

Carlos A Canchaya

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8838974/carlos-a-canchaya-publications-by-year.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

53
papers

5,647
citations

37
h-index

58
g-index

58
ext. papers

6,551
ext. citations

5
avg, IF

5.23
L-index

#	Paper	IF	Citations
53	The network structure of intertidal meiofaunal communities from environmental DNA metabarcoding surveys in Northwest Iberia. <i>Aquatic Sciences</i> , 2021 , 83, 1	2.5	2
52	Meiofauna metabarcoding in Lima estuary (Portugal) suggests high taxon replacement within a background of network stability. <i>Regional Studies in Marine Science</i> , 2020 , 38, 101341	1.5	3
51	Small-scale spatial variation of meiofaunal communities in Lima estuary (NW Portugal) assessed through metabarcoding. <i>Estuarine, Coastal and Shelf Science</i> , 2020 , 238, 106683	2.9	8
50	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020 , 21, 275	18.3	42
49	Population genomic footprints of environmental pollution pressure in natural populations of the Mediterranean mussel. <i>Marine Genomics</i> , 2019 , 45, 11-15	1.9	1
48	Draft genome sequence of LMTR 21 isolated from Lima bean () in Peru. <i>Genomics Data</i> , 2017 , 13, 38-40		3
47	Genome sequence of sp. LMTR 3, a diazotrophic symbiont of Lima bean (). <i>Genomics Data</i> , 2017 , 13, 35-37		3
46	A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016 , 11, e0151561	3.7	90
45	Genome of <i>Rhizobium leucaenae</i> strains CFN 299(T) and CPAO 29.8: searching for genes related to a successful symbiotic performance under stressful conditions. <i>BMC Genomics</i> , 2016 , 17, 534	4.5	10
44	RNA-Seq in <i>Mytilus galloprovincialis</i> : comparative transcriptomics and expression profiles among different tissues. <i>BMC Genomics</i> , 2015 , 16, 728	4.5	70
43	Mosaic-like sequences containing transposon, phage, and plasmid elements among <i>Listeria monocytogenes</i> plasmids. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 4851-7	4.8	17
42	Comparative genomics and proteomics of <i>Helicobacter mustelae</i> , an ulcerogenic and carcinogenic gastric pathogen. <i>BMC Genomics</i> , 2010 , 11, 164	4.5	31
41	Microbial diversity in the human intestine and novel insights from metagenomics. <i>Frontiers in Bioscience - Landmark</i> , 2009 , 14, 3214-21	2.8	60
40	The <i>Bifidobacterium dentium</i> Bd1 genome sequence reflects its genetic adaptation to the human oral cavity. <i>PLoS Genetics</i> , 2009 , 5, e1000785	6	120
39	Isolation of lactobacilli with probiotic properties from the human stomach. <i>Letters in Applied Microbiology</i> , 2008 , 47, 269-74	2.9	47
38	<i>Lactobacillus hordei</i> sp. nov., a bacteriocinogenic strain isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008 , 58, 2013-7	2.2	20
37	Comparative analyses of prophage-like elements present in two <i>Lactococcus lactis</i> strains. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 7771-80	4.8	37

36	Genomics of Actinobacteria: tracing the evolutionary history of an ancient phylum. <i>Microbiology and Molecular Biology Reviews</i> , 2007 , 71, 495-548	13.2	680
35	Exploiting Bifidobacterium genomes: the molecular basis of stress response. <i>International Journal of Food Microbiology</i> , 2007 , 120, 13-24	5.8	46
34	Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2007 , 91, 351-72	2.1	87
33	Distribution of megaplastids in <i>Lactobacillus salivarius</i> and other lactobacilli. <i>Journal of Bacteriology</i> , 2007 , 189, 6128-39	3.5	50
32	Molecular characterization of hsp20, encoding a small heat shock protein of bifidobacterium breve UCC2003. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4695-703	4.8	38
31	GANNPhos: a new phosphorylation site predictor based on a genetic algorithm integrated neural network. <i>Protein Engineering, Design and Selection</i> , 2007 , 20, 405-12	1.9	50
30	Complete genome sequence of the prototype lactic acid bacterium <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363. <i>Journal of Bacteriology</i> , 2007 , 189, 3256-70	3.5	314
29	Comparative and functional analysis of sortase-dependent proteins in the predicted secretome of <i>Lactobacillus salivarius</i> UCC118. <i>Applied and Environmental Microbiology</i> , 2006 , 72, 4143-53	4.8	114
28	Analysis of bifidobacterial evolution using a multilocus approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2783-2792	2.2	136
27	Multireplicon genome architecture of <i>Lactobacillus salivarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 6718-23	11.5	183
26	Diversity of the genus <i>Lactobacillus</i> revealed by comparative genomics of five species. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 3185-3196	2.9	102
25	Comparative genomics and transcriptional analysis of prophages identified in the genomes of <i>Lactobacillus gasseri</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006 , 72, 3130-46	4.8	57
24	Sequence and comparative genomic analysis of lactococcal bacteriophages jj50, 712 and P008: evolutionary insights into the 936 phage species. <i>FEMS Microbiology Letters</i> , 2006 , 261, 253-61	2.9	61
23	How high G+C Gram-positive bacteria and in particular bifidobacteria cope with heat stress: protein players and regulators. <i>FEMS Microbiology Reviews</i> , 2006 , 30, 734-59	15.1	41
22	Polyphasic analysis indicates that <i>Lactobacillus salivarius</i> subsp. <i>salivarius</i> and <i>Lactobacillus salivarius</i> subsp. <i>salicinius</i> do not merit separate subspecies status. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2397-2403	2.2	21
21	The ClgR protein regulates transcription of the <i>clpP</i> operon in <i>Bifidobacterium breve</i> UCC 2003. <i>Journal of Bacteriology</i> , 2005 , 187, 8411-26	3.5	38
20	Genetic characterization of the <i>Bifidobacterium breve</i> UCC 2003 <i>hrcA</i> locus. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8998-9007	4.8	27
19	Prophage-like elements in bifidobacteria: insights from genomics, transcription, integration, distribution, and phylogenetic analysis. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8692-705	4.8	55

18	Bifidobacterium lactis DSM 10140: identification of the atp (atpBEFHAGDC) operon and analysis of its genetic structure, characteristics, and phylogeny. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 3110-21	4.8	83
17	Comparative genomics of the T4-Like Escherichia coli phage JS98: implications for the evolution of T4 phages. <i>Journal of Bacteriology</i> , 2004 , 186, 8276-86	3.5	40
16	Characterization of the groEL and groES loci in Bifidobacterium breve UCC 2003: genetic, transcriptional, and phylogenetic analyses. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 6197-209	4.8	82
15	The impact of prophages on bacterial chromosomes. <i>Molecular Microbiology</i> , 2004 , 53, 9-18	4.1	264
14	The prophages of Lactobacillus johnsonii NCC 533: comparative genomics and transcription analysis. <i>Virology</i> , 2004 , 320, 229-42	3.6	40
13	Phages and the evolution of bacterial pathogens: from genomic rearrangements to lysogenic conversion. <i>Microbiology and Molecular Biology Reviews</i> , 2004 , 68, 560-602, table of contents	13.2	1118
12	Prophage Genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2003 , 67, 473-473	13.2	2
11	Analysis, characterization, and loci of the tuf genes in lactobacillus and bifidobacterium species and their direct application for species identification. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 6908-22	4.8	134
10	The prophage sequences of Lactobacillus plantarum strain WCFS1. <i>Virology</i> , 2003 , 316, 245-55	3.6	58
9	Prophage genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2003 , 67, 238-76, table of contents	13.2	508
8	Phage as agents of lateral gene transfer. <i>Current Opinion in Microbiology</i> , 2003 , 6, 417-24	7.9	360
7	Integration and distribution of Lactobacillus johnsonii prophages. <i>Journal of Bacteriology</i> , 2003 , 185, 4603-8	3.5	40
6	Transcription mapping as a tool in phage genomics: the case of the temperate Streptococcus thermophilus phage Sfi21. <i>Virology</i> , 2002 , 296, 62-76	3.6	39
5	Genome analysis of an inducible prophage and prophage remnants integrated in the Streptococcus pyogenes strain SF370. <i>Virology</i> , 2002 , 302, 245-58	3.6	62
4	Transcription analysis of Streptococcus thermophilus phages in the lysogenic state. <i>Virology</i> , 2002 , 302, 21-32	3.6	37
3	Comparative genomics of phages and prophages in lactic acid bacteria. <i>Antonie Van Leeuwenhoek</i> , 2002 , 82, 73-91	2.1	80
2	Comparative genomics of phages and prophages in lactic acid bacteria 2002 , 73-91		8
1	Massive gene presence/absence variation in the mussel genome as an adaptive strategy: first evidence of a pan-genome in Metazoa		11

