293.	1.6	10
44	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. <i>Environmental Microbiology</i> , 2019, 21, 1331-1343.	1.8	60
45	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. <i>International Journal of Food Microbiology</i> , 2019, 294, 1-9.	2.1	26
46	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	11
47	<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.	1.8	47
48	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.	1.6	13
49	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. <i>Genome Biology</i> , 2019, 20, 96.	3.8	44
50	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019, 10, 1286.	5.8	46
51	Reply: Letter to the editor Re: Diaz M., et al. <i>Nutrients</i> 2018, 10, 1481. <i>Nutrients</i> , 2019, 11, 476.	1.7	1
52	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5755.	1.6	22
53	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.	0.4	0
54	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, .	1.4	44

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55	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. <i>Microorganisms</i> , 2019, 7, 599.	1.6	8
56	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.	0.8	45
57	Phylogenetic classification of six novel species belonging to the genus <i>Bifidobacterium</i> comprising <i>Bifidobacterium anseris</i> sp. nov., <i>Bifidobacterium criceti</i> sp. nov., <i>Bifidobacterium imperatoris</i> sp. nov., <i>Bifidobacterium italicum</i> sp. nov., <i>Bifidobacterium margollesii</i> sp. nov. and <i>Bifidobacterium parmae</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 173-183.	1.2	58
58	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, .	1.4	16
59	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.	6.1	130
60	Bifidobacteria and the infant gut: an example of co-evolution and natural selection. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 103-118.	2.4	129
61	Tracking the Taxonomy of the Genus <i>Bifidobacterium</i> Based on a Phylogenomic Approach. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	58
62	Fecal microbiota profile in a group of myasthenia gravis patients. <i>Scientific Reports</i> , 2018, 8, 14384.	1.6	45
63	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.	1.7	40
64	<i>Bifidobacterium bifidum</i> PRL2010 alleviates intestinal ischemia/reperfusion injury. <i>PLoS ONE</i> , 2018, 13, e0202670.	1.1	16
65	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	1.6	148
66	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.	5.1	822
67	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. <i>Microbiome</i> , 2018, 6, 145.	4.9	54
68	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	1.8	153
69	Ancient bacteria of the ‘zai’ microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	4.9	45
70	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.	2.1	27
71	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017, 19, 4771-4783.	1.8	49
72	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	4.4	96

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73	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	1.6	146
74	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
75	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, .	1.4	31
76	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, .	2.9	1,118
77	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240
78	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived <i>Bifidobacteria</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	88
79	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
80	Comparative genomic and phylogenomic analyses of the <i>Bifidobacteriaceae</i> family. <i>BMC Genomics</i> , 2017, 18, 568.	1.2	98
81	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. <i>Frontiers in Microbiology</i> , 2017, 8, 1749.	1.5	86
82	<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.	0.8	32
83	The Role of <i>Bifidobacteria</i> in Ulcerative Colitis: Preliminary Results. <i>American Journal of Gastroenterology</i> , 2016, 111, S325-S326.	0.2	0
84	Modulation of the <i>Bifidobacterial</i> Communities of the Dog Microbiota by Zeolite. <i>Frontiers in Microbiology</i> , 2016, 7, 1491.	1.5	10
85	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
86	Evaluation of genetic diversity among strains of the human gut commensal <i>Bifidobacterium adolescentis</i> . <i>Scientific Reports</i> , 2016, 6, 23971.	1.6	97
87	Elucidating the gut microbiome of ulcerative colitis: <i>bifidobacteria</i> as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw191.	1.3	102
88	Gut microbiota composition and <i>Clostridium difficile</i> infection in hospitalized elderly individuals: a metagenomic study. <i>Scientific Reports</i> , 2016, 6, 25945.	1.6	207
89	Prophages of the genus <i>Bifidobacterium</i> as modulating agents of the infant gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 2196-2213.	1.8	66
90	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw049.	0.7	94

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91	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. <i>ISME Journal</i> , 2016, 10, 1656-1668.	4.4	145
92	Modulation of the <i>eps</i> -ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , 2016, 92, f1w056.	1.3	44
93	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.	1.4	165
94	<i>Bifidobacteria</i> exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	1.6	233
95	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. <i>Frontiers in Microbiology</i> , 2015, 6, 1030.	1.5	74
96	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , 2015, 6, 1331.	1.5	45
97	A genome-based identification approach for members of the genus <i>Bifidobacterium</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	12
98	Exploring Vertical Transmission of <i>Bifidobacteria</i> from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	1.4	191
99	Evidence for cholesterol-lowering activity by <i>Bifidobacterium bifidum</i> PRL2010 through gut microbiota modulation. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6813-6829.	1.7	64
100	Insights into teichoic acid biosynthesis by <i>Bifidobacterium bifidum</i> PRL2010. <i>FEMS Microbiology Letters</i> , 2015, 362, f1v141.	0.7	15
101	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . <i>Environmental Microbiology</i> , 2015, 17, 2515-2531.	1.8	80
102	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203
103	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.	1.3	71
104	Investigation of the Evolutionary Development of the Genus <i>Bifidobacterium</i> by Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6383-6394.	1.4	117