

# Gabriele Andrea Lugli

## List of Publications by Year in descending order

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131  
papers

8,409  
citations

57631

44  
h-index

51492

86  
g-index

132  
all docs

132  
docs citations

132  
times ranked

8834  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome diversity of domesticated <i>Acinetobacter baumannii</i> ATCC 19606T strains. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
2	Needle in a Whey-Stack: PhRACS as a Discovery Tool for Unknown Phage-Host Combinations. <i>MBio</i> , 2022, 13, e0333421.	1.8	5
3	Brussowvirus SW13 Requires a Cell Surface-Associated Polysaccharide To Recognize Its <i>Streptococcus thermophilus</i> Host. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0172321.	1.4	8
4	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
5	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
6	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	1.2	6
7	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. <i>Environmental Microbiology</i> , 2022, , .	1.8	5
8	Dairy streptococcal cell wall and exopolysaccharide genome diversity. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
9	Phageome Analysis of Bifidobacteria-Rich Samples. <i>Methods in Molecular Biology</i> , 2021, 2278, 71-85.	0.4	0
10	Five novel bifidobacterial species isolated from faeces of primates in two Czech zoos: <i>Bifidobacterium erythrocebi</i> sp. nov., <i>Bifidobacterium moraviense</i> sp. nov., <i>Bifidobacterium oedipodis</i> sp. nov., <i>Bifidobacterium olomucense</i> sp. nov. and <i>Bifidobacterium panos</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	26
11	Draft Genome Sequence and Secondary Metabolite Biosynthetic Potential of the <i>Lysobacter niastensis</i> Type Strain DSM 18481. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
12	Assembly, Annotation, and Comparative Analysis of Bifidobacterial Genomes. <i>Methods in Molecular Biology</i> , 2021, 2278, 31-44.	0.4	0
13	Vaginitypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
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	Draft Genome Sequence and Polyhydroxyalkanoate Biosynthetic Potential of <i>Jeongeupia naejangsanensis</i> Type Strain DSM 24253. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	1
17	Phylogenomic analysis and characterization of carbon monoxide utilization genes in the family Phyllobacteriaceae with reclassification of <i>Aminobacter carboxidus</i> (Meyer et al. 1993, Hårdt et al.) Tj ETQq1 1 0.784314 rgBT /Over <i>Microbiology</i> , 2021, 44, 126199.	1.2	1
18	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

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19	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
20	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35
21	Phylogenomic Reconstruction and Metabolic Potential of the Genus <i>Aminobacter</i> . <i>Microorganisms</i> , 2021, 9, 1332.	1.6	7
22	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
23	Lactic Acid Bacteria Diversity and Characterization of Probiotic Candidates in Fermented Meats. <i>Foods</i> , 2021, 10, 1519.	1.9	23
24	In Vitro and In Vivo Assessment of the Potential of <i>Escherichia coli</i> Phages to Treat Infections and Survive Gastric Conditions. <i>Microorganisms</i> , 2021, 9, 1869.	1.6	4
25	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
26	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
27	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
28	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
29	Editorial: Role of <i>Bifidobacteria</i> in Human and Animal Health and Biotechnological Applications. <i>Frontiers in Microbiology</i> , 2021, 12, 785664.	1.5	4
30	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	1.5	11
31	The microbial community of a biofilm lining the wall of a pristine cave in Western New Guinea. <i>Microbiological Research</i> , 2020, 241, 126584.	2.5	20
32	<i>Bifidobacterial</i> biofilm formation is a multifactorial adaptive phenomenon in response to bile exposure. <i>Scientific Reports</i> , 2020, 10, 11598.	1.6	37
33	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	1.7	13
34	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
35	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
36	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

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37	Bifidobacterium adolescentis as a key member of the human gut microbiota in the production of GABA. Scientific Reports, 2020, 10, 14112.	1.6	140
38	Draft Genome Sequence of the Carboxydrotrophic Alphaproteobacterium Aminobacter carboxidus Type Strain DSM 1086. Microbiology Resource Announcements, 2020, 9, .	0.3	3
39	Decoding the Genomic Variability among Members of the Bifidobacterium dentium Species. Microorganisms, 2020, 8, 1720.	1.6	18
40	Lysogenization of a Lactococcal Host with Three Distinct Temperate Phages Provides Homologous and Heterologous Phage Resistance. Microorganisms, 2020, 8, 1685.	1.6	13
41	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. Environmental Microbiology, 2020, 22, 3375-3393.	1.8	17
42	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. FEMS Microbiology Ecology, 2020, 96, .	1.3	33
43	The infant gut microbiome as a microbial organ influencing host well-being. Italian Journal of Pediatrics, 2020, 46, 16.	1.0	93
44	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. Applied and Environmental Microbiology, 2020, 86, .	1.4	9
45	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
46	Bifidobacterium canis sp. nov., a novel member of the Bifidobacterium pseudolongum phylogenetic group isolated from faeces of a dog (Canis lupus f. familiaris). International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5040-5047.	0.8	14
47	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. Applied and Environmental Microbiology, 2020, 86, .	1.4	30
48	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. Microorganisms, 2020, 8, 131.	1.6	26
49	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. FEMS Microbiology Ecology, 2019, 95, .	1.3	29
50	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
51	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. Microorganisms, 2019, 7, 535.	1.6	10
52	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. Microorganisms, 2019, 7, 293.	1.6	10
53	A Quest of Great Importance-Developing a Broad Spectrum Escherichia coli Phage Collection. Viruses, 2019, 11, 899.	1.5	9
54	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. Environmental Microbiology, 2019, 21, 1331-1343.	1.8	60

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55	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
56	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
57	<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
58	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. <i>Genome Biology</i> , 2019, 20, 96.	3.8	44
59	Isolation and Characterization of <i>Lactobacillus brevis</i> Phages. <i>Viruses</i> , 2019, 11, 393.	1.5	22
60	The <i>Lactococcus lactis</i> Pan-Plasmidome. <i>Frontiers in Microbiology</i> , 2019, 10, 707.	1.5	22
61	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019, 10, 1286.	5.8	46
62	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
63	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. <i>Microorganisms</i> , 2019, 7, 544.	1.6	70
64	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. <i>Microorganisms</i> , 2019, 7, 599.	1.6	8
65	Mobilome and Resistome Reconstruction from Genomes Belonging to Members of the <i>Bifidobacterium</i> Genus. <i>Microorganisms</i> , 2019, 7, 638.	1.6	25
66	Health benefits conferred by the human gut microbiota during infancy. <i>Microbial Biotechnology</i> , 2019, 12, 243-248.	2.0	7
67	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
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.. <i>Systematic and Applied Microbiology</i> , 2018, 41, 173-183.	1.2	58
69	Impact of gut-associated bifidobacteria and their phages on health: two sides of the same coin?. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2091-2099.	1.7	14
70	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
71	Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. <i>Cut</i> , 2018, 67, 2097-2106.	6.1	130
72	A Decade of <i>Streptococcus thermophilus</i> Phage Evolution in an Irish Dairy Plant. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	35

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73	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
74	Tracking the Taxonomy of the Genus Bifidobacterium Based on a Phylogenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	1.4	58
75	Biodiversity of Streptococcus thermophilus Phages in Global Dairy Fermentations. Viruses, 2018, 10, 577.	1.5	29
76	Functional carbohydrate binding modules identified in evolved dits from siphophages infecting various Gramâ€positive bacteria. Molecular Microbiology, 2018, 110, 777-795.	1.2	32
77	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
78	Characterization and induction of prophages in human gut-associated Bifidobacterium hosts. Scientific Reports, 2018, 8, 12772.	1.6	26
79	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
80	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
81	Metaâ€analysis of the human gut microbiome from urbanized and preâ€agricultural populations. Environmental Microbiology, 2017, 19, 1379-1390.	1.8	153
82	Ancient bacteria of the Ã–tziâ€™s microbiome: a genomic tale from the Copper Age. Microbiome, 2017, 5, 5.	4.9	45
83	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
84	Genome Sequence of Serratia marcescens Phage BF. Genome Announcements, 2017, 5, .	0.8	11
85	Complete Genome Sequence of Bifidobacterium longum W11 (LMG P-21586), Used as a Probiotic Strain. Genome Announcements, 2017, 5, .	0.8	3
86	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. Environmental Microbiology, 2017, 19, 4771-4783.	1.8	49
87	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. ISME Journal, 2017, 11, 2834-2847.	4.4	96
88	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. Scientific Reports, 2017, 7, 11102.	1.6	146
89	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. Scientific Reports, 2017, 7, 9879.	1.6	123
90	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

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91	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
92	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240
93	Genetic and functional characterisation of the lactococcal P335 phage-host interactions. <i>BMC Genomics</i> , 2017, 18, 146.	1.2	29
94	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	88
95	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
96	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
97	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , 2017, 18, 568.	1.2	98
98	Phage Biodiversity in Artisanal Cheese Wheys Reflects the Complexity of the Fermentation Process. <i>Viruses</i> , 2017, 9, 45.	1.5	21
99	Biocidal Inactivation of <i>Lactococcus lactis</i> Bacteriophages: Efficacy and Targets of Commonly Used Sanitizers. <i>Frontiers in Microbiology</i> , 2017, 8, 107.	1.5	23
100	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
101	Global Survey and Genome Exploration of Bacteriophages Infecting the Lactic Acid Bacterium <i>Streptococcus thermophilus</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1754.	1.5	27
102	<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
103	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152
104	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
105	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw191.	1.3	102
106	Genome Sequences of Eight Prophages Isolated from <i>Lactococcus lactis</i> Dairy Strains. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
107	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
108	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



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109	Cloning, expression and characterization of a $\beta$ -D-xylosidase from <i>Lactobacillus rossiae</i> DSM 15814T. <i>Microbial Cell Factories</i> , 2016, 15, 72.	1.9	24
110	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw049.	0.7	94
111	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
112	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
113	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
114	<i>Bifidobacteria</i> exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	1.6	233
115	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , 2015, 6, 1331.	1.5	45
116	Occurrence and Diversity of CRISPR-Cas Systems in the Genus <i>Bifidobacterium</i> . <i>PLoS ONE</i> , 2015, 10, e0133661.	1.1	73
117	A genome-based identification approach for members of the genus <i>Bifidobacterium</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	12
118	Exploring Vertical Transmission of <i>Bifidobacteria</i> from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	1.4	191
119	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
120	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
121	Comparative genomics of the <i>Bifidobacterium brevetaxon</i> . <i>BMC Genomics</i> , 2014, 15, 170.	1.2	113
122	<i>Bifidobacterium bifidum</i> PRL2010 Modulates the Host Innate Immune Response. <i>Applied and Environmental Microbiology</i> , 2014, 80, 730-740.	1.4	67
123	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
124	<i>Bifidobacteria</i> 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
125	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
126	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203



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127	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
128	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
129	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
130	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	1.1	257
131	<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