

Christian Milani

List of Publications by Year in descending order

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141
papers

12,345
citations

26567

56
h-index

28224

105
g-index

143
all docs

143
docs citations

143
times ranked

13568
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, .	2.9	1,118
2	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
3	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
4	Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus. <i>MBio</i> , 2014, 5, e01548-14.	1.8	500
5	Intestinal Microbiota Development in Preterm Neonates and Effect of Perinatal Antibiotics. <i>Journal of Pediatrics</i> , 2015, 166, 538-544.	0.9	329
6	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	1.1	257
7	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240
8	Ageing 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
9	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	1.6	233
10	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
11	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
12	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203
13	Antibiotics in Early Life Alter the Gut Microbiome and Increase Disease Incidence in a Spontaneous Mouse Model of Autoimmune Insulin-Dependent Diabetes. <i>PLoS ONE</i> , 2015, 10, e0125448.	1.1	194
14	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	1.4	191
15	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
16	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. <i>Trends in Microbiology</i> , 2018, 26, 339-350.	3.5	182
17	Modulation of Fecal Clostridiales Bacteria and Butyrate by Probiotic Intervention with <i>Lactobacillus paracasei</i> DC Varies among Healthy Adults. <i>Journal of Nutrition</i> , 2014, 144, 1787-1796.	1.3	169
18	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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19	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
20	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
21	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	1.8	153
22	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
23	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	1.6	148
24	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	1.6	146
25	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
26	<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
27	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
28	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
29	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
30	<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
31	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
32	Comparative genomics of the <i>Bifidobacterium</i> <i>brevetaxon</i> . <i>BMC Genomics</i> , 2014, 15, 170.	1.2	113
33	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
34	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, f1w191.	1.3	102
35	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. <i>Microbiome</i> , 2019, 7, 100.	4.9	101
36	Comparative genomic and phylogenomic analyses of the <i>Bifidobacteriaceae</i> family. <i>BMC Genomics</i> , 2017, 18, 568.	1.2	98

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37	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
38	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	4.4	96
39	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw049.	0.7	94
40	The infant gut microbiome as a microbial organ influencing host well-being. <i>Italian Journal of Pediatrics</i> , 2020, 46, 16.	1.0	93
41	Allergic Patients with Long-Term Asthma Display Low Levels of <i>Bifidobacterium adolescentis</i> . <i>PLoS ONE</i> , 2016, 11, e0147809.	1.1	90
42	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	88
43	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
44	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
45	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
46	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
47	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. <i>Frontiers in Microbiology</i> , 2015, 6, 1030.	1.5	74
48	Occurrence and Diversity of CRISPR-Cas Systems in the Genus <i>Bifidobacterium</i> . <i>PLoS ONE</i> , 2015, 10, e0133661.	1.1	73
49	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
50	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. <i>Microorganisms</i> , 2019, 7, 544.	1.6	70
51	Ranking the impact of human health disorders on gut metabolism: Systemic lupus erythematosus and obesity as study cases. <i>Scientific Reports</i> , 2015, 5, 8310.	1.6	68
52	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
53	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
54	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

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55	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
56	Kefir fermented milk and kefiran promote growth of <i>Bifidobacterium bifidum</i> PRL2010 and modulate its gene expression. <i>International Journal of Food Microbiology</i> , 2014, 178, 50-59.	2.1	59
57	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
58	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
59	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
60	Bacterial diversity of the Colombian fermented milk "Suero Costeño" assessed by culturing and high-throughput sequencing and DGGE analysis of 16S rRNA gene amplicons. <i>Food Microbiology</i> , 2017, 68, 129-136.	2.1	54
61	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
62	Microbial and metabolic multi-omic correlations in systemic sclerosis patients. <i>Annals of the New York Academy of Sciences</i> , 2018, 1421, 97-109.	1.8	50
63	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017, 19, 4771-4783.	1.8	49
64	<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
65	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019, 10, 1286.	5.8	46
66	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , 2015, 6, 1331.	1.5	45
67	Ancient bacteria of the "Tzitzis" microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	4.9	45
68	Fecal microbiota profile in a group of myasthenia gravis patients. <i>Scientific Reports</i> , 2018, 8, 14384.	1.6	45
69	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
70	Modulation of the <i>eps</i> -ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw056.	1.3	44
71	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. <i>Genome Biology</i> , 2019, 20, 96.	3.8	44
72	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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73	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
74	<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
75	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
76	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
77	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35
78	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
79	<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
80	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
81	Vaginotypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
82	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	30
83	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
84	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	29
85	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
86	Early-Life Development of the Bifidobacterial Community in the Infant Gut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3382.	1.8	28
87	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
88	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
89	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
90	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

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91	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
92	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5755.	1.6	22
93	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
94	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
95	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
96	A Gene Homologous to rRNA Methylase Genes Confers Erythromycin and Clindamycin Resistance in <i>Bifidobacterium breve</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	19
97	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
98	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
99	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	1.8	17
100	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
101	<i>Bifidobacterium bifidum</i> PRL2010 alleviates intestinal ischemia/reperfusion injury. <i>PLoS ONE</i> , 2018, 13, e0202670.	1.1	16
102	Reconstruction of the Bifidobacterial Pan-Secretome Reveals the Network of Extracellular Interactions between Bifidobacteria and the Infant Gut. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	16
103	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
104	<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
105	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
106	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
107	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
108	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	1.7	13

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109	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
110	A genome-based identification approach for members of the genus <i>Bifidobacterium</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	12
111	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
112	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	1.5	11
113	Modulation of the Bifidobacterial Communities of the Dog Microbiota by Zeolite. <i>Frontiers in Microbiology</i> , 2016, 7, 1491.	1.5	10
114	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
115	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. <i>Microorganisms</i> , 2019, 7, 535.	1.6	10
116	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. <i>Microorganisms</i> , 2019, 7, 293.	1.6	10
117	Gastric microbiota composition in patients with corpus atrophic gastritis. <i>Digestive and Liver Disease</i> , 2021, 53, 1580-1587.	0.4	10
118	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
119	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
120	Investigation of the Ecological Link between Recurrent Microbial Human Gut Communities and Physical Activity. <i>Microbiology Spectrum</i> , 2022, 10, e0042022.	1.2	9
121	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
122	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. <i>Microorganisms</i> , 2019, 7, 599.	1.6	8
123	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
124	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
125	Health benefits conferred by the human gut microbiota during infancy. <i>Microbial Biotechnology</i> , 2019, 12, 243-248.	2.0	7
126	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

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127	The Genome Sequence of <i>Bifidobacterium moukalabense</i> DSM 27321 Highlights the Close Phylogenetic Relatedness with the <i>Bifidobacterium dentium</i> Taxon. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
128	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	1.2	6
129	Human Colon-Derived Soluble Factors Modulate Gut Microbiota Composition. <i>Frontiers in Oncology</i> , 2015, 5, 86.	1.3	5
130	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
131	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. <i>Environmental Microbiology</i> , 2022, , .	1.8	5
132	<i>Bifidobacteria: Ecology and Coevolution With the Host.</i> , 2018, , 213-220.		4
133	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
134	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
135	Envisioning emerging frontiers on human gut microbiota and its applications. <i>Microbial Biotechnology</i> , 2021, 14, 12-17.	2.0	2
136	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.	1.0	2
137	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
138	<i>Gut Microbiome in the Elderly Hospitalized Patient.</i> , 2019, , 287-296.		1
139	Metagenomic Analyses of <i>Bifidobacterial</i> Communities. <i>Methods in Molecular Biology</i> , 2021, 2278, 183-193.	0.4	1
140	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
141	Phageome Analysis of <i>Bifidobacteria</i> -Rich Samples. <i>Methods in Molecular Biology</i> , 2021, 2278, 71-85.	0.4	0