

Francesca Bottacini

List of Publications by Year in descending order

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74
papers

5,208
citations

117453

34
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88477

70
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76
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docs citations

76
times ranked

5377
citing authors

#	ARTICLE	IF	CITATIONS
1	Galacto-oligosaccharides as infant prebiotics: production, application, bioactive activities and future perspectives. <i>Critical Reviews in Food Science and Nutrition</i> , 2023, 63, 753-766.	5.4	30
2	A Proposed Framework to Identify Dispensable and Essential Functions in Bifidobacteria: Case Study of <i>Bifidobacterium breve</i> UCC2003 as a Prototype of Its Genus. <i>Methods in Molecular Biology</i> , 2022, 2377, 273-302.	0.4	0
3	Selective Isolation of <i>Eggerthella lenta</i> from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	1.6	9
4	Insights into Gene Transcriptional Regulation of Kayvirus Bacteriophages Obtained from Therapeutic Mixtures. <i>Viruses</i> , 2022, 14, 626.	1.5	4
5	Comparative Genomics of <i>Lactiplantibacillus plantarum</i> : Insights Into Probiotic Markers in Strains Isolated From the Human Gastrointestinal Tract and Fermented Foods. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	9
6	Maximum depth sequencing reveals an ON/OFF replication slippage switch and apparent in vivo selection for bifidobacterial pilus expression. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
7	<i>Bifidobacterium</i> Genome Assembly and Methylome Analysis Using Pacbio SMRT Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2278, 225-232.	0.4	0
8	<i>Bifidobacterium</i> Transformation. <i>Methods in Molecular Biology</i> , 2021, 2278, 13-19.	0.4	2
9	Broad Purpose Vector for Site-Directed Insertional Mutagenesis in <i>Bifidobacterium breve</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 636822.	1.5	7
10	Infant-Associated Bifidobacterial β -Galactosidases and Their Ability to Synthesize Galacto-Oligosaccharides. <i>Frontiers in Microbiology</i> , 2021, 12, 662959.	1.5	9
11	<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
12	Bifidobacterial β -Galactosidase-Mediated Production of Galacto-Oligosaccharides: Structural and Preliminary Functional Assessments. <i>Frontiers in Microbiology</i> , 2021, 12, 750635.	1.5	3
13	Diversity of Human-Associated Bifidobacterial Prophage Sequences. <i>Microorganisms</i> , 2021, 9, 2559.	1.6	5
14	Riboflavin Biosynthesis and Overproduction by a Derivative of the Human Gut Commensal <i>Bifidobacterium longum</i> subsp. <i>infantis</i> ATCC 15697. <i>Frontiers in Microbiology</i> , 2020, 11, 573335.	1.5	18
15	<i>Bifidobacterium</i> biofilm formation is a multifactorial adaptive phenomenon in response to bile exposure. <i>Scientific Reports</i> , 2020, 10, 11598.	1.6	37
16	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
17	The Infant-Derived <i>Bifidobacterium bifidum</i> Strain CNCM I-4319 Strengthens Gut Functionality. <i>Microorganisms</i> , 2020, 8, 1313.	1.6	10
18	Biochemical analysis of cross-feeding behaviour between two common gut commensals when cultivated on plant-derived arabinogalactan. <i>Microbial Biotechnology</i> , 2020, 13, 1733-1747.	2.0	20

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19	A cell wall-associated polysaccharide is required for bacteriophage adsorption to the <i>Streptococcus thermophilus</i> cell surface. <i>Molecular Microbiology</i> , 2020, 114, 31-45.	1.2	22
20	Characterization of GH2 and GH42 β -galactosidases derived from bifidobacterial infant isolates. <i>AMB Express</i> , 2019, 9, 9.	1.4	24
21	Metabolism of the predominant human milk oligosaccharide fucosyllactose by an infant gut commensal. <i>Scientific Reports</i> , 2019, 9, 15427.	1.6	58
22	The <i>Lactococcus lactis</i> Pan-Plasmidome. <i>Frontiers in Microbiology</i> , 2019, 10, 707.	1.5	22
23	Impact of a bathing tradition on shared gut microbes among Japanese families. <i>Scientific Reports</i> , 2019, 9, 4380.	1.6	16
24	Ability of bifidobacteria to metabolize chitin-glucan and its impact on the gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5755.	1.6	22
25	Complete Genome Sequence of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> 3107, Host for the Model Lactococcal P335 Bacteriophage TP901-1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
26	Genomic diversity and distribution of <i>Bifidobacterium longum</i> subsp. <i>longum</i> across the human lifespan. <i>Scientific Reports</i> , 2018, 8, 85.	1.6	99
27	Comparative genome and methylome analysis reveals restriction/modification system diversity in the gut commensal <i>Bifidobacterium breve</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1860-1877.	6.5	46
28	Staying alive: growth and survival of <i>Bifidobacterium animalis</i> subsp. <i>animalis</i> under in vitro and in vivo conditions. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10645-10663.	1.7	3
29	Comparative genomics and genotype-phenotype associations in <i>Bifidobacterium breve</i> . <i>Scientific Reports</i> , 2018, 8, 10633.	1.6	37
30	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.	1.2	74
31	Characterization and induction of prophages in human gut-associated <i>Bifidobacterium</i> hosts. <i>Scientific Reports</i> , 2018, 8, 12772.	1.6	26
32	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
33	Comparative and functional genomics of the <i>Lactococcus lactis</i> taxon; insights into evolution and niche adaptation. <i>BMC Genomics</i> , 2017, 18, 267.	1.2	117
34	The essential genomic landscape of the commensal <i>Bifidobacterium breve</i> UCC2003. <i>Scientific Reports</i> , 2017, 7, 5648.	1.6	26
35	Omics of bifidobacteria: research and insights into their health-promoting activities. <i>Biochemical Journal</i> , 2017, 474, 4137-4152.	1.7	107
36	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

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37	Global transcriptional landscape and promoter mapping of the gut commensal <i>Bifidobacterium breve</i> UCC2003. <i>BMC Genomics</i> , 2017, 18, 991.	1.2	24
38	Genome-Wide Search for Genes Required for <i>Bifidobacterium</i> Growth under Iron-Limitation. <i>Frontiers in Microbiology</i> , 2017, 8, 964.	1.5	17
39	Genome Analysis and Characterisation of the Exopolysaccharide Produced by <i>Bifidobacterium longum</i> subsp. <i>longum</i> 35624. <i>PLoS ONE</i> , 2016, 11, e0162983.	1.1	76
40	<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.	1.6	118
41	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
42	Comparative genomics and functional analysis of the 936 group of lactococcal Siphoviridae phages. <i>Scientific Reports</i> , 2016, 6, 21345.	1.6	64
43	Glycoside hydrolase family 13 α -glucosidases encoded by <i>Bifidobacterium breve</i> UCC2003; A comparative analysis of function, structure and phylogeny. <i>International Journal of Food Microbiology</i> , 2016, 224, 55-65.	2.1	20
44	Pangenome analysis of <i>Bifidobacterium longum</i> and site-directed mutagenesis through by-pass of restriction-modification systems. <i>BMC Genomics</i> , 2015, 16, 832.	1.2	89
45	Discovery of a Conjugative Megaplasmid in <i>Bifidobacterium breve</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 166-176.	1.4	22
46	Identification of Restriction-Modification Systems of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> CNCM I-2494 by SMRT Sequencing and Associated Methylome Analysis. <i>PLoS ONE</i> , 2014, 9, e94875.	1.1	25
47	Autoinducer-2 Plays a Crucial Role in Gut Colonization and Probiotic Functionality of <i>Bifidobacterium breve</i> UCC2003. <i>PLoS ONE</i> , 2014, 9, e98111.	1.1	67
48	<i>Bifidobacterium bifidum</i> as an example of a specialized human gut commensal. <i>Frontiers in Microbiology</i> , 2014, 5, 437.	1.5	92
49	Comparative genomics of the <i>Bifidobacterium brevetaxon</i> . <i>BMC Genomics</i> , 2014, 15, 170.	1.2	113
50	Diversity, ecology and intestinal function of bifidobacteria. <i>Microbial Cell Factories</i> , 2014, 13, S4.	1.9	106
51	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
52	Molecular Characterization of Three <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> Phages. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5623-5635.	1.4	23
53	The <i>Lactococcus lactis</i> plasmidome: much learnt, yet still lots to discover. <i>FEMS Microbiology Reviews</i> , 2014, 38, 1066-1088.	3.9	56
54	Genomic Encyclopedia of Type Strains of the Genus <i>Bifidobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 6290-6302.	1.4	203

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55	Progress in lactic acid bacterial phage research. <i>Microbial Cell Factories</i> , 2014, 13, S1.	1.9	35
56	<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.	1.1	74
57	Exploration of the Genomic Diversity and Core Genome of the <i>Bifidobacterium adolescentis</i> Phylogenetic Group by Means of a Polyphasic Approach. <i>Applied and Environmental Microbiology</i> , 2013, 79, 336-346.	1.4	19
58	Comparative Genomics of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> Reveals a Strict Monophyletic <i>Bifidobacterial</i> Taxon. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4304-4315.	1.4	74
59	Complete Genome Sequence of <i>Lactobacillus plantarum</i> Strain 16, a Broad-Spectrum Antifungal-Producing Lactic Acid Bacterium. <i>Genome Announcements</i> , 2013, 1, .	0.8	41
60	Complete Genome of <i>Lactococcus lactis</i> subsp. <i>cremoris</i> UC509.9, Host for a Model Lactococcal P335 Bacteriophage. <i>Genome Announcements</i> , 2013, 1, .	0.8	39
61	Draft Genome Sequence of <i>Lactobacillus crispatus</i> EM-LC1, an Isolate with Antimicrobial Activity Cultured from an Elderly Subject. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
62	Genome Sequence of <i>Parascardovia denticolens</i> IPLA 20019, Isolated from Human Breast Milk. <i>Journal of Bacteriology</i> , 2012, 194, 4776-4777.	1.0	9
63	<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
64	Insights into Physiological and Genetic Mupirocin Susceptibility in <i>Bifidobacteria</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 3141-3146.	1.4	37
65	Genetic analysis and morphological identification of pilus-like structures in members of the genus <i>Bifidobacterium</i> . <i>Microbial Cell Factories</i> , 2011, 10, S16.	1.9	84
66	Complete Genome Sequence of <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> BLC1. <i>Journal of Bacteriology</i> , 2011, 193, 6387-6388.	1.0	19
67	Ability of <i>Bifidobacterium breve</i> To Grow on Different Types of Milk: Exploring the Metabolism of Milk through Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7408-7417.	1.4	42
68	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
69	Analyses of <i>bifidobacterial</i> prophage-like sequences. <i>Antonie Van Leeuwenhoek</i> , 2010, 98, 39-50.	0.7	17
70	Characterization of the Serpin-Encoding Gene of <i>Bifidobacterium breve</i> 210B. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3206-3219.	1.4	66
71	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
72	Comparative genomics of the genus <i>Bifidobacterium</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3243-3254.	0.7	116

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73	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. Applied and Environmental Microbiology, 2009, 75, 6929-6936.	1.4	45
74	The Bifidobacterium dentium Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. PLoS Genetics, 2009, 5, e1000785.	1.5	141