

# 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	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	19.8	312
2	A detailed comparative analysis on the overall codon usage patterns in West Nile virus. <i>Infection, Genetics and Evolution</i> , 2013, 14, 396-400.	2.3	75
3	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
4	Codon Usage Bias: An Endless Tale. <i>Journal of Molecular Evolution</i> , 2021, 89, 589-593.	1.9	53
5	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
6	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
7	Pandemic influenza A virus codon usage revisited: biases, adaptation and implications for vaccine strain development. <i>Virology Journal</i> , 2012, 9, 263.	3.6	43
8	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
9	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
10	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
11	Small <i>Klebsiella pneumoniae</i> Plasmids: Neglected Contributors to Antibiotic Resistance. <i>Frontiers in Microbiology</i> , 2019, 10, 2182.	3.5	26
12	<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
13	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
14	Developmental expression of high molecular weight tropomyosin isoforms in <i>Mesocestoides corti</i> . <i>Molecular and Biochemical Parasitology</i> , 2011, 175, 181-191.	1.1	20
15	Translational selection on codon usage in the genus <i>Aspergillus</i> . <i>Gene</i> , 2012, 506, 98-105.	2.3	20
16	Stage-specific transcriptomic analysis of the model cestode <i>Hymenolepis microstoma</i> . <i>Genomics</i> , 2021, 113, 620-632.	2.9	17
17	Identification of novel glutathione transferases in <i>Echinococcus granulosus</i> . An evolutionary perspective. <i>Acta Tropica</i> , 2012, 123, 208-216.	2.0	16
18	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

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19	<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
20	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
21	Imported One-Day-Old Chicks as Trojan Horses for Multidrug-Resistant Priority Pathogens Harboring <i>mcr-9</i> , <i>rmtG</i> , and Extended-Spectrum $\beta$ -Lactamase Genes. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0167521.	3.2	13
22	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
23	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
24	Est10: A Novel Alkaline Esterase Isolated from Bovine Rumen Belonging to the New Family XV of Lipolytic Enzymes. <i>PLoS ONE</i> , 2015, 10, e0126651.	2.5	10
25	Draft Genome Sequence of a Taxonomically Unique <i>Acinetobacter</i> Clinical Strain with Proteolytic and Hemolytic Activities. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
26	Conservation of CFTR codon frequency through primates suggests synonymous mutations could have a functional effect. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2015, 775, 19-25.	1.0	10
27	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
28	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
29	Comparison of transcriptomic landscapes of different lamb muscles using RNA-Seq. <i>PLoS ONE</i> , 2018, 13, e0200732.	2.5	10
30	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
31	Metagenomic analysis of <i>Raphidiopsis raciborskii</i> microbiome: beyond the individual. <i>Biodiversity Data Journal</i> , 2021, 9, e72514.	0.6	9
32	Characterization of a putative hsp70 pseudogene transcribed in protoscolecids and adult worms of <i>Echinococcus granulosus</i> . <i>Gene</i> , 2009, 443, 1-11.	2.3	8
33	Evolution of optimal codon choices in the family Enterobacteriaceae. <i>Microbiology (United Kingdom)</i> , 2013, 159, 555-564.	1.7	8
34	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
35	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
36	General Trends in Selectively Driven Codon Usage Biases in the Domain Archaea. <i>Journal of Molecular Evolution</i> , 2014, 79, 105-110.	1.9	6

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37	Draft Genome Sequence of an Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Indigo-Pigmented Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
38	Whole-Genome Analysis of an Extensively Drug-Resistance <i>Empedobacter falsenii</i> Strain Reveals Distinct Features and the Presence of a Novel Metallo- $\beta$ -Lactamase (EBR-2). <i>Current Microbiology</i> , 2018, 75, 1084-1089.	2.2	6
39	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
40	The complex pattern of codon usage evolution in the family Comamonadaceae. <i>Ecological Genetics and Genomics</i> , 2018, 6, 1-8.	0.5	6
41	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
42	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
43	Revealing the genetic basis of eyelid pigmentation in Hereford cattle. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	6
44	Selected codon usage bias in members of the class Mollicutes. <i>Gene</i> , 2011, 473, 110-118.	2.3	5
45	Draft Genome Sequence of <i>Cupriavidus</i> UYMMa02A, a Novel Beta-Rhizobium Species. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
46	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
47	Draft Genome Sequence of <i>Paraburkholderia</i> sp. UYCP14C, a Rhizobium Strain Isolated from Root Nodules of <i>Calliandra parvifolia</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	1.1	5
48	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
49	<i>Staphylococcus aureus</i> $\beta$ -Toxin Effect on <i>Acinetobacter baumannii</i> Behavior. <i>Biology</i> , 2022, 11, 570.	2.9	5
50	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
51	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
52	Effects of 5-azacytidine on lymphocyte-metaphases of Creole cows carrying the rob(1;29). <i>Research in Veterinary Science</i> , 2010, 88, 263-266.	2.0	3
53	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
54	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

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55	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
56	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
57	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
58	Genomics and transcriptomics insights into luteolin effects on the beta-hemolytic rhizobial strain <i>Cupriavidus necator</i> UYPR2.512. <i>Environmental Microbiology</i> , 2022, 24, 240-264.	3.8	3
59	Trends in amino acid usage across the class Mollicutes. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 65-74.	3.5	2
60	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
61	Transcriptomic analysis of eyelid pigmentation in Hereford cattle. <i>Animal Genetics</i> , 2020, 51, 935-939.	1.7	2
62	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
63	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
64	Molecular characterization of KPC-2-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
65	Molecular detection of coccidian Apicomplexa Parasites isolated from wild crab-eating and pampas foxes through novel TaqMan probes: a contribution to their molecular epidemiology. <i>Molecular Biology Reports</i> , 2021, 48, 5013-5021.	2.4	1
66	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
67	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
68	Identification of Long Noncoding RNAs Involved in Eyelid Pigmentation of Hereford Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	0
69	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
70	Evolutionary analysis of species-specific duplications in flatworm genomes. <i>Molecular Phylogenetics and Evolution</i> , 2024, , 108141.	2.9	0