

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	The use of ITS1 rDNA PCR in detecting pathogenic African trypanosomes. <i>Parasitology Research</i> , 2005, 95, 186-192.	0.6	225
2	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
3	Enzootiology of <i>Trypanosoma evansi</i> in Pantanal, Brazil. <i>Veterinary Parasitology</i> , 2004, 125, 263-275.	0.7	166
4	Detection and identification of <i>Trypanosoma</i> of African livestock through a single PCR based on internal transcribed spacer 1 of rDNA. <i>International Journal for Parasitology</i> , 2001, 31, 610-614.	1.3	160
5	Applications of PCR-based tools for detection and identification of animal trypanosomes: a review and perspectives. <i>Veterinary Parasitology</i> , 2002, 109, 213-231.	0.7	138
6	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
7	<i>Bothrops jararaca</i> venom gland transcriptome: Analysis of the gene expression pattern. <i>Toxicon</i> , 2006, 48, 437-461.	0.8	118
8	<i>Trypanosoma vivax</i> “out of Africa. <i>Trends in Parasitology</i> , 2001, 17, 99-101.	1.5	96
9	Animal Trypanosomiasis in South America: Current Status, Partnership, and Information Technology. <i>Annals of the New York Academy of Sciences</i> , 2000, 916, 199-212.	1.8	72
10	Global ocean resistome revealed: Exploring antibiotic resistance gene abundance and distribution in TARA Oceans samples. <i>GigaScience</i> , 2020, 9, .	3.3	60
11	Outbreak of trypanosomiasis due to <i>Trypanosoma vivax</i> (Ziemann, 1905) in bovines of the Pantanal, Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 1996, 91, 561-562.	0.8	57
12	Using PCR for unraveling the cryptic epizootiology of livestock trypanosomosis in the Pantanal, Brazil. <i>Veterinary Parasitology</i> , 2003, 117, 1-13.	0.7	56
13	Internal-transcribed-spacer (ITS) sequences used to explore phylogenetic relationships within <i>Leishmania</i> . <i>Annals of Tropical Medicine and Parasitology</i> , 2000, 94, 651-654.	1.6	53
14	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
15	Internal-transcribed-spacer (ITS) sequences used to explore phylogenetic relationships within <i>Leishmania</i> . <i>Annals of Tropical Medicine and Parasitology</i> , 2000, 94, 651-654.	1.6	45
16	Hematology of natural bovine trypanosomosis in the Brazilian Pantanal and Bolivian wetlands. <i>Veterinary Parasitology</i> , 1999, 85, 87-93.	0.7	40
17	Transcriptomic analyses of the avirulent protozoan parasite <i>Trypanosoma rangeli</i> . <i>Molecular and Biochemical Parasitology</i> , 2010, 174, 18-25.	0.5	32
18	Recovering Genomics Clusters of Secondary Metabolites from Lakes Using Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2018, 9, 251.	1.5	32

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19	The Transcriptome of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) Male Reproductive Organs. PLoS ONE, 2012, 7, e34495.	1.1	32
20	Internal transcribed spacers (ITS) of <i>Trypanosoma rangeli</i> ribosomal DNA (rDNA): a useful marker for inter-specific differentiation. Infection, Genetics and Evolution, 2005, 5, 17-28.	1.0	29
21	EST sequencing of blood-fed and <i>Leishmania</i> -infected midgut of <i>Lutzomyia longipalpis</i> , the principal visceral leishmaniasis vector in the Americas. Molecular Genetics and Genomics, 2009, 282, 307-317.	1.0	27
22	SparkBLAST: scalable BLAST processing using in-memory operations. BMC Bioinformatics, 2017, 18, 318.	1.2	27
23	SciPhy: A Cloud-Based Workflow for Phylogenetic Analysis of Drug Targets in Protozoan Genomes. Lecture Notes in Computer Science, 2011, , 66-70.	1.0	26
24	Estimated Financial Impact of <i>Trypanosoma vivax</i> on the Brazilian Pantanal and Bolivian Lowlands. Memórias Do Instituto Oswaldo Cruz, 1999, 94, 269-272.	0.8	24
25	Transcriptome analysis of <i>Taenia solium</i> <i>cysticerci</i> using Open Reading Frame ESTs (ORESTES). Parasites and Vectors, 2009, 2, 35.	1.0	24
26	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. Evolutionary Bioinformatics, 2014, 10, EBO.S13759.	0.6	23
27	GARSA: genomic analysis resources for sequence annotation. Bioinformatics, 2005, 21, 4302-4303.	1.8	20
28	Molecular diversity of disintegrin-like domains within metalloproteinase precursors of <i>Bothrops jararaca</i> . Toxicon, 2006, 48, 590-599.	0.8	20
29	Improving model construction of profile HMMs for remote homology detection through structural alignment. BMC Bioinformatics, 2007, 8, 435.	1.2	20
30	The Seroprevalence of Equine Trypanosomosis in the Pantanal. Memórias Do Instituto Oswaldo Cruz, 1999, 94, 199-202.	0.8	18
31	Assessment of drug resistance related genes as candidate markers for treatment outcome prediction of cutaneous leishmaniasis in Brazil. Acta Tropica, 2013, 126, 132-141.	0.9	18
32	ProtozoaDB: dynamic visualization and exploration of protozoan genomes. Nucleic Acids Research, 2007, 36, D547-D552.	6.5	17
33	Multilocus Analysis Resolves the European Finch Epidemic Strain of <i>Trichomonas gallinae</i> and Suggests Introgression from Divergent Trichomonads. Genome Biology and Evolution, 2019, 11, 2391-2402.	1.1	17
34	Detection and characterization of rabies virus in Southern Brazil by PCR amplification and sequencing of the nucleoprotein gene. Archives of Virology, 2005, 150, 695-708.	0.9	16
35	Data parallelism in bioinformatics workflows using Hydra. , 2010, , .		15
36	Bovine Trypanosomiasis in Bolivian and Brazilian Lowlands. Memórias Do Instituto Oswaldo Cruz, 1998, 93, 29-32.	0.8	15

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37	Comparative genomics to uncover the secrets of tsetse and livestock-infective trypanosomes. Trends in Parasitology, 2003, 19, 436-439.	1.5	13
38	Distribution and Classification of Serine $\hat{2}$ -Lactamases in Brazilian Hospital Sewage and Other Environmental Metagenomes Deposited in Public Databases. Frontiers in Microbiology, 2016, 7, 1790.	1.5	13
39	Metagenomic Analysis of Upwelling-Affected Brazilian Coastal Seawater Reveals Sequence Domains of Type I PKS and Modular NRPS. International Journal of Molecular Sciences, 2015, 16, 28285-28295.	1.8	11
40	Core of the saliva microbiome: an analysis of the MG-RAST data. BMC Oral Health, 2021, 21, 351.	0.8	11
41	Morphological and Biometrical Differences among Trypanosoma vivax Isolates from Brazil and Bolivia. Memorias Do Instituto Oswaldo Cruz, 1997, 92, 357-358.	0.8	11
42	Measurements of Trypanosoma evansi from the Pantanal. Memorias Do Instituto Oswaldo Cruz, 1997, 92, 483-484.	0.8	10
43	Picoplankton Bloom in Global South? A High Fraction of Aerobic Anoxygenic Phototrophic Bacteria in Metagenomes from a Coastal Bay (Arraial do Cabo "Brazil). OMICS A Journal of Integrative Biology, 2016, 20, 76-87.	1.0	9
44	Many task computing for orthologous genes identification in protozoan genomes using Hydra. Concurrency Computation Practice and Experience, 2011, 23, 2326-2337.	1.4	8
45	Phylogenomics-Based Reconstruction of Protozoan Species Tree. Evolutionary Bioinformatics, 2011, 7, EBO.S6861.	0.6	8
46	An Orthology-Based Analysis of Pathogenic Protozoa Impacting Global Health: An Improved Comparative Genomics Approach with Prokaryotes and Model Eukaryote Orthologs. OMICS A Journal of Integrative Biology, 2014, 18, 524-538.	1.0	8
47	Aporã virus, a novel mammarenavirus (Bunyavirales: Arenaviridae) related to highly pathogenic virus from South America. Memorias Do Instituto Oswaldo Cruz, 2019, 114, e180586.	0.8	7
48	Genomic and temporal analyses of Mycobacterium bovis in southern Brazil. Microbial Genomics, 2021, 7, .	1.0	7
49	OrthoSearch. , 2008, , .		6
50	Bacterial and Archaeal Communities Variability Associated with Upwelling and Anthropogenic Pressures in the Protection Area of Arraial do Cabo (Cabo Frio region - RJ). Anais Da Academia Brasileira De Ciencias, 2015, 87, 1737-1750.	0.3	6
51	Putative mobilized colistin resistance genes in the human gut microbiome. BMC Microbiology, 2021, 21, 220.	1.3	6
52	Detecting distant homologies on protozoans metabolic pathways using scientific workflows. International Journal of Data Mining and Bioinformatics, 2010, 4, 256.	0.1	5
53	STINGRAY: system for integrated genomic resources and analysis. BMC Research Notes, 2014, 7, 132.	0.6	5
54	Biometrical alterations of Trypanosoma evansi isolate in laboratory rodents. Veterinary Parasitology, 1998, 76, 149-152.	0.7	4

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55	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
56	Exploring the Genome of <i>Trypanosoma vivax</i> through GSS and In Silico Comparative Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 116-128.	1.0	4
57	Towards a framework for the evolutionary genomics of Kinetoplastids: what kind of data and how much?. <i>Parasites and Vectors</i> , 2003, 2, 16.	1.9	3
58	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
59	Towards a Comprehensive Search of Putative Chitinases Sequences in Environmental Metagenomic Databases. <i>Natural Science</i> , 2014, 06, 323-337.	0.2	3
60	Virtual Tools Against Trypanosomatids. <i>Parasitology Today</i> , 2000, 16, 327-328.	3.1	2
61	Combating Kinetoplastid diseases. , 2002, 1, 6.		2
62	Continuing tsetse and <i>Trypanosoma</i> genome sequencing projects. <i>Trends in Parasitology</i> , 2004, 20, 308-309.	1.5	2
63	Improved orthologous databases to ease protozoan targets inference. <i>Parasites and Vectors</i> , 2015, 8, 494.	1.0	2
64	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
65	In Services: Data Management for In Silico Workflows. , 0, , .		1
66	ProtozoaDB 2.0: A <i>Trypanosoma Brucei</i> Case Study. <i>Pathogens</i> , 2017, 6, 32.	1.2	1
67	Homology Inference Based on a Reconciliation Approach for the Comparative Genomics of Protozoa. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431878513.	0.6	1
68	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
69	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
70	Codes for Labelling Salivarian Trypanosomes in the New World. <i>Memorias Do Instituto Oswaldo Cruz</i> , 1998, 93, 301-301.	0.8	1
71	Response to Hertz-Fowler and Berriman: Continuing tsetse and <i>Trypanosoma</i> genome sequencing projects. <i>Trends in Parasitology</i> , 2004, 20, 309-310.	1.5	0
72	A framework for readapting and running bioinformatics applications in the cloud. , 2012, , .		0

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73	Rethinking Omics Education in Brazil and South America: From Genomics to Multiomics and Critical Policy Studies. OMICS A Journal of Integrative Biology, 2020, 24, 391-393.	1.0	0
74	Methodological aspects concerning the reuse of ontologies: a study based on genomic annotations in the domain of trypanosomatids. Revista Electronica De Comunicacao, Informacao & Inovacao Em Saude: RECIIS, 2009, 3, .	0.2	0
75	Aspectos metodol&3gicos no reuso de ontologias: um estudo a partir das anota&3µes gen&3micas no dom&3nio dos tripanosomat&3deos. Revista Electronica De Comunicacao, Informacao & Inovacao Em Saude: RECIIS, 2009, 3, .	0.2	0