

Eduardo Castro-Nallar

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,593
citations

236925

25
h-index

223800

46
g-index

79
all docs

79
docs citations

79
times ranked

4150
citing authors

#	ARTICLE	IF	CITATIONS
1	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. PeerJ, 2015, 3, e1140.	2.0	222
2	PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. Microbiome, 2014, 2, 33.	11.1	206
3	A global metagenomic map of urban microbiomes and antimicrobial resistance. Cell, 2021, 184, 3376-3393.e17.	28.9	164
4	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. Infection, Genetics and Evolution, 2013, 16, 38-53.	2.3	157
5	<i>Pathoscope</i> : Species identification and strain attribution with unassembled sequencing data. Genome Research, 2013, 23, 1721-1729.	5.5	132
6	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	30.7	130
7	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. PLoS ONE, 2015, 10, e0131819.	2.5	87
8	The evolution of HIV: Inferences using phylogenetics. Molecular Phylogenetics and Evolution, 2012, 62, 777-792.	2.7	79
9	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. Frontiers in Microbiology, 2016, 7, 484.	3.5	78
10	Single-Molecule Long-Read 16S Sequencing To Characterize the Lung Microbiome from Mechanically Ventilated Patients with Suspected Pneumonia. Journal of Clinical Microbiology, 2014, 52, 3913-3921.	3.9	69
11	Cyclic AMP Regulates Bacterial Persistence through Repression of the Oxidative Stress Response and SOS-Dependent DNA Repair in Uropathogenic <i>Escherichia coli</i> . MBio, 2018, 9, .	4.1	64
12	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. BMC Medical Genomics, 2015, 8, 50.	1.5	63
13	Redefining Healthy Urine: A Cross-Sectional Exploratory Metagenomic Study of People With and Without Bladder Dysfunction. Journal of Urology, 2016, 196, 579-587.	0.4	58
14	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. BMC Bioinformatics, 2014, 15, 262.	2.6	55
15	Comparative Genomics Analysis of a New Exiguobacterium Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. Frontiers in Microbiology, 2017, 8, 456.	3.5	55
16	Microbial sequence typing in the genomic era. Infection, Genetics and Evolution, 2018, 63, 346-359.	2.3	50
17	Phage cluster relationships identified through single gene analysis. BMC Genomics, 2013, 14, 410.	2.8	47
18	Monitoring the occurrence of microplastic ingestion in Otariids along the Peruvian and Chilean coasts. Marine Pollution Bulletin, 2020, 153, 110966.	5.0	47

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19	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , The, 2021, 2, e135-e136.	7.3	47
20	Population Genomics and Phylogeography of an Australian Dairy Factory Derived Lytic Bacteriophage. <i>Genome Biology and Evolution</i> , 2012, 4, 382-393.	2.5	36
21	In-Depth Genomic and Phenotypic Characterization of the Antarctic Psychrotolerant Strain <i>Pseudomonas</i> sp. MPC6 Reveals Unique Metabolic Features, Plasticity, and Biotechnological Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1154.	3.5	36
22	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. <i>Infection, Genetics and Evolution</i> , 2018, 63, 295-306.	2.3	32
23	Androgen Receptor Gene CAG and GGN Repeat Polymorphisms in Chilean Men With Primary Severe Spermatogenic Failure. <i>Journal of Andrology</i> , 2010, 31, 552-559.	2.0	31
24	Comparative genomic analysis of a new tellurite-resistant <i>Psychrobacter</i> strain isolated from the Antarctic Peninsula. <i>PeerJ</i> , 2018, 6, e4402.	2.0	30
25	Draft Genome Sequence of a Multi-Metal Resistant Bacterium <i>Pseudomonas putida</i> ATH-43 Isolated from Greenwich Island, Antarctica. <i>Frontiers in Microbiology</i> , 2016, 7, 1777.	3.5	27
26	Genomic Analysis of 48 <i>Paenibacillus</i> larvae Bacteriophages. <i>Viruses</i> , 2018, 10, 377.	3.3	26
27	Genomic and Physiological Traits of the Marine Bacterium <i>Alcaligenes aquatilis</i> QD168 Isolated From Quintero Bay, Central Chile, Reveal a Robust Adaptive Response to Environmental Stressors. <i>Frontiers in Microbiology</i> , 2019, 10, 528.	3.5	25
28	The temporal dynamics of the tracheal microbiome in tracheostomised patients with and without lower respiratory infections. <i>PLoS ONE</i> , 2017, 12, e0182520.	2.5	24
29	Nasopharyngeal metatranscriptome profiles of infants with bronchiolitis and risk of childhood asthma: a multicentre prospective study. <i>European Respiratory Journal</i> , 2022, 60, 2102293.	6.7	23
30	Biotransformation of 2,4,6-Trinitrotoluene by <i>Pseudomonas</i> sp. TNT3 isolated from Deception Island, Antarctica. <i>Environmental Pollution</i> , 2020, 262, 113922.	7.5	22
31	Copper-induced concomitant increases in photosynthesis, respiration, and C, N and S assimilation revealed by transcriptomic analyses in <i>Ulva compressa</i> (Chlorophyta). <i>BMC Plant Biology</i> , 2020, 20, 25.	3.6	21
32	The transcription factor SlyA from <i>Salmonella Typhimurium</i> regulates genes in response to hydrogen peroxide and sodium hypochlorite. <i>Research in Microbiology</i> , 2018, 169, 263-278.	2.1	20
33	Arsenic Response of Three Altiplanic <i>Exiguobacterium</i> Strains With Different Tolerance Levels Against the Metalloid Species: A Proteomics Study. <i>Frontiers in Microbiology</i> , 2019, 10, 2161.	3.5	20
34	Whole genome single-nucleotide variation profile-based phylogenetic tree building methods for analysis of viral, bacterial and human genomes. <i>Genomics</i> , 2014, 104, 1-7.	2.9	19
35	Altered Middle Ear Microbiome in Children With Chronic Otitis Media With Effusion and Respiratory Illnesses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 339.	3.9	19
36	Variability in Genomic and Virulent Properties of <i>Porphyromonas gingivalis</i> Strains Isolated From Healthy and Severe Chronic Periodontitis Individuals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 246.	3.9	19

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37	Copper-induced increased expression of genes involved in photosynthesis, carotenoid synthesis and C assimilation in the marine alga <i>Ulva compressa</i> . <i>BMC Genomics</i> , 2018, 19, 829.	2.8	18
38	A first insight into the structure and function of rhizosphere microbiota in Antarctic plants using shotgun metagenomic. <i>Polar Biology</i> , 2019, 42, 1825-1835.	1.2	18
39	The Transcription Factor ArcA Modulates <i>Salmonella</i> ™s Metabolism in Response to Neutrophil Hypochlorous Acid-Mediated Stress. <i>Frontiers in Microbiology</i> , 2019, 10, 2754.	3.5	17
40	Living to the High Extreme: Unraveling the Composition, Structure, and Functional Insights of Bacterial Communities Thriving in the Arsenic-Rich Salar de Huasco Altiplanic Ecosystem. <i>Microbiology Spectrum</i> , 2021, 9, e0044421.	3.0	16
41	DNA Barcoding analysis of seafood accuracy in Washington, D.C. restaurants. <i>PeerJ</i> , 2017, 5, e3234.	2.0	15
42	Exon 1 Exhibits Functional Diversity during HIV-1 Subtype C Primary Infection. <i>Journal of Virology</i> , 2013, 87, 5732-5745.	3.4	14
43	Genomic Variation and Arsenic Tolerance Emerged as Niche Specific Adaptations by Different <i>Exiguobacterium</i> Strains Isolated From the Extreme Salar de Huasco Environment in Chilean "Altiplano". <i>Frontiers in Microbiology</i> , 2020, 11, 1632.	3.5	14
44	Radiation-induced toxicity in rectal epithelial stem cell contributes to acute radiation injury in rectum. <i>Stem Cell Research and Therapy</i> , 2021, 12, 63.	5.5	14
45	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020, 8, e9688.	2.0	14
46	Tracheal Microbiota in Patients With a Tracheostomy Before, During and After an Acute Respiratory Infection. <i>Pediatric Infectious Disease Journal</i> , 2018, 37, e269-e271.	2.0	13
47	Multilocus Sequence Typing of Pathogens. , 2017, , 383-404.		12
48	Predicting climate change-related genetic offset for the endangered southern South American conifer <i>Araucaria araucana</i> . <i>Forest Ecology and Management</i> , 2022, 504, 119856.	3.2	12
49	Genetic diversity and molecular epidemiology of HIV transmission. <i>Future Virology</i> , 2012, 7, 239-252.	1.8	11
50	Phosphate-Arsenic Interactions in Halophilic Microorganisms of the Microbial Mat from Laguna Tebenquiche: from the Microenvironment to the Genomes. <i>Microbial Ecology</i> , 2021, 81, 941-953.	2.8	11
51	Patterns of the fecal microbiota in the Juan Fernández fur seal (<i>Arctocephalus philippii</i>). <i>MicrobiologyOpen</i> , 2021, 10, e1215.	3.0	11
52	Influence of Physical-Chemical Soil Parameters on Microbiota Composition and Diversity in a Deep Hyperarid Core of the Atacama Desert. <i>Frontiers in Microbiology</i> , 2021, 12, 794743.	3.5	11
53	Molecular phylodynamics and protein modeling of infectious salmon anemia virus (ISAV). <i>BMC Evolutionary Biology</i> , 2011, 11, 349.	3.2	10
54	<i>Rhodococcus</i> comparative genomics reveals a phylogenomic-dependent non-ribosomal peptide synthetase distribution: insights into biosynthetic gene cluster connection to an orphan metabolite. <i>Microbial Genomics</i> , 2021, 7, .	2.0	10

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55	Complete genome sequence of the marine <i>Rhodococcus</i> sp. H-CA8f isolated from Comau fjord in Northern Patagonia, Chile. <i>Marine Genomics</i> , 2018, 40, 13-17.	1.1	9
56	In infants with severe bronchiolitis: dual-transcriptomic profiling of nasopharyngeal microbiome and host response. <i>Pediatric Research</i> , 2020, 88, 144-146.	2.3	9
57	Genetic Characterization of <i>Salmonella</i> <i>Infantis</i> with Multiple Drug Resistance Profiles Isolated from a Poultry-Farm in Chile. <i>Microorganisms</i> , 2021, 9, 2370.	3.6	9
58	The Genome of the Marine Alga <i>Ulva compressa</i> (Chlorophyta) Reveals Protein-Coding Genes with Similarity to Plants and Green Microalgae, but Also to Animal, Bacterial, and Fungal Genes. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7279.	4.1	8
59	Annotating unknown species of urban microorganisms on a global scale unveils novel functional diversity and local environment association. <i>Environmental Research</i> , 2022, 207, 112183.	7.5	7
60	Origin, genomic diversity and microevolution of the <i>Clostridium difficile</i> B1/NAP1/RT027/ST01 strain in Costa Rica, Chile, Honduras and Mexico. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
61	Genome Sequence of <i>Streptomyces</i> sp. H-KF8, a Marine Actinobacterium Isolated from a Northern Chilean Patagonian Fjord. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
62	Concordance and discordance of sequence survey methods for molecular epidemiology. <i>PeerJ</i> , 2015, 3, e761.	2.0	5
63	Computational Methods for Human Microbiome Analysis. <i>Current Protocols in Microbiology</i> , 2017, 47, 1E.14.1-1E.14.17.	6.5	4
64	Composition and structure of the skin microbiota of roquales off the Eastern South Pacific. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	4
65	Rapid sequence modification in the highly polymorphic region (HPR) of the hemagglutinin gene of the infectious salmon anaemia virus (ISAV) suggests intra-segmental template switching recombination. <i>Journal of Fish Diseases</i> , 2020, 43, 1483-1496.	1.9	3
66	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
67	MP20-08 PYURIA AND ASYMPTOMATIC BACTERIURIA IS ASSOCIATED WITH NOVEL AND SPECIFIC URINE MICROBIOMES. <i>Journal of Urology</i> , 2015, 193, .	0.4	2
68	Sequences of Endophytic Fungal and Bacterial Communities from <i>Araucaria araucana</i> [(Molina) K. Koch, 1869] in the Coastal and Andes Mountain Ranges, Chile. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
69	Genome Sequence of <i>Clostridium paraputrificum</i> 373-A1 Isolated in Chile from a Patient Infected with <i>Clostridium difficile</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	1
70	Draft Genome Sequences of Five <i>Enterococcus</i> Species Isolated from the Gut of Patients with Suspected <i>Clostridium difficile</i> Infection. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
71	MP20-07 ALL ASYMPTOMATIC BACTERIURIA, ALL THE TIME. <i>Journal of Urology</i> , 2015, 193, .	0.4	0
72	Genome sequence of two members of the chloroaromatic-degrading MT community: <i>Pseudomonas reinekei</i> MT1 and <i>Achromobacter xylosoxidans</i> MT3. <i>Journal of Biotechnology</i> , 2018, 275, 13-16.	3.8	0