

Andrés Iriarte

List of Publications by Year in descending order

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70
papers

1,201
citations

511338

15
h-index

423188

30
g-index

74
all docs

74
docs citations

74
times ranked

2259
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary analysis of species-specific duplications in flatworm genomes. <i>Molecular Phylogenetics and Evolution</i> , 2024, , 108141.	2.9	0
2	Trans-splicing in the cestode <i>Hymenolepis microstoma</i> is constitutive across the life cycle and depends on gene structure and composition. <i>International Journal for Parasitology</i> , 2023, , .	3.2	0
3	Transcriptomic analysis reveals gene expression changes in peripheral white blood cells of cows after embryo transfer: Implications for pregnancy tolerance. <i>Reproduction in Domestic Animals</i> , 2023, 58, 946-954.	1.4	2
4	Imported One-Day-Old Chicks as Trojan Horses for Multidrug-Resistant Priority Pathogens Harboring <i>mcr-9</i> , <i>rmtG</i> , and Extended-Spectrum β -Lactamase Genes. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0167521.	3.2	13
5	Genotyping and Multivariate Regression Trees Reveal Ecological Diversification within the <i>Microcystis aeruginosa</i> Complex along a Wide Environmental Gradient. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0147521.	3.2	2
6	Genomics and transcriptomics insights into luteolin effects on the beta- ϵ -rhizobial strain <i>Cupriavidus necator</i> UYPR2.512. <i>Environmental Microbiology</i> , 2022, 24, 240-264.	3.8	3
7	Codon usage in the flatworm <i>Schistosoma mansoni</i> is shaped by the mutational bias towards A+T and translational selection, which increases GC-ending codons in highly expressed genes. <i>Molecular and Biochemical Parasitology</i> , 2022, 247, 111445.	1.1	6
8	Revealing the genetic basis of eyelid pigmentation in Hereford cattle. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	6
9	<i>Staphylococcus aureus</i> β -Toxin Effect on <i>Acinetobacter baumannii</i> Behavior. <i>Biology</i> , 2022, 11, 570.	2.9	5
10	Identification of Long Noncoding RNAs Involved in Eyelid Pigmentation of Hereford Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	0
11	Stage-specific transcriptomic analysis of the model cestode <i>Hymenolepis microstoma</i> . <i>Genomics</i> , 2021, 113, 620-632.	2.9	17
12	Full characterization of plasmids from <i>Achromobacter ruhlandii</i> isolates recovered from a single patient with cystic fibrosis (CF). <i>Revista Argentina De Microbiologia</i> , 2021, , .	0.6	0
13	Molecular detection of coccidian Apicomplexa Parasites isolated from wild crab-eating and pampas foxes through novel TaqMan Δ , ϵ probes: a contribution to their molecular epidemiology. <i>Molecular Biology Reports</i> , 2021, 48, 5013-5021.	2.4	1
14	Codon Usage Bias: An Endless Tale. <i>Journal of Molecular Evolution</i> , 2021, 89, 589-593.	1.9	53
15	Metagenomic analysis of <i>Raphidiopsis raciborskii</i> microbiome: beyond the individual. <i>Biodiversity Data Journal</i> , 2021, 9, e72514.	0.6	9
16	Plasmidome of a multiresistant <i>Salmonella enterica</i> serovar Typhimurium isolate from Uruguay. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 20, 84-86.	2.5	0
17	Transcriptomic analysis of eyelid pigmentation in Hereford cattle. <i>Animal Genetics</i> , 2020, 51, 935-939.	1.7	2
18	Genomic analysis of two <i>Acinetobacter baumannii</i> strains belonging to two different sequence types (ST172 and ST25). <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 154-161.	2.5	6

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19	SLFinder, a pipeline for the novel identification of splice-leader sequences: a good enough solution for a complex problem. <i>BMC Bioinformatics</i> , 2020, 21, 293.	2.6	3
20	Comparative genomics of <i>Salmonella enterica</i> serovar Enteritidis ST-11 isolated in Uruguay reveals lineages associated with particular epidemiological traits. <i>Scientific Reports</i> , 2020, 10, 3638.	3.4	3
21	Biogeography of the cyanobacterium <i>Raphidiopsis (Cylindrospermopsis) raciborskii</i> : Integrating genomics, phylogenetic and toxicity data. <i>Molecular Phylogenetics and Evolution</i> , 2020, 148, 106824.	2.9	32
22	<i>Bacillus natronophilus</i> sp. nov., an alkaliphilic bacterium isolated from a soda lake. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 562-568.	1.8	15
23	Proteomic analysis of plasma exosomes from Cystic Echinococcosis patients provides in vivo support for distinct immune response profiles in active vs inactive infection and suggests potential biomarkers. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008586.	2.4	27
24	Small <i>Klebsiella pneumoniae</i> Plasmids: Neglected Contributors to Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2019, 10, 2182.	3.5	26
25	Genetic and Phenotypic Features of a Novel <i>Acinetobacter</i> Species, Strain A47, Isolated From the Clinical Setting. <i>Frontiers in Microbiology</i> , 2019, 10, 1375.	3.5	4
26	ICE SXT vs. ICESh95: Co-existence of Integrative and Conjugative Elements and Competition for a New Host. <i>Scientific Reports</i> , 2019, 9, 8045.	3.4	3
27	Draft Genome Sequence of <i>Paraburkholderia</i> sp. UYCP14C, a <i>Rhizobium</i> Strain Isolated from Root Nodules of <i>Calliandra parvifolia</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	1.1	5
28	A pair of non-optimal codons are necessary for the correct biosynthesis of the <i>Aspergillus nidulans</i> urea transporter, UreA. <i>Royal Society Open Science</i> , 2019, 6, 190773.	2.5	5
29	Interspecies DNA acquisition by a naturally competent <i>Acinetobacter baumannii</i> strain. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 483-490.	3.3	15
30	<i>Nesterenkonia natronophila</i> sp. nov., an alkaliphilic actinobacterium isolated from a soda lake, and emended description of the genus <i>Nesterenkonia</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1960-1966.	1.8	23
31	Whole-Genome Analysis of an Extensively Drug-Resistance <i>Empedobacter falsenii</i> Strain Reveals Distinct Features and the Presence of a Novel Metallo- β -Lactamase (EBR-2). <i>Current Microbiology</i> , 2018, 75, 1084-1089.	2.2	6
32	Expansion of cap superfamily proteins in the genome of <i>Mesocestoides corti</i> : An extreme case of a general bilaterian trend. <i>Gene Reports</i> , 2018, 11, 110-120.	0.8	6
33	A Naturally Occurring Deletion in FljE from <i>Salmonella enterica</i> Serovar Dublin Results in an Aflagellate Phenotype and Defective Proinflammatory Properties. <i>Infection and Immunity</i> , 2018, 86, .	2.3	5
34	The complex pattern of codon usage evolution in the family Comamonadaceae. <i>Ecological Genetics and Genomics</i> , 2018, 6, 1-8.	0.5	6
35	Genome sequence analysis of an extensively drug-resistant <i>Acinetobacter baumannii</i> indigo-pigmented strain depicts evidence of increase genome plasticity. <i>Scientific Reports</i> , 2018, 8, 16961.	3.4	29
36	Analysis of classical neurotransmitter markers in tapeworms: Evidence for extensive loss of neurotransmitter pathways. <i>International Journal for Parasitology</i> , 2018, 48, 979-992.	3.2	13

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37	Human serum albumin alters specific genes that can play a role in survival and persistence in <i>Acinetobacter baumannii</i> . <i>Scientific Reports</i> , 2018, 8, 14741.	3.4	51
38	Whole-genome analysis and description of an outbreak due to carbapenem-resistant <i>Ochrobactrum anthropi</i> causing pseudo-bacteraemias. <i>New Microbes and New Infections</i> , 2018, 26, 100-106.	1.7	3
39	Draft Genome Sequences of Two Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhimurium Clinical Isolates from Uruguay. <i>Microbiology Resource Announcements</i> , 2018, 7, .	1.1	3
40	Comparison of transcriptomic landscapes of different lamb muscles using RNA-Seq.. <i>PLoS ONE</i> , 2018, 13, e0200732.	2.5	10
41	Molecular characterization of KPC-2â€“positive <i>Klebsiella pneumoniae</i> isolates from a neurosurgical centre in Argentina. <i>New Microbes and New Infections</i> , 2018, 24, 32-34.	1.7	1
42	Genomics helps to decipher the resistance mechanisms present in a <i>Pseudomonas chlororaphis</i> strain recovered in an HIV patient. <i>New Microbes and New Infections</i> , 2018, 25, 45-47.	1.7	7
43	Genomic insights into the broad antifungal activity, plant-probiotic properties, and their regulation, in <i>Pseudomonas donghuensis</i> strain SVBP6. <i>PLoS ONE</i> , 2018, 13, e0194088.	2.5	47
44	Temporal evolution of anti- <i>Clostridium</i> antibody responses in sheep after vaccination with polyvalent clostridial vaccines. <i>Veterinary Immunology and Immunopathology</i> , 2018, 202, 46-51.	1.2	11
45	A novel prophage identified in strains from <i>Salmonella enterica</i> serovar Enteritidis is a phylogenetic signature of the lineage ST-1974. <i>Microbial Genomics</i> , 2018, 4, .	2.1	9
46	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Infantis Strain SPE101, Isolated from a Chronic Human Infection. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
47	Genetic analysis of a PER-2-producing <i>Shewanella</i> sp. strain harbouring a variety of mobile genetic elements and antibiotic resistance determinants. <i>Journal of Global Antimicrobial Resistance</i> , 2017, 11, 81-86.	2.5	10
48	An Isochore-Like Structure in the Genome of the Flatworm <i>Schistosoma mansoni</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 2312-2318.	2.6	12
49	Use of next-generation molecular tools in archaeological neotropical deer sample analysis. <i>Journal of Archaeological Science: Reports</i> , 2016, 10, 403-410.	0.6	4
50	Draft Genome Sequence of <i>Cupriavidus</i> UYMMa02A, a Novel Beta-Rhizobium Species. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
51	Draft Genome of <i>Shewanella frigidimarina</i> Ag06-30, a Marine Bacterium Isolated from Potter Peninsula, King George Island, Antarctica. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
52	Novel <i>Cupriavidus</i> Strains Isolated from Root Nodules of Native Uruguayan <i>Mimosa</i> Species. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3150-3164.	3.2	67
53	Genome analysis of a clinical isolate of <i>Shewanella</i> sp. uncovered an active hybrid integrative and conjugative element carrying an integron platform inserted in a novel genomic locus. <i>Microbiology (United Kingdom)</i> , 2016, 162, 1335-1345.	1.7	8
54	Revealing the biotechnological potential of <i>Delftia</i> sp. JD2 by a genomic approach. <i>AIMS Bioengineering</i> , 2016, 3, 156-175.	1.1	23

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55	Est10: A Novel Alkaline Esterase Isolated from Bovine Rumen Belonging to the New Family XV of Lipolytic Enzymes. PLoS ONE, 2015, 10, e0126651.	2.5	10
56	Draft Genome Sequence of a Taxonomically Unique Acinetobacter Clinical Strain with Proteolytic and Hemolytic Activities. Genome Announcements, 2015, 3, .	0.8	10
57	Conservation of CFTR codon frequency through primates suggests synonymous mutations could have a functional effect. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 775, 19-25.	1.0	10
58	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	19.8	312
59	General Trends in Selectively Driven Codon Usage Biases in the Domain Archaea. Journal of Molecular Evolution, 2014, 79, 105-110.	1.9	6
60	Trends in amino acid usage across the class Mollicutes. Journal of Biomolecular Structure and Dynamics, 2014, 32, 65-74.	3.5	2
61	Draft Genome Sequence of an Extensively Drug-Resistant Acinetobacter baumannii Indigo-Pigmented Strain. Genome Announcements, 2014, 2, .	0.8	6
62	A detailed comparative analysis on the overall codon usage patterns in West Nile virus. Infection, Genetics and Evolution, 2013, 14, 396-400.	2.3	75
63	Evolution of optimal codon choices in the family Enterobacteriaceae. Microbiology (United Kingdom), 2013, 159, 555-564.	1.7	8
64	Identification of novel glutathione transferases in Echinococcus granulosus. An evolutionary perspective. Acta Tropica, 2012, 123, 208-216.	2.0	16
65	Translational selection on codon usage in the genus Aspergillus. Gene, 2012, 506, 98-105.	2.3	20
66	Pandemic influenza A virus codon usage revisited: biases, adaptation and implications for vaccine strain development. Virology Journal, 2012, 9, 263.	3.6	43
67	Selected codon usage bias in members of the class Mollicutes. Gene, 2011, 473, 110-118.	2.3	5
68	Developmental expression of high molecular weight tropomyosin isoforms in Mesocostoides corti. Molecular and Biochemical Parasitology, 2011, 175, 181-191.	1.1	20
69	Effects of 5-azacytidine on lymphocyte-metaphases of Creole cows carrying the rob(1;29). Research in Veterinary Science, 2010, 88, 263-266.	2.0	3
70	Characterization of a putative hsp70 pseudogene transcribed in protoscoleces and adult worms of Echinococcus granulosus. Gene, 2009, 443, 1-11.	2.3	8