

Francesca Turroni

List of Publications by Year in descending order

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Version: 2024-02-01

156
papers

13,819
citations

18465

62
h-index

23514

111
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158
all docs

158
docs citations

158
times ranked

12909
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	Insights into endogenous <i>Bifidobacterium</i> species in the human gut microbiota during adulthood. <i>Trends in Microbiology</i> , 2022, 30, 940-947.	3.5	56
8	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
9	Envisioning emerging frontiers on human gut microbiota and its applications. <i>Microbial Biotechnology</i> , 2021, 14, 12-17.	2.0	2
10	Vaginotypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
11	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
12	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
13	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
14	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
15	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35
16	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
17	Exploring the Ecology of <i>Bifidobacteria</i> and Their Genetic Adaptation to the Mammalian Gut. <i>Microorganisms</i> , 2021, 9, 8.	1.6	21
18	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

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19	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
20	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
21	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
22	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	1.5	11
23	Bifidobacterial biofilm formation is a multifactorial adaptive phenomenon in response to bile exposure. <i>Scientific Reports</i> , 2020, 10, 11598.	1.6	37
24	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	1.7	13
25	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
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	Microbiota and Cancer: The Emerging Beneficial Role of Bifidobacteria in Cancer Immunotherapy. <i>Frontiers in Microbiology</i> , 2020, 11, 575072.	1.5	40
29	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
30	<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
31	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
32	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
33	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	1.8	17
34	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
35	The infant gut microbiome as a microbial organ influencing host well-being. <i>Italian Journal of Pediatrics</i> , 2020, 46, 16.	1.0	93
36	Ecology of <i>Lactobacilli</i> Present in Italian Cheeses Produced from Raw Milk. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9

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37	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 leontopitheci</i> sp. nov.. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2288-2297.	0.8	22
38	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. Applied and Environmental Microbiology, 2020, 86, .	1.4	30
39	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. Microorganisms, 2020, 8, 131.	1.6	26
40	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. FEMS Microbiology Ecology, 2019, 95, .	1.3	29
41	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
42	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. Microorganisms, 2019, 7, 535.	1.6	10
43	Exploring the effects of COLOSTRONONI on the mammalian gut microbiota composition. PLoS ONE, 2019, 14, e0217609.	1.1	6
44	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. Microorganisms, 2019, 7, 293.	1.6	10
45	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. Environmental Microbiology, 2019, 21, 1331-1343.	1.8	60
46	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
47	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
48	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host coevolution. Environmental Microbiology, 2019, 21, 3683-3695.	1.8	47
49	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. Genome Biology, 2019, 20, 96.	3.8	44
50	Colonization of the human gut by bovine bacteria present in Parmesan cheese. Nature Communications, 2019, 10, 1286.	5.8	46
51	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. Scientific Reports, 2019, 9, 5755.	1.6	22
52	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
53	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. Microorganisms, 2019, 7, 544.	1.6	70
54	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. Microorganisms, 2019, 7, 599.	1.6	8

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55	Mobilome and Resistome Reconstruction from Genomes Belonging to Members of the Bifidobacterium Genus. <i>Microorganisms</i> , 2019, 7, 638.	1.6	25
56	Characterization of the phylogenetic diversity of five novel species belonging to the genus Bifidobacterium: Bifidobacterium castoris sp. nov., Bifidobacterium callimiconis sp. nov., Bifidobacterium goeldii sp. nov., Bifidobacterium samirii sp. nov. and Bifidobacterium dolichotidis 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 Bifidobacterium comprising Bifidobacterium anseris sp. nov., Bifidobacterium criceti sp. nov., Bifidobacterium imperatoris sp. nov., Bifidobacterium italicum sp. nov., Bifidobacterium margollesii sp. nov. and Bifidobacterium parmae sp. nov.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 173-183.	1.2	58
58	Bifidobacteria: Ecology and Coevolution With the Host. , 2018, , 213-220.		4
59	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
60	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
61	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. <i>Trends in Microbiology</i> , 2018, 26, 339-350.	3.5	182
62	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
63	Tracking the Taxonomy of the Genus Bifidobacterium Based on a Phylogenomic Approach. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	58
64	Bifidobacterium bifidum 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	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
69	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	1.8	153
70	Ancient bacteria of the <i>Ä-tzi</i> ™s microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	4.9	45
71	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
72	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017, 19, 4771-4783.	1.8	49

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73	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	4.4	96
74	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	1.6	146
75	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
76	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
77	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
78	Obesity and microbiota: an example of an intricate relationship. <i>Genes and Nutrition</i> , 2017, 12, 18.	1.2	86
79	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240
80	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived <i>Bifidobacteria</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	88
81	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
82	Comparative genomic and phylogenomic analyses of the <i>Bifidobacteriaceae</i> family. <i>BMC Genomics</i> , 2017, 18, 568.	1.2	98
83	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
84	<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
85	The Role of <i>Bifidobacteria</i> in Ulcerative Colitis: Preliminary Results. <i>American Journal of Gastroenterology</i> , 2016, 111, S325-S326.	0.2	0
86	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
87	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
88	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, f1w191.	1.3	102
89	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
90	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 837-890.	2.9	487

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91	Prophages of the genus <i>Bacteriophage</i> as modulating agents of the infant gut microbiota. <i>Environmental Microbiology</i> , 2016, 18, 2196-2213.	1.8	66
92	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
93	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
94	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
95	Editorial: Bifidobacteria and Their Role in the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 2148.	1.5	17
96	Allergic Patients with Long-Term Asthma Display Low Levels of <i>Bifidobacterium adolescentis</i> . <i>PLoS ONE</i> , 2016, 11, e0147809.	1.1	90
97	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	1.6	233
98	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
99	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. <i>Frontiers in Microbiology</i> , 2015, 6, 1030.	1.5	74
100	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , 2015, 6, 1331.	1.5	45
101	Occurrence and Diversity of CRISPR-Cas Systems in the Genus <i>Bifidobacterium</i> . <i>PLoS ONE</i> , 2015, 10, e0133661.	1.1	73
102	A genome-based identification approach for members of the genus <i>Bifidobacterium</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	12
103	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	1.4	191
104	Bifidobacteria of the Human Gut. , 2015, , 41-51.		13
105	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
106	Insights into teichoic acid biosynthesis by <i>Bifidobacterium bifidum</i> PRL2010. <i>FEMS Microbiology Letters</i> , 2015, 362, fnv141.	0.7	15
107	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
108	Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus. <i>MBio</i> , 2014, 5, e01548-14.	1.8	500

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109	Bifidobacterium bifidum as an example of a specialized human gut commensal. <i>Frontiers in Microbiology</i> , 2014, 5, 437.	1.5	92
110	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
111	Comparative genomics of the <i>Bifidobacterium brevetaxon</i> . <i>BMC Genomics</i> , 2014, 15, 170.	1.2	113
112	<i>Bifidobacterium bifidum</i> PRL2010 Modulates the Host Innate Immune Response. <i>Applied and Environmental Microbiology</i> , 2014, 80, 730-740.	1.4	67
113	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
114	Bifidobacteria and humans: our special friends, from ecological to genomics perspectives. <i>Journal of the Science of Food and Agriculture</i> , 2014, 94, 163-168.	1.7	96
115	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
116	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
117	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203
118	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
119	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
120	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
121	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
122	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
123	Evaluation of adhesion properties and antibacterial activities of the infant gut commensal <i>Bifidobacterium bifidum</i> PRL2010. <i>Anaerobe</i> , 2013, 21, 9-17.	1.0	67
124	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
125	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	1.1	257
126	Analysis of Predicted Carbohydrate Transport Systems Encoded by <i>Bifidobacterium bifidum</i> PRL2010. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5002-5012.	1.4	63

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127	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
128	Probiogenomics as a tool to obtain genetic insights into adaptation of probiotic bacteria to the human gut. <i>Bioengineered</i> , 2012, 3, 73-79.	1.4	54
129	Role of Extracellular Transaldolase from <i>Bifidobacterium bifidum</i> in Mucin Adhesion and Aggregation. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3992-3998.	1.4	109
130	Diversity of <i>Bifidobacteria</i> within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	1.1	512
131	Host-microbe interactions that facilitate gut colonization by commensal bifidobacteria. <i>Trends in Microbiology</i> , 2012, 20, 467-476.	3.5	164
132	An efficient and reproducible method for transformation of genetically recalcitrant bifidobacteria. <i>FEMS Microbiology Letters</i> , 2012, 333, 146-152.	0.7	23
133	<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
134	Insights into Physiological and Genetic Mupirocin Susceptibility in <i>Bifidobacteria</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 3141-3146.	1.4	37
135	Genomics and ecological overview of the genus <i>Bifidobacterium</i> . <i>International Journal of Food Microbiology</i> , 2011, 149, 37-44.	2.1	140
136	The impact of bacteriophages on probiotic bacteria and gut microbiota diversity. <i>Genes and Nutrition</i> , 2011, 6, 205-207.	1.2	52
137	Genetic analysis and morphological identification of pilus-like structures in members of the genus <i>Bifidobacterium</i> . <i>Microbial Cell Factories</i> , 2011, 10, S16.	1.9	84
138	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
139	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
140	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
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
142	Stress Responses of <i>Bifidobacteria</i> . , 2011, , 323-347.		3
143	Analyses of bifidobacterial prophage-like sequences. <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 39-50.	0.7	17
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