

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	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
2	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
3	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
4	Comparative Analysis of Metagenomics and Metataxonomics for the Characterization of Vermicompost Microbiomes. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	3
5	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
6	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
7	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
8	Composition and structure of the skin microbiota of roborals off the Eastern South Pacific. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	4
9	COVID-19 drug practices risk antimicrobial resistance evolution. <i>Lancet Microbe</i> , The, 2021, 2, e135-e136.	7.3	47
10	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
11	Patterns of the fecal microbiota in the Juan Fernández fur seal (<i>Arctocephalus philippii</i>). <i>MicrobiologyOpen</i> , 2021, 10, e1215.	3.0	11
12	Rhodococcus 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
13	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
14	Genetic Characterization of <i>Salmonella Infantis</i> with Multiple Drug Resistance Profiles Isolated from a Poultry-Farm in Chile. <i>Microorganisms</i> , 2021, 9, 2370.	3.6	9
15	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
16	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
17	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
18	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

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19	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
20	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
21	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. <i>Nature Medicine</i> , 2020, 26, 941-951.	30.7	130
22	Monitoring the occurrence of microplastic ingestion in Otariids along the Peruvian and Chilean coasts. <i>Marine Pollution Bulletin</i> , 2020, 153, 110966.	5.0	47
23	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
24	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
25	Evaluation of computational methods for human microbiome analysis using simulated data. <i>PeerJ</i> , 2020, 8, e9688.	2.0	14
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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
34	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
35	Cyclic AMP Regulates Bacterial Persistence through Repression of the Oxidative Stress Response and SOS-Dependent DNA Repair in Uropathogenic <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	4.1	64
36	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

#	ARTICLE	IF	CITATIONS
37	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. <i>Infection, Genetics and Evolution</i> , 2018, 63, 295-306.	2.3	32
38	Microbial sequence typing in the genomic era. <i>Infection, Genetics and Evolution</i> , 2018, 63, 346-359.	2.3	50
39	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
40	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
41	Genomic Analysis of 48 <i>Paenibacillus</i> larvae Bacteriophages. <i>Viruses</i> , 2018, 10, 377.	3.3	26
42	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
43	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
44	Computational Methods for Human Microbiome Analysis. <i>Current Protocols in Microbiology</i> , 2017, 47, 1E.14.1-1E.14.17.	6.5	4
45	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
46	Comparative Genomics Analysis of a New <i>Exiguobacterium</i> Strain from Salar de Huasco Reveals a Repertoire of Stress-Related Genes and Arsenic Resistance. <i>Frontiers in Microbiology</i> , 2017, 8, 456.	3.5	55
47	Multilocus Sequence Typing of Pathogens. , 2017, , 383-404.		12
48	DNA Barcoding analysis of seafood accuracy in Washington, D.C. restaurants. <i>PeerJ</i> , 2017, 5, e3234.	2.0	15
49	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
50	Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. <i>Frontiers in Microbiology</i> , 2016, 7, 484.	3.5	78
51	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
52	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
53	Redefining Healthy Urine: A Cross-Sectional Exploratory Metagenomic Study of People With and Without Bladder Dysfunction. <i>Journal of Urology</i> , 2016, 196, 579-587.	0.4	58
54	MP20-08 PYURIA AND ASYMPTOMATIC BACTERIURIA IS ASSOCIATED WITH NOVEL AND SPECIFIC URINE MICROBIOMES. <i>Journal of Urology</i> , 2015, 193, .	0.4	2

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55	MP20-07 ALL ASYMPTOMATIC BACTERIURIA, ALL THE TIME. <i>Journal of Urology</i> , 2015, 193, .	0.4	0
56	Integrating microbial and host transcriptomics to characterize asthma-associated microbial communities. <i>BMC Medical Genomics</i> , 2015, 8, 50.	1.5	63
57	Dual Transcriptomic Profiling of Host and Microbiota during Health and Disease in Pediatric Asthma. <i>PLoS ONE</i> , 2015, 10, e0131819.	2.5	87
58	Composition, taxonomy and functional diversity of the oropharynx microbiome in individuals with schizophrenia and controls. <i>PeerJ</i> , 2015, 3, e1140.	2.0	222
59	Concordance and discordance of sequence survey methods for molecular epidemiology. <i>PeerJ</i> , 2015, 3, e761.	2.0	5
60	PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. <i>Microbiome</i> , 2014, 2, 33.	11.1	206
61	Single-Molecule Long-Read 16S Sequencing To Characterize the Lung Microbiome from Mechanically Ventilated Patients with Suspected Pneumonia. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3913-3921.	3.9	69
62	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
63	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. <i>BMC Bioinformatics</i> , 2014, 15, 262.	2.6	55
64	Phage cluster relationships identified through single gene analysis. <i>BMC Genomics</i> , 2013, 14, 410.	2.8	47
65	Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2013, 16, 38-53.	2.3	157
66	<i>Pathoscope</i> : Species identification and strain attribution with unassembled sequencing data. <i>Genome Research</i> , 2013, 23, 1721-1729.	5.5	132
67	<i>tat</i> Exon 1 Exhibits Functional Diversity during HIV-1 Subtype C Primary Infection. <i>Journal of Virology</i> , 2013, 87, 5732-5745.	3.4	14
68	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
69	Genetic diversity and molecular epidemiology of HIV transmission. <i>Future Virology</i> , 2012, 7, 239-252.	1.8	11
70	The evolution of HIV: Inferences using phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 777-792.	2.7	79
71	Molecular phylodynamics and protein modeling of infectious salmon anemia virus (ISAV). <i>BMC Evolutionary Biology</i> , 2011, 11, 349.	3.2	10
72	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