Daniel Garrido

List of Publications by Year
in descending order

45 papers	2,645 citations	236833 25 h-index	289141 40 g-index
45 all docs	45 docs citations	45 times ranked	2730 citing authors

#	Article	IF	Citations
1	Bifidobacterium longum subsp. infantis ATCC 15697 Î±-Fucosidases Are Active on Fucosylated Human Milk Oligosaccharides. Applied and Environmental Microbiology, 2012, 78, 795-803.	1.4	204
2	Variation in Consumption of Human Milk Oligosaccharides by Infant Gut-Associated Strains of Bifidobacterium breve. Applied and Environmental Microbiology, 2013, 79, 6040-6049.	1.4	203
3	Consumption of human milk glycoconjugates by infant-associated bifidobacteria: mechanisms and implications. Microbiology (United Kingdom), 2013, 159, 649-664.	0.7	187
4	Oligosaccharide Binding Proteins from Bifidobacterium longum subsp. infantis Reveal a Preference for Host Glycans. PLoS ONE, 2011, 6, e17315.	1.1	179
5	Human milk oligosaccharides and infant gut bifidobacteria: Molecular strategies for their utilization. Food Microbiology, 2018, 75, 37-46.	2.1	161
6	Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. Scientific Reports, 2015, 5, 13517.	1.6	144
7	A novel gene cluster allows preferential utilization of fucosylated milk oligosaccharides in Bifidobacterium longum subsp. longum SC596. Scientific Reports, 2016, 6, 35045.	1.6	137
8	A Molecular Basis for Bifidobacterial Enrichment in the Infant Gastrointestinal Tract. Advances in Nutrition, 2012, 3, 415S-421S.	2.9	128
9	Endo-Î²-N-acetylglucosaminidases from Infant Gut-associated Bifidobacteria Release Complex N-glycans from Human Milk Glycoproteins. Molecular and Cellular Proteomics, 2012, 11, 775-785.	2.5	121
10	Effect of a Milk Formula With Prebiotics on the Intestinal Microbiota of Infants After an Antibiotic Treatment. Pediatric Research, 2006, 59, 451-456.	1.1	118
11	Utilization of galactooligosaccharides by Bifidobacterium longum subsp. infantis isolates. Food Microbiology, 2013, 33, 262-270.	2.1	94
12	Release and utilization of N-acetyl-d-glucosamine from human milk oligosaccharides by Bifidobacterium longum subsp. infantis. Anaerobe, 2012, 18, 430-435.	1.0	88
13	Distinct patterns in the gut microbiota after surgical or medical therapy in obese patients. PeerJ, 2017, 5, e3443.	0.9	85
14	Species Deletions from Microbiome Consortia Reveal Key Metabolic Interactions between Gut Microbes. MSystems, 2019, 4, .	1.7	79
15	Identification of Oligosaccharides in Feces of Breast-fed Infants and Their Correlation with the Gut Microbial Community. Molecular and Cellular Proteomics, 2016, 15, 2987-3002.	2.5	77
16	Proteomic Analysis of Bifidobacterium longum subsp. infantis Reveals the Metabolic Insight on Consumption of Prebiotics and Host Glycans. PLoS ONE, 2013, 8, e57535.	1.1	74
17	Short-term impact of sucralose consumption on the metabolic response and gut microbiome of healthy adults. British Journal of Nutrition, 2019, 122, 856-862.	1.2	63
18	Engineered Probiotics for Detection and Treatment of Inflammatory Intestinal Diseases. Frontiers in Bioengineering and Biotechnology, 2020, 8, 265.	2.0	51

#	Article	IF	Citations
19	Modulation of the fecal microbiota by the intake of aLactobacillus johnsoniiLa1-containing product in human volunteers. FEMS Microbiology Letters, 2005, 248, 249-256.	0.7	44
20	Characterization of human intestinal bifidobacteria using competitive PCR and PCR-TTGE. FEMS Microbiology Ecology, 2006, 55, 28-37.	1.3	41
21	Study of the coumarate decarboxylase and vinylphenol reductase activities of *Dekkera bruxellensis* (anamorph *Brettanomyces bruxellensis*) isolates. Letters in Applied Microbiology, 2009, 48, 452-457.	1.0	37
22	Anti-inflammatory effect of microbial consortia during the utilization of dietary polysaccharides. Food Research International, 2018, 109, 14-23.	2.9	37
23	Hydrolysis of milk gangliosides by infant€gut associated bifidobacteria determined by microfluidic chips and high€resolution mass spectrometry. Electrophoresis, 2014, 35, 1742-1750.	1.3	35
24	Prebiotics Mediate Microbial Interactions in a Consortium of the Infant Gut Microbiome. International Journal of Molecular Sciences, 2017, 18, 2095.	1.8	34
25	Taqman real-time PCR for the detection and enumeration of Saccharomyces cerevisiae in wine. Food Microbiology, 2009, 26, 328-332.	2.1	33
26	Molecular Insights Into O-Linked Glycan Utilization by Gut Microbes. Frontiers in Microbiology, 2020, 11, 591568.	1.5	27
27	Modeling Metabolic Interactions in a Consortium of the Infant Gut Microbiome. Frontiers in Microbiology, 2017, 8, 2507.	1.5	26
28	Evaluating the Capacity of Human Gut Microorganisms to Colonize the Zebrafish Larvae (Danio rerio). Frontiers in Microbiology, 2018, 9, 1032.	1.5	26
29	Modeling approaches for probing cross-feeding interactions in the human gut microbiome. Computational and Structural Biotechnology Journal, 2022, 20, 79-89.	1.9	19
30	Inferring composition and function of the human gut microbiome in time and space: A review of genome-scale metabolic modelling tools. Computational and Structural Biotechnology Journal, 2020, 18, 3897-3904.	1.9	15
31	Assessment of Changes in the Oral Microbiome That Occur in Dogs with Periodontal Disease. Veterinary Sciences, 2021, 8, 291.	0.6	15
32	Comparative Genomic Analysis of Novel Bifidobacterium longum subsp. longum Strains Reveals Functional Divergence in the Human Gut Microbiota. Microorganisms, 2021, 9, 1906.	1.6	11
33	Stochastic simulation of multiscale complex systems with PISKaS: AÂrule-based approach. Biochemical and Biophysical Research Communications, 2018, 498, 342-351.	1.0	9
34	*Atlas*: automatic modeling of regulation of bacterial gene expression and metabolism using rule-based languages. Bioinformatics, 2021, 36, 5473-5480.	1.8	7
35	Simulation and modeling of dietary changes in the infant gut microbiome. FEMS Microbiology Ecology, 2018, 94, .	1.3	6
36	Comparative Genomics of Clostridium baratii Reveals Strain-Level Diversity in Toxin Abundance. Microorganisms, 2022, 10, 213.	1.6	6

#	ARTICLE	IF	CITATIONS
37	Differences in the composition and predicted functions of the intestinal microbiome of obese and normal weight adult dogs. PeerJ, 2022, 10, e12695.	0.9	6
38	Glycosylated proteins preserved over millennia: N-glycan analysis of Tyrolean Iceman, Scythian Princess and Warrior. Scientific Reports, 2014, 4, 4963.	1.6	5
39	Draft genome sequences of Cylindrospermopsis raciborskii strains CS-508 and MVCC14, isolated from freshwater bloom events in Australia and Uruguay. Standards in Genomic Sciences, 2018, 13, 26.	1.5	4
40	Pleione: A tool for statistical and multi-objective calibration of Rule-based models. Scientific Reports, 2019, 9, 15104.	1.6	4
41	The Gut Microbiome After Bariatric Surgery. , 2019, , 235-242.		2
42	Probiotics, Microbiome and the Concept of Cross-Feeding. , 2022, , 199-220.		2
43	Human Milk Oligosaccharides and Health Promotion Through the Gut Microbiome. , 2017, , 73-86.		1
44	Recent advances in the infant gut microbiome and health. , 2020, , 33-38.		0
45	Human Milk Oligosaccharides and Microbiome Homeostasis. , 2021, , 372-388.		0