Manuel ZÃºÃ±iga

List of Publications by Year
in descending order

62 papers	2,916 citations	172457 29 h-index	175258 52 g-index
62 all docs	62 docs citations	62 times ranked	3397 citing authors

#	Article	IF	Citations
1	Stress Physiology of Lactic Acid Bacteria. Microbiology and Molecular Biology Reviews, 2016, 80, 837-890.	6.6	487
2	Amino Acid Catabolic Pathways of Lactic Acid Bacteria. Critical Reviews in Microbiology, 2006, 32, 155-183.	6.1	346
3	Complete Genome Sequence of the Probiotic <i>Lactobacillus casei</i> Strain BL23. Journal of Bacteriology, 2010, 192, 2647-2648.	2.2	144
4	Evolution of arginine deiminase (ADI) pathway genes. Molecular Phylogenetics and Evolution, 2002, 25, 429-444.	2.7	123
5	Relationships between arginine degradation, pH and survival in Lactobacillus sakei. FEMS Microbiology Letters, 1999, 180, 297-304.	1.8	83
6	Utilization of Host-Derived Glycans by Intestinal Lactobacillus and Bifidobacterium Species. Frontiers in Microbiology, 2018, 9, 1917.	3.5	82
7	Proteomic and transcriptomic analysis of the response to bile stress of Lactobacillus casei BL23. Microbiology (United Kingdom), 2012, 158, 1206-1218.	1.8	81
8	Accumulation of Polyphosphate in Lactobacillus spp. and Its Involvement in Stress Resistance. Applied and Environmental Microbiology, 2014, 80, 1650-1659.	3.1	70
9	Identification of a Gene Cluster Enabling<i>Lactobacillus casei</i>BL23 To Utilize<i>myo</i>-Inositol. Applied and Environmental Microbiology, 2007, 73, 3850-3858.	3.1	69
10	The Phosphotransferase System of <i>Lactobacillus casei</i>: Regulation of Carbon Metabolism and Connection to Cold Shock Response. Journal of Molecular Microbiology and Biotechnology, 2007, 12, 20-32.	1.0	65
11	An improved medium for distinguishing between homofermentative and heterofermentative lactic acid bacteria. International Journal of Food Microbiology, 1993, 18, 37-42.	4.7	64
12	Requirement of the<i>Lactobacillus casei</i>MaeKR Two-Component System for<scp>l</scp>-Malic Acid Utilization via a Malic Enzyme Pathway. Applied and Environmental Microbiology, 2010, 76, 84-95.	3.1	59
13	Changes in Cecal Microbiota and Mucosal Gene Expression Revealed New Aspects of Epizootic Rabbit Enteropathy. PLoS ONE, 2014, 9, e105707.	2.5	58
14	The Product of arcR, the Sixth Gene of the arc Operon of Lactobacillus sakei, Is Essential for Expression of the Arginine Deiminase Pathway. Applied and Environmental Microbiology, 2002, 68, 6051-6058.	3.1	54
15	Defence against antimicrobial peptides: different strategies in <scp><i>F</i></scp><i>irmicutes</i>. Environmental Microbiology, 2014, 16, 1225-1237.	3.8	54
16	Horizontal Gene Transfer in the Molecular Evolution of Mannose PTS Transporters. Molecular Biology and Evolution, 2005, 22, 1673-1685.	8.9	50
17	Dietary supplementation with sorbitol results in selective enrichment of lactobacilli in rat intestine. Research in Microbiology, 2007, 158, 694-701.	2.1	47
18	Construction of Compatible Wide-Host-Range Shuttle Vectors for Lactic Acid Bacteria and Escherichia coli. Plasmid, 2001, 46, 106-116.	1.4	46

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19	Characterization of faecal enterococci from rabbits for the selection of probiotic strains. Journal of Applied Microbiology, 2004, 96, 761-771.	3.1	46
20	Malic Enzyme and Malolactic Enzyme Pathways Are Functionally Linked but Independently Regulated in Lactobacillus casei BL23. Applied and Environmental Microbiology, 2013, 79, 5509-5518.	3.1	45
21	Characterization of Lactobacillus from Algerian goat's milk based on phenotypic, 16S rDNA sequencing and their technological properties. Brazilian Journal of Microbiology, 2011, 42, 158-171.	2.0	44
22	Use of lactic acid bacteria and yeasts to reduce exposure to chemical food contaminants and toxicity. Critical Reviews in Food Science and Nutrition, 2019, 59, 1534-1545.	10.3	44
23	Influence of Two-Component Signal Transduction Systems of <i>Lactobacillus casei</i> BL23 on Tolerance to Stress Conditions. Applied and Environmental Microbiology, 2011, 77, 1516-1519.	3.1	43
24	Dynamics of Microbial Populations during Fermentation of Wines from the Utiel-Requena Region of Spain. Applied and Environmental Microbiology, 1989, 55, 539-541.	3.1	42
25	Characterization of a Regulatory Network of Peptide Antibiotic Detoxification Modules in Lactobacillus casei BL23. Applied and Environmental Microbiology, 2013, 79, 3160-3170.	3.1	41
26	The use of lactic acid bacteria to reduce mercury bioaccessibility. Food Chemistry, 2017, 228, 158-166.	8.2	36
27	Lactobacillus paracasei and Lactobacillus plantarum strains downregulate proinflammatory genes in an ex vivo system of cultured human colonic mucosa. Genes and Nutrition, 2013, 8, 165-180.	2.5	35
28	Peptide and amino acid metabolism is controlled by an OmpRâ€family response regulator in <i>Lactobacillus casei</i>. Molecular Microbiology, 2016, 100, 25-41.	2.5	35
29	Molecular analysis of the glucose-specific phosphoenolpyruvateâ€Š:â€Šsugar phosphotransferase system from Lactobacillus casei and its links with the control of sugar metabolism. Microbiology (United) Tj ETQq1 1 0.784314 rgBT /Overlock	1.8	31
30	Bacterial and Eukaryotic Phosphoketolases: Phylogeny, Distribution and Evolution. Journal of Molecular Microbiology and Biotechnology, 2010, 18, 37-51.	1.0	31
31	Characterization of a novel Lactobacillus species closely related to Lactobacillus johnsonii using a combination of molecular and comparative genomics methods. BMC Genomics, 2010, 11, 504.	2.8	29
32	Sublethally damaged cells of Escherichia coli by Pulsed Electric Fields: The chance of transformation and proteomic assays. Food Research International, 2013, 54, 1120-1127.	6.2	28
33	Complex Oligosaccharide Utilization Pathways in <i>Lactobacillus</i>. Current Issues in Molecular Biology, 2021, 40, 49-80.	2.4	27
34	Physiological Role of Two-Component Signal Transduction Systems in Food-Associated Lactic Acid Bacteria. Advances in Applied Microbiology, 2017, 99, 1-51.	2.4	27
35	P40 and P75 Are Singular Functional Muramidases Present in the Lactobacillus casei /paracasei/rhamnosus Taxon. Frontiers in Microbiology, 2019, 10, 1420.	3.5	26
36	Unraveling the evolutionary history of the phosphoryl-transfer chain of the phosphoenolpyruvate:phosphotransferase system through phylogenetic analyses and genome context. BMC Evolutionary Biology, 2008, 8, 147.	3.2	23

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37	Response of Lactobacillus casei BL23 to phenolic compounds. Journal of Applied Microbiology, 2011, 111, 1473-1481.	3.1	23
38	Comparative Genomic and Phylogenetic Analyses of Gammaproteobacterial glg Genes Traced the Origin of the Escherichia coli Glycogen glgBXCAP Operon to the Last Common Ancestor of the Sister Orders Enterobacteriales and Pasteurellales. PLoS ONE, 2015, 10, e0115516.	2.5	23
39	Characterization of the binding capacity of mercurial species in <i>Lactobacillus</i> strains. Journal of the Science of Food and Agriculture, 2017, 97, 5107-5113.	3.5	23
40	Conjugative plasmid pIP501 undergoes specific deletions after transfer from Lactococcus lactis to Oenococcus oeni. Archives of Microbiology, 2003, 180, 367-373.	2.2	22
41	In vivo evaluation of the effect of arsenite on the intestinal epithelium and associated microbiota in mice. Archives of Toxicology, 2019, 93, 2127-2139.	4.2	21
42	Lactic Acid Bacteria in Spanish Red Rose and White Musts and Wines under Cellar Conditions. Journal of Food Science, 1992, 57, 392-395.	3.1	19
43	Nucleotide Sequence of Plasmid p4028, a Cryptic Plasmid fromLeuconostoc oenos. Plasmid, 1996, 36, 67-74.	1.4	17
44	Polyphosphate in Lactobacillus and Its Link to Stress Tolerance and Probiotic Properties. Frontiers in Microbiology, 2018, 9, 1944.	3.5	17
45	In Vitro Evaluation of the Protective Role of Lactobacillus StrainsAgainst Inorganic Arsenic Toxicity. Probiotics and Antimicrobial Proteins, 2020, 12, 1484-1491.	3.9	15
46	Unique Microbial Catabolic Pathway for the Human Core <i>N</i> -Glycan Constituent Fucosyl-Î±-1,6- <i>N</i> -Acetylglucosamine-Asparagine. MBio, 2020, 11, .	4.1	15
47	TransposonsTn916andTn925can transfer fromEnterococcus faecalistoLeuconostoc oenos. FEMS Microbiology Letters, 1996, 135, 179-185.	1.8	13
48	Characterization of the Putative Replisome Organizer of the Lactococcal Bacteriophage r1t. Journal of Virology, 2002, 76, 10234-10244.	3.4	13
49	Effect of lactic acid bacteria on mercury toxicokinetics. Food and Chemical Toxicology, 2019, 128, 147-153.	3.6	12
50	Evolutionary history of the OmpR/IIIA family of signal transduction two component systems in Lactobacillaceae and Leuconostocaceae. BMC Evolutionary Biology, 2011, 11, 34.	3.2	11
51	Growth and Metabolism of L-malic Acid by Lactobacillus plantarum CECT 220 in a Defined Medium. Journal of Food Science, 1992, 57, 778-780.	3.1	10
52	Characterization of the response to low pH of<i>Lactobacillus casei</i>Î”RR12, a mutant strain with low D-alanylation activity and sensitivity to low pH. Journal of Applied Microbiology, 2014, 116, 1250-1261.	3.1	10
53	Lipoteichoic acid depletion in <i>Lactobacillus</i> impacts cell morphology and stress response but does not abolish mercury surface binding. Beneficial Microbes, 2020, 11, 791-802.	2.4	8
54	Differences in the expression of cell envelope proteinases (CEP) in two <i>Lactobacillus paracasei</i> probiotic strains. FEMS Microbiology Letters, 2020, 367, .	1.8	6

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55	In vitro evaluation of the efficacy of lactobacilli and yeasts in reducing bioavailability of inorganic arsenic. LWT - Food Science and Technology, 2020, 126, 109272.	5.2	6
56	Core and Accessory Genome Analysis of Vibrio mimicus. Microorganisms, 2021, 9, 191.	3.6	6
57	The malate sensing two-component system MaeKR is a non-canonical class of sensory complex for C4-dicarboxylates. Scientific Reports, 2017, 7, 2708.	3.3	5
58	ABC Transporter DerAB of Lactobacillus casei Mediates Resistance against Insect-Derived Defensins. Applied and Environmental Microbiology, 2020, 86, .	3.1	3
59	A selective medium for the isolation of malolactic mutants of Leuconostoc oenos. Letters in Applied Microbiology, 1994, 19, 451-453.	2.2	2
60	Adaptation potential of microorganisms treated by pulsed electric fields. , 2007, , 156-164.		1
61	Cysteine induces resistance of lactobacilli to erythromycin and azithromycin. International Journal of Antimicrobial Agents, 2019, 53, 352-353.	2.5	0
62	Complex Oligosaccharide Utilization Pathways in Lactobacillus. , 2019, , .		0