

Carlos A Canchaya

List of Publications by Year in descending order

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52
papers

6,992
citations

81900

39
h-index

168389

53
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58
all docs

58
docs citations

58
times ranked

7596
citing authors

#	ARTICLE	IF	CITATIONS
1	Phages and the Evolution of Bacterial Pathogens: from Genomic Rearrangements to Lysogenic Conversion. <i>Microbiology and Molecular Biology Reviews</i> , 2004, 68, 560-602.	6.6	1,412
2	Genomics of <i>Actinobacteria</i> : Tracing the Evolutionary History of an Ancient Phylum. <i>Microbiology and Molecular Biology Reviews</i> , 2007, 71, 495-548.	6.6	852
3	Prophage Genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2003, 67, 238-276.	6.6	594
4	Phage as agents of lateral gene transfer. <i>Current Opinion in Microbiology</i> , 2003, 6, 417-424.	5.1	437
5	The impact of prophages on bacterial chromosomes. <i>Molecular Microbiology</i> , 2004, 53, 9-18.	2.5	366
6	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, 3256-3270.	2.2	362
7	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, 6718-6723.	7.1	216
8	Analysis of bifidobacterial evolution using a multilocus approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2783-2792.	1.7	154
9	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, 6908-6922.	3.1	150
10	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, 4143-4153.	3.1	145
11	The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	3.5	141
12	A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016, 11, e0151561.	2.5	124
13	Diversity of the genus <i>Lactobacillus</i> revealed by comparative genomics of five species. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3185-3196.	1.8	118
14	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275.	8.8	105
15	Comparative genomics of phages and prophages in lactic acid bacteria. <i>Antonie Van Leeuwenhoek</i> , 2002, 82, 73-91.	1.7	96
16	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, 6197-6209.	3.1	95
17	Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria. <i>Antonie Van Leeuwenhoek</i> , 2007, 91, 351-372.	1.7	95
18	<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, 3110-3121.	3.1	94

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19	RNA-Seq in <i>Mytilus galloprovincialis</i> : comparative transcriptomics and expression profiles among different tissues. <i>BMC Genomics</i> , 2015, 16, 728.	2.8	86
20	Comparative Genomics and Transcriptional Analysis of Prophages Identified in the Genomes of <i>Lactobacillus gasser</i> , <i>Lactobacillus salivarius</i> , and <i>Lactobacillus casei</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3130-3146.	3.1	75
21	Microbial diversity in the human intestine and novel insights from metagenomics. <i>Frontiers in Bioscience - Landmark</i> , 2009, Volume, 3214.	3.0	72
22	Genome Analysis of an Inducible Prophage and Prophage Remnants Integrated in the <i>Streptococcus pyogenes</i> Strain SF370. <i>Virology</i> , 2002, 302, 245-258.	2.4	70
23	Prophage-Like Elements in Bifidobacteria: Insights from Genomics, Transcription, Integration, Distribution, and Phylogenetic Analysis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8692-8705.	3.1	70
24	Isolation of lactobacilli with probiotic properties from the human stomach. <i>Letters in Applied Microbiology</i> , 2008, 47, 269-274.	2.2	67
25	The prophage sequences of <i>Lactobacillus plantarum</i> strain WCFS1. <i>Virology</i> , 2003, 316, 245-255.	2.4	65
26	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, 253-261.	1.8	63
27	GANNPhos: a new phosphorylation site predictor based on a genetic algorithm integrated neural network. <i>Protein Engineering, Design and Selection</i> , 2007, 20, 405-412.	2.1	56
28	Exploiting Bifidobacterium genomes: The molecular basis of stress response. <i>International Journal of Food Microbiology</i> , 2007, 120, 13-24.	4.7	55
29	Integration and Distribution of <i>Lactobacillus johnsonii</i> Prophages. <i>Journal of Bacteriology</i> , 2003, 185, 4603-4608.	2.2	54
30	The prophages of <i>Lactobacillus johnsonii</i> NCC 533: comparative genomics and transcription analysis. <i>Virology</i> , 2004, 320, 229-242.	2.4	53
31	Distribution of Megaplastids in <i>Lactobacillus salivarius</i> and Other Lactobacilli. <i>Journal of Bacteriology</i> , 2007, 189, 6128-6139.	2.2	53
32	Comparative Analyses of Prophage-Like Elements Present in Two <i>Lactococcus lactis</i> Strains. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7771-7780.	3.1	52
33	Molecular Characterization of hsp20 , Encoding a Small Heat Shock Protein of <i>Bifidobacterium breve</i> UCC2003. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4695-4703.	3.1	51
34	Polyphasic analysis indicates that <i>Lactobacillus salivarius</i> subsp. <i>salivarius</i> and <i>Lactobacillus salivarius</i> subsp. <i>salicin</i> do not merit separate subspecies status. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2397-2403.	1.7	50
35	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, 734-759.	8.6	48
36	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, 8276-8286.	2.2	41

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37	The ClgR Protein Regulates Transcription of the clpP Operon in <i>Bifidobacterium breve</i> UCC 2003. <i>Journal of Bacteriology</i> , 2005, 187, 8411-8426.	2.2	41
38	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.	2.4	40
39	Comparative genomics and proteomics of <i>Helicobacter mustelae</i> , an ulcerogenic and carcinogenic gastric pathogen. <i>BMC Genomics</i> , 2010, 11, 164.	2.8	40
40	Transcription Analysis of <i>Streptococcus thermophilus</i> Phages in the Lysogenic State. <i>Virology</i> , 2002, 302, 21-32.	2.4	39
41	Genetic Characterization of the <i>Bifidobacterium breve</i> UCC 2003 hrcA Locus. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8998-9007.	3.1	29
42	<i>Lactobacillus hordei</i> sp. nov., a bacteriocinogenic strain isolated from malted barley. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2013-2017.	1.7	29
43	Mosaic-Like Sequences Containing Transposon, Phage, and Plasmid Elements among <i>Listeria monocytogenes</i> Plasmids. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4851-4857.	3.1	21
44	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.	2.1	20
45	Comparative genomics of phages and prophages in lactic acid bacteria. , 2002, , 73-91.		14
46	Genome of <i>Rhizobium leucaenae</i> strains CFN 299T and CPAO 29.8: searching for genes related to a successful symbiotic performance under stressful conditions. <i>BMC Genomics</i> , 2016, 17, 534.	2.8	13
47	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.	0.7	8
48	The network structure of intertidal meiofaunal communities from environmental DNA metabarcoding surveys in Northwest Iberia. <i>Aquatic Sciences</i> , 2021, 83, 1.	1.5	7
49	Population genomic footprints of environmental pollution pressure in natural populations of the Mediterranean mussel. <i>Marine Genomics</i> , 2019, 45, 11-15.	1.1	5
50	Draft genome sequence of <i>Bradyrhizobium paxllaeri</i> LMTR 21 T isolated from Lima bean (<i>Phaseolus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.3	4
51	Genome sequence of <i>Bradyrhizobium</i> sp. LMTR 3, a diazotrophic symbiont of Lima bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.3 3	1.3	3
52	Patterns of spatial and temporal variation in estuarine meiofaunal communities assessed through DNA metabarcoding: a case study in the Lima estuary (NW Portugal). <i>Frontiers in Marine Science</i> , 0, 6, .	2.5	0