

Marco Ventura

List of Publications by Year in descending order

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Version: 2024-02-01

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	Creating an atlas to visualize the biodiversity of the mammalian gut microbiota. <i>Current Opinion in Biotechnology</i> , 2022, 73, 28-33.	3.3	5
2	The human gut microbiota during the initial stages of life: insights from bifidobacteria. <i>Current Opinion in Biotechnology</i> , 2022, 73, 81-87.	3.3	29
3	Editorial overview: Biotechnological insights of marine and terrestrial microbiome. <i>Current Opinion in Biotechnology</i> , 2022, 73, vii-ix.	3.3	0
4	Genome diversity of domesticated <i>Acinetobacter baumannii</i> ATCC 19606T strains. <i>Microbial Genomics</i> , 2022, 8, .	1.0	7
5	Needle in a Whey-Stack: PhRACS as a Discovery Tool for Unknown Phage-Host Combinations. <i>MBio</i> , 2022, 13, e0333421.	1.8	5
6	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
7	Interaction Between Diet and Microbiota in the Pathophysiology of Alzheimer's Disease: Focus on Polyphenols and Dietary Fibers. <i>Journal of Alzheimer's Disease</i> , 2022, 86, 961-982.	1.2	15
8	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
9	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
10	Mapping bacterial diversity and metabolic functionality of the human respiratory tract microbiome. <i>Journal of Oral Microbiology</i> , 2022, 14, 2051336.	1.2	6
11	Tap water as a natural vehicle for microorganisms shaping the human gut microbiome. <i>Environmental Microbiology</i> , 2022, , .	1.8	5
12	Investigation of the Ecological Link between Recurrent Microbial Human Gut Communities and Physical Activity. <i>Microbiology Spectrum</i> , 2022, 10, e0042022.	1.2	9
13	Dairy streptococcal cell wall and exopolysaccharide genome diversity. <i>Microbial Genomics</i> , 2022, 8, .	1.0	2
14	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
15	Effect of antibiotics in the first week of life on faecal microbiota development. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2022, 107, 603-610.	1.4	9
16	Exploring the Ecological Effects of Naturally Antibiotic-Insensitive <i>Bifidobacteria</i> in the Recovery of the Resilience of the Gut Microbiota during and after Antibiotic Treatment. <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	4
17	Interaction Between Diet and Microbiota in the Pathophysiology of Alzheimer's Disease: Focus on Polyphenols and Dietary Fibers. <i>Advances in Alzheimer's Disease</i> , 2022, , .	0.2	0
18	Envisioning emerging frontiers on human gut microbiota and its applications. <i>Microbial Biotechnology</i> , 2021, 14, 12-17.	2.0	2

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19	Impact of Extreme Obesity and Diet-Induced Weight Loss on the Fecal Metabolome and Gut Microbiota. <i>Molecular Nutrition and Food Research</i> , 2021, 65, e2000030.	1.5	19
20	Phageome Analysis of Bifidobacteria-Rich Samples. <i>Methods in Molecular Biology</i> , 2021, 2278, 71-85.	0.4	0
21	The genus <i>Bifidobacterium</i> : from genomics to functionality of an important component of the mammalian gut microbiota. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1472-1487.	1.9	49
22	Protocol to Select <i>Bifidobacterium</i> from Fecal and Environmental Samples. <i>Methods in Molecular Biology</i> , 2021, 2278, 61-70.	0.4	1
23	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
24	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
25	Vaginotypes of the human vaginal microbiome. <i>Environmental Microbiology</i> , 2021, 23, 1780-1792.	1.8	30
26	Early-Life Development of the Bifidobacterial Community in the Infant Gut. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3382.	1.8	28
27	Amoxicillin-Clavulanic Acid Resistance in the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	16
28	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
29	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
30	Phylogenomic analysis and characterization of carbon monoxide utilization genes in the family Phyllobacteriaceae with reclassification of <i>Aminobacter carboxidus</i> (Meyer et al. 1993, HÄrrdt et al.) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> <i>Microbiology</i> , 2021, 44, 126199.	1.2	8
31	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
32	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
33	METAnnotatorX2: a Comprehensive Tool for Deep and Shallow Metagenomic Data Set Analyses. <i>MSystems</i> , 2021, 6, e0058321.	1.7	35
34	Phylogenomic Reconstruction and Metabolic Potential of the Genus <i>Aminobacter</i> . <i>Microorganisms</i> , 2021, 9, 1332.	1.6	7
35	<i>Bifidobacterium breve</i> Exopolysaccharide Blocks Dendritic Cell Maturation and Activation of CD4+ T Cells. <i>Frontiers in Microbiology</i> , 2021, 12, 653587.	1.5	14
36	Gastric microbiota composition in patients with corpus atrophic gastritis. <i>Digestive and Liver Disease</i> , 2021, 53, 1580-1587.	0.4	10

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37	Phylogenomic disentangling of the <i>Bifidobacterium longum</i> subsp. <i>infantis</i> taxon. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
38	Lactic Acid Bacteria Diversity and Characterization of Probiotic Candidates in Fermented Meats. <i>Foods</i> , 2021, 10, 1519.	1.9	23
39	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
40	Effect of Intrapartum Antibiotics Prophylaxis on the Bifidobacterial Establishment within the Neonatal Gut. <i>Microorganisms</i> , 2021, 9, 1867.	1.6	8
41	Exploring the Ecology of Bifidobacteria and Their Genetic Adaptation to the Mammalian Gut. <i>Microorganisms</i> , 2021, 9, 8.	1.6	21
42	Phylogenetic classification of ten novel species belonging to the genus <i>Bifidobacterium</i> comprising <i>B. phasiani</i> sp. nov., <i>B. pongonis</i> sp. nov., <i>B. saguiniicoloris</i> sp. nov., <i>B. colobi</i> sp. nov., <i>B. simiiventris</i> sp. nov., <i>B. santillanense</i> sp. nov., <i>B. miconis</i> sp. nov., <i>B. amazonense</i> sp. nov., <i>B. pluvialisilvae</i> sp. nov., and <i>B. miconisargentati</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126273.	1.2	42
43	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
44	Unraveling the Microbiome of Necrotizing Enterocolitis: Insights in Novel Microbial and Metabolomic Biomarkers. <i>Microbiology Spectrum</i> , 2021, 9, e0117621.	1.2	30
45	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
46	Editorial: Role of Bifidobacteria in Human and Animal Health and Biotechnological Applications. <i>Frontiers in Microbiology</i> , 2021, 12, 785664.	1.5	4
47	The Probiotic Identity Card: A Novel "Probiogenomics" Approach to Investigate Probiotic Supplements. <i>Frontiers in Microbiology</i> , 2021, 12, 790881.	1.5	11
48	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
49	Bifidobacterial biofilm formation is a multifactorial adaptive phenomenon in response to bile exposure. <i>Scientific Reports</i> , 2020, 10, 11598.	1.6	37
50	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
51	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020, 5, .	1.7	13
52	Special Issue "Bifidobacteria: Insights from Ecology to Genomics of a Key Microbial Group of the Mammalian Gut Microbiota". <i>Microorganisms</i> , 2020, 8, 1660.	1.6	0
53	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
54	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

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55	Microbiota and Cancer: The Emerging Beneficial Role of Bifidobacteria in Cancer Immunotherapy. <i>Frontiers in Microbiology</i> , 2020, 11, 575072.	1.5	40
56	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
57	<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
58	Catching a glimpse of the bacterial gut community of companion animals: a canine and feline perspective. <i>Microbial Biotechnology</i> , 2020, 13, 1708-1732.	2.0	38
59	Draft Genome Sequence of the Carboxydrotrophic Alphaproteobacterium <i>Aminobacter carboxidus</i> Type Strain DSM 1086. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
60	Decoding the Genomic Variability among Members of the <i>Bifidobacterium dentium</i> Species. <i>Microorganisms</i> , 2020, 8, 1720.	1.6	18
61	Lysogenization of a Lactococcal Host with Three Distinct Temperate Phages Provides Homologous and Heterologous Phage Resistance. <i>Microorganisms</i> , 2020, 8, 1685.	1.6	13
62	<i>Bifidobacterium mongoliense</i> genome seems particularly adapted to milk oligosaccharide digestion leading to production of antivirulent metabolites. <i>BMC Microbiology</i> , 2020, 20, 111.	1.3	14
63	Evolutionary development and co-phylogeny of primate-associated bifidobacteria. <i>Environmental Microbiology</i> , 2020, 22, 3375-3393.	1.8	17
64	Investigating bifidobacteria and human milk oligosaccharide composition of lactating mothers. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	33
65	In Vitro Evaluation of Different Prebiotics on the Modulation of Gut Microbiota Composition and Function in Morbid Obese and Normal-Weight Subjects. <i>International Journal of Molecular Sciences</i> , 2020, 21, 906.	1.8	29
66	The infant gut microbiome as a microbial organ influencing host well-being. <i>Italian Journal of Pediatrics</i> , 2020, 46, 16.	1.0	93
67	Ecology of Lactobacilli Present in Italian Cheeses Produced from Raw Milk. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	9
68	Characterization of the phylogenetic diversity of two novel species belonging to the genus <i>Bifidobacterium</i> : <i>Bifidobacterium cebidarum</i> sp. nov. and <i>Bifidobacterium leontopithecii</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 2288-2297.	0.8	22
69	<i>Bifidobacterium canis</i> sp. nov., a novel member of the <i>Bifidobacterium pseudolongum</i> phylogenetic group isolated from faeces of a dog (<i>Canis lupus f. familiaris</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5040-5047.	0.8	14
70	Deciphering the Bifidobacterial Populations within the Canine and Feline Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	30
71	The Impact of Primer Design on Amplicon-Based Metagenomic Profiling Accuracy: Detailed Insights into Bifidobacterial Community Structure. <i>Microorganisms</i> , 2020, 8, 131.	1.6	26
72	Donated Human Milk as a Determinant Factor for the Gut Bifidobacterial Ecology in Premature Babies. <i>Microorganisms</i> , 2020, 8, 760.	1.6	13

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73	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. FEMS Microbiology Ecology, 2019, 95, .	1.3	29
74	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. Microbiome, 2019, 7, 100.	4.9	101
75	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
76	Uncovering Bifidobacteria via Targeted Sequencing of the Mammalian Gut Microbiota. Microorganisms, 2019, 7, 535.	1.6	10
77	Bifidobacterial Dialogue With Its Human Host and Consequent Modulation of the Immune System. Frontiers in Immunology, 2019, 10, 2348.	2.2	81
78	Exploring the effects of COLOSTRONONI on the mammalian gut microbiota composition. PLoS ONE, 2019, 14, e0217609.	1.1	6
79	Bifidobacterial Transfer from Mother to Child as Examined by an Animal Model. Microorganisms, 2019, 7, 293.	1.6	10
80	A Quest of Great Importance-Developing a Broad Spectrum Escherichia coli Phage Collection. Viruses, 2019, 11, 899.	1.5	9
81	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. Environmental Microbiology, 2019, 21, 1331-1343.	1.8	60
82	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. International Journal of Food Microbiology, 2019, 294, 1-9.	2.1	26
83	Dissecting the Evolutionary Development of the Species <i>Bifidobacterium animalis</i> through Comparative Genomics Analyses. Applied and Environmental Microbiology, 2019, 85, .	1.4	11
84	<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
85	The Influence of Fungicide Treatments on Mycobiota of Grapes and Its Evolution during Fermentation Evaluated by Metagenomic and Culture-Dependent Methods. Microorganisms, 2019, 7, 114.	1.6	13
86	Isolation of novel gut bifidobacteria using a combination of metagenomic and cultivation approaches. Genome Biology, 2019, 20, 96.	3.8	44
87	Isolation and Characterization of Lactobacillus brevis Phages. Viruses, 2019, 11, 393.	1.5	22
88	The Lactococcus lactis Pan-Plasmidome. Frontiers in Microbiology, 2019, 10, 707.	1.5	22
89	Colonization of the human gut by bovine bacteria present in Parmesan cheese. Nature Communications, 2019, 10, 1286.	5.8	46
90	Reply: Letter to the editor Re: Diaz M., et al. Nutrients 2018, 10, 1481. Nutrients, 2019, 11, 476.	1.7	1

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91	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. Scientific Reports, 2019, 9, 5755.	1.6	22
92	Gut Microbiome in the Elderly Hospitalized Patient. , 2019, , 287-296.		1
93	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
94	<i>Bifidobacterium bifidum</i> : A Key Member of the Early Human Gut Microbiota. Microorganisms, 2019, 7, 544.	1.6	70
95	Bifidobacterial Distribution Across Italian Cheeses Produced from Raw Milk. Microorganisms, 2019, 7, 599.	1.6	8
96	Mobilome and Resistome Reconstruction from Genomes Belonging to Members of the <i>Bifidobacterium</i> Genus. Microorganisms, 2019, 7, 638.	1.6	25
97	Health benefits conferred by the human gut microbiota during infancy. Microbial Biotechnology, 2019, 12, 243-248.	2.0	7
98	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.. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1288-1298.	0.8	45
99	A Gene Homologous to rRNA Methylase Genes Confers Erythromycin and Clindamycin Resistance in <i>Bifidobacterium breve</i> . Applied and Environmental Microbiology, 2018, 84, .	1.4	19
100	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.. Systematic and Applied Microbiology, 2018, 41, 173-183.	1.2	58
101	Claimed effects, outcome variables and methods of measurement for health claims on foods related to the gastrointestinal tract proposed under regulation (EC) 1924/2006. International Journal of Food Sciences and Nutrition, 2018, 69, 771-804.	1.3	6
102	Impact of gut-associated bifidobacteria and their phages on health: two sides of the same coin?. Applied Microbiology and Biotechnology, 2018, 102, 2091-2099.	1.7	14
103	<i>Bifidobacteria</i> : Ecology and Coevolution With the Host. , 2018, , 213-220.		4
104	<i>Staphylococcus aureus</i> undergoes major transcriptional reorganization during growth with <i>Enterococcus faecalis</i> in milk. Food Microbiology, 2018, 73, 17-28.	2.1	15
105	Claimed effects, outcome variables and methods of measurement for health claims proposed under Regulation (EC) 1924/2006 in the framework of bone health. PharmaNutrition, 2018, 6, 17-36.	0.8	4
106	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, .	1.4	16
107	Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. Gut, 2018, 67, 2097-2106.	6.1	130
108	A Decade of <i>Streptococcus thermophilus</i> Phage Evolution in an Irish Dairy Plant. Applied and Environmental Microbiology, 2018, 84, .	1.4	35

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109	Claimed effects, outcome variables and methods of measurement for health claims on foods proposed under Regulation (EC) 1924/2006 in the area of oral health. NFS Journal, 2018, 10, 10-25.	1.9	7
110	Glycan Utilization and Cross-Feeding Activities by Bifidobacteria. Trends in Microbiology, 2018, 26, 339-350.	3.5	182
111	Claimed effects, outcome variables and methods of measurement for health claims on foods proposed under European Community Regulation 1924/2006 in the area of appetite ratings and weight management. International Journal of Food Sciences and Nutrition, 2018, 69, 389-409.	1.3	13
112	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
113	Selected aspects of the human gut microbiota. Cellular and Molecular Life Sciences, 2018, 75, 81-82.	2.4	19
114	Tracking the Taxonomy of the Genus Bifidobacterium Based on a Phylogenomic Approach. Applied and Environmental Microbiology, 2018, 84, .	1.4	58
115	GP/EFSA/NUTRI/2014/01 Scientific substantiation of health claims made on food: collection, collation and critical analysis of information in relation to claimed effects, outcome variables and methods of measurement. EFSA Supporting Publications, 2018, 15, 1272E.	0.3	1
116	Fecal microbiota profile in a group of myasthenia gravis patients. Scientific Reports, 2018, 8, 14384.	1.6	45
117	Biodiversity of Streptococcus thermophilus Phages in Global Dairy Fermentations. Viruses, 2018, 10, 577.	1.5	29
118	Microbiota and Derived Parameters in Fecal Samples of Infants with Non-IgE Cowâ€™s Milk Protein Allergy under a Restricted Diet. Nutrients, 2018, 10, 1481.	1.7	40
119	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. Scientific Reports, 2018, 8, 13974.	1.6	148
120	Functional carbohydrate binding modules identified in evolved dits from siphophages infecting various Gramâ€™positive bacteria. Molecular Microbiology, 2018, 110, 777-795.	1.2	32
121	Pre- and probiotic overview. Current Opinion in Pharmacology, 2018, 43, 87-92.	1.7	97
122	Claimed Effects, Outcome Variables and Methods of Measurement for Health Claims Proposed Under European Community Regulation 1924/2006 in the Framework of Maintenance of Skin Function. Nutrients, 2018, 10, 7.	1.7	18
123	Claimed Effects, Outcome Variables and Methods of Measurement for Health Claims on Foods Related to Vision Proposed Under Regulation (EC) 1924/2006. Nutrients, 2018, 10, 211.	1.7	0
124	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
125	Microbial and metabolic multiâ€™omic correlations in systemic sclerosis patients. Annals of the New York Academy of Sciences, 2018, 1421, 97-109.	1.8	50
126	Claimed effects, outcome variables and methods of measurement for health claims proposed under European Community Regulation 1924/2006 in the area of blood glucose and insulin concentrations. Acta Diabetologica, 2018, 55, 391-404.	1.2	2

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127	Characterization and induction of prophages in human gut-associated Bifidobacterium hosts. <i>Scientific Reports</i> , 2018, 8, 12772.	1.6	26
128	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
129	Reconstruction of the Bifidobacterial Pan-Secretome Reveals the Network of Extracellular Interactions between Bifidobacteria and the Infant Gut. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	16
130	Meta-analysis of the human gut microbiome from urbanized and pre-agricultural populations. <i>Environmental Microbiology</i> , 2017, 19, 1379-1390.	1.8	153
131	Ancient bacteria of the <i>Å-tzi</i> ™s microbiome: a genomic tale from the Copper Age. <i>Microbiome</i> , 2017, 5, 5.	4.9	45
132	Next generation sequencing-based multigene panel for high throughput detection of food-borne pathogens. <i>International Journal of Food Microbiology</i> , 2017, 256, 20-29.	2.1	27
133	Genome Sequence of <i>Serratia marcescens</i> Phage BF. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
134	Complete Genome Sequence of <i>Bifidobacterium longum</i> W11 (LMG P-21586), Used as a Probiotic Strain. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
135	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017, 19, 4771-4783.	1.8	49
136	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017, 11, 2834-2847.	4.4	96
137	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017, 7, 11102.	1.6	146
138	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017, 7, 9879.	1.6	123
139	The Sortase-Dependent Fimbriome of the Genus <i>Bifidobacterium</i> : Extracellular Structures with Potential To Modulate Microbe-Host Dialogue. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	31
140	Bacterial diversity of the Colombian fermented milk <i>œSuero Coste</i> 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
141	Omics of bifidobacteria: research and insights into their health-promoting activities. <i>Biochemical Journal</i> , 2017, 474, 4137-4152.	1.7	107
142	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
143	Obesity and microbiota: an example of an intricate relationship. <i>Genes and Nutrition</i> , 2017, 12, 18.	1.2	86
144	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017, 5, 66.	4.9	240

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145	Genetic and functional characterisation of the lactococcal P335 phage-host interactions. <i>BMC Genomics</i> , 2017, 18, 146.	1.2	29
146	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	88
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