

Marco Ventura

List of Publications by Year in descending order

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295
papers

23,169
citations

6592

79
h-index

10708

138
g-index

299
all docs

299
docs citations

299
times ranked

19733
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	Genomics of <i>Actinobacteria</i> : Tracing the Evolutionary History of an Ancient Phylum. <i>Microbiology and Molecular Biology Reviews</i> , 2007, 71, 495-548.	2.9	852
4	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
5	Diversity of Bifidobacteria within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	1.1	512
6	Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus. <i>MBio</i> , 2014, 5, e01548-14.	1.8	500
7	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 837-890.	2.9	487
8	Genome-scale analyses of health-promoting bacteria: probiogenomics. <i>Nature Reviews Microbiology</i> , 2009, 7, 61-71.	13.6	400
9	Complete Genome Sequence of the Prototype Lactic Acid Bacterium <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363. <i>Journal of Bacteriology</i> , 2007, 189, 3256-3270.	1.0	362
10	Stable Engraftment of <i>Bifidobacterium longum</i> AH1206 in the Human Gut Depends on Individualized Features of the Resident Microbiome. <i>Cell Host and Microbe</i> , 2016, 20, 515-526.	5.1	337
11	Intestinal Microbiota Development in Preterm Neonates and Effect of Perinatal Antibiotics. <i>Journal of Pediatrics</i> , 2015, 166, 538-544.	0.9	329
12	Functional genome analysis of <i>Bifidobacterium breve</i> UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11217-11222.	3.3	328
13	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
14	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
15	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
16	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	1.1	257
17	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240
18	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

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19	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	1.6	233
20	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
21	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
22	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203
23	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
24	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	1.4	191
25	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	191
26	Human gut microbiota and bifidobacteria: from composition to functionality. <i>Antonie Van Leeuwenhoek</i> , 2008, 94, 35-50.	0.7	182
27	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. <i>Trends in Microbiology</i> , 2018, 26, 339-350.	3.5	182
28	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
29	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
30	Insights into the taxonomy, genetics and physiology of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2004, 86, 205-223.	0.7	164
31	Host-microbe interactions that facilitate gut colonization by commensal bifidobacteria. <i>Trends in Microbiology</i> , 2012, 20, 467-476.	3.5	164
32	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
33	Cross-feeding by <i>Bifidobacterium breve</i> UCC2003 during co-cultivation with <i>Bifidobacterium bifidum</i> PRL2010 in a mucin-based medium. <i>BMC Microbiology</i> , 2014, 14, 282.	1.3	158
34	Analysis of bifidobacterial evolution using a multilocus approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2783-2792.	0.8	154
35	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	1.8	153
36	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	1.8	152

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37	Analysis, Characterization, and Loci of the <i>tuf</i> Genes in <i>Lactobacillus</i> and <i>Bifidobacterium</i> Species and Their Direct Application for Species Identification. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6908-6922.	1.4	150
38	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	1.6	148
39	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	1.6	146
40	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
41	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
42	Genomics and ecological overview of the genus <i>Bifidobacterium</i> . <i>International Journal of Food Microbiology</i> , 2011, 149, 37-44.	2.1	140
43	<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
44	Specific Identification and Targeted Characterization of <i>Bifidobacterium lactis</i> from Different Environmental Isolates by a Combined Multiplex-PCR Approach. <i>Applied and Environmental Microbiology</i> , 2001, 67, 2760-2765.	1.4	136
45	Polyphasic taxonomic analysis of <i>Bifidobacterium animalis</i> and <i>Bifidobacterium lactis</i> reveals relatedness at the subspecies level: reclassification of <i>Bifidobacterium animalis</i> as <i>Bifidobacterium animalis</i> subsp. <i>animalis</i> subsp. nov. and <i>Bifidobacterium lactis</i> as <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1137-1143.	0.8	136
46	Metabolism of Sialic Acid by <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4414-4426.	1.4	130
47	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
48	<i>Bifidobacteria</i> 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
49	Microbiomic analysis of the bifidobacterial population in the human distal gut. <i>ISME Journal</i> , 2009, 3, 745-751.	4.4	128
50	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
51	<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
52	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
53	Comparative genomics of the genus <i>Bifidobacterium</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3243-3254.	0.7	116
54	Comparative genomics of the <i>Bifidobacterium</i> <i>brevetax</i> on. <i>BMC Genomics</i> , 2014, 15, 170.	1.2	113

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55	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
56	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
57	Omics of bifidobacteria: research and insights into their health-promoting activities. <i>Biochemical Journal</i> , 2017, 474, 4137-4152.	1.7	107
58	Diversity, ecology and intestinal function of bifidobacteria. <i>Microbial Cell Factories</i> , 2014, 13, S4.	1.9	106
59	Identification and Characterization of Novel Surface Proteins in <i>Lactobacillus johnsonii</i> and <i>Lactobacillus gasseri</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 6172-6181.	1.4	104
60	Molecular microbial analysis of <i>Bifidobacterium</i> isolates from different environments by the species-specific amplified ribosomal DNA restriction analysis (ARDRA). <i>FEMS Microbiology Ecology</i> , 2001, 36, 113-121.	1.3	103
61	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw191.	1.3	102
62	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. <i>Microbiome</i> , 2019, 7, 100.	4.9	101
63	Rapid Identification, Differentiation, and Proposed New Taxonomic Classification of <i>Bifidobacterium lactis</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 6429-6434.	1.4	100
64	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , 2017, 18, 568.	1.2	98
65	Specific identification and molecular typing analysis of <i>Lactobacillus johnsonii</i> by using PCR-based methods and pulsed-field gel electrophoresis. <i>FEMS Microbiology Letters</i> , 2002, 217, 141-154.	0.7	97
66	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
67	Pre- and probiotic overview. <i>Current Opinion in Pharmacology</i> , 2018, 43, 87-92.	1.7	97
68	Comparative genomics of phages and prophages in lactic acid bacteria. <i>Antonie Van Leeuwenhoek</i> , 2002, 82, 73-91.	0.7	96
69	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
70	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	4.4	96
71	Characterization of the groEL and groES Loci in <i>Bifidobacterium breve</i> UCC 2003: Genetic, Transcriptional, and Phylogenetic Analyses. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6197-6209.	1.4	95
72	Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2007, 91, 351-372.	0.7	95

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73	Bifidobacterium lactis DSM 10140: Identification of the atp (atpBEFHAGDC) Operon and Analysis of Its Genetic Structure, Characteristics, and Phylogeny. Applied and Environmental Microbiology, 2004, 70, 3110-3121.	1.4	94
74	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. FEMS Microbiology Letters, 2016, 363, fnw049.	0.7	94
75	The infant gut microbiome as a microbial organ influencing host well-being. Italian Journal of Pediatrics, 2020, 46, 16.	1.0	93
76	Bifidobacterium bifidum as an example of a specialized human gut commensal. Frontiers in Microbiology, 2014, 5, 437.	1.5	92
77	Allergic Patients with Long-Term Asthma Display Low Levels of Bifidobacterium adolescentis. PLoS ONE, 2016, 11, e0147809.	1.1	90
78	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. Applied and Environmental Microbiology, 2017, 83, .	1.4	88
79	Obesity and microbiota: an example of an intricate relationship. Genes and Nutrition, 2017, 12, 18.	1.2	86
80	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. Frontiers in Microbiology, 2017, 8, 1749.	1.5	86
81	Genetic analysis and morphological identification of pilus-like structures in members of the genus Bifidobacterium. Microbial Cell Factories, 2011, 10, S16.	1.9	84
82	Bifidobacterial Dialogue With Its Human Host and Consequent Modulation of the Immune System. Frontiers in Immunology, 2019, 10, 2348.	2.2	81
83	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . Environmental Microbiology, 2015, 17, 2515-2531.	1.8	80
84	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of Lactobacillus gasseri, Lactobacillus salivarius, and Lactobacillus casei. Applied and Environmental Microbiology, 2006, 72, 3130-3146.	1.4	75
85	Comparative Genomics of Bifidobacterium animalis subsp. lactis Reveals a Strict Monophyletic Bifidobacterial Taxon. Applied and Environmental Microbiology, 2013, 79, 4304-4315.	1.4	74
86	Genomic Characterization and Transcriptional Studies of the Starch-Utilizing Strain Bifidobacterium adolescentis 22L. Applied and Environmental Microbiology, 2014, 80, 6080-6090.	1.4	74
87	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. Frontiers in Microbiology, 2015, 6, 1030.	1.5	74
88	Lactobacillus rossiae, a Vitamin B12 Producer, Represents a Metabolically Versatile Species within the Genus Lactobacillus. PLoS ONE, 2014, 9, e107232.	1.1	74
89	Occurrence and Diversity of CRISPR-Cas Systems in the Genus Bifidobacterium. PLoS ONE, 2015, 10, e0133661.	1.1	73
90	Microbial diversity in the human intestine and novel insights from metagenomics. Frontiers in Bioscience - Landmark, 2009, Volume, 3214.	3.0	72

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91	Progress in genomics, metabolism and biotechnology of bifidobacteria. International Journal of Food Microbiology, 2011, 149, 4-18.	2.1	72
92	Contribution of Aggregation-Promoting Factor to Maintenance of Cell Shape in <i>Lactobacillus gasseri</i> 4B2. Journal of Bacteriology, 2003, 185, 3288-3296.	1.0	71
93	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
94	Prophage-Like Elements in Bifidobacteria: Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. Applied and Environmental Microbiology, 2005, 71, 8692-8705.	1.4	70
95	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. Microorganisms, 2019, 7, 544.	1.6	70
96	Gene Structure and Transcriptional Organization of the <i>dnaK</i> Operon of <i>Bifidobacterium breve</i> UCC 2003 and Application of the Operon in Bifidobacterial Tracing. Applied and Environmental Microbiology, 2005, 71, 487-500.	1.4	69
97	Ranking the impact of human health disorders on gut metabolism: Systemic lupus erythematosus and obesity as study cases. Scientific Reports, 2015, 5, 8310.	1.6	68
98	Rapid Amplified Ribosomal DNA Restriction Analysis (ARDRA) Identification of <i>Lactobacillus</i> spp. Isolated from Fecal and Vaginal Samples. Systematic and Applied Microbiology, 2000, 23, 504-509.	1.2	67
99	From bacterial genome to functionality; case bifidobacteria. International Journal of Food Microbiology, 2007, 120, 2-12.	2.1	67
100	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
101	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
102	<i>Bifidobacterium bifidum</i> PRL2010 Modulates the Host Innate Immune Response. Applied and Environmental Microbiology, 2014, 80, 730-740.	1.4	67
103	Characterization of the Serpin-Encoding Gene of <i>Bifidobacterium breve</i> 210B. Applied and Environmental Microbiology, 2010, 76, 3206-3219.	1.4	66
104	Prophages of the genus <i>Bifidobacterium</i> as modulating agents of the infant gut microbiota. Environmental Microbiology, 2016, 18, 2196-2213.	1.8	66
105	The prophage sequences of <i>Lactobacillus plantarum</i> strain WCFS1. Virology, 2003, 316, 245-255.	1.1	65
106	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
107	Sequence and comparative genomic analysis of lactococcal bacteriophages jj50, 712 and P008: evolutionary insights into the 936 phage species. FEMS Microbiology Letters, 2006, 261, 253-261.	0.7	63
108	Analysis of Predicted Carbohydrate Transport Systems Encoded by <i>Bifidobacterium bifidum</i> PRL2010. Applied and Environmental Microbiology, 2012, 78, 5002-5012.	1.4	63

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109	Comparative Sequence Analysis of the <i>tuf</i> and <i>recA</i> Genes and Restriction Fragment Length Polymorphism of the Internal Transcribed Spacer Region Sequences Supply Additional Tools for Discriminating <i>Bifidobacterium lactis</i> from <i>Bifidobacterium animalis</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 7517-7522.	1.4	61
110	Identification and Tracing of <i>Bifidobacterium</i> Species by Use of Enterobacterial Repetitive Intergenic Consensus Sequences. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4296-4301.	1.4	61
111	An Interactive Regulatory Network Controls Stress Response in <i>Bifidobacterium breve</i> UCC2003. <i>Journal of Bacteriology</i> , 2009, 191, 7039-7049.	1.0	60
112	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
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	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
115	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
116	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
117	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
118	Exploiting <i>Bifidobacterium</i> genomes: The molecular basis of stress response. <i>International Journal of Food Microbiology</i> , 2007, 120, 13-24.	2.1	55
119	Integration and Distribution of <i>Lactobacillus johnsonii</i> Prophages. <i>Journal of Bacteriology</i> , 2003, 185, 4603-4608.	1.0	54
120	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
121	Metabolism of Four α -Glycosidic Linkage-Containing Oligosaccharides by <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6280-6292.	1.4	54
122	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
123	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
124	The prophages of <i>Lactobacillus johnsonii</i> NCC 533: comparative genomics and transcription analysis. <i>Virology</i> , 2004, 320, 229-242.	1.1	53
125	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
126	The impact of bacteriophages on probiotic bacteria and gut microbiota diversity. <i>Genes and Nutrition</i> , 2011, 6, 205-207.	1.2	52

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127	Molecular Characterization of hsp20 , Encoding a Small Heat Shock Protein of Bifidobacterium breve UCC2003. Applied and Environmental Microbiology, 2007, 73, 4695-4703.	1.4	51
128	Expression of sortase-dependent pili of <i>Bifidobacterium bifidum</i> PRL2010 in response to environmental gut conditions. FEMS Microbiology Letters, 2014, 357, 23-33.	0.7	50
129	Microbial and metabolic multi-omic correlations in systemic sclerosis patients. Annals of the New York Academy of Sciences, 2018, 1421, 97-109.	1.8	50
130	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. Environmental Microbiology, 2017, 19, 4771-4783.	1.8	49
131	The genus Bifidobacterium: from genomics to functionality of an important component of the mammalian gut microbiota. Computational and Structural Biotechnology Journal, 2021, 19, 1472-1487.	1.9	49
132	How high G+C Gram-positive bacteria and in particular bifidobacteria cope with heat stress: protein players and regulators. FEMS Microbiology Reviews, 2006, 30, 734-759.	3.9	48
133	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host co-evolution. Environmental Microbiology, 2019, 21, 3683-3695.	1.8	47
134	Colonization of the human gut by bovine bacteria present in Parmesan cheese. Nature Communications, 2019, 10, 1286.	5.8	46
135	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. Applied and Environmental Microbiology, 2009, 75, 6929-6936.	1.4	45
136	Exploring Amino Acid Auxotrophy in Bifidobacterium bifidum PRL2010. Frontiers in Microbiology, 2015, 6, 1331.	1.5	45
137	Ancient bacteria of the <i>Å-tzi</i> ™s microbiome: a genomic tale from the Copper Age. Microbiome, 2017, 5, 5.	4.9	45
138	Fecal microbiota profile in a group of myasthenia gravis patients. Scientific Reports, 2018, 8, 14384.	1.6	45
139	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., International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1288-1298.	0.8	45
140	Modulation of the <i>eps</i> -ome transcription of bifidobacteria through simulation of human intestinal environment. FEMS Microbiology Ecology, 2016, 92, fiw056.	1.3	44
141	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. Genome Biology, 2019, 20, 96.	3.8	44
142	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
143	Ability of Bifidobacterium breve To Grow on Different Types of Milk: Exploring the Metabolism of Milk through Genome Analysis. Applied and Environmental Microbiology, 2011, 77, 7408-7417.	1.4	42
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291	Claimed Effects, Outcome Variables and Methods of Measurement for Health Claims on Foods Related to Vision Proposed Under Regulation (EC) 1924/2006. <i>Nutrients</i> , 2018, 10, 211.	1.7	0
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294	Editorial overview: Biotechnological insights of marine and terrestrial microbiome. <i>Current Opinion in Biotechnology</i> , 2022, 73, vii-ix.	3.3	0
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