

Alberto DÃ¡vila

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

2,287
citations

279487

23
h-index

223531

46
g-index

81
all docs

81
docs citations

81
times ranked

2842
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic analysis of an outbreak of bovine tuberculosis in a man-made multi-host species system: A call for action on wildlife in Brazil. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	1
2	Genetic Diversity and Potential Paths of Transmission of <i>Mycobacterium bovis</i> in the Amazon: The Discovery of <i>M. bovis</i> Lineage Lb1 Circulating in South America. <i>Frontiers in Veterinary Science</i> , 2021, 8, 630989.	0.9	3
3	Genomic and temporal analyses of <i>Mycobacterium bovis</i> in southern Brazil. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
4	Putative mobilized colistin resistance genes in the human gut microbiome. <i>BMC Microbiology</i> , 2021, 21, 220.	1.3	6
5	Core of the saliva microbiome: an analysis of the MG-RAST data. <i>BMC Oral Health</i> , 2021, 21, 351.	0.8	11
6	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	0.9	184
7	Rethinking Omics Education in Brazil and South America: From Genomics to Multiomics and Critical Policy Studies. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 391-393.	1.0	0
8	Global ocean resistome revealed: Exploring antibiotic resistance gene abundance and distribution in TARA Oceans samples. <i>GigaScience</i> , 2020, 9, .	3.3	60
9	Aporã virus, a novel mammarenavirus (Bunyavirales: Arenaviridae) related to highly pathogenic virus from South America. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180586.	0.8	7
10	Multilocus Analysis Resolves the European Finch Epidemic Strain of <i>Trichomonas gallinae</i> and Suggests Introgression from Divergent Trichomonads. <i>Genome Biology and Evolution</i> , 2019, 11, 2391-2402.	1.1	17
11	Recovering Genomics Clusters of Secondary Metabolites from Lakes Using Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 251.	1.5	32
12	Homology Inference Based on a Reconciliation Approach for the Comparative Genomics of Protozoa. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431878513.	0.6	1
13	SparkBLAST: scalable BLAST processing using in-memory operations. <i>BMC Bioinformatics</i> , 2017, 18, 318.	1.2	27
14	Managing workflows on top of a cloud computing orchestrator for using heterogeneous environments on e-Science. <i>International Journal of Web and Grid Services</i> , 2017, 13, 375.	0.4	2
15	ProtozoaDB 2.0: A <i>Trypanosoma Brucei</i> Case Study. <i>Pathogens</i> , 2017, 6, 32.	1.2	1
16	Distribution and Classification of Serine β -Lactamases in Brazilian Hospital Sewage and Other Environmental Metagenomes Deposited in Public Databases. <i>Frontiers in Microbiology</i> , 2016, 7, 1790.	1.5	13
17	Picoplankton Bloom in Global South? A High Fraction of Aerobic Anoxygenic Phototrophic Bacteria in Metagenomes from a Coastal Bay (Arraial do Cabo, Brazil). <i>OMICS A Journal of Integrative Biology</i> , 2016, 20, 76-87.	1.0	9
18	Improved orthologous databases to ease protozoan targets inference. <i>Parasites and Vectors</i> , 2015, 8, 494.	1.0	2

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19	Bacterial and Archaeal Communities Variability Associated with Upwelling and Anthropogenic Pressures in the Protection Area of Arraial do Cabo (Cabo Frio region - RJ). <i>Anais Da Academia Brasileira De Ciencias</i> , 2015, 87, 1737-1750.	0.3	6
20	Metagenomic Analysis of Upwelling-Affected Brazilian Coastal Seawater Reveals Sequence Domains of Type I PKS and Modular NRPS. <i>International Journal of Molecular Sciences</i> , 2015, 16, 28285-28295.	1.8	11
21	An Orthology-Based Analysis of Pathogenic Protozoa Impacting Global Health: An Improved Comparative Genomics Approach with Prokaryotes and Model Eukaryote Orthologs. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 524-538.	1.0	8
22	STINGRAY: system for integrated genomic resources and analysis. <i>BMC Research Notes</i> , 2014, 7, 132.	0.6	5
23	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13759.	0.6	23
24	Towards a Comprehensive Search of Putative Chitinases Sequences in Environmental Metagenomic Databases. <i>Natural Science</i> , 2014, 06, 323-337.	0.2	3
25	Assessment of drug resistance related genes as candidate markers for treatment outcome prediction of cutaneous leishmaniasis in Brazil. <i>Acta Tropica</i> , 2013, 126, 132-141.	0.9	18
26	Information Sciences Methodological Aspects Applied to Ontology Reuse Tools: A Study Based on Genomic Annotations in the Domain of Trypanosomatides. <i>Knowledge Organization</i> , 2013, 40, 50-61.	0.1	1
27	A framework for readapting and running bioinformatics applications in the cloud. , 2012, , .		0
28	The Transcriptome of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) Male Reproductive Organs. <i>PLoS ONE</i> , 2012, 7, e34495.	1.1	32
29	Multiresistance, beta-lactamase-encoding genes and bacterial diversity in hospital wastewater in Rio de Janeiro, Brazil. <i>Journal of Applied Microbiology</i> , 2011, 111, 572-581.	1.4	135
30	Many task computing for orthologous genes identification in protozoan genomes using Hydra. <i>Concurrency Computation Practice and Experience</i> , 2011, 23, 2326-2337.	1.4	8
31	Microbial Diversity of a Brazilian Coastal Region Influenced by an Upwelling System and Anthropogenic Activity. <i>PLoS ONE</i> , 2011, 6, e16553.	1.1	47
32	Phylogenomics-Based Reconstruction of Protozoan Species Tree. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S6861.	0.6	8
33	SciPhy: A Cloud-Based Workflow for Phylogenetic Analysis of Drug Targets in Protozoan Genomes. <i>Lecture Notes in Computer Science</i> , 2011, , 66-70.	1.0	26
34	Detecting distant homologies on protozoans metabolic pathways using scientific workflows. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 256.	0.1	5
35	Transcriptomic analyses of the avirulent protozoan parasite <i>Trypanosoma rangeli</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 174, 18-25.	0.5	32
36	Data parallelism in bioinformatics workflows using Hydra. , 2010, , .		15

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37	EST sequencing of blood-fed and Leishmania-infected midgut of Lutzomyia longipalpis, the principal visceral leishmaniasis vector in the Americas. <i>Molecular Genetics and Genomics</i> , 2009, 282, 307-317.	1.0	27
38	Transcriptome analysis of Taenia solium cysticerci using Open Reading Frame ESTs (ORESTES). <i>Parasites and Vectors</i> , 2009, 2, 35.	1.0	24
39	Methodological aspects concerning the reuse of ontologies: a study based on genomic annotations in the domain of trypanosomatids. <i>Revista Electronica De Comunicacao, Informacao & Inovacao Em Saude: RECIIS</i> , 2009, 3, .	0.2	0
40	Aspectos metodolégicos no reuso de ontologias: um estudo a partir das anotaães genãmicas no domãnio dos tripanosomatãdeos. <i>Revista Electronica De Comunicacao, Informacao & Inovacao Em Saude: RECIIS</i> , 2009, 3, .	0.2	0
41	OrthoSearch. , 2008, , .		6
42	ProtozoaDB: dynamic visualization and exploration of protozoan genomes. <i>Nucleic Acids Research</i> , 2007, 36, D547-D552.	6.5	17
43	Improving model construction of profile HMMs for remote homology detection through structural alignment. <i>BMC Bioinformatics</i> , 2007, 8, 435.	1.2	20
44	Bothrops jararaca venom gland transcriptome: Analysis of the gene expression pattern. <i>Toxicon</i> , 2006, 48, 437-461.	0.8	118
45	Molecular diversity of disintegrin-like domains within metalloproteinase precursors of Bothrops jararaca. <i>Toxicon</i> , 2006, 48, 590-599.	0.8	20
46	Internal transcribed spacers (ITS) of Trypanosoma rangeli ribosomal DNA (rDNA): a useful marker for inter-specific differentiation. <i>Infection, Genetics and Evolution</i> , 2005, 5, 17-28.	1.0	29
47	The use of ITS1 rDNA PCR in detecting pathogenic African trypanosomes. <i>Parasitology Research</i> , 2005, 95, 186-192.	0.6	225
48	Detection and characterization of rabies virus in Southern Brazil by PCR amplification and sequencing of the nucleoprotein gene. <i>Archives of Virology</i> , 2005, 150, 695-708.	0.9	16
49	GARSA: genomic analysis resources for sequence annotation. <i>Bioinformatics</i> , 2005, 21, 4302-4303.	1.8	20
50	Exploring the Genome of Trypanosoma vivax through GSS and In Silico Comparative Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 116-128.	1.0	4
51	Continuing tsetse and Trypanosoma genome sequencing projects. <i>Trends in Parasitology</i> , 2004, 20, 308-309.	1.5	2
52	Response to Hertz-Fowler and Berriman: Continuing tsetse and Trypanosoma genome sequencing projects. <i>Trends in Parasitology</i> , 2004, 20, 309-310.	1.5	0
53	Tropical Diseases, Pathogens, and Vectors Biodiversity in Developing Countries: Need for Development of Genomics and Bioinformatics Approaches. <i>Annals of the New York Academy of Sciences</i> , 2004, 1026, 41-46.	1.8	4
54	Enzootiology of Trypanosoma evansi in Pantanal, Brazil. <i>Veterinary Parasitology</i> , 2004, 125, 263-275.	0.7	166

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55	Comparative genomics to uncover the secrets of tsetse and livestock-infective trypanosomes. Trends in Parasitology, 2003, 19, 436-439.	1.5	13
56	Using PCR for unraveling the cryptic epizootiology of livestock trypanosomosis in the Pantanal, Brazil. Veterinary Parasitology, 2003, 117, 1-13.	0.7	56
57	Towards a framework for the evolutionary genomics of Kinetoplastids: what kind of data and how much?. Parasites and Vectors, 2003, 2, 16.	1.9	3
58	Combating Kinetoplastid diseases. , 2002, 1, 6.		2
59	Applications of PCR-based tools for detection and identification of animal trypanosomes: a review and perspectives. Veterinary Parasitology, 2002, 109, 213-231.	0.7	138
60	Detection and identification of Trypanosoma of African livestock through a single PCR based on internal transcribed spacer 1 of rDNA. International Journal for Parasitology, 2001, 31, 610-614.	1.3	160
61	Trypanosoma vivax " out of Africa. Trends in Parasitology, 2001, 17, 99-101.	1.5	96
62	Internal-transcribed-spacer (ITS) sequences used to explore phylogenetic relationships within <i>Leishmania</i> . Annals of Tropical Medicine and Parasitology, 2000, 94, 651-654.	1.6	45
63	Virtual Tools Against Trypanosomatids. Parasitology Today, 2000, 16, 327-328.	3.1	2
64	Animal Trypanosomiasis in South America: Current Status, Partnership, and Information Technology. Annals of the New York Academy of Sciences, 2000, 916, 199-212.	1.8	72
65	Internal-transcribed-spacer (ITS) sequences used to explore phylogenetic relationships within <i>Leishmania</i> . Annals of Tropical Medicine and Parasitology, 2000, 94, 651-654.	1.6	53
66	Estimated Financial Impact of Trypanosoma vivax on the Brazilian Pantanal and Bolivian Lowlands. Memórias Do Instituto Oswaldo Cruz, 1999, 94, 269-272.	0.8	24
67	The Seroprevalence of Equine Trypanosomosis in the Pantanal. Memórias Do Instituto Oswaldo Cruz, 1999, 94, 199-202.	0.8	18
68	Hematology of natural bovine trypanosomosis in the Brazilian Pantanal and Bolivian wetlands. Veterinary Parasitology, 1999, 85, 87-93.	0.7	40
69	Biometrical alterations of Trypanosoma evansi isolate in laboratory rodents. Veterinary Parasitology, 1998, 76, 149-152.	0.7	4
70	Bovine Trypanosomiasis in Bolivian and Brazilian Lowlands. Memórias Do Instituto Oswaldo Cruz, 1998, 93, 29-32.	0.8	15
71	Codes for Labelling Salivarian Trypanosomes in the New World. Memórias Do Instituto Oswaldo Cruz, 1998, 93, 301-301.	0.8	1
72	Morphological and Biometrical Differences among Trypanosoma vivax Isolates from Brazil and Bolivia. Memórias Do Instituto Oswaldo Cruz, 1997, 92, 357-358.	0.8	11

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73	Measurements of Trypanosoma evansi from the Pantanal. Memorias Do Instituto Oswaldo Cruz, 1997, 92, 483-484.	0.8	10
74	Outbreak of trypanosomiasis due to Trypanosoma vivax (Ziemann, 1905) in bovines of the Pantanal, Brazil. Memorias Do Instituto Oswaldo Cruz, 1996, 91, 561-562.	0.8	57
75	In Services: Data Management for In Silico Workflows. , 0, , .		1