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	Core and Accessory Genome Analysis of Vibrio mimicus. Microorganisms, 2021, 9, 191.	3.6	6
2	Complex Oligosaccharide Utilization Pathways in <i>Lactobacillus</i>. Current Issues in Molecular Biology, 2021, 40, 49-80.	2.4	27
3	ABC Transporter DerAB of Lactobacillus casei Mediates Resistance against Insect-Derived Defensins. Applied and Environmental Microbiology, 2020, 86, .	3.1	3
4	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
5	In Vitro Evaluation of the Protective Role of Lactobacillus StrainsAgainst Inorganic Arsenic Toxicity. Probiotics and Antimicrobial Proteins, 2020, 12, 1484-1491.	3.9	15
6	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
7	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
8	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
9	P40 and P75 Are Singular Functional Muramidases Present in the Lactobacillus casei /paracasei/rhamnosus Taxon. Frontiers in Microbiology, 2019, 10, 1420.	3.5	26
10	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
11	Effect of lactic acid bacteria on mercury toxicokinetics. Food and Chemical Toxicology, 2019, 128, 147-153.	3.6	12
12	Cysteine induces resistance of lactobacilli to erythromycin and azithromycin. International Journal of Antimicrobial Agents, 2019, 53, 352-353.	2.5	0
13	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
14	Complex Oligosaccharide Utilization Pathways in Lactobacillus. , 2019, , .		0
15	Polyphosphate in Lactobacillus and Its Link to Stress Tolerance and Probiotic Properties. Frontiers in Microbiology, 2018, 9, 1944.	3.5	17
16	Utilization of Host-Derived Glycans by Intestinal Lactobacillus and Bifidobacterium Species. Frontiers in Microbiology, 2018, 9, 1917.	3.5	82
17	The use of lactic acid bacteria to reduce mercury bioaccessibility. Food Chemistry, 2017, 228, 158-166.	8.2	36
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Stress Physiology of Lactic Acid Bacteria. Microbiology and Molecular Biology Reviews, 2016, 80, 837-890.	6.6	487
22	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
23	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
24	Changes in Cecal Microbiota and Mucosal Gene Expression Revealed New Aspects of Epizootic Rabbit Enteropathy. PLoS ONE, 2014, 9, e105707.	2.5	58
25	Defence against antimicrobial peptides: different strategies in <scp><i>F</i></scp><i>irmicutes</i>. Environmental Microbiology, 2014, 16, 1225-1237.	3.8	54
26	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
27	Accumulation of Polyphosphate in Lactobacillus spp. and Its Involvement in Stress Resistance. Applied and Environmental Microbiology, 2014, 80, 1650-1659.	3.1	70
28	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
29	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
30	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
31	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
32	Proteomic and transcriptomic analysis of the response to bile stress of Lactobacillus casei BL23. Microbiology (United Kingdom), 2012, 158, 1206-1218.	1.8	81
33	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
34	Response of Lactobacillus casei BL23 to phenolic compounds. Journal of Applied Microbiology, 2011, 111, 1473-1481.	3.1	23
35	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
36	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

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37	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
38	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
39	Complete Genome Sequence of the Probiotic <i>Lactobacillus casei</i> Strain BL23. Journal of Bacteriology, 2010, 192, 2647-2648.	2.2	144
40	Bacterial and Eukaryotic Phosphoketolases: Phylogeny, Distribution and Evolution. Journal of Molecular Microbiology and Biotechnology, 2010, 18, 37-51.	1.0	31
41	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
42	Adaptation potential of microorganisms treated by pulsed electric fields. , 2007, , 156-164.		1
43	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
44	Dietary supplementation with sorbitol results in selective enrichment of lactobacilli in rat intestine. Research in Microbiology, 2007, 158, 694-701.	2.1	47
45	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
46	Amino Acid Catabolic Pathways of Lactic Acid Bacteria. Critical Reviews in Microbiology, 2006, 32, 155-183.	6.1	346
47	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	30
48	Horizontal Gene Transfer in the Molecular Evolution of Mannose PTS Transporters. Molecular Biology and Evolution, 2005, 22, 1673-1685.	8.9	50
49	Characterization of faecal enterococci from rabbits for the selection of probiotic strains. Journal of Applied Microbiology, 2004, 96, 761-771.	3.1	46
50	Conjugative plasmid pIP501 undergoes specific deletions after transfer from Lactococcus lactis to Oenococcus oeni. Archives of Microbiology, 2003, 180, 367-373.	2.2	22
51	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
52	Characterization of the Putative Replisome Organizer of the Lactococcal Bacteriophage r1t. Journal of Virology, 2002, 76, 10234-10244.	3.4	13
53	Evolution of arginine deiminase (ADI) pathway genes. Molecular Phylogenetics and Evolution, 2002, 25, 429-444.	2.7	123
54	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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55	Relationships between arginine degradation, pH and survival in Lactobacillus sakei. FEMS Microbiology Letters, 1999, 180, 297-304.	1.8	83
56	Nucleotide Sequence of Plasmid p4028, a Cryptic Plasmid fromLeuconostoc oenos. Plasmid, 1996, 36, 67-74.	1.4	17
57	TransposonsTn916andTn925can transfer fromEnterococcus faecalistoLeuconostoc oenos. FEMS Microbiology Letters, 1996, 135, 179-185.	1.8	13
58	A selective medium for the isolation of malolactic mutants of Leuconostoc oenos. Letters in Applied Microbiology, 1994, 19, 451-453.	2.2	2
59	An improved medium for distinguishing between homofermentative and heterofermentative lactic acid bacteria. International Journal of Food Microbiology, 1993, 18, 37-42.	4.7	64
60	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
61	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
62	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