

Christian Milani

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

12,345
citations

26610

56
h-index

28275

105
g-index

143
all docs

143
docs citations

143
times ranked

13568
citing authors

#	ARTICLE	IF	CITATIONS
1	The human gut microbiota during the initial stages of life: insights from bifidobacteria. <i>Current Opinion in Biotechnology</i> , 2022, 73, 81-87.	3.3	29
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	Effect of antibiotics in the first week of life on faecal microbiota development. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2022, 107, 603-610.	1.4	9
8	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, .	1.4	4
9	Envisioning emerging frontiers on human gut microbiota and its applications. <i>Microbial Biotechnology</i> , 2021, 14, 12-17.	2.0	2
10	Phageome Analysis of Bifidobacteria-Rich Samples. <i>Methods in Molecular Biology</i> , 2021, 2278, 71-85.	0.4	0
11	Metagenomic Analyses of Bifidobacterial Communities. <i>Methods in Molecular Biology</i> , 2021, 2278, 183-193.	0.4	1
12	Vaginotypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
13	Early-Life Development of the Bifidobacterial Community in the Infant Gut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3382.	1.8	28
14	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
15	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
16	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
17	Investigating the infant gut microbiota in developing countries: worldwide metagenomic meta-analysis involving infants living in suburban areas of CÔte d'Ivoire. <i>Environmental Microbiology Reports</i> , 2021, 13, 626-636.	1.0	2
18	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35

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19	Gastric microbiota composition in patients with corpus atrophic gastritis. <i>Digestive and Liver Disease</i> , 2021, 53, 1580-1587.	0.4	10
20	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
21	Phylogenetic classification of ten novel species belonging to the genus <i>Bifidobacterium</i> comprising <i>B. phasiani</i> sp. nov., <i>B. pongonis</i> sp. nov., <i>B. saguinibicoloris</i> sp. nov., <i>B. colobi</i> sp. nov., <i>B. simiiventris</i> sp. nov., <i>B. santillanense</i> sp. nov., <i>B. miconis</i> sp. nov., <i>B. amazonense</i> sp. nov., <i>B. pluvialisilvae</i> sp. nov., and <i>B. miconisargentati</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126273.	1.2	42
22	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
23	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
24	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
25	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	1.5	11
26	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
27	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	1.7	13
28	Special Issue "Bifidobacteria: Insights from Ecology to Genomics of a Key Microbial Group of the Mammalian Gut Microbiota". <i>Microorganisms</i> , 2020, 8, 1660.	1.6	0
29	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
30	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
31	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
32	<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
33	Catching a glimpse of the bacterial gut community of companion animals: a canine and feline perspective. <i>Microbial Biotechnology</i> , 2020, 13, 1708-1732.	2.0	38
34	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
35	<i>Bifidobacterium mongoliense</i> genome seems particularly adapted to milk oligosaccharide digestion leading to production of antivirulent metabolites. <i>BMC Microbiology</i> , 2020, 20, 111.	1.3	14
36	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	1.8	17

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37	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. FEMS Microbiology Ecology, 2020, 96, .	1.3	33
38	The infant gut microbiome as a microbial organ influencing host well-being. Italian Journal of Pediatrics, 2020, 46, 16.	1.0	93
39	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. Applied and Environmental Microbiology, 2020, 86, .	1.4	9
40	Characterization of the phylogenetic diversity of two novel species belonging to the genus Bifidobacterium: Bifidobacterium cebidarum sp. nov. and Bifidobacterium leontopithecii sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2288-2297.	0.8	22
41	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. Applied and Environmental Microbiology, 2020, 86, .	1.4	30
42	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. Microorganisms, 2020, 8, 131.	1.6	26
43	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. FEMS Microbiology Ecology, 2019, 95, .	1.3	29
44	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. Microbiome, 2019, 7, 100.	4.9	101
45	A microbiome reality check: limitations of <i>in silico</i> -based metagenomic approaches to study complex bacterial communities. Environmental Microbiology Reports, 2019, 11, 840-847.	1.0	10
46	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. Microorganisms, 2019, 7, 535.	1.6	10
47	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. Microorganisms, 2019, 7, 293.	1.6	10
48	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. Environmental Microbiology, 2019, 21, 1331-1343.	1.8	60
49	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. International Journal of Food Microbiology, 2019, 294, 1-9.	2.1	26
50	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
51	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host co-evolution. Environmental Microbiology, 2019, 21, 3683-3695.	1.8	47
52	The Influence of Fungicide Treatments on Mycobiota of Grapes and Its Evolution during Fermentation Evaluated by Metagenomic and Culture-Dependent Methods. Microorganisms, 2019, 7, 114.	1.6	13
53	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. Genome Biology, 2019, 20, 96.	3.8	44
54	Colonization of the human gut by bovine bacteria present in Parmesan cheese. Nature Communications, 2019, 10, 1286.	5.8	46

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55	Reply: "Letter to the editor Re: Diaz M., et al. Nutrients 2018, 10, 1481" Nutrients, 2019, 11, 476.	1.7	1
56	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. Scientific Reports, 2019, 9, 5755.	1.6	22
57	Gut Microbiome in the Elderly Hospitalized Patient. , 2019, , 287-296.		1
58	Unveiling Genomic Diversity among Members of the Species <i>Bifidobacterium pseudolongum</i> , a Widely Distributed Gut Commensal of the Animal Kingdom. Applied and Environmental Microbiology, 2019, 85, .	1.4	44
59	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. Microorganisms, 2019, 7, 544.	1.6	70
60	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. Microorganisms, 2019, 7, 599.	1.6	8
61	Health benefits conferred by the human gut microbiota during infancy. Microbial Biotechnology, 2019, 12, 243-248.	2.0	7
62	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.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1288-1298.	0.8	45
63	A Gene Homologous to rRNA Methylase Genes Confers Erythromycin and Clindamycin Resistance in <i>Bifidobacterium breve</i> . Applied and Environmental Microbiology, 2018, 84, .	1.4	19
64	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.. Systematic and Applied Microbiology, 2018, 41, 173-183.	1.2	58
65	Bifidobacteria: Ecology and Coevolution With the Host. , 2018, , 213-220.		4
66	Phylotype-Level Profiling of Lactobacilli in Highly Complex Environments by Means of an Internal Transcribed Spacer-Based Metagenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	1.4	16
67	Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. Gut, 2018, 67, 2097-2106.	6.1	130
68	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. Trends in Microbiology, 2018, 26, 339-350.	3.5	182
69	Bifidobacteria and the infant gut: an example of co-evolution and natural selection. Cellular and Molecular Life Sciences, 2018, 75, 103-118.	2.4	129
70	Tracking the Taxonomy of the Genus <i>Bifidobacterium</i> Based on a Phylogenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	1.4	58
71	Fecal microbiota profile in a group of myasthenia gravis patients. Scientific Reports, 2018, 8, 14384.	1.6	45
72	Microbiota and Derived Parameters in Fecal Samples of Infants with Non-IgE Cow's Milk Protein Allergy under a Restricted Diet. Nutrients, 2018, 10, 1481.	1.7	40

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73	Bifidobacterium bifidum PRL2010 alleviates intestinal ischemia/reperfusion injury. PLoS ONE, 2018, 13, e0202670.	1.1	16
74	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. Scientific Reports, 2018, 8, 13974.	1.6	148
75	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. Cell Host and Microbe, 2018, 24, 133-145.e5.	5.1	822
76	Microbial and metabolic multi-omic correlations in systemic sclerosis patients. Annals of the New York Academy of Sciences, 2018, 1421, 97-109.	1.8	50
77	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. Microbiome, 2018, 6, 145.	4.9	54
78	Reconstruction of the Bifidobacterial Pan-Secretome Reveals the Network of Extracellular Interactions between Bifidobacteria and the Infant Gut. Applied and Environmental Microbiology, 2018, 84, .	1.4	16
79	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. Environmental Microbiology, 2017, 19, 1379-1390.	1.8	153
80	Ancient bacteria of the <i>Å-tzi</i> ™s microbiome: a genomic tale from the Copper Age. Microbiome, 2017, 5, 5.	4.9	45
81	Next generation sequencing-based multigene panel for high throughput detection of food-borne pathogens. International Journal of Food Microbiology, 2017, 256, 20-29.	2.1	27
82	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. Environmental Microbiology, 2017, 19, 4771-4783.	1.8	49
83	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. ISME Journal, 2017, 11, 2834-2847.	4.4	96
84	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. Scientific Reports, 2017, 7, 11102.	1.6	146
85	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. Scientific Reports, 2017, 7, 9879.	1.6	123
86	The Sortase-Dependent Fimbriome of the Genus Bifidobacterium: Extracellular Structures with Potential To Modulate Microbe-Host Dialogue. Applied and Environmental Microbiology, 2017, 83, .	1.4	31
87	Bacterial diversity of the Colombian fermented milk <i>Åœo Coste</i> ± assessed by culturing and high-throughput sequencing and DGGE analysis of 16S rRNA gene amplicons. Food Microbiology, 2017, 68, 129-136.	2.1	54
88	The First Microbial Colonizers of the Human Gut: Composition, Activities, and Health Implications of the Infant Gut Microbiota. Microbiology and Molecular Biology Reviews, 2017, 81, .	2.9	1,118
89	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. Microbiome, 2017, 5, 66.	4.9	240
90	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. Applied and Environmental Microbiology, 2017, 83, .	1.4	88

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91	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
92	Global transcriptional landscape and promoter mapping of the gut commensal <i>Bifidobacterium breve</i> UCC2003. <i>BMC Genomics</i> , 2017, 18, 991.	1.2	24
93	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , 2017, 18, 568.	1.2	98
94	Aging Gut Microbiota at the Cross-Road between Nutrition, Physical Frailty, and Sarcopenia: Is There a Gut-Muscle Axis?. <i>Nutrients</i> , 2017, 9, 1303.	1.7	237
95	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
96	Impact of intrapartum antimicrobial prophylaxis upon the intestinal microbiota and the prevalence of antibiotic resistance genes in vaginally delivered full-term neonates. <i>Microbiome</i> , 2017, 5, 93.	4.9	165
97	<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
98	Modulation of the Bifidobacterial Communities of the Dog Microbiota by Zeolite. <i>Frontiers in Microbiology</i> , 2016, 7, 1491.	1.5	10
99	Impact of Prematurity and Perinatal Antibiotics on the Developing Intestinal Microbiota: A Functional Inference Study. <i>International Journal of Molecular Sciences</i> , 2016, 17, 649.	1.8	109
100	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
101	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
102	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv191.	1.3	102
103	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
104	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
105	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw049.	0.7	94
106	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
107	Modulation of the <i>eps</i> -ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv056.	1.3	44
108	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

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109	Allergic Patients with Long-Term Asthma Display Low Levels of Bifidobacterium adolescentis. PLoS ONE, 2016, 11, e0147809.	1.1	90
110	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. Scientific Reports, 2015, 5, 15782.	1.6	233
111	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. Frontiers in Microbiology, 2015, 6, 1030.	1.5	74
112	Exploring Amino Acid Auxotrophy in Bifidobacterium bifidum PRL2010. Frontiers in Microbiology, 2015, 6, 1331.	1.5	45
113	Antibiotics in Early Life Alter the Gut Microbiome and Increase Disease Incidence in a Spontaneous Mouse Model of Autoimmune Insulin-Dependent Diabetes. PLoS ONE, 2015, 10, e0125448.	1.1	194
114	Occurrence and Diversity of CRISPR-Cas Systems in the Genus Bifidobacterium. PLoS ONE, 2015, 10, e0133661.	1.1	73
115	Human Colon-Derived Soluble Factors Modulate Gut Microbiota Composition. Frontiers in Oncology, 2015, 5, 86.	1.3	5
116	A genome-based identification approach for members of the genus Bifidobacterium. FEMS Microbiology Ecology, 2015, 91, .	1.3	12
117	Intestinal Microbiota Development in Preterm Neonates and Effect of Perinatal Antibiotics. Journal of Pediatrics, 2015, 166, 538-544.	0.9	329
118	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. Applied and Environmental Microbiology, 2015, 81, 7078-7087.	1.4	191
119	Ranking the impact of human health disorders on gut metabolism: Systemic lupus erythematosus and obesity as study cases. Scientific Reports, 2015, 5, 8310.	1.6	68
120	Evidence for cholesterol-lowering activity by Bifidobacterium bifidum PRL2010 through gut microbiota modulation. Applied Microbiology and Biotechnology, 2015, 99, 6813-6829.	1.7	64
121	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . Environmental Microbiology, 2015, 17, 2515-2531.	1.8	80
122	Modulation of Fecal Clostridiales Bacteria and Butyrate by Probiotic Intervention with Lactobacillus paracasei DG Varies among Healthy Adults. Journal of Nutrition, 2014, 144, 1787-1796.	1.3	169
123	Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus. MBio, 2014, 5, e01548-14.	1.8	500
124	The Genome Sequence of Bifidobacterium moukalabense DSM 27321 Highlights the Close Phylogenetic Relatedness with the Bifidobacterium dentium Taxon. Genome Announcements, 2014, 2, .	0.8	6
125	Comparative genomics of the Bifidobacterium brevetaxon. BMC Genomics, 2014, 15, 170.	1.2	113
126	Kefir fermented milk and kefiran promote growth of Bifidobacterium bifidum PRL2010 and modulate its gene expression. International Journal of Food Microbiology, 2014, 178, 50-59.	2.1	59

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127	Genomic Overview and Biological Functions of Exopolysaccharide Biosynthesis in <i>Bifidobacterium</i> spp. <i>Applied and Environmental Microbiology</i> , 2014, 80, 9-18.	1.4	159
128	Genomic Characterization and Transcriptional Studies of the Starch-Utilizing Strain <i>Bifidobacterium adolescentis</i> 22L. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6080-6090.	1.4	74
129	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203
130	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
131	TgaA, a VirB1-Like Component Belonging to a Putative Type IV Secretion System of <i>Bifidobacterium bifidum</i> MIMBb75. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5161-5169.	1.4	13
132	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
133	Role of sortase-dependent pili of <i>Bifidobacterium bifidum</i> PRL2010 in modulating bacterium-host interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11151-11156.	3.3	217
134	Exploration of the Genomic Diversity and Core Genome of the <i>Bifidobacterium adolescentis</i> Phylogenetic Group by Means of a Polyphasic Approach. <i>Applied and Environmental Microbiology</i> , 2013, 79, 336-346.	1.4	19
135	Bacteria as vitamin suppliers to their host: a gut microbiota perspective. <i>Current Opinion in Biotechnology</i> , 2013, 24, 160-168.	3.3	1,101
136	Comparative Genomics of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Reveals a Strict Monophyletic Bifidobacterial Taxon. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4304-4315.	1.4	74
137	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	1.1	257
138	<i>Lactococcus garvieae</i> : Where Is It From? A First Approach to Explore the Evolutionary History of This Emerging Pathogen. <i>PLoS ONE</i> , 2013, 8, e84796.	1.1	40
139	<i>Bifidobacterium asteroides</i> PRL2011 Genome Analysis Reveals Clues for Colonization of the Insect Gut. <i>PLoS ONE</i> , 2012, 7, e44229.	1.1	123
140	Complete Genome Sequence of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BLC1. <i>Journal of Bacteriology</i> , 2011, 193, 6387-6388.	1.0	19
141	Genetic strategies for mucin metabolism in <i>Bifidobacterium bifidum</i> PRL2010: An example of possible human-microbe co-evolution. <i>Gut Microbes</i> , 2011, 2, 183-189.	4.3	67