

Gregorio Iraola

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

1,608
citations

304743

22
h-index

330143

37
g-index

62
all docs

62
docs citations

62
times ranked

2122
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	Pangenome analysis reveals genetic isolation in <i>Campylobacter hyointestinalis</i> subspecies adapted to different mammalian hosts. <i>Scientific Reports</i> , 2021, 11, 3431.	3.3	7
3	Accurate and fast identification of <i>Campylobacter fetus</i> in bulls by real-time PCR targeting a 16S rRNA gene sequence. <i>Veterinary and Animal Science</i> , 2021, 11, 100163.	1.5	4
4	Case Report: Early Transcontinental Import of SARS-CoV-2 Variant of Concern 202012/01 (B.1.1.7) From Europe to Uruguay. <i>Frontiers in Virology</i> , 2021, 1, .	1.4	1
5	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
6	An object-oriented framework for evolutionary pangenome analysis. <i>Cell Reports Methods</i> , 2021, 1, 100085.	2.9	11
7	Protocol for post-processing of bacterial pangenome data using Pagoo pipeline. <i>STAR Protocols</i> , 2021, 2, 100802.	1.2	5
8	simurg: simulate bacterial pangenomes in R. <i>Bioinformatics</i> , 2020, 36, 1273-1274.	4.1	5
9	Occurrence and diversity of <i>Campylobacter</i> species in captive chelonians. <i>Veterinary Microbiology</i> , 2020, 241, 108567.	1.9	6
10	Schwann cell reprogramming into repair cells increases exosome-loaded miRNA-21 promoting axonal growth. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	46
11	Integrated genomic epidemiology and phenotypic profiling of <i>Clostridium difficile</i> across intra-hospital and community populations in Colombia. <i>Scientific Reports</i> , 2019, 9, 11293.	3.3	12
12	Polyclonal <i>Campylobacter fetus</i> Infections Among Unrelated Patients, Montevideo, Uruguay, 2013–2018. <i>Clinical Infectious Diseases</i> , 2019, 70, 1236-1239.	5.8	3
13	Comparative genomics identifies potential virulence factors in <i>Clostridium tertium</i> and <i>C. paraputrificum</i> . <i>Virulence</i> , 2019, 10, 657-676.	4.4	13
14	Pathogenomics of Emerging <i>Campylobacter</i> Species. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	13.6	107
15	The Trityps Comparative Repeatome: Insights on Repetitive Element Evolution in Trypanosomatid Pathogens. <i>Genome Biology and Evolution</i> , 2019, 11, 546-551.	2.5	24
16	Nanopore Sequencing Significantly Improves Genome Assembly of the Protozoan Parasite <i>Trypanosoma cruzi</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 1952-1957.	2.5	38
17	Urban metagenomics uncover antibiotic resistance reservoirs in coastal beach and sewage waters. <i>Microbiome</i> , 2019, 7, 35.	11.1	109
18	The fecal, oral, and skin microbiota of children with Chagas disease treated with benznidazole. <i>PLoS ONE</i> , 2019, 14, e0212593.	2.5	21

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19	Draft Genome Sequences of 40 Pathogenic <i>Leptospira</i> Strains Isolated from Cattle in Uruguay. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
20	Inter- and intracontinental migrations and local differentiation have shaped the contemporary epidemiological landscape of canine parvovirus in South America. <i>Virus Evolution</i> , 2018, 4, vey011.	4.9	38
21	First Release of the Bacterial Biobank of the Urban Environment (BBUE). <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
22	Biodiversity of Environmental <i>Leptospira</i> : Improving Identification and Revisiting the Diagnosis. <i>Frontiers in Microbiology</i> , 2018, 9, 816.	3.5	143
23	Whole genome sequencing of the monomorphic pathogen <i>Mycobacterium bovis</i> reveals local differentiation of cattle clinical isolates. <i>BMC Genomics</i> , 2018, 19, 2.	2.8	36
24	Surveying what's flushed away. <i>Nature Reviews Microbiology</i> , 2018, 16, 456-456.	28.6	7
25	<i>Leptospira venezuelensis</i> sp. nov., a new member of the intermediate group isolated from rodents, cattle and humans. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 513-517.	1.7	45
26	Deciphering the unexplored <i>Leptospira</i> diversity from soils uncovers genomic evolution to virulence. <i>Microbial Genomics</i> , 2018, 4, .	2.0	91
27	Phylen: automatic phylogenetic reconstruction using the EggNOG database. <i>Journal of Open Source Software</i> , 2018, 3, 593.	4.6	5
28	MLSTar: automatic multilocus sequence typing of bacterial genomes in R. <i>PeerJ</i> , 2018, 6, e5098.	2.0	21
29	Genomic and clinical evidence uncovers the enterohepatic species <i>Helicobacter valdiviensis</i> as a potential human intestinal pathogen. <i>Helicobacter</i> , 2017, 22, e12425.	3.5	9
30	Distinct <i>Campylobacter fetus</i> lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota. <i>Nature Communications</i> , 2017, 8, 1367.	12.8	56
31	Assessing the intra-species genetic variability in the clonal pathogen <i>Campylobacter fetus</i> : CRISPRs are highly polymorphic DNA markers. <i>Journal of Microbiological Methods</i> , 2017, 132, 86-94.	1.6	16
32	<i>Campylobacter ornithocola</i> sp. nov., a novel member of the <i>Campylobacter lari</i> group isolated from wild bird faecal samples. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 1643-1649.	1.7	19
33	A novel real-time PCR assay for quantitative detection of <i>Campylobacter fetus</i> based on ribosomal sequences. <i>BMC Veterinary Research</i> , 2016, 12, 286.	1.9	25
34	Transcriptome Sequencing Reveals Wide Expression Reprogramming of Basal and Unknown Genes in <i>Leptospira biflexa</i> Biofilms. <i>MSphere</i> , 2016, 1, .	2.9	26
35	<i>Campylobacter geochelonis</i> sp. nov. isolated from the western Hermann's tortoise (<i>Testudo hermanni</i>) Tj ETQq1 1 0.784314 49 BT / Over	1.7	42
36	Whole-Genome Sequences of <i>Mycobacterium bovis</i> Strain MbURU-001, Isolated from Fresh Bovine Infected Samples. <i>Genome Announcements</i> , 2015, 3, .	0.8	3

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37	Phyldynamic analysis of avian infectious bronchitis virus in South America. <i>Journal of General Virology</i> , 2015, 96, 1340-1346.	2.9	39
38	Genetic characterization of South American infectious bursal disease virus reveals the existence of a distinct worldwide-spread genetic lineage. <i>Avian Pathology</i> , 2015, 44, 212-221.	2.0	33
39	Molecular phylogeography of canine distemper virus: Geographic origin and global spreading. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 147-154.	2.7	53
40	A rural worker infected with a bovine-prevalent genotype of <i>Campylobacter fetus</i> subsp. <i>fetus</i> supports zoonotic transmission and inconsistency of MLST and whole-genome typing. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2015, 34, 1593-1596.	2.9	25
41	Phylogenetic and Genome-Wide Deep-Sequencing Analyses of Canine Parvovirus Reveal Co-Infection with Field Variants and Emergence of a Recent Recombinant Strain. <i>PLoS ONE</i> , 2014, 9, e111779.	2.5	73
42	Genomic Evidence for the Emergence and Evolution of Pathogenicity and Niche Preferences in the Genus <i>Campylobacter</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 2392-2405.	2.5	32
43	Complete Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain MtURU-001, Isolated from a Rapidly Progressing Outbreak in Uruguay. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
44	Whole-Genome Sequencing of an Isoniazid-Resistant Clinical Isolate of <i>Mycobacterium tuberculosis</i> Strain MtURU-002 from Uruguay. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
45	Phyldynamics analysis of canine parvovirus in Uruguay: evidence of two successive invasions by different variants. <i>Archives of Virology</i> , 2013, 158, 1133-1141.	2.1	37
46	High local genetic diversity of canine parvovirus from Ecuador. <i>Veterinary Microbiology</i> , 2013, 166, 214-219.	1.9	38
47	Differential Expression of Glycerol-3-Phosphate Dehydrogenase Isoforms in Flight Muscles of the Chagas Disease Vector <i>Triatoma infestans</i> (Hemiptera, Reduviidae). <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 88, 1146-1151.	1.4	6
48	Complete Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> Biovar Intermedius, Isolated from the Prepuce of a Bull. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
49	Reduced Set of Virulence Genes Allows High Accuracy Prediction of Bacterial Pathogenicity in Humans. <i>PLoS ONE</i> , 2012, 7, e42144.	2.5	17
50	Application of a multiplex PCR assay for <i>Campylobacter fetus</i> detection and subspecies differentiation in uncultured samples of aborted bovine fetuses. <i>Journal of Veterinary Science</i> , 2012, 13, 371.	1.3	36
51	Pagoo: An Encapsulated and Object-Oriented Framework for Evolutionary Analysis of Bacterial Pangenomes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0