

Douwe Van Sinderen

List of Publications by Year in descending order

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502
papers

39,971
citations

2675

95
h-index

4432

172
g-index

510
all docs

510
docs citations

510
times ranked

29922
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota composition correlates with diet and health in the elderly. <i>Nature</i> , 2012, 488, 178-184.	27.8	2,618
2	Composition, variability, and temporal stability of the intestinal microbiota of the elderly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4586-4591.	7.1	1,418
3	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, .	6.6	1,118
4	Bacteria as vitamin suppliers to their host: a gut microbiota perspective. <i>Current Opinion in Biotechnology</i> , 2013, 24, 160-168.	6.6	1,101
5	Genomics of <i>Actinobacteria</i> : Tracing the Evolutionary History of an Ancient Phylum. <i>Microbiology and Molecular Biology Reviews</i> , 2007, 71, 495-548.	6.6	852
6	T-cell activation by transitory neo-antigens derived from distinct microbial pathways. <i>Nature</i> , 2014, 509, 361-365.	27.8	731
7	Carbohydrate metabolism in <i>Bifidobacteria</i> . <i>Genes and Nutrition</i> , 2011, 6, 285-306.	2.5	628
8	<i>Bifidobacteria</i> and Their Role as Members of the Human Gut Microbiota. <i>Frontiers in Microbiology</i> , 2016, 7, 925.	3.5	627
9	Diversity of <i>Bifidobacteria</i> within the Infant Gut Microbiota. <i>PLoS ONE</i> , 2012, 7, e36957.	2.5	512
10	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 837-890.	6.6	487
11	<i>Bifidobacterial</i> surface-exopolysaccharide facilitates commensal-host interaction through immune modulation and pathogen protection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2108-2113.	7.1	450
12	Genome-scale analyses of health-promoting bacteria: probiogenomics. <i>Nature Reviews Microbiology</i> , 2009, 7, 61-71.	28.6	400
13	Fermented functional foods based on probiotics and their biogenic metabolites. <i>Current Opinion in Biotechnology</i> , 2005, 16, 198-203.	6.6	375
14	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.	2.2	362
15	B-Group vitamin production by lactic acid bacteria - current knowledge and potential applications. <i>Journal of Applied Microbiology</i> , 2011, 111, 1297-1309.	3.1	359
16	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.	11.0	337
17	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.	7.1	328
18	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.	7.1	324

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19	Sequence and analysis of the genetic locus responsible for surfactin synthesis in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1993, 8, 821-831.	2.5	308
20	Improvement of the quality and shelf life of wheat bread by fermentation with the antifungal strain <i>Lactobacillus plantarum</i> FST 1.7. <i>Journal of Cereal Science</i> , 2007, 45, 309-318.	3.7	278
21	Getting better with bifidobacteria. <i>Journal of Applied Microbiology</i> , 2005, 98, 1303-1315.	3.1	274
22	Exploring the Diversity of the Bifidobacterial Population in the Human Intestinal Tract. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1534-1545.	3.1	270
23	Shaping the Future of Probiotics and Prebiotics. <i>Trends in Microbiology</i> , 2021, 29, 667-685.	7.7	270
24	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.	5.4	265
25	Assessing the Fecal Microbiota: An Optimized Ion Torrent 16S rRNA Gene-Based Analysis Protocol. <i>PLoS ONE</i> , 2013, 8, e68739.	2.5	257
26	Characterization of the genetic locus responsible for the production of ABP-118, a novel bacteriocin produced by the probiotic bacterium <i>Lactobacillus salivarius</i> subsp. <i>salivarius</i> UCC118 The GenBank accession number for the sequence reported in this paper is AF408405.. <i>Microbiology (United Kingdom)</i> 182, 2018, 250-259.	1.8	250
27	Current perspectives on antifungal lactic acid bacteria as natural bio-preservatives. <i>Trends in Food Science and Technology</i> , 2013, 33, 93-109.	15.1	243
28	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	11.1	240
29	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015, 5, 15782.	3.3	233
30	comK encodes the competence transcription factor, the key regulatory protein for competence development in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1995, 15, 455-462.	2.5	225
31	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.	7.1	217
32	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6718-6723.	7.1	216
33	Riboflavin Production in <i>Lactococcus lactis</i> : Potential for In Situ Production of Vitamin-Enriched Foods. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5769-5777.	3.1	209
34	Gut microbiota composition and <i>Clostridium difficile</i> infection in hospitalized elderly individuals: a metagenomic study. <i>Scientific Reports</i> , 2016, 6, 25945.	3.3	207
35	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	3.1	203
36	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7078-7087.	3.1	191

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37	Identification of universal gut microbial biomarkers of common human intestinal diseases by meta-analysis. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	191
38	Bacteriophage Orphan DNA Methyltransferases: Insights from Their Bacterial Origin, Function, and Occurrence. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7547-7555.	3.1	190
39	Sequence analysis and molecular characterization of the temperate lactococcal bacteriophage r1t. <i>Molecular Microbiology</i> , 1996, 19, 1343-1355.	2.5	182
40	Human gut microbiota and bifidobacteria: from composition to functionality. <i>Antonie Van Leeuwenhoek</i> , 2008, 94, 35-50.	1.7	182
41	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. <i>Trends in Microbiology</i> , 2018, 26, 339-350.	7.7	182
42	Selective carbohydrate utilization by lactobacilli and bifidobacteria. <i>Journal of Applied Microbiology</i> , 2013, 114, 1132-1146.	3.1	181
43	Bacteriophages as biocontrol agents of food pathogens. <i>Current Opinion in Biotechnology</i> , 2011, 22, 157-163.	6.6	169
44	Characterization of virus-like particles associated with the human faecal and caecal microbiota. <i>Research in Microbiology</i> , 2014, 165, 803-812.	2.1	169
45	A small gene, designated comS, located within the coding region of the fourth amino acid-activation domain of srfA, is required for competence development in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1995, 15, 55-63.	2.5	165
46	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.	3.1	165
47	Insights into the taxonomy, genetics and physiology of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2004, 86, 205-223.	1.7	164
48	Host-microbe interactions that facilitate gut colonization by commensal bifidobacteria. <i>Trends in Microbiology</i> , 2012, 20, 467-476.	7.7	164
49	Human milk oligosaccharides: Shaping the infant gut microbiota and supporting health. <i>Journal of Functional Foods</i> , 2020, 72, 104074.	3.4	159
50	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.	3.3	158
51	The genus <i>Lactobacillus</i> a genomic basis for understanding its diversity. <i>FEMS Microbiology Letters</i> , 2007, 269, 22-28.	1.8	157
52	Lactic acid bacteria with potential to eliminate fungal spoilage in foods. <i>Journal of Applied Microbiology</i> , 2008, 104, 915-923.	3.1	157
53	Enhancing the Microbiological Stability of Malt and Beer - A Review. <i>Journal of the Institute of Brewing</i> , 2005, 111, 355-371.	2.3	155
54	Analysis of bifidobacterial evolution using a multilocus approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2783-2792.	1.7	154

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55	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	3.8	153
56	Screening for and Identification of Starch-, Amylopectin-, and Pullulan-Degrading Activities in Bifidobacterial Strains. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5289-5296.	3.1	152
57	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016, 18, 4727-4738.	3.8	152
58	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 13974.	3.3	148
59	Comparative and Functional Analysis of Sortase-Dependent Proteins in the Predicted Secretome of <i>Lactobacillus salivarius</i> UCC118. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4143-4153.	3.1	145
60	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. <i>ISME Journal</i> , 2016, 10, 1656-1668.	9.8	145
61	The Bifidobacterium dentium Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	3.5	141
62	Bacterial vitamin B2, B11 and B12 overproduction: An overview. <i>International Journal of Food Microbiology</i> , 2009, 133, 1-7.	4.7	140
63	Genomics and ecological overview of the genus Bifidobacterium. <i>International Journal of Food Microbiology</i> , 2011, 149, 37-44.	4.7	140
64	Characterization of bacteriocin-like inhibitory substances (BLIS) from sourdough lactic acid bacteria and evaluation of their in vitro and in situ activity. <i>Journal of Applied Microbiology</i> , 2004, 96, 521-534.	3.1	139
65	Metabolism of Sialic Acid by Bifidobacterium breve UCC2003. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4414-4426.	3.1	130
66	Comparative Genomics Reveals Close Genetic Relationships between Phages from Dairy Bacteria and Pathogenic Streptococci: Evolutionary Implications for Prophage-Host Interactions. <i>Virology</i> , 2001, 288, 325-341.	2.4	129
67	Bifidobacteria and the infant gut: an example of co-evolution and natural selection. <i>Cellular and Molecular Life Sciences</i> , 2018, 75, 103-118.	5.4	129
68	Microbiomic analysis of the bifidobacterial population in the human distal gut. <i>ISME Journal</i> , 2009, 3, 745-751.	9.8	128
69	The Surface-Associated Exopolysaccharide of Bifidobacterium longum 35624 Plays an Essential Role in Dampening Host Proinflammatory Responses and Repressing Local T _H 17 Responses. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7185-7196.	3.1	126
70	Feeding the microbiota: transducer of nutrient signals for the host. <i>Gut</i> , 2017, 66, 1709-1717.	12.1	124
71	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	3.3	123
72	Bifidobacterium asteroides PRL2011 Genome Analysis Reveals Clues for Colonization of the Insect Gut. <i>PLoS ONE</i> , 2012, 7, e44229.	2.5	123

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73	Identification and characterization of phage-resistance genes in temperate lactococcal bacteriophages. <i>Molecular Microbiology</i> , 2002, 43, 509-520.	2.5	122
74	Biotechnological Production of Vitamin B2-Enriched Bread and Pasta. <i>Journal of Agricultural and Food Chemistry</i> , 2011, 59, 8013-8020.	5.2	121
75	Structure of the phage TP901-1 1.8ÅMDa baseplate suggests an alternative host adhesion mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8954-8958.	7.1	121
76	A general method for selection of riboflavin-overproducing food grade micro-organisms. <i>Microbial Cell Factories</i> , 2006, 5, 24.	4.0	119
77	Diversity of the genus <i>Lactobacillus</i> revealed by comparative genomics of five species. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3185-3196.	1.8	118
78	<i>Bifidobacterium breve</i> UCC2003 metabolises the human milk oligosaccharides lacto-N-tetraose and lacto-N-neo-tetraose through overlapping, yet distinct pathways. <i>Scientific Reports</i> , 2016, 6, 38560.	3.3	118
79	Multivitamin production in <i>Lactococcus lactis</i> using metabolic engineering. <i>Metabolic Engineering</i> , 2004, 6, 109-115.	7.0	117
80	Investigation of the Evolutionary Development of the Genus <i>Bifidobacterium</i> by Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6383-6394.	3.1	117
81	Comparative and functional genomics of the <i>Lactococcus lactis</i> taxon; insights into evolution and niche adaptation. <i>BMC Genomics</i> , 2017, 18, 267.	2.8	117
82	Comparative genomics of the genus <i>Bifidobacterium</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3243-3254.	1.8	116
83	High Resolution In Vivo Bioluminescent Imaging for the Study of Bacterial Tumour Targeting. <i>PLoS ONE</i> , 2012, 7, e30940.	2.5	116
84	Comparative genomics of the <i>Bifidobacterium brevetaxon</i> . <i>BMC Genomics</i> , 2014, 15, 170.	2.8	113
85	Metabolic engineering of lactic acid bacteria for the production of nutraceuticals. <i>Antonie Van Leeuwenhoek</i> , 2002, 82, 217-235.	1.7	112
86	Sequence analysis and characterization of ÅQ1205, a temperate bacteriophage infecting <i>Streptococcus thermophilus</i> CNRZ1205. <i>Microbiology (United Kingdom)</i> , 1997, 143, 3417-3429.	1.8	111
87	Two groups of bacteriophages infecting <i>Streptococcus thermophilus</i> can be distinguished on the basis of mode of packaging and genetic determinants for major structural proteins. <i>Applied and Environmental Microbiology</i> , 1997, 63, 3246-3253.	3.1	110
88	The Dilemma of Phage Taxonomy Illustrated by Comparative Genomics of Sfi21-Like Siphoviridae in Lactic Acid Bacteria. <i>Journal of Bacteriology</i> , 2002, 184, 6026-6036.	2.2	108
89	Omics of bifidobacteria: research and insights into their health-promoting activities. <i>Biochemical Journal</i> , 2017, 474, 4137-4152.	3.7	107
90	Diversity, ecology and intestinal function of bifidobacteria. <i>Microbial Cell Factories</i> , 2014, 13, S4.	4.0	106

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91	Improvement and Optimization of Two Engineered Phage Resistance Mechanisms in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2001, 67, 608-616.	3.1	105
92	Transcriptional Regulation and Characterization of a Novel Î²-Fructofuranosidase-Encoding Gene from <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3475-3482.	3.1	104
93	Characterization of ApuB, an Extracellular Type II Amylopullulanase from <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6271-6279.	3.1	102
94	Overcoming the restriction barrier to plasmid transformation and targeted mutagenesis in <i>Bifidobacterium breve</i> UCC2003. <i>Microbial Biotechnology</i> , 2009, 2, 321-332.	4.2	102
95	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016, 92, f1w191.	2.7	102
96	Orally Administered Bifidobacteria as Vehicles for Delivery of Agents to Systemic Tumors. <i>Molecular Therapy</i> , 2010, 18, 1397-1407.	8.2	101
97	Investigation of the Relationship between Lactococcal Host Cell Wall Polysaccharide Genotype and 936 Phage Receptor Binding Protein Phylogeny. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4385-4392.	3.1	99
98	Genomic diversity and distribution of <i>Bifidobacterium longum</i> subsp. <i>longum</i> across the human lifespan. <i>Scientific Reports</i> , 2018, 8, 85.	3.3	99
99	Differences in Lactococcal Cell Wall Polysaccharide Structure Are Major Determining Factors in Bacteriophage Sensitivity. <i>MBio</i> , 2014, 5, e00880-14.	4.1	98
100	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , 2017, 18, 568.	2.8	98
101	Metagenomic Approaches to Assess Bacteriophages in Various Environmental Niches. <i>Viruses</i> , 2017, 9, 127.	3.3	98
102	Evaluation of genetic diversity among strains of the human gut commensal <i>Bifidobacterium adolescentis</i> . <i>Scientific Reports</i> , 2016, 6, 23971.	3.3	97
103	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.	3.5	96
104	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	9.8	96
105	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.	3.1	95
106	Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2007, 91, 351-372.	1.7	95
107	Identification and Characterization of Lactococcal-Prophage-Carried Superinfection Exclusion Genes. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6206-6215.	3.1	95
108	<i>Lactobacillus</i> phylogenomics - towards a reclassification of the genus. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2945-2954.	1.7	95

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109	<i>Bifidobacterium lactis</i> DSM 10140: Identification of the <i>atpB</i> (<i>atpB</i> BEFHAGDC) Operon and Analysis of Its Genetic Structure, Characteristics, and Phylogeny. Applied and Environmental Microbiology, 2004, 70, 3110-3121.	3.1	94
110	MEGAnnotator: a user-friendly pipeline for microbial genomes assembly and annotation. FEMS Microbiology Letters, 2016, 363, fnw049.	1.8	94
111	The infant gut microbiome as a microbial organ influencing host well-being. Italian Journal of Pediatrics, 2020, 46, 16.	2.6	93
112	<i>Bifidobacterium bifidum</i> as an example of a specialized human gut commensal. Frontiers in Microbiology, 2014, 5, 437.	3.5	92
113	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived <i>Bifidobacteria</i> . Applied and Environmental Microbiology, 2017, 83, .	3.1	88
114	Obesity and microbiota: an example of an intricate relationship. Genes and Nutrition, 2017, 12, 18.	2.5	86
115	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. Frontiers in Microbiology, 2017, 8, 1749.	3.5	86
116	An analysis of bacteriocins produced by lactic acid bacteria isolated from malted barley. Journal of Applied Microbiology, 2001, 91, 131-138.	3.1	85
117	Genetic analysis and morphological identification of pilus-like structures in members of the genus <i>Bifidobacterium</i> . Microbial Cell Factories, 2011, 10, S16.	4.0	84
118	Bacteriophage Tuc2009 Encodes a Tail-Associated Cell Wall-Degrading Activity. Journal of Bacteriology, 2004, 186, 3480-3491.	2.2	83
119	<i>Lactobacillus rossii</i> sp. nov., isolated from wheat sourdough. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 35-40.	1.7	83
120	Identification and Characterization of a Fructose Phosphotransferase System in <i>Bifidobacterium breve</i> UCC2003. Applied and Environmental Microbiology, 2007, 73, 545-553.	3.1	83
121	Metabolism of a plant derived galactose-containing polysaccharide by <i>Bifidobacterium breve</i> UCC2003. Microbial Biotechnology, 2011, 4, 403-416.	4.2	82
122	<i>Bifidobacterium</i> Dialogue With Its Human Host and Consequent Modulation of the Immune System. Frontiers in Immunology, 2019, 10, 2348.	4.8	81
123	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . Environmental Microbiology, 2015, 17, 2515-2531.	3.8	80
124	The Lactococcal Phages Tuc2009 and TP901-1 Incorporate Two Alternate Forms of Their Tail Fiber into Their Virions for Infection Specialization*. Journal of Biological Chemistry, 2013, 288, 5581-5590.	3.4	79
125	Functional Characterization of a Composite Bacteriocin Locus from Malt Isolate <i>Lactobacillus sakei</i> 5. Applied and Environmental Microbiology, 2003, 69, 7194-7203.	3.1	78
126	Genome Analysis and Characterisation of the Exopolysaccharide Produced by <i>Bifidobacterium longum</i> subsp. <i>longum</i> 35624. PLoS ONE, 2016, 11, e0162983.	2.5	76

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127	In Vitro Characteristics of Phages to Guide "Real Life"™ Phage Therapy Suitability. <i>Viruses</i> , 2018, 10, 163.	3.3	76
128	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of <i>Lactobacillus gasseri</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3130-3146.	3.1	75
129	Functional and structural dissection of the tape measure protein of lactococcal phage TP901-1. <i>Scientific Reports</i> , 2016, 6, 36667.	3.3	75
130	Discovering lactic acid bacteria by genomics. , 2002, 82, 29-58.		74
131	Cellodextrin Utilization by <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1681-1690.	3.1	74
132	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.	3.1	74
133	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.	3.1	74
134	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. <i>Frontiers in Microbiology</i> , 2015, 6, 1030.	3.5	74
135	Gene-trait matching across the <i>Bifidobacterium longum</i> pan-genome reveals considerable diversity in carbohydrate catabolism among human infant strains. <i>BMC Genomics</i> , 2018, 19, 33.	2.8	74
136	<i>Lactobacillus rossiae</i> , a Vitamin B12 Producer, Represents a Metabolically Versatile Species within the Genus <i>Lactobacillus</i> . <i>PLoS ONE</i> , 2014, 9, e107232.	2.5	74
137	Transcriptional and functional characterization of genetic elements involved in galacto-oligosaccharide utilization by <i>Bifidobacterium breve</i> UCC2003. <i>Microbial Biotechnology</i> , 2013, 6, 67-79.	4.2	73
138	Occurrence and Diversity of CRISPR-Cas Systems in the Genus <i>Bifidobacterium</i> . <i>PLoS ONE</i> , 2015, 10, e0133661.	2.5	73
139	Six putative two-component regulatory systems isolated from <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363 The GenBank accession numbers for the sequences of the six 2CSs and surrounding ORFs determined in this work are AF172649, AF176556, AF178425, AF172650, AF176557 and AF176809 for systems A-F, respectively. <i>Microbiology (United Kingdom)</i> , 2000, 146, 935-947.	1.8	72
140	Anatomy of a Lactococcal Phage Tail. <i>Journal of Bacteriology</i> , 2006, 188, 3972-3982.	2.2	72
141	Microbial diversity in the human intestine and novel insights from metagenomics. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 3214.	3.0	72
142	Progress in genomics, metabolism and biotechnology of bifidobacteria. <i>International Journal of Food Microbiology</i> , 2011, 149, 4-18.	4.7	72
143	The Riboflavin Transporter RibU in <i>Lactococcus lactis</i> : Molecular Characterization of Gene Expression and the Transport Mechanism. <i>Journal of Bacteriology</i> , 2006, 188, 2752-2760.	2.2	71
144	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.	2.7	71

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145	Prophage-Like Elements in Bifidobacteria: Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8692-8705.	3.1	70
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150	From bacterial genome to functionality; case bifidobacteria. <i>International Journal of Food Microbiology</i> , 2007, 120, 2-12.	4.7	67
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