

# Francesca Turroni

## List of Publications by Year in descending order

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156  
papers

13,819  
citations

18465

62  
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23514

111  
g-index

158  
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158  
docs citations

158  
times ranked

12909  
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	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
3	Diversity of Bifidobacteria within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	1.1	512
4	Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus. <i>MBio</i> , 2014, 5, e01548-14.	1.8	500
5	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 837-890.	2.9	487
6	Genome-scale analyses of health-promoting bacteria: probiogenomics. <i>Nature Reviews Microbiology</i> , 2009, 7, 61-71.	13.6	400
7	Genome analysis of <i>Bifidobacterium bifidum</i> PRL2010 reveals metabolic pathways for host-derived glycan foraging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19514-19519.	3.3	324
8	Exploring the Diversity of the Bifidobacterial Population in the Human Intestinal Tract. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1534-1545.	1.4	270
9	Molecular dialogue between the human gut microbiota and the host: a <i>Lactobacillus</i> and <i>Bifidobacterium</i> perspective. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 183-203.	2.4	265
10	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	1.1	257
11	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240
12	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	1.6	233
13	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
14	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
15	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203
16	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	1.4	191
17	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
18	Human gut microbiota and bifidobacteria: from composition to functionality. <i>Antonie Van Leeuwenhoek</i> , 2008, 94, 35-50.	0.7	182

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19	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. <i>Trends in Microbiology</i> , 2018, 26, 339-350.	3.5	182
20	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
21	Host-microbe interactions that facilitate gut colonization by commensal bifidobacteria. <i>Trends in Microbiology</i> , 2012, 20, 467-476.	3.5	164
22	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	1.8	153
23	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
24	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	1.6	148
25	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	1.6	146
26	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
27	The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	1.5	141
28	Genomics and ecological overview of the genus <i>Bifidobacterium</i> . <i>International Journal of Food Microbiology</i> , 2011, 149, 37-44.	2.1	140
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	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
31	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
32	Microbiomic analysis of the bifidobacterial population in the human distal gut. <i>ISME Journal</i> , 2009, 3, 745-751.	4.4	128
33	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
34	<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
35	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
36	Comparative genomics of the genus <i>Bifidobacterium</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3243-3254.	0.7	116

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37	Comparative genomics of the <i>Bifidobacterium brevetaxon</i> . BMC Genomics, 2014, 15, 170.	1.2	113
38	Role of Extracellular Transaldolase from <i>Bifidobacterium bifidum</i> in Mucin Adhesion and Aggregation. Applied and Environmental Microbiology, 2012, 78, 3992-3998.	1.4	109
39	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. FEMS Microbiology Ecology, 2016, 92, fiw191.	1.3	102
40	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. BMC Genomics, 2017, 18, 568.	1.2	98
41	Evaluation of genetic diversity among strains of the human gut commensal <i>Bifidobacterium adolescentis</i> . Scientific Reports, 2016, 6, 23971.	1.6	97
42	Bifidobacteria and humans: our special friends, from ecological to genomics perspectives. Journal of the Science of Food and Agriculture, 2014, 94, 163-168.	1.7	96
43	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. ISME Journal, 2017, 11, 2834-2847.	4.4	96
44	The infant gut microbiome as a microbial organ influencing host well-being. Italian Journal of Pediatrics, 2020, 46, 16.	1.0	93
45	<i>Bifidobacterium bifidum</i> as an example of a specialized human gut commensal. Frontiers in Microbiology, 2014, 5, 437.	1.5	92
46	Allergic Patients with Long-Term Asthma Display Low Levels of <i>Bifidobacterium adolescentis</i> . PLoS ONE, 2016, 11, e0147809.	1.1	90
47	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. Applied and Environmental Microbiology, 2017, 83, .	1.4	88
48	Obesity and microbiota: an example of an intricate relationship. Genes and Nutrition, 2017, 12, 18.	1.2	86
49	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. Frontiers in Microbiology, 2017, 8, 1749.	1.5	86
50	Genetic analysis and morphological identification of pilus-like structures in members of the genus <i>Bifidobacterium</i> . Microbial Cell Factories, 2011, 10, S16.	1.9	84
51	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . Environmental Microbiology, 2015, 17, 2515-2531.	1.8	80
52	Comparative Genomics of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Reveals a Strict Monophyletic Bifidobacterial Taxon. Applied and Environmental Microbiology, 2013, 79, 4304-4315.	1.4	74
53	Genomic Characterization and Transcriptional Studies of the Starch-Utilizing Strain <i>Bifidobacterium adolescentis</i> 22L. Applied and Environmental Microbiology, 2014, 80, 6080-6090.	1.4	74
54	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. Frontiers in Microbiology, 2015, 6, 1030.	1.5	74

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55	Occurrence and Diversity of CRISPR-Cas Systems in the Genus <i>Bifidobacterium</i> . PLoS ONE, 2015, 10, e0133661.	1.1	73
56	Microbial diversity in the human intestine and novel insights from metagenomics. Frontiers in Bioscience - Landmark, 2009, Volume, 3214.	3.0	72
57	Evaluation of bifidobacterial community composition in the human gut by means of a targeted amplicon sequencing (ITS) protocol. FEMS Microbiology Ecology, 2014, 90, n/a-n/a.	1.3	71
58	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. Microorganisms, 2019, 7, 544.	1.6	70
59	Genetic strategies for mucin metabolism in <i>Bifidobacterium bifidum</i> PRL2010: An example of possible human-microbe co-evolution. Gut Microbes, 2011, 2, 183-189.	4.3	67
60	Evaluation of adhesion properties and antibacterial activities of the infant gut commensal <i>Bifidobacterium bifidum</i> PRL2010. Anaerobe, 2013, 21, 9-17.	1.0	67
61	<i>Bifidobacterium bifidum</i> PRL2010 Modulates the Host Innate Immune Response. Applied and Environmental Microbiology, 2014, 80, 730-740.	1.4	67
62	Characterization of the Serpin-Encoding Gene of <i>Bifidobacterium breve</i> 210B. Applied and Environmental Microbiology, 2010, 76, 3206-3219.	1.4	66
63	Prophages of the genus <i>Bifidobacterium</i> as modulating agents of the infant gut microbiota. Environmental Microbiology, 2016, 18, 2196-2213.	1.8	66
64	Evidence for cholesterol-lowering activity by <i>Bifidobacterium bifidum</i> PRL2010 through gut microbiota modulation. Applied Microbiology and Biotechnology, 2015, 99, 6813-6829.	1.7	64
65	Analysis of Predicted Carbohydrate Transport Systems Encoded by <i>Bifidobacterium bifidum</i> PRL2010. Applied and Environmental Microbiology, 2012, 78, 5002-5012.	1.4	63
66	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. Environmental Microbiology, 2019, 21, 1331-1343.	1.8	60
67	Kefir fermented milk and kefiran promote growth of <i>Bifidobacterium bifidum</i> PRL2010 and modulate its gene expression. International Journal of Food Microbiology, 2014, 178, 50-59.	2.1	59
68	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
69	Tracking the Taxonomy of the Genus <i>Bifidobacterium</i> Based on a Phylogenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	1.4	58
70	Insights into endogenous <i>Bifidobacterium</i> species in the human gut microbiota during adulthood. Trends in Microbiology, 2022, 30, 940-947.	3.5	56
71	Probiogenomics as a tool to obtain genetic insights into adaptation of probiotic bacteria to the human gut. Bioengineered, 2012, 3, 73-79.	1.4	54
72	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

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73	Comparative Analyses of Prophage-Like Elements Present in Two <i>Lactococcus lactis</i> Strains. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7771-7780.	1.4	52
74	The impact of bacteriophages on probiotic bacteria and gut microbiota diversity. <i>Genes and Nutrition</i> , 2011, 6, 205-207.	1.2	52
75	Expression of sortase-dependent pili of <i>Bifidobacterium bifidum</i> PRL2010 in response to environmental gut conditions. <i>FEMS Microbiology Letters</i> , 2014, 357, 23-33.	0.7	50
76	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017, 19, 4771-4783.	1.8	49
77	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host coevolution. <i>Environmental Microbiology</i> , 2019, 21, 3683-3695.	1.8	47
78	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019, 10, 1286.	5.8	46
79	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6929-6936.	1.4	45
80	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , 2015, 6, 1331.	1.5	45
81	Ancient bacteria of the $\tilde{\text{tzi}}$ 's microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	4.9	45
82	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
83	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
84	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. <i>Genome Biology</i> , 2019, 20, 96.	3.8	44
85	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
86	Ability of <i>Bifidobacterium breve</i> To Grow on Different Types of Milk: Exploring the Metabolism of Milk through Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7408-7417.	1.4	42
87	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. saguiniicoloris</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
88	Microbiota and Cancer: The Emerging Beneficial Role of Bifidobacteria in Cancer Immunotherapy. <i>Frontiers in Microbiology</i> , 2020, 11, 575072.	1.5	40
89	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
90	Insights into Physiological and Genetic Mupirocin Susceptibility in Bifidobacteria. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3141-3146.	1.4	37

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91	Bifidobacterial biofilm formation is a multifactorial adaptive phenomenon in response to bile exposure. <i>Scientific Reports</i> , 2020, 10, 11598.	1.6	37
92	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35
93	Bifidobacteria: from ecology to genomics. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 4673.	3.0	33
94	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
95	<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
96	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
97	Vaginitypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
98	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	30
99	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
100	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	29
101	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
102	Global Genome Transcription Profiling of <i>Bifidobacterium bifidum</i> PRL2010 under <i>In Vitro</i> Conditions and Identification of Reference Genes for Quantitative Real-Time PCR. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8578-8587.	1.4	27
103	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
104	A Two-Component Regulatory System Controls Autoregulated Serpin Expression in <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7032-7041.	1.4	26
105	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
106	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
107	Multimorbidity in elderly hospitalised patients and risk of <i>Clostridium difficile</i> infection: a retrospective study with the Cumulative Illness Rating Scale (CIRS). <i>BMJ Open</i> , 2015, 5, e009316.	0.8	25
108	Mobilome and Resistome Reconstruction from Genomes Belonging to Members of the <i>Bifidobacterium</i> Genus. <i>Microorganisms</i> , 2019, 7, 638.	1.6	25

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109	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
110	An efficient and reproducible method for transformation of genetically recalcitrant bifidobacteria. <i>FEMS Microbiology Letters</i> , 2012, 333, 146-152.	0.7	23
111	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5755.	1.6	22
112	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
113	Exploring the Ecology of Bifidobacteria and Their Genetic Adaptation to the Mammalian Gut. <i>Microorganisms</i> , 2021, 9, 8.	1.6	21
114	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
115	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
116	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
117	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
118	Analyses of bifidobacterial prophage-like sequences. <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 39-50.	0.7	17
119	Editorial: Bifidobacteria and Their Role in the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 2148.	1.5	17
120	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	1.8	17
121	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
122	<i>Bifidobacterium bifidum</i> PRL2010 alleviates intestinal ischemia/reperfusion injury. <i>PLoS ONE</i> , 2018, 13, e0202670.	1.1	16
123	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
124	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
125	Insights into teichoic acid biosynthesis by <i>Bifidobacterium bifidum</i> PRL2010. <i>FEMS Microbiology Letters</i> , 2015, 362, fmv141.	0.7	15
126	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



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127	Bifidobacteria of the Human Gut. , 2015, , 41-51.		13
128	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. MSystems, 2020, 5, .	1.7	13
129	Probiogenomics Analysis of 97 Lactobacillus crispatus Strains as a Tool for the Identification of Promising Next-Generation Probiotics. Microorganisms, 2021, 9, 73.	1.6	13
130	A genome-based identification approach for members of the genus Bifidobacterium. FEMS Microbiology Ecology, 2015, 91, .	1.3	12
131	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
132	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. Frontiers in Microbiology, 2021, 12, 790881.	1.5	11
133	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
134	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. Microorganisms, 2019, 7, 535.	1.6	10
135	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. Microorganisms, 2019, 7, 293.	1.6	10
136	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. Applied and Environmental Microbiology, 2020, 86, .	1.4	9
137	Phylogenomic disentangling of the Bifidobacterium longum subsp. infantis taxon. Microbial Genomics, 2021, 7, .	1.0	9
138	Investigation of the Ecological Link between Recurrent Microbial Human Gut Communities and Physical Activity. Microbiology Spectrum, 2022, 10, e0042022.	1.2	9
139	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. Microorganisms, 2019, 7, 599.	1.6	8
140	Assessing the Genomic Variability of Gardnerella vaginalis through Comparative Genomic Analyses: Evolutionary and Ecological Implications. Applied and Environmental Microbiology, 2020, 87, .	1.4	8
141	Comparative Genome Analyses of Lactobacillus crispatus Isolates from Different Ecological Niches Reveal an Adaptation of This Species to the Human Vaginal Environment. Applied and Environmental Microbiology, 2021, 87, .	1.4	8
142	Free DNA and Metagenomics Analyses: Evaluation of Free DNA Inactivation Protocols for Shotgun Metagenomics Analysis of Human Biological Matrices. Frontiers in Microbiology, 2021, 12, 749373.	1.5	7
143	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
144	Exploring the effects of COLOSTRONONI on the mammalian gut microbiota composition. PLoS ONE, 2019, 14, e0217609.	1.1	6

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145	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	1.2	6
146	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
147	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. <i>Environmental Microbiology</i> , 2022, , .	1.8	5
148	Bifidobacteria: Ecology and Coevolution With the Host. , 2018, , 213-220.		4
149	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
150	Stress Responses of Bifidobacteria. , 2011, , 323-347.		3
151	Bifi dobacteria: the Model Human Gut Commensal. , 0, , 35-50.		3
152	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
153	Envisioning emerging frontiers on human gut microbiota and its applications. <i>Microbial Biotechnology</i> , 2021, 14, 12-17.	2.0	2
154	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
155	The Role of Bifidobacteria in Ulcerative Colitis: Preliminary Results. <i>American Journal of Gastroenterology</i> , 2016, 111, S325-S326.	0.2	0
156	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