

Marta Mangifesta

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

3,110
citations

32
h-index

47
g-index

47
ext. papers

4,165
ext. citations

6.8
avg, IF

4.62
L-index

#	Paper	IF	Citations
47	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , 2020 , 5,	7.6	3
46	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,	4.8	8
45	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. <i>Environmental Microbiology</i> , 2019 , 21, 1331-1343	5.2	36
44	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. <i>International Journal of Food Microbiology</i> , 2019 , 294, 1-9	5.8	17
43	Dissecting the Evolutionary Development of the Species through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	7
42	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host co-evolution. <i>Environmental Microbiology</i> , 2019 , 21, 3683-3695	5.2	35
41	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , 2019 , 10, 1286	17.4	26
40	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , 2019 , 95,	4.3	18
39	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. <i>Microbiome</i> , 2019 , 7, 100	16.6	42
38	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 parvae</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2018 , 41, 173-183	4.2	28
37	Phylotype-Level Profiling of Lactobacilli in Highly Complex Environments by Means of an Internal Transcribed Spacer-Based Metagenomic Approach. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	12
36	Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. <i>Gut</i> , 2018 , 67, 2097-2106	19.2	71
35	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018 , 24, 133-145.e5	23.4	435
34	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. <i>Microbiome</i> , 2018 , 6, 145	16.6	36
33	Tracking the Taxonomy of the Genus <i>Bifidobacterium</i> Based on a Phylogenomic Approach. <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	38
32	<i>Bifidobacterium bifidum</i> PRL2010 alleviates intestinal ischemia/reperfusion injury. <i>PLoS ONE</i> , 2018 , 13, e0202670	3.7	6
31	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , 2018 , 8, 13974	4.9	65

30	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	5.8	16
29	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , 2017 , 19, 4771-4783	5.2	33
28	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , 2017 , 11, 2834-2847	11.9	66
27	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , 2017 , 7, 11102	4.9	99
26	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , 2017 , 7, 9879	4.9	67
25	The Sortase-Dependent Fimbriome of the Genus Bifidobacterium: Extracellular Structures with Potential To Modulate Microbe-Host Dialogue. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	19
24	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , 2017 , 5, 66	16.6	163
23	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	56
22	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , 2017 , 18, 568	4.5	62
21	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. <i>Frontiers in Microbiology</i> , 2017 , 8, 1749	5.7	54
20	Bifidobacterium vansinderenii sp. nov., isolated from faeces of emperor tamarin (Saguinus imperator). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017 , 67, 3987-3995	2.2	26
19	Gut microbiota composition and Clostridium difficile infection in hospitalized elderly individuals: a metagenomic study. <i>Scientific Reports</i> , 2016 , 6, 25945	4.9	132
18	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. <i>ISME Journal</i> , 2016 , 10, 1656-68	11.9	107
17	Modulation of the eps-ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , 2016 , 92, fiw056	4.3	33
16	The human gut microbiota and its interactive connections to diet. <i>Journal of Human Nutrition and Dietetics</i> , 2016 , 29, 539-46	3.1	40
15	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , 2016 , 18, 4727-4738	5.2	89
14	Evaluation of genetic diversity among strains of the human gut commensal Bifidobacterium adolescentis. <i>Scientific Reports</i> , 2016 , 6, 23971	4.9	70
13	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	75

12	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7078-87	4.8	150
11	Insights from genomes of representatives of the human gut commensal Bifidobacterium bifidum. <i>Environmental Microbiology</i> , 2015 , 17, 2515-31	5.2	61
10	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , 2015 , 5, 15782	4.9	168
9	Exploring Amino Acid Auxotrophy in Bifidobacterium bifidum PRL2010. <i>Frontiers in Microbiology</i> , 2015 , 6, 1331	5.7	31
8	A genome-based identification approach for members of the genus Bifidobacterium. <i>FEMS Microbiology Ecology</i> , 2015 , 91,	4.3	12
7	Expression of sortase-dependent pili of Bifidobacterium bifidum PRL2010 in response to environmental gut conditions. <i>FEMS Microbiology Letters</i> , 2014 , 357, 23-33	2.9	41
6	Genomic characterization and transcriptional studies of the starch-utilizing strain Bifidobacterium adolescentis 22L. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 6080-90	4.8	60
5	Genomic encyclopedia of type strains of the genus Bifidobacterium. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 6290-302	4.8	162
4	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, 493-503	4.3	62
3	Investigation of the evolutionary development of the genus Bifidobacterium by comparative genomics. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 6383-94	4.8	95
2	The Genome Sequence of Bifidobacterium moukalabense DSM 27321 Highlights the Close Phylogenetic Relatedness with the Bifidobacterium dentium Taxon. <i>Genome Announcements</i> , 2014 , 2,		6
1	Role of sortase-dependent pili of Bifidobacterium bifidum PRL2010 in modulating bacterium-host interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 11151-6	11.5	172