

Carlos A Canchaya

List of Publications by Citations

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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	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
52	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
51	Prophage genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2003 , 67, 238-76, table of contents	13.2	508
50	Phage as agents of lateral gene transfer. <i>Current Opinion in Microbiology</i> , 2003 , 6, 417-24	7.9	360
49	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
48	The impact of prophages on bacterial chromosomes. <i>Molecular Microbiology</i> , 2004 , 53, 9-18	4.1	264
47	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
46	Analysis of bifidobacterial evolution using a multilocus approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006 , 56, 2783-2792	2.2	136
45	Analysis, characterization, and loci of the <i>tuf</i> genes in <i>Lactobacillus</i> and <i>Bifidobacterium</i> species and their direct application for species identification. <i>Applied and Environmental Microbiology</i> , 2003 , 69, 6908-12	4.8	134
44	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
43	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
42	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
41	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
40	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
39	<i>Bifidobacterium lactis</i> DSM 10140: identification of the <i>atp</i> (<i>atpBEFHAGDC</i>) operon and analysis of its genetic structure, characteristics, and phylogeny. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 3110-21	4.8	83
38	Characterization of the <i>groEL</i> and <i>groES</i> loci in <i>Bifidobacterium breve</i> UCC 2003: genetic, transcriptional, and phylogenetic analyses. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 6197-209	4.8	82
37	Comparative genomics of phages and prophages in lactic acid bacteria. <i>Antonie Van Leeuwenhoek</i> , 2002 , 82, 73-91	2.1	80

36	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
35	Genome analysis of an inducible prophage and prophage remnants integrated in the <i>Streptococcus pyogenes</i> strain SF370. <i>Virology</i> , 2002 , 302, 245-58	3.6	62
34	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
33	Microbial diversity in the human intestine and novel insights from metagenomics. <i>Frontiers in Bioscience - Landmark</i> , 2009 , 14, 3214-21	2.8	60
32	The prophage sequences of <i>Lactobacillus plantarum</i> strain WCFS1. <i>Virology</i> , 2003 , 316, 245-55	3.6	58
31	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
30	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
29	Distribution of megaplastids in <i>Lactobacillus salivarius</i> and other lactobacilli. <i>Journal of Bacteriology</i> , 2007 , 189, 6128-39	3.5	50
28	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
27	Isolation of lactobacilli with probiotic properties from the human stomach. <i>Letters in Applied Microbiology</i> , 2008 , 47, 269-74	2.9	47
26	Exploiting <i>Bifidobacterium</i> genomes: the molecular basis of stress response. <i>International Journal of Food Microbiology</i> , 2007 , 120, 13-24	5.8	46
25	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020 , 21, 275	18.3	42
24	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
23	Comparative genomics of the T4-Like <i>Escherichia coli</i> phage JS98: implications for the evolution of T4 phages. <i>Journal of Bacteriology</i> , 2004 , 186, 8276-86	3.5	40
22	The prophages of <i>Lactobacillus johnsonii</i> NCC 533: comparative genomics and transcription analysis. <i>Virology</i> , 2004 , 320, 229-42	3.6	40
21	Integration and distribution of <i>Lactobacillus johnsonii</i> prophages. <i>Journal of Bacteriology</i> , 2003 , 185, 4603-8	3.5	40
20	Transcription mapping as a tool in phage genomics: the case of the temperate <i>Streptococcus thermophilus</i> phage Sfi21. <i>Virology</i> , 2002 , 296, 62-76	3.6	39
19	Molecular characterization of hsp20, encoding a small heat shock protein of <i>bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 4695-703	4.8	38

18	The ClgR protein regulates transcription of the clpP operon in <i>Bifidobacterium breve</i> UCC 2003. <i>Journal of Bacteriology</i> , 2005 , 187, 8411-26	3.5	38
17	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
16	Transcription analysis of <i>Streptococcus thermophilus</i> phages in the lysogenic state. <i>Virology</i> , 2002 , 302, 21-32	3.6	37
15	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
14	Genetic characterization of the <i>Bifidobacterium breve</i> UCC 2003 hrcA locus. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8998-9007	4.8	27
13	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
12	<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
11	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
10	Massive gene presence/absence variation in the mussel genome as an adaptive strategy: first evidence of a pan-genome in Metazoa		11
9	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
8	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
7	Comparative genomics of phages and prophages in lactic acid bacteria 2002 , 73-91		8
6	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
5	Draft genome sequence of LMTR 21 isolated from Lima bean () in Peru. <i>Genomics Data</i> , 2017 , 13, 38-40		3
4	Genome sequence of sp. LMTR 3, a diazotrophic symbiont of Lima bean (). <i>Genomics Data</i> , 2017 , 13, 35-37		3
3	Prophage Genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2003 , 67, 473-473	13.2	2
2	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
1	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

