

# Marta Mangifesta

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/2841820/marta-mangifesta-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , <b>2018</b> , 24, 133-145.e5	23.4	435
46	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> , <b>2013</b> , 110, 11151-6	11.5	172
45	Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. <i>Scientific Reports</i> , <b>2015</b> , 5, 15782	4.9	168
44	Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. <i>Microbiome</i> , <b>2017</b> , 5, 66	16.6	163
43	Genomic encyclopedia of type strains of the genus Bifidobacterium. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 6290-302	4.8	162
42	Exploring Vertical Transmission of Bifidobacteria from Mother to Child. <i>Applied and Environmental Microbiology</i> , <b>2015</b> , 81, 7078-87	4.8	150
41	Gut microbiota composition and Clostridium difficile infection in hospitalized elderly individuals: a metagenomic study. <i>Scientific Reports</i> , <b>2016</b> , 6, 25945	4.9	132
40	Deciphering bifidobacterial-mediated metabolic interactions and their impact on gut microbiota by a multi-omics approach. <i>ISME Journal</i> , <b>2016</b> , 10, 1656-68	11.9	107
39	Gut microbiota composition is associated with polypharmacy in elderly hospitalized patients. <i>Scientific Reports</i> , <b>2017</b> , 7, 11102	4.9	99
38	Investigation of the evolutionary development of the genus Bifidobacterium by comparative genomics. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 6383-94	4.8	95
37	Insights into the biodiversity of the gut microbiota of broiler chickens. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 4727-4738	5.2	89
36	Elucidating the gut microbiome of ulcerative colitis: bifidobacteria as novel microbial biomarkers. <i>FEMS Microbiology Ecology</i> , <b>2016</b> , 92,	4.3	75
35	Understanding the gut-kidney axis in nephrolithiasis: an analysis of the gut microbiota composition and functionality of stone formers. <i>Gut</i> , <b>2018</b> , 67, 2097-2106	19.2	71
34	Evaluation of genetic diversity among strains of the human gut commensal Bifidobacterium adolescentis. <i>Scientific Reports</i> , <b>2016</b> , 6, 23971	4.9	70
33	Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. <i>Scientific Reports</i> , <b>2017</b> , 7, 9879	4.9	67
32	Unveiling bifidobacterial biogeography across the mammalian branch of the tree of life. <i>ISME Journal</i> , <b>2017</b> , 11, 2834-2847	11.9	66
31	Mucosal microbiota of intestinal polyps reveals putative biomarkers of colorectal cancer. <i>Scientific Reports</i> , <b>2018</b> , 8, 13974	4.9	65

30	Evaluation of bifidobacterial community composition in the human gut by means of a targeted amplicon sequencing (ITS) protocol. <i>FEMS Microbiology Ecology</i> , <b>2014</b> , 90, 493-503	4.3	62
29	Comparative genomic and phylogenomic analyses of the Bifidobacteriaceae family. <i>BMC Genomics</i> , <b>2017</b> , 18, 568	4.5	62
28	Insights from genomes of representatives of the human gut commensal <i>Bifidobacterium bifidum</i> . <i>Environmental Microbiology</i> , <b>2015</b> , 17, 2515-31	5.2	61
27	Genomic characterization and transcriptional studies of the starch-utilizing strain <i>Bifidobacterium adolescentis</i> 22L. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 6080-90	4.8	60
26	Prevalence of Antibiotic Resistance Genes among Human Gut-Derived Bifidobacteria. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	56
25	How to Feed the Mammalian Gut Microbiota: Bacterial and Metabolic Modulation by Dietary Fibers. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1749	5.7	54
24	The human gallbladder microbiome is related to the physiological state and the biliary metabolic profile. <i>Microbiome</i> , <b>2019</b> , 7, 100	16.6	42
23	Expression of sortase-dependent pili of <i>Bifidobacterium bifidum</i> PRL2010 in response to environmental gut conditions. <i>FEMS Microbiology Letters</i> , <b>2014</b> , 357, 23-33	2.9	41
22	The human gut microbiota and its interactive connections to diet. <i>Journal of Human Nutrition and Dietetics</i> , <b>2016</b> , 29, 539-46	3.1	40
21	Tracking the Taxonomy of the Genus <i>Bifidobacterium</i> Based on a Phylogenomic Approach. <i>Applied and Environmental Microbiology</i> , <b>2018</b> , 84,	4.8	38
20	Metagenomic dissection of the canine gut microbiota: insights into taxonomic, metabolic and nutritional features. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 1331-1343	5.2	36
19	Tracing mother-infant transmission of bacteriophages by means of a novel analytical tool for shotgun metagenomic datasets: METAnnotatorX. <i>Microbiome</i> , <b>2018</b> , 6, 145	16.6	36
18	<i>Bifidobacterium bifidum</i> and the infant gut microbiota: an intriguing case of microbe-host co-evolution. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 3683-3695	5.2	35
17	Untangling the cecal microbiota of feral chickens by culturomic and metagenomic analyses. <i>Environmental Microbiology</i> , <b>2017</b> , 19, 4771-4783	5.2	33
16	Modulation of the eps-ome transcription of bifidobacteria through simulation of human intestinal environment. <i>FEMS Microbiology Ecology</i> , <b>2016</b> , 92, fiw056	4.3	33
15	Exploring Amino Acid Auxotrophy in <i>Bifidobacterium bifidum</i> PRL2010. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1331	5.7	31
14	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. <i>Systematic and Applied Microbiology</i> , <b>2018</b> , 41, 173-183	4.2	28
13	Colonization of the human gut by bovine bacteria present in Parmesan cheese. <i>Nature Communications</i> , <b>2019</b> , 10, 1286	17.4	26

12	Bifidobacterium vansinderenii sp. nov., isolated from faeces of emperor tamarin (Saguinus imperator). <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2017</b> , 67, 3987-3995	2.2	26
11	The Sortase-Dependent Fimbriome of the Genus Bifidobacterium: Extracellular Structures with Potential To Modulate Microbe-Host Dialogue. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	19
10	The impact of human-facilitated selection on the gut microbiota of domesticated mammals. <i>FEMS Microbiology Ecology</i> , <b>2019</b> , 95,	4.3	18
9	Compositional assessment of bacterial communities in probiotic supplements by means of metagenomic techniques. <i>International Journal of Food Microbiology</i> , <b>2019</b> , 294, 1-9	5.8	17
8	Next generation sequencing-based multigene panel for high throughput detection of food-borne pathogens. <i>International Journal of Food Microbiology</i> , <b>2017</b> , 256, 20-29	5.8	16
7	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> , <b>2018</b> , 84,	4.8	12
6	A genome-based identification approach for members of the genus Bifidobacterium. <i>FEMS Microbiology Ecology</i> , <b>2015</b> , 91,	4.3	12
5	Multi-omics Approaches To Decipher the Impact of Diet and Host Physiology on the Mammalian Gut Microbiome. <i>Applied and Environmental Microbiology</i> , <b>2020</b> , 86,	4.8	8
4	Dissecting the Evolutionary Development of the Species through Comparative Genomics Analyses. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	7
3	The Genome Sequence of Bifidobacterium moukalabense DSM 27321 Highlights the Close Phylogenetic Relatedness with the Bifidobacterium dentium Taxon. <i>Genome Announcements</i> , <b>2014</b> , 2,		6
2	Bifidobacterium bifidum PRL2010 alleviates intestinal ischemia/reperfusion injury. <i>PLoS ONE</i> , <b>2018</b> , 13, e0202670	3.7	6
1	Untangling Species-Level Composition of Complex Bacterial Communities through a Novel Metagenomic Approach. <i>MSystems</i> , <b>2020</b> , 5,	7.6	3