

# Mary O'connell Motherway

## List of Publications by Year in descending order

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42  
papers

3,736  
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172457

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265206

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docs citations

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times ranked

3486  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of GH2 and GH42 Î²-galactosidases derived from bifidobacterial infant isolates. <i>AMB Express</i> , 2019, 9, 9.	3.0	24
2	Metabolism of the predominant human milk oligosaccharide fucosyllactose by an infant gut commensal. <i>Scientific Reports</i> , 2019, 9, 15427.	3.3	58
3	A Bifidobacterial pilus-associated protein promotes colonic epithelial proliferation. <i>Molecular Microbiology</i> , 2019, 111, 287-301.	2.5	62
4	<i>Bifidobacterium breve</i> UCC2003 Employs Multiple Transcriptional Regulators To Control Metabolism of Particular Human Milk Oligosaccharides. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	23
5	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.	14.5	46
6	Identification of probiotic effector molecules: present state and future perspectives. <i>Current Opinion in Biotechnology</i> , 2018, 49, 217-223.	6.6	204
7	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.	3.6	3
8	Comparative genomics and genotype-phenotype associations in <i>Bifidobacterium breve</i> . <i>Scientific Reports</i> , 2018, 8, 10633.	3.3	37
9	Carbohydrate Syntrophy enhances the establishment of <i>Bifidobacterium breve</i> UCC2003 in the neonatal gut. <i>Scientific Reports</i> , 2018, 8, 10627.	3.3	19
10	Genome-Wide Search for Genes Required for Bifidobacterial Growth under Iron-Limitation. <i>Frontiers in Microbiology</i> , 2017, 8, 964.	3.5	17
11	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.	2.5	76
12	<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
13	Glycosulfatase-Encoding Gene Cluster in <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6611-6623.	3.1	40
14	The Surface-Associated Exopolysaccharide of <i>Bifidobacterium longum</i> 35624 Plays an Essential Role in Dampening Host Proinflammatory Responses and Repressing Local T <sub>H</sub> 17 Responses. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7185-7196.	3.1	126
15	Cloning, expression and characterization of a Î²-d-xylosidase from <i>Lactobacillus rossiae</i> DSM 15814T. <i>Microbial Cell Factories</i> , 2016, 15, 72.	4.0	24
16	Glycoside hydrolase family 13 Î±-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.	4.7	20
17	A GntR-type transcriptional repressor controls sialic acid utilization in <i>Bifidobacterium breve</i> UCC2003. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-9.	1.8	17
18	Carbohydrate catabolic diversity of bifidobacteria and lactobacilli of human origin. <i>International Journal of Food Microbiology</i> , 2015, 203, 109-121.	4.7	63

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19	Discovery of a Conjugative Megaplasmid in <i>Bifidobacterium breve</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 166-176.	3.1	22
20	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.	2.5	67
21	Comparative genomics of the <i>Bifidobacterium</i> brevetaxon. <i>BMC Genomics</i> , 2014, 15, 170.	2.8	113
22	Diversity, ecology and intestinal function of bifidobacteria. <i>Microbial Cell Factories</i> , 2014, 13, S4.	4.0	106
23	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
24	Metabolism of Sialic Acid by <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4414-4426.	3.1	130
25	Transcription of Two Adjacent Carbohydrate Utilization Gene Clusters in <i>Bifidobacterium breve</i> UCC2003 Is Controlled by LacI- and Repressor Open Reading Frame Kinase (ROK)-Type Regulators. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3604-3614.	3.1	29
26	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
27	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
28	Metabolism of Four $\alpha$ -Glycosidic Linkage-Containing Oligosaccharides by <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6280-6292.	3.1	54
29	Transcriptional and functional characterization of genetic elements involved in galactooligosaccharide utilization by <i>Bifidobacterium breve</i> UCC2003. <i>Microbial Biotechnology</i> , 2013, 6, 67-79.	4.2	73
30	Identification and characterization of an oleate hydratase-encoding gene from <i>Bifidobacterium breve</i> . <i>Bioengineered</i> , 2013, 4, 313-321.	3.2	40
31	Transposon Mutagenesis in <i>Bifidobacterium breve</i> : Construction and Characterization of a Tn5 Transposon Mutant Library for <i>Bifidobacterium breve</i> UCC2003. <i>PLoS ONE</i> , 2013, 8, e64699.	2.5	41
32	In Silico Assigned Resistance Genes Confer <i>Bifidobacterium</i> with Partial Resistance to Aminoglycosides but Not to $\beta$ -Lactams. <i>PLoS ONE</i> , 2013, 8, e82653.	2.5	17
33	A Two-Component Regulatory System Controls Autoregulated Serpin Expression in <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7032-7041.	3.1	26
34	Host-microbe interactions that facilitate gut colonization by commensal bifidobacteria. <i>Trends in Microbiology</i> , 2012, 20, 467-476.	7.7	164
35	<i>Bifidobacterium</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
36	An efficient and reproducible method for transformation of genetically recalcitrant bifidobacteria. <i>FEMS Microbiology Letters</i> , 2012, 333, 146-152.	1.8	23

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37	Metabolism of a plant derived galactose-containing polysaccharide by <i>Bifidobacterium breve</i> UCC2003. <i>Microbial Biotechnology</i> , 2011, 4, 403-416.	4.2	82
38	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.	4.0	84
39	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
40	Characterization of the Serpin-Encoding Gene of <i>Bifidobacterium breve</i> 210B. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3206-3219.	3.1	66
41	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
42	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