Manuel Carmona

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35	1,313	17	36
papers	citations	h-index	g-index
37 ext. papers	1,536 ext. citations	4.8 avg, IF	4.05 L-index

#	Paper	IF	Citations
35	Motility, Adhesion and c-di-GMP Influence the Endophytic Colonization of Rice by sp. CIB. <i>Microorganisms</i> , 2021 , 9,	4.9	6
34	Comparative Genomics Provides Insights into the Taxonomy of and Reveals Separate Origins of Genes in the Proposed and Genera. <i>Genes</i> , 2021 , 12,	4.2	3
33	Enhancing the Rice Seedlings Growth Promotion Abilities of sp. CIB by Heterologous Expression of ACC Deaminase to Improve Performance of Plants Exposed to Cadmium Stress. <i>Microorganisms</i> , 2020 , 8,	4.9	8
32	ArxA From sp. CIB, an Anaerobic Arsenite Oxidase From an Obligate Heterotrophic and Mesophilic Bacterium. <i>Frontiers in Microbiology</i> , 2019 , 10, 1699	5.7	9
31	Bioremediation of Soil Contaminated with Arsenic. Microorganisms for Sustainability, 2019, 321-351	1.1	2
30	Transcriptional Regulation of the Peripheral Pathway for the Anaerobic Catabolism of Toluene and -Xylene in sp. CIB. <i>Frontiers in Microbiology</i> , 2018 , 9, 506	5.7	16
29	Engineering a bzd cassette for the anaerobic bioconversion of aromatic compounds. <i>Microbial Biotechnology</i> , 2017 , 10, 1418-1425	6.3	5
28	Speeding up bioproduction of selenium nanoparticles by using Vibrio natriegens as microbial factory. <i>Scientific Reports</i> , 2017 , 7, 16046	4.9	47
27	Biosynthesis of selenium nanoparticles by Azoarcus sp. CIB. <i>Microbial Cell Factories</i> , 2016 , 15, 109	6.4	60
26	Refactoring the [phage lytic/lysogenic decision with a synthetic regulator. <i>MicrobiologyOpen</i> , 2016 , 5, 575-81	3.4	8
25	Whole-genome analysis of Azoarcus sp. strain CIB provides genetic insights to its different lifestyles and predicts novel metabolic features. <i>Systematic and Applied Microbiology</i> , 2015 , 38, 462-71	4.2	49
24	Unraveling the specific regulation of the central pathway for anaerobic degradation of 3-methylbenzoate. <i>Journal of Biological Chemistry</i> , 2015 , 290, 12165-83	5.4	12
23	AccR is a master regulator involved in carbon catabolite repression of the anaerobic catabolism of aromatic compounds in Azoarcus sp. CIB. <i>Journal of Biological Chemistry</i> , 2014 , 289, 1892-904	5.4	16
22	Azoarcus sp. CIB, an anaerobic biodegrader of aromatic compounds shows an endophytic lifestyle. <i>PLoS ONE</i> , 2014 , 9, e110771	3.7	33
21	Characterization of the mbd cluster encoding the anaerobic 3-methylbenzoyl-CoA central pathway. <i>Environmental Microbiology</i> , 2013 , 15, 148-66	5.2	32
20	Identification of a missing link in the evolution of an enzyme into a transcriptional regulator. <i>PLoS ONE</i> , 2013 , 8, e57518	3.7	11
19	Bacterial degradation of benzoate: cross-regulation between aerobic and anaerobic pathways. Journal of Biological Chemistry, 2012 , 287, 10494-10508	5.4	66

(1991-2010)

18	transcription of the Geobacter metallireducens bamVW two-component system, involved in transcriptional regulation of aromatic degradation. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 383-5	4.8	16
17	Biochemical characterization of the transcriptional regulator BzdR from Azoarcus sp. CIB. <i>Journal of Biological Chemistry</i> , 2010 , 285, 35694-705	5.4	23
16	Anaerobic catabolism of aromatic compounds: a genetic and genomic view. <i>Microbiology and Molecular Biology Reviews</i> , 2009 , 73, 71-133	13.2	312
15	Identification and analysis of a glutaryl-CoA dehydrogenase-encoding gene and its cognate transcriptional regulator from Azoarcus sp. CIB. <i>Environmental Microbiology</i> , 2008 , 10, 474-82	5.2	16
14	New insights into the BzdR-mediated transcriptional regulation of the anaerobic catabolism of benzoate in Azoarcus sp. CIB. <i>Microbiology (United Kingdom)</i> , 2008 , 154, 306-316	2.9	11
13	Oxygen-dependent regulation of the central pathway for the anaerobic catabolism of aromatic compounds in Azoarcus sp. strain CIB. <i>Journal of Bacteriology</i> , 2006 , 188, 2343-54	3.5	16
12	Iron-reducing bacteria unravel novel strategies for the anaerobic catabolism of aromatic compounds. <i>Molecular Microbiology</i> , 2005 , 58, 1210-5	4.1	15
11	m-xylene-responsive Pu-PnifH hybrid sigma54 promoters that overcome physiological control in Pseudomonas putida KT2442. <i>Journal of Bacteriology</i> , 2005 , 187, 125-34	3.5	14
10	BzdR, a repressor that controls the anaerobic catabolism of benzoate in Azoarcus sp. CIB, is the first member of a new subfamily of transcriptional regulators. <i>Journal of Biological Chemistry</i> , 2005 , 280, 10683-94	5.4	58
9	The bzd gene cluster, coding for anaerobic benzoate catabolism, in Azoarcus sp. strain CIB. <i>Journal of Bacteriology</i> , 2004 , 186, 5762-74	3.5	92
8	Genetic clues on the evolution of anaerobic catabolism of aromatic compounds. <i>Microbiology</i> (United Kingdom), 2004 , 150, 2018-2021	2.9	15
7	In vivo and in vitro effects of (p)ppGpp on the sigma(54) promoter Pu of the TOL plasmid of Pseudomonas putida. <i>Journal of Bacteriology</i> , 2000 , 182, 4711-8	3.5	54
6	Recruitment of RNA polymerase is a rate-limiting step for the activation of the sigma(54) promoter Pu of Pseudomonas putida. <i>Journal of Biological Chemistry</i> , 1999 , 274, 33790-4	5.4	30
5	Involvement of the FtsH (HflB) protease in the activity of sigma 54 promoters. <i>Molecular Microbiology</i> , 1999 , 31, 261-70	4.1	35
4	DNA bending and the initiation of transcription at sigma54-dependent bacterial promoters. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 9568-72	11.5	38
3	Activation of transcription at sigma 54-dependent promoters on linear templates requires intrinsic or induced bending of the DNA. <i>Journal of Molecular Biology</i> , 1996 , 261, 348-56	6.5	60
2	Escherichia coli hha mutants, DNA supercoiling and expression of the haemolysin genes from the recombinant plasmid pANN202-312. <i>Molecular Microbiology</i> , 1993 , 9, 1011-8	4.1	40
1	The hha gene modulates haemolysin expression in Escherichia coli. <i>Molecular Microbiology</i> , 1991 , 5, 1285	4913	85