Mary O'connell Motherway

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10865505/publications.pdf

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42 papers 3,736 citations

172457 29 h-index 265206 42 g-index

42 all docs 42 docs citations

times ranked

42

3486 citing authors

#	Article	IF	CITATIONS
1	Bifidobacterial surface-exopolysaccharide facilitates commensal-host interaction through immune modulation and pathogen protection. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2108-2113.	7.1	450
2	Functional genome analysis of <i>Bifidobacterium breve</i> UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11217-11222.	7.1	328
3	Molecular dialogue between the human gut microbiota and the host: a Lactobacillus and Bifidobacterium perspective. Cellular and Molecular Life Sciences, 2014, 71, 183-203.	5.4	265
4	Role of sortase-dependent pili of <i>Bifidobacterium bifidum</i> PRL2010 in modulating bacterium–host interactions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11151-11156.	7.1	217
5	Identification of probiotic effector molecules: present state and future perspectives. Current Opinion in Biotechnology, 2018, 49, 217-223.	6.6	204
6	Host–microbe interactions that facilitate gut colonization by commensal bifidobacteria. Trends in Microbiology, 2012, 20, 467-476.	7.7	164
7	Cross-feeding by Bifidobacterium breve UCC2003 during co-cultivation with Bifidobacterium bifidum PRL2010 in a mucin-based medium. BMC Microbiology, 2014, 14, 282.	3.3	158
8	Metabolism of Sialic Acid by Bifidobacterium breve UCC2003. Applied and Environmental Microbiology, 2014, 80, 4414-4426.	3.1	130
9	The Surface-Associated Exopolysaccharide of Bifidobacterium longum 35624 Plays an Essential Role in Dampening Host Proinflammatory Responses and Repressing Local T _H 17 Responses. Applied and Environmental Microbiology, 2016, 82, 7185-7196.	3.1	126
10	Bifidobacterium breve UCC2003 metabolises the human milk oligosaccharides lacto-N-tetraose and lacto-N-neo-tetraose through overlapping, yet distinct pathways. Scientific Reports, 2016, 6, 38560.	3.3	118
11	Comparative genomics of the Bifidobacterium brevetaxon. BMC Genomics, 2014, 15, 170.	2.8	113
12	Diversity, ecology and intestinal function of bifidobacteria. Microbial Cell Factories, 2014, 13, S4.	4.0	106
13	Characterization of ApuB, an Extracellular Type II Amylopullulanase from <i>Bifidobacterium breve</i> UCC2003. Applied and Environmental Microbiology, 2008, 74, 6271-6279.	3.1	102
14	Overcoming the restriction barrier to plasmid transformation and targeted mutagenesis in <i>Bifidobacterium breve</i> UCC2003. Microbial Biotechnology, 2009, 2, 321-332.	4.2	102
15	Genetic analysis and morphological identification of pilus-like structures in members of the genus Bifidobacterium. Microbial Cell Factories, 2011, 10, S16.	4.0	84
16	Metabolism of a plant derived galactoseâ€containing polysaccharide by <i>Bifidobacterium breve</i> UCC2003. Microbial Biotechnology, 2011, 4, 403-416.	4.2	82
17	Genome Analysis and Characterisation of the Exopolysaccharide Produced by Bifidobacterium longum subsp. longum 35624â,,¢. PLoS ONE, 2016, 11, e0162983.	2.5	76
18	Transcriptional and functional characterization of genetic elements involved in galactoâ€oligosaccharide utilization by <i><scp>B</scp>ifidobacterium breve</i> àâ€ <scp>UCC</scp> 2003. Microbial Biotechnology, 2013, 6, 67-79.	4.2	73

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19	Autoinducer-2 Plays a Crucial Role in Gut Colonization and Probiotic Functionality of Bifidobacterium breve UCC2003. PLoS ONE, 2014, 9, e98111.	2.5	67
20	Characterization of the Serpin-Encoding Gene of <i>Bifidobacterium breve</i> 210B. Applied and Environmental Microbiology, 2010, 76, 3206-3219.	3.1	66
21	Carbohydrate catabolic diversity of bifidobacteria and lactobacilli of human origin. International Journal of Food Microbiology, 2015, 203, 109-121.	4.7	63
22	A Bifidobacterial pilusâ€associated protein promotes colonic epithelial proliferation. Molecular Microbiology, 2019, 111, 287-301.	2.5	62
23	Metabolism of the predominant human milk oligosaccharide fucosyllactose by an infant gut commensal. Scientific Reports, 2019, 9, 15427.	3.3	58
24	Metabolism of Four \hat{l}_{\pm} -Glycosidic Linkage-Containing Oligosaccharides by Bifidobacterium breve UCC2003. Applied and Environmental Microbiology, 2013, 79, 6280-6292.	3.1	54
25	Comparative genome and methylome analysis reveals restriction/modification system diversity in the gut commensal Bifidobacterium breve. Nucleic Acids Research, 2018, 46, 1860-1877.	14.5	46
26	Transposon Mutagenesis in Bifidobacterium breve: Construction and Characterization of a Tn5 Transposon Mutant Library for Bifidobacterium breve UCC2003. PLoS ONE, 2013, 8, e64699.	2.5	41
27	Identification and characterization of an oleate hydratase-encoding gene from <i><i>Bifidobacterium breve</i></i> /i>. Bioengineered, 2013, 4, 313-321.	3.2	40
28	Glycosulfatase-Encoding Gene Cluster in Bifidobacterium breve UCC2003. Applied and Environmental Microbiology, 2016, 82, 6611-6623.	3.1	40
29	Comparative genomics and genotype-phenotype associations in Bifidobacterium breve. Scientific Reports, 2018, 8, 10633.	3.3	37
30	Transcription of Two Adjacent Carbohydrate Utilization Gene Clusters in Bifidobacterium breve UCC2003 Is Controlled by LacI- and Repressor Open Reading Frame Kinase (ROK)-Type Regulators. Applied and Environmental Microbiology, 2014, 80, 3604-3614.	3.1	29
31	A Two-Component Regulatory System Controls Autoregulated Serpin Expression in Bifidobacterium breve UCC2003. Applied and Environmental Microbiology, 2012, 78, 7032-7041.	3.1	26
32	Cloning, expression and characterization of a \hat{l}^2 -d-xylosidase from Lactobacillus rossiae DSM 15814T. Microbial Cell Factories, 2016, 15, 72.	4.0	24
33	Characterization of GH2 and GH42 \hat{l}^2 -galactosidases derived from bifidobacterial infant isolates. AMB Express, 2019, 9, 9.	3.0	24
34	An efficient and reproducible method for transformation of genetically recalcitrant bifidobacteria. FEMS Microbiology Letters, 2012, 333, 146-152.	1.8	23
35	Bifidobacterium breve UCC2003 Employs Multiple Transcriptional Regulators To Control Metabolism of Particular Human Milk Oligosaccharides. Applied and Environmental Microbiology, 2018, 84, .	3.1	23
36	Discovery of a Conjugative Megaplasmid in Bifidobacterium breve. Applied and Environmental Microbiology, 2015, 81, 166-176.	3.1	22

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37	Glycoside hydrolase family 13 α-glucosidases encoded by Bifidobacterium breve UCC2003; A comparative analysis of function, structure and phylogeny. International Journal of Food Microbiology, 2016, 224, 55-65.	4.7	20
38	Carbohydrate Syntrophy enhances the establishment of Bifidobacterium breve UCC2003 in the neonatal gut. Scientific Reports, 2018, 8, 10627.	3.3	19
39	In Silico Assigned Resistance Genes Confer Bifidobacterium with Partial Resistance to Aminoglycosides but Not to Î'-Lactams. PLoS ONE, 2013, 8, e82653.	2.5	17
40	A GntR-type transcriptional repressor controls sialic acid utilization in Bifidobacterium breve UCC2003. FEMS Microbiology Letters, 2015, 362, 1-9.	1.8	17
41	Genome-Wide Search for Genes Required for Bifidobacterial Growth under Iron-Limitation. Frontiers in Microbiology, 2017, 8, 964.	3.5	17
42	Staying alive: growth and survival of Bifidobacterium animalis subsp. animalis under in vitro and in vivo conditions. Applied Microbiology and Biotechnology, 2018, 102, 10645-10663.	3.6	3