List of Publications by Year in descending order

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DOLINE VAN SINDEREN

#	Article	IF	CITATIONS
1	Galacto-oligosaccharides as infant prebiotics: production, application, bioactive activities and future perspectives. Critical Reviews in Food Science and Nutrition, 2023, 63, 753-766.	10.3	30
2	Creating an atlas to visualize the biodiversity of the mammalian gut microbiota. Current Opinion in Biotechnology, 2022, 73, 28-33.	6.6	5
3	Virome studies of food production systems: time for †farm to fork' analyses. Current Opinion in Biotechnology, 2022, 73, 22-27.	6.6	11
4	The human gut microbiota during the initial stages of life: insights from bifidobacteria. Current Opinion in Biotechnology, 2022, 73, 81-87.	6.6	29
5	A Proposed Framework to Identify Dispensable and Essential Functions in Bifidobacteria: Case Study of Bifidobacterium breve UCC2003 as a Prototype of Its Genus. Methods in Molecular Biology, 2022, 2377, 273-302.	0.9	0
6	Novel Siphoviridae phage PMBT4 belonging to the group b Lactobacillus delbrueckii subsp. bulgaricus phages. Virus Research, 2022, 308, 198635.	2.2	5
7	Needle in a Whey-Stack: PhRACS as a Discovery Tool for Unknown Phage-Host Combinations. MBio, 2022, 13, e0333421.	4.1	5
8	Diet and mental health in pregnancy: Nutrients of importance based on large observational cohort data. Nutrition, 2022, 96, 111582.	2.4	15
9	Brussowvirus SW13 Requires a Cell Surface-Associated Polysaccharide To Recognize Its Streptococcus thermophilus Host. Applied and Environmental Microbiology, 2022, 88, AEM0172321.	3.1	8
10	Natural Transformation in Gram-Positive Bacteria and Its Biotechnological Relevance to Lactic Acid Bacteria. Annual Review of Food Science and Technology, 2022, 13, 409-431.	9.9	6
11	Disclosing the Genomic Diversity among Members of the <i>Bifidobacterium</i> Genus of Canine and Feline Origin with Respect to Those from Human. Applied and Environmental Microbiology, 2022, 88, e0203821.	3.1	3
12	Evaluation of Modulatory Activities of Lactobacillus crispatus Strains in the Context of the Vaginal Microbiota. Microbiology Spectrum, 2022, 10, e0273321.	3.0	14
13	Human milk oligosaccharide-sharing by a consortium of infant derived Bifidobacterium species. Scientific Reports, 2022, 12, 4143.	3.3	20
14	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. Journal of Oral Microbiology, 2022, 14, 2051336.	2.7	6
15	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. Environmental Microbiology, 2022, , .	3.8	5
16	Dairy streptococcal cell wall and exopolysaccharide genome diversity. Microbial Genomics, 2022, 8, .	2.0	2
17	Insights into endogenous Bifidobacterium species in the human gut microbiota during adulthood. Trends in Microbiology, 2022, 30, 940-947.	7.7	56
18	Comparative Genomics of Lactiplantibacillus plantarum: Insights Into Probiotic Markers in Strains Isolated From the Human Gastrointestinal Tract and Fermented Foods. Frontiers in Microbiology, 2022, 13, .	3.5	9

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19	Exploring the Ecological Effects of Naturally Antibiotic-Insensitive Bifidobacteria in the Recovery of the Resilience of the Gut Microbiota during and after Antibiotic Treatment. Applied and Environmental Microbiology, 2022, 88, .	3.1	4
20	Maximum depth sequencing reveals an ON/OFF replication slippage switch and apparent in vivo selection for bifidobacterial pilus expression. Scientific Reports, 2022, 12, .	3.3	2
21	Priority effects shape the structure of infant-type <i>Bifidobacterium</i> communities on human milk oligosaccharides. ISME Journal, 2022, 16, 2265-2279.	9.8	34
22	Maternal gut microbiota Bifidobacterium promotes placental morphogenesis, nutrient transport and fetal growth in mice. Cellular and Molecular Life Sciences, 2022, 79, .	5.4	19
23	Envisioning emerging frontiers on human gut microbiota and its applications. Microbial Biotechnology, 2021, 14, 12-17.	4.2	2
24	Measuring Conjugated Linoleic Acid (CLA) Production by Bifidobacteria. Methods in Molecular Biology, 2021, 2278, 87-100.	0.9	2
25	Phageome Analysis of Bifidobacteria-Rich Samples. Methods in Molecular Biology, 2021, 2278, 71-85.	0.9	0
26	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.	4.1	49
27	A Resource for Cloning and Expression Vectors Designed for Bifidobacteria: Overview of Available Tools and Biotechnological Applications. Methods in Molecular Biology, 2021, 2278, 157-182.	0.9	1
28	Protocol to Select Bifidobacteria from Fecal and Environmental Samples. Methods in Molecular Biology, 2021, 2278, 61-70.	0.9	1
29	Isolation of Chromosomal and Plasmid DNA from Bifidobacteria. Methods in Molecular Biology, 2021, 2278, 21-29.	0.9	1
30	Determination of Bifidobacterial Carbohydrate Utilization Abilities and Associated Metabolic End Products. Methods in Molecular Biology, 2021, 2278, 117-129.	0.9	2
31	Bifidobacterium Genome Assembly and Methylome Analysis Using Pacbio SMRT Sequencing. Methods in Molecular Biology, 2021, 2278, 225-232.	0.9	0
32	Bifidobacterium Transformation. Methods in Molecular Biology, 2021, 2278, 13-19.	0.9	2
33	Viral Genomics and Evolution: The Fascinating Story of Dairy Phages. , 2021, , 171-187.		1
34	Vaginotypes of the human vaginal microbiome. Environmental Microbiology, 2021, 23, 1780-1792.	3.8	30
35	Broad Purpose Vector for Site-Directed Insertional Mutagenesis in Bifidobacterium breve. Frontiers in Microbiology, 2021, 12, 636822.	3.5	7
36	Analysis of Selection Methods to Develop Novel Phage Therapy Cocktails Against Antimicrobial Resistant Clinical Isolates of Bacteria. Frontiers in Microbiology, 2021, 12, 613529.	3.5	42

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37	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . Applied and Environmental Microbiology, 2021, 87, .	3.1	16
38	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, .	3.1	8
39	Genetic Dissection of a Prevalent Plasmid-Encoded Conjugation System in Lactococcus lactis. Frontiers in Microbiology, 2021, 12, 680920.	3.5	8
40	Genetic insights into the dark matter of the mammalian gut microbiota through targeted genome reconstruction. Environmental Microbiology, 2021, 23, 3294-3305.	3.8	5
41	Molecular analysis of the replication functions of the bifidobacterial conjugative megaplasmid pMP7017. Microbial Biotechnology, 2021, 14, 1494-1511.	4.2	0
42	Infant-Associated Bifidobacterial β-Galactosidases and Their Ability to Synthesize Galacto-Oligosaccharides. Frontiers in Microbiology, 2021, 12, 662959.	3.5	9
43	A comprehensive review on the impact of β-glucan metabolism by Bacteroides and Bifidobacterium species as members of the gut microbiota. International Journal of Biological Macromolecules, 2021, 181, 877-889.	7.5	40
44	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. MSystems, 2021, 6, e0058321.	3.8	35
45	Bifidobacterium breve Exopolysaccharide Blocks Dendritic Cell Maturation and Activation of CD4+ T Cells. Frontiers in Microbiology, 2021, 12, 653587.	3.5	14
46	Phylogenomic disentangling of the Bifidobacterium longum subsp. infantis taxon. Microbial Genomics, 2021, 7, .	2.0	9
47	Lactic Acid Bacteria Diversity and Characterization of Probiotic Candidates in Fermented Meats. Foods, 2021, 10, 1519.	4.3	23
48	Shaping the Future of Probiotics and Prebiotics. Trends in Microbiology, 2021, 29, 667-685.	7.7	270
49	Biodiversity of Phages Infecting the Dairy Bacterium Streptococcus thermophilus. Microorganisms, 2021, 9, 1822.	3.6	7
50	In Vitro and In Vivo Assessment of the Potential of Escherichia coli Phages to Treat Infections and Survive Gastric Conditions. Microorganisms, 2021, 9, 1869.	3.6	4
51	Cell wall polysaccharides of Gram positive ovococcoid bacteria and their role as bacteriophage receptors. Computational and Structural Biotechnology Journal, 2021, 19, 4018-4031.	4.1	9
52	Site-Directed Mutagenesis of Bifidobacterium Strains. Methods in Molecular Biology, 2021, 2278, 45-60.	0.9	1
53	Plant Glycan Metabolism by Bifidobacteria. Frontiers in Microbiology, 2021, 12, 609418.	3.5	40
54	Exploring the Ecology of Bifidobacteria and Their Genetic Adaptation to the Mammalian Gut. Microorganisms, 2021, 9, 8.	3.6	21

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55	Bifidobacterial β-Galactosidase-Mediated Production of Galacto-Oligosaccharides: Structural and Preliminary Functional Assessments. Frontiers in Microbiology, 2021, 12, 750635.	3.5	3
56	Editorial: Role of Bifidobacteria in Human and Animal Health and Biotechnological Applications. Frontiers in Microbiology, 2021, 12, 785664.	3.5	4
57	Simultaneous Production of Multiple Antimicrobial Compounds by Bacillus velezensis ML122-2 Isolated From Assam Tea Leaf [Camellia sinensis var. assamica (J.W.Mast.) Kitam.]. Frontiers in Microbiology, 2021, 12, 789362.	3.5	8
58	The Probiotic Identity Card: A Novel "Probiogenomics―Approach to Investigate Probiotic Supplements. Frontiers in Microbiology, 2021, 12, 790881.	3.5	11
59	Diversity of Human-Associated Bifidobacterial Prophage Sequences. Microorganisms, 2021, 9, 2559.	3.6	5
60	Metabolism of biosynthetic oligosaccharides by human-derived Bifidobacterium breve UCC2003 and Bifidobacterium longum NCIMB 8809. International Journal of Food Microbiology, 2020, 316, 108476.	4.7	16
61	The impact of probiotic supplementation on metabolic health in healthy women of reproductive age: a systematic review. Food and Function, 2020, 11, 10279-10289.	4.6	3
62	Riboflavin Biosynthesis and Overproduction by a Derivative of the Human Gut Commensal Bifidobacterium longum subsp. infantis ATCC 15697. Frontiers in Microbiology, 2020, 11, 573335.	3.5	18
63	214: Lifestyle, metabolic health and the gut microbiome in early pregnancy. American Journal of Obstetrics and Gynecology, 2020, 222, S148-S149.	1.3	0
64	Bifidobacterial biofilm formation is a multifactorial adaptive phenomenon in response to bile exposure. Scientific Reports, 2020, 10, 11598.	3.3	37
65	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. MSystems, 2020, 5, .	3.8	13
66	Special Issue "Bifidobacteria: Insights from Ecology to Genomics of a Key Microbial Group of the Mammalian Gut Microbiota― Microorganisms, 2020, 8, 1660.	3.6	0
67	Multi-population cohort meta-analysis of human intestinal microbiota in early life reveals the existence of infant community state types (ICSTs). Computational and Structural Biotechnology Journal, 2020, 18, 2480-2493.	4.1	19
68	The Infant-Derived Bifidobacterium bifidum Strain CNCM I-4319 Strengthens Gut Functionality. Microorganisms, 2020, 8, 1313.	3.6	10
69	Microbiota and Cancer: The Emerging Beneficial Role of Bifidobacteria in Cancer Immunotherapy. Frontiers in Microbiology, 2020, 11, 575072.	3.5	40
70	Multi-omics Approaches To Decipher the Impact of Diet and Host Physiology on the Mammalian Gut Microbiome. Applied and Environmental Microbiology, 2020, 86, .	3.1	24
71	Catching a glimpse of the bacterial gut community of companion animals: a canine and feline perspective. Microbial Biotechnology, 2020, 13, 1708-1732.	4.2	38
72	Evaluation of methods for the reduction of contaminating host reads when performing shotgun metagenomic sequencing of the milk microbiome. Scientific Reports, 2020, 10, 21665.	3.3	33

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73	Lysogenization of a Lactococcal Host with Three Distinct Temperate Phages Provides Homologous and Heterologous Phage Resistance. Microorganisms, 2020, 8, 1685.	3.6	13
74	Can a probiotic supplement in pregnancy result in transfer to the neonatal gut: A systematic review. Acta Obstetricia Et Gynecologica Scandinavica, 2020, 99, 1269-1277.	2.8	11
75	Biochemical analysis of crossâ€feeding behaviour between two common gut commensals when cultivated on plantâ€derived arabinogalactan. Microbial Biotechnology, 2020, 13, 1733-1747.	4.2	20
76	Evolutionary development and coâ€phylogeny of primateâ€associated bifidobacteria. Environmental Microbiology, 2020, 22, 3375-3393.	3.8	17
77	Revisiting the host adhesion determinants of <i>Streptococcus thermophilus</i> siphophages. Microbial Biotechnology, 2020, 13, 1765-1779.	4.2	20
78	Beer spoilage and low pH tolerance is linked to manganese homeostasis in selected <i>Lactobacillus brevis</i> strains. Journal of Applied Microbiology, 2020, 129, 1309-1320.	3.1	10
79	Maternal and infant factors that shape neonatal gut colonization by bacteria. Expert Review of Gastroenterology and Hepatology, 2020, 14, 651-664.	3.0	16
80	The CWPS Rubik's cube: Linking diversity of cell wall polysaccharide structures with the encoded biosynthetic machinery of selected <i>Lactococcus lactis</i> strains. Molecular Microbiology, 2020, 114, 582-596.	2.5	19
81	From lab bench to formulated ingredient: Characterization, production, and commercialization of human milk oligosaccharides. Journal of Functional Foods, 2020, 72, 104052.	3.4	44
82	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. FEMS Microbiology Ecology, 2020, 96, .	2.7	33
83	Three distinct glycosylation pathways are involved in the decoration of Lactococcus lactis cell wall glycopolymers. Journal of Biological Chemistry, 2020, 295, 5519-5532.	3.4	13
84	Human milk oligosaccharides: Shaping the infant gut microbiota and supporting health. Journal of Functional Foods, 2020, 72, 104074.	3.4	159
85	Bifidobacterium breve UCC2003 Induces a Distinct Global Transcriptomic Program in Neonatal Murine Intestinal Epithelial Cells. IScience, 2020, 23, 101336.	4.1	23
86	The Impact and Applications of Phages in the Food Industry and Agriculture. Viruses, 2020, 12, 210.	3.3	4
87	A cell wallâ€associated polysaccharide is required for bacteriophage adsorption to the <i>Streptococcus thermophilus</i> cell surface. Molecular Microbiology, 2020, 114, 31-45.	2.5	22
88	A Plasmid-Encoded Putative Glycosyltransferase Is Involved in Hop Tolerance and Beer Spoilage in Lactobacillus brevis. Applied and Environmental Microbiology, 2020, 86, .	3.1	12
89	The infant gut microbiome as a microbial organ influencing host well-being. Italian Journal of Pediatrics, 2020, 46, 16.	2.6	93
90	Ecological Importance of Cross-Feeding of the Intermediate Metabolite 1,2-Propanediol between Bacterial Gut Symbionts. Applied and Environmental Microbiology, 2020, 86, .	3.1	40

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91	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. Applied and Environmental Microbiology, 2020, 86, .	3.1	9
92	Bifidobacterium breve UCC2003 Exopolysaccharide Modulates the Early Life Microbiota by Acting as a Potential Dietary Substrate. Nutrients, 2020, 12, 948.	4.1	22
93	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. Applied and Environmental Microbiology, 2020, 86, .	3.1	30
94	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. Microorganisms, 2020, 8, 131.	3.6	26
95	Identification of a Prophage-encoded Abortive Infection System in Levilactobacillus brevis. Microbiology and Biotechnology Letters, 2020, 48, 322-327.	0.4	1
96	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. FEMS Microbiology Ecology, 2019, 95, .	2.7	29
97	Characterization of GH2 and GH42 β-galactosidases derived from bifidobacterial infant isolates. AMB Express, 2019, 9, 9.	3.0	24
98	Ubiquitous Carbohydrate Binding Modules Decorate 936 Lactococcal Siphophage Virions. Viruses, 2019, 11, 631.	3.3	19
99	A microbiome reality check: limitations of <i>in silico</i> â€based metagenomic approaches to study complex bacterial communities. Environmental Microbiology Reports, 2019, 11, 840-847.	2.4	10
100	A dual-chain assembly pathway generates the high structural diversity of cell-wall polysaccharides in Lactococcus lactis. Journal of Biological Chemistry, 2019, 294, 17612-17625.	3.4	25
101	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. Microorganisms, 2019, 7, 535.	3.6	10
102	Biodiversity and Classification of Phages Infecting Lactobacillus brevis. Frontiers in Microbiology, 2019, 10, 2396.	3.5	9
103	Bifidobacterial Dialogue With Its Human Host and Consequent Modulation of the Immune System. Frontiers in Immunology, 2019, 10, 2348.	4.8	81
104	Metabolism of the predominant human milk oligosaccharide fucosyllactose by an infant gut commensal. Scientific Reports, 2019, 9, 15427.	3.3	58
105	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. Microorganisms, 2019, 7, 293.	3.6	10
106	A Quest of Great Importance-Developing a Broad Spectrum Escherichia coli Phage Collection. Viruses, 2019, 11, 899.	3.3	9
107	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. Environmental Microbiology, 2019, 21, 1331-1343.	3.8	60
108	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. International Journal of Food Microbiology, 2019, 294, 1-9.	4.7	26

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109	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, .	3.1	11
110	Implementation of Transposon Mutagenesis in Bifidobacterium. Methods in Molecular Biology, 2019, 2016, 51-62.	0.9	2
111	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbeâ€host coâ€evolution. Environmental Microbiology, 2019, 21, 3683-3695.	3.8	47
112	Comparative genome analysis of the Lactobacillus brevis species. BMC Genomics, 2019, 20, 416.	2.8	45
113	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. Genome Biology, 2019, 20, 96.	8.8	44
114	Isolation and Characterization of Lactobacillus brevis Phages. Viruses, 2019, 11, 393.	3.3	22
115	The Lactococcus lactis Pan-Plasmidome. Frontiers in Microbiology, 2019, 10, 707.	3.5	22
116	Colonization of the human gut by bovine bacteria present in Parmesan cheese. Nature Communications, 2019, 10, 1286.	12.8	46
117	Impact of a bathing tradition on shared gut microbes among Japanese families. Scientific Reports, 2019, 9, 4380.	3.3	16
118	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. Scientific Reports, 2019, 9, 5755.	3.3	22
119	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, .	3.1	44
120	Bifidobacterium bifidum: A Key Member of the Early Human Gut Microbiota. Microorganisms, 2019, 7, 544.	3.6	70
121	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. Microorganisms, 2019, 7, 599.	3.6	8
122	Mobilome and Resistome Reconstruction from Genomes Belonging to Members of the Bifidobacterium Genus. Microorganisms, 2019, 7, 638.	3.6	25
123	Transcriptional control of central carbon metabolic flux in Bifidobacteria by two functionally similar, yet distinct Lacl-type regulators. Scientific Reports, 2019, 9, 17851.	3.3	13
124	Health benefits conferred by the human gut microbiota during infancy. Microbial Biotechnology, 2019, 12, 243-248.	4.2	7
125	Complete Genome Sequence of Lactococcus lactis subsp. cremoris 3107, Host for the Model Lactococcal P335 Bacteriophage TP901-1. Microbiology Resource Announcements, 2019, 8, .	0.6	4
126	A Bifidobacterial pilusâ€associated protein promotes colonic epithelial proliferation. Molecular Microbiology, 2019, 111, 287-301.	2.5	62

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127	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.	1.7	45
128	Bifidobacteria. , 2019, , 125-137.		0
129	Assessing the functionality and genetic diversity of lactococcal prophages. International Journal of Food Microbiology, 2018, 272, 29-40.	4.7	26
130	Bifidobacterium breve UCC2003 Employs Multiple Transcriptional Regulators To Control Metabolism of Particular Human Milk Oligosaccharides. Applied and Environmental Microbiology, 2018, 84, .	3.1	23
131	Determination of the cell wall polysaccharide and teichoic acid structures from Lactococcus lactis IL1403. Carbohydrate Research, 2018, 462, 39-44.	2.3	21
132	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 Systematic and Applied Microbiology, 2018, 41, 173-183.	2.8	58
133	Impact of gut-associated bifidobacteria and their phages on health: two sides of the same coin?. Applied Microbiology and Biotechnology, 2018, 102, 2091-2099.	3.6	14
134	Carbohydrate Metabolism inÂBifidobacteria. , 2018, , 145-164.		15
135	Bifidobacteria: Ecology and Coevolution With the Host. , 2018, , 213-220.		4
136	Genomic diversity and distribution of Bifidobacterium longum subsp. longum across the human lifespan. Scientific Reports, 2018, 8, 85.	3.3	99
137	Comparative genome and methylome analysis reveals restriction/modification system diversity in the gut commensal Bifidobacterium breve. Nucleic Acids Research, 2018, 46, 1860-1877.	14.5	46
138	Phylotype-Level Profiling of Lactobacilli in Highly Complex Environments by Means of an Internal Transcribed Spacer-Based Metagenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	3.1	16
139	Extraction of the same novel homoglycan mixture from two different strains of Bifidobacterium animalis and three strains of Bifidobacterium breve. Beneficial Microbes, 2018, 9, 663-674.	2.4	3
140	Structural studies of the cell wall polysaccharide from Lactococcus lactis UC509.9. Carbohydrate Research, 2018, 461, 25-31.	2.3	16
141	A Decade of Streptococcus thermophilus Phage Evolution in an Irish Dairy Plant. Applied and Environmental Microbiology, 2018, 84, .	3.1	35
142	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. Trends in Microbiology, 2018, 26, 339-350.	7.7	182
143	Plantaricyclin A, a Novel Circular Bacteriocin Produced by Lactobacillus plantarum NI326: Purification, Characterization, and Heterologous Production. Applied and Environmental Microbiology, 2018, 84, .	3.1	64
144	Bifidobacteria and the infant gut: an example of co-evolution and natural selection. Cellular and Molecular Life Sciences, 2018, 75, 103-118.	5.4	129

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145	Selected aspects of the human gut microbiota. Cellular and Molecular Life Sciences, 2018, 75, 81-82.	5.4	19
146	Generation of Bacteriophage-Insensitive Mutants of Streptococcus thermophilus via an Antisense RNA CRISPR-Cas Silencing Approach. Applied and Environmental Microbiology, 2018, 84, .	3.1	18
147	Tracking the Taxonomy of the Genus Bifidobacterium Based on a Phylogenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	3.1	58
148	Biodiversity of bacteriophages infecting Lactococcus lactis starter cultures. Journal of Dairy Science, 2018, 101, 96-105.	3.4	31
149	Identification of DNA Base Modifications by Means of Pacific Biosciences RS Sequencing Technology. Methods in Molecular Biology, 2018, 1681, 127-137.	0.9	10
150	Characterisation of a Hydroxycinnamic Acid Esterase From the Bifidobacterium longum subsp. longum Taxon. Frontiers in Microbiology, 2018, 9, 2690.	3.5	20
151	Identification of Dual Receptor Binding Protein Systems in Lactococcal 936 Group Phages. Viruses, 2018, 10, 668.	3.3	12
152	Staying alive: growth and survival of Bifidobacterium animalis subsp. animalis under in vitro and in vivo conditions. Applied Microbiology and Biotechnology, 2018, 102, 10645-10663.	3.6	3
153	Biodiversity of Streptococcus thermophilus Phages in Global Dairy Fermentations. Viruses, 2018, 10, 577.	3.3	29
154	Bifidobacterium bifidum PRL2010 alleviates intestinal ischemia/reperfusion injury. PLoS ONE, 2018, 13, e0202670.	2.5	16
155	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. Scientific Reports, 2018, 8, 13974.	3.3	148
156	Functional carbohydrate binding modules identified in evolved dits from siphophages infecting various Gramâ€positive bacteria. Molecular Microbiology, 2018, 110, 777-795.	2.5	32
157	Comparative Genomics Reveals the Regulatory Complexity of Bifidobacterial Arabinose and Arabino-Oligosaccharide Utilization. Frontiers in Microbiology, 2018, 9, 776.	3.5	45
158	Comparative genomics and genotype-phenotype associations in Bifidobacterium breve. Scientific Reports, 2018, 8, 10633.	3.3	37
159	Carbohydrate Syntrophy enhances the establishment of Bifidobacterium breve UCC2003 in the neonatal gut. Scientific Reports, 2018, 8, 10627.	3.3	19
160	In Vitro Characteristics of Phages to Guide â€~Real Life' Phage Therapy Suitability. Viruses, 2018, 10, 163.	3.3	76
161	Gene-trait matching across the Bifidobacterium longum pan-genome reveals considerable diversity in carbohydrate catabolism among human infant strains. BMC Genomics, 2018, 19, 33.	2.8	74
162	Characterization and induction of prophages in human gut-associated Bifidobacterium hosts. Scientific Reports, 2018, 8, 12772.	3.3	26

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163	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. Microbiome, 2018, 6, 145.	11.1	54
164	Exopolysaccharide from Bifidobacterium longum subsp. longum 35624â,,¢ modulates murine allergic airway responses. Beneficial Microbes, 2018, 9, 761-773.	2.4	35
165	Reconstruction of the Bifidobacterial Pan-Secretome Reveals the Network of Extracellular Interactions between Bifidobacteria and the Infant Gut. Applied and Environmental Microbiology, 2018, 84, .	3.1	16
166	Metaâ€analysis of the human gut microbiome from urbanized and preâ€agricultural populations. Environmental Microbiology, 2017, 19, 1379-1390.	3.8	153
167	Ancient bacteria of the Ötzi's microbiome: a genomic tale from the Copper Age. Microbiome, 2017, 5, 5.	11.1	45
168	<i>Bifidobacterium breve</i> reduces apoptotic epithelial cell shedding in an exopolysaccharide and MyD88-dependent manner. Open Biology, 2017, 7, 160155.	3.6	65
169	Next generation sequencing-based multigene panel for high throughput detection of food-borne pathogens. International Journal of Food Microbiology, 2017, 256, 20-29.	4.7	27
170	Bacteriophages Infecting Lactic Acid Bacteria. , 2017, , 249-272.		5
171	Comparative and functional genomics of the Lactococcus lactis taxon; insights into evolution and niche adaptation. BMC Genomics, 2017, 18, 267.	2.8	117
172	Genome Sequence of Serratia marcescens Phage BF. Genome Announcements, 2017, 5, .	0.8	11
173	Sourdough authentication: quantitative PCR to detect the lactic acid bacterial microbiota in breads. Scientific Reports, 2017, 7, 624.	3.3	24
174	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. Environmental Microbiology, 2017, 19, 4771-4783.	3.8	49
175	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. ISME Journal, 2017, 11, 2834-2847.	9.8	96
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