

Carlos A Canchaya

List of Publications by Year in descending order

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52
papers

6,992
citations

81743

39
h-index

168136

53
g-index

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. | 2.9 | 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. | 2.9 | 852 |
| 3 | Prophage Genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2003, 67, 238-276. | 2.9 | 594 |
| 4 | Phage as agents of lateral gene transfer. <i>Current Opinion in Microbiology</i> , 2003, 6, 417-424. | 2.3 | 437 |
| 5 | The impact of prophages on bacterial chromosomes. <i>Molecular Microbiology</i> , 2004, 53, 9-18. | 1.2 | 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. | 1.0 | 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. | 3.3 | 216 |
| 8 | Analysis of bifidobacterial evolution using a multilocus approach. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 2783-2792. | 0.8 | 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. | 1.4 | 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. | 1.4 | 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. | 1.5 | 141 |
| 12 | A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016, 11, e0151561. | 1.1 | 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. | 0.7 | 118 |
| 14 | Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. <i>Genome Biology</i> , 2020, 21, 275. | 3.8 | 105 |
| 15 | Comparative genomics of phages and prophages in lactic acid bacteria. <i>Antonie Van Leeuwenhoek</i> , 2002, 82, 73-91. | 0.7 | 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. | 1.4 | 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. | 0.7 | 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. | 1.4 | 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. | 1.2 | 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. | 1.4 | 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. | 1.1 | 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. | 1.4 | 70 |
| 24 | Isolation of lactobacilli with probiotic properties from the human stomach. <i>Letters in Applied Microbiology</i> , 2008, 47, 269-274. | 1.0 | 67 |
| 25 | The prophage sequences of <i>Lactobacillus plantarum</i> strain WCFS1. <i>Virology</i> , 2003, 316, 245-255. | 1.1 | 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. | 0.7 | 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. | 1.0 | 56 |
| 28 | Exploiting Bifidobacterium genomes: The molecular basis of stress response. <i>International Journal of Food Microbiology</i> , 2007, 120, 13-24. | 2.1 | 55 |
| 29 | Integration and Distribution of <i>Lactobacillus johnsonii</i> Prophages. <i>Journal of Bacteriology</i> , 2003, 185, 4603-4608. | 1.0 | 54 |
| 30 | The prophages of <i>Lactobacillus johnsonii</i> NCC 533: comparative genomics and transcription analysis. <i>Virology</i> , 2004, 320, 229-242. | 1.1 | 53 |
| 31 | Distribution of Megaplastids in <i>Lactobacillus salivarius</i> and Other Lactobacilli. <i>Journal of Bacteriology</i> , 2007, 189, 6128-6139. | 1.0 | 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. | 1.4 | 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. | 1.4 | 51 |
| 34 | 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. | 0.8 | 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. | 3.9 | 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. | 1.0 | 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. | 1.0 | 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. | 1.1 | 40 |
| 39 | Comparative genomics and proteomics of <i>Helicobacter mustelae</i> , an ulcerogenic and carcinogenic gastric pathogen. <i>BMC Genomics</i> , 2010, 11, 164. | 1.2 | 40 |
| 40 | Transcription Analysis of <i>Streptococcus thermophilus</i> Phages in the Lysogenic State. <i>Virology</i> , 2002, 302, 21-32. | 1.1 | 39 |
| 41 | Genetic Characterization of the <i>Bifidobacterium breve</i> UCC 2003 <i>hrcA</i> Locus. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8998-9007. | 1.4 | 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. | 0.8 | 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. | 1.4 | 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. | 0.9 | 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. | 1.2 | 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. | 0.4 | 8 |
| 48 | The network structure of intertidal meiofaunal communities from environmental DNA metabarcoding surveys in Northwest Iberia. <i>Aquatic Sciences</i> , 2021, 83, 1. | 0.6 | 7 |
| 49 | Population genomic footprints of environmental pollution pressure in natural populations of the Mediterranean mussel. <i>Marine Genomics</i> , 2019, 45, 11-15. | 0.4 | 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 | 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, . | 1.2 | 0 |