Daniella Castanheira Bartholomeu

List of Publications by Year
in descending order

120 papers	8,928 citations	87843 38 h-index	43868 91 g-index
122 all docs	122 docs citations	122 times ranked	9324 citing authors

#	Article	IF	Citations
1	Disruption of Active Trans-Sialidase Genes Impairs Egress from Mammalian Host Cells and Generates Highly Attenuated Trypanosoma cruzi Parasites. MBio, 2022, 13, e0347821.	1.8	8
2	Trypanosoma cruzi Genomic Variability: Array Comparative Genomic Hybridization Analysis of Clone and Parental Strain. Frontiers in Cellular and Infection Microbiology, 2022, 12, 760830.	1.8	0
3	Trypanosoma cruzi genetic diversity: impact on transmission cycles and Chagas disease. Memorias Do Instituto Oswaldo Cruz, 2022, 117, e210193.	0.8	25
4	Antigenic diversity of MASP gene family of Trypanosoma cruzi. Microbes and Infection, 2022, 24, 104982.	1.0	3
5	Nitric oxide contributes to liver inflammation and parasitic burden control in Ascaris suum infection. Experimental Parasitology, 2022, 238, 108267.	0.5	2
6	Trypanosoma cruzi iron superoxide dismutases: insights from phylogenetics to chemotherapeutic target assessment. Parasites and Vectors, 2022, 15, .	1.0	2
7	Vaccination with chimeric protein induces protection in murine model against ascariasis. Vaccine, 2021, 39, 394-401.	1.7	14
8	Genomics and functional genomics in Leishmania and Trypanosoma cruzi: statuses, challenges and perspectives. Memorias Do Instituto Oswaldo Cruz, 2021, 116, e200634.	0.8	11
9	Diagnosis and identification of Leishmania species in patients with cutaneous leishmaniasis in the state of Roraima, Brazil's Amazon Region. Parasites and Vectors, 2021, 14, 32.	1.0	14
10	Repeat-Driven Generation of Antigenic Diversity in a Major Human Pathogen,ÂTrypanosoma cruzi. Frontiers in Cellular and Infection Microbiology, 2021, 11, 614665.	1.8	25
11	Unraveling Ascaris suum experimental infection in humans. Microbes and Infection, 2021, 23, 104836.	1.0	14
12	Comparative genomics of Leishmania isolates from Brazil confirms the presence of Leishmania major in the Americas. International Journal for Parasitology, 2021, 51, 1047-1057.	1.3	7
13	Phenotypic, functional and serological aspects of genotypic-specific immune response of experimental T. cruzi infection. Acta Tropica, 2021, 222, 106021.	0.9	1
14	Targeted Deletion of Centrin in Leishmania braziliensis Using CRISPR-Cas9-Based Editing. Frontiers in Cellular and Infection Microbiology, 2021, 11, 790418.	1.8	8
15	A multiplex PCR protocol for rapid differential identification of four families of trematodes with medical and veterinary importance transmitted by Biomphalaria Preston, 1910 snails. Acta Tropica, 2020, 211, 105655.	0.9	4
16	Ketamine can be produced by Pochonia chlamydosporia: an old molecule and a new anthelmintic?. Parasites and Vectors, 2020, 13, 527.	1.0	13
17	Diagnostic accuracy of tests using recombinant protein antigens of Mycobacterium leprae for leprosy: A systematic review. Journal of Infection and Public Health, 2020, 13, 1078-1088.	1.9	3
18	The gut anti-complement activity of Aedes aegypti: Investigating new ways to control the major human arboviruses vector in the Americas. Insect Biochemistry and Molecular Biology, 2020, 120, 103338.	1.2	9

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19	Conditional knockout of RAD51-related genes in Leishmania major reveals a critical role for homologous recombination during genome replication. PLoS Genetics, 2020, 16, e1008828.	1.5	21
20	Amblyomma sculptum Salivary Protease Inhibitors as Potential Anti-Tick Vaccines. Frontiers in Immunology, 2020, 11, 611104.	2.2	9
21	Parasitological and molecular diagnosis of cutaneous leishmaniasis among indigenous peoples in the state of Roraima, Brazil.. Revista Da Sociedade Brasileira De Medicina Tropical, 2020, 53, e20200006.	0.4	3
22	Next-Generation Analysis of Trypanosomatid Genome Stability and Instability. Methods in Molecular Biology, 2020, 2116, 225-262.	0.4	2
23	Title is missing!. , 2020, 16, e1008828.		0
24	Title is missing!. , 2020, 16, e1008828.		0
25	Title is missing!. , 2020, 16, e1008828.		0
26	Title is missing!. , 2020, 16, e1008828.		0
27	ProphET, prophage estimation tool: A stand-alone prophage sequence prediction tool with self-updating reference database. PLoS ONE, 2019, 14, e0223364.	1.1	45
28	Mapping benznidazole resistance in trypanosomatids and exploring evolutionary histories of nitroreductases and ABCG transporter protein sequences. Acta Tropica, 2019, 200, 105161.	0.9	11
29	The Use of Specific Serological Biomarkers to Detect CaniLeish Vaccination in Dogs. Frontiers in Veterinary Science, 2019, 6, 373.	0.9	6
30	Leishmania infantum recombinant kinesin degenerated derived repeat (rKDDR): A novel potential antigen for serodiagnosis of visceral leishmaniasis. PLoS ONE, 2019, 14, e0211719.	1.1	27
31	Efficacy of sulfadiazine and pyrimetamine for treatment of experimental toxoplasmosis with strains obtained from human cases of congenital disease in Brazil. Experimental Parasitology, 2019, 202, 7-14.	0.5	21
32	Trypanosoma cruzi Genome Assemblies: Challenges and Milestones of Assembling a Highly Repetitive and Complex Genome. Methods in Molecular Biology, 2019, 1955, 1-22.	0.4	8
33	Detection of multiple circulating Leishmania species in Lutzomyia longipalpis in the city of Governador Valadares, southeastern Brazil. PLoS ONE, 2019, 14, e0211831.	1.1	11
34	Identification of B-Cell Epitopes with Potential to Serologicaly Discrimnate Dengue from Zika Infections. Viruses, 2019, 11, 1079.	1.5	6
35	Comorbidity associated to Ascaris suum infection during pulmonary fibrosis exacerbates chronic lung and liver inflammation and dysfunction but not affect the parasite cycle in mice. PLoS Neglected Tropical Diseases, 2019, 13, e0007896.	1.3	16
36	IgG Induced by Vaccination With Ascaris suum Extracts Is Protective Against Infection. Frontiers in Immunology, 2018, 9, 2535.	2.2	36

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37	Conditional genome engineering reveals canonical and divergent roles for the Hus1 component of the 9â€“1â€–1 complex in the maintenance of the plastic genome ofLeishmania. Nucleic Acids Research, 2018, 46, 11835-11846.	6.5	24
38	Whole genome sequencing of Trypanosoma cruzi field isolates reveals extensive genomic variability and complex aneuploidy patterns within TcII DTU. BMC Genomics, 2018, 19, 816.	1.2	45
39	Assembly of highly repetitive genomes using short reads: the genome of discrete typing unit III Trypanosoma cruzi strain 231. Microbial Genomics, 2018, 4, .	1.0	24
40	Chromosomal copy number variation analysis by next generation sequencing confirms ploidy stability in Trypanosoma brucei subspecies. Microbial Genomics, 2018, 4, .	1.0	18
41	Gene and Chromosomal Copy Number Variations as an Adaptive Mechanism Towards a Parasitic Lifestyle in Trypanosomatids. Current Genomics, 2018, 19, 87-97.	0.7	44
42	Development of the PraziCalc mobile device-app to calculate praziquantel dosage in the treatment of schistosomiasis. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2018, 60, e42.	0.5	0
43	Comparative genomics of canine-isolated Leishmania (Leishmania) amazonensis from an endemic focus of visceral leishmaniasis in Governador Valadares, southeastern Brazil. Scientific Reports, 2017, 7, 40804.	1.6	65
44	TipMT: Identification of PCR-based taxon-specific markers. BMC Bioinformatics, 2017, 18, 104.	1.2	2
45	Regulatory monocytes in helminth infections: insights from the modulation during human hookworm infection. BMC Infectious Diseases, 2017, 17, 253.	1.3	14
46	On the cytokine/chemokine network during Plasmodium vivax malaria: new insights to understand the disease. Malaria Journal, 2017, 16, 42.	0.8	24
47	Virus-like Particle Display of the Î±-Gal Carbohydrate for Vaccination against Leishmania Infection. ACS Central Science, 2017, 3, 1026-1031.	5.3	67
48	Genetic Polymorphisms and Phenotypic Profiles of Sulfadiazine-Resistant and Sensitive Toxoplasma gondii Isolates Obtained from Newborns with Congenital Toxoplasmosis in Minas Gerais, Brazil. PLoS ONE, 2017, 12, e0170689.	1.1	20
49	Comparative transcriptome profiling of virulent and non-virulent Trypanosoma cruzi underlines the role of surface proteins during infection. PLoS Pathogens, 2017, 13, e1006767.	2.1	52
50	Structure of SALO, a leishmaniasis vaccine candidate from the sand fly Lutzomyia longipalpis. PLoS Neglected Tropical Diseases, 2017, 11, e0005374.	1.3	11
51	Application of rapid in vitro co-culture system of macrophages and T-cell subsets to assess the immunogenicity of dogs vaccinated with live attenuated Leishmania donovani centrin deleted parasites (LdCenâ^'/â^'). Parasites and Vectors, 2016, 9, 250.	1.0	10
52	TLR9 is required for MAPK/NF-ÎºB activation but does not cooperate with TLR2 or TLR6 to induce host resistance to Brucella abortus. Journal of Leukocyte Biology, 2016, 99, 771-780.	1.5	51
53	The Leishmania metaphylome: a comprehensive survey of Leishmania protein phylogenetic relationships. BMC Genomics, 2015, 16, 887.	1.2	21
54	A New Methodology for Evaluation of Nematode Viability. BioMed Research International, 2015, 2015, 1-7.	0.9	30

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55	ProGeRF: Proteome and Genome Repeat Finder Utilizing a Fast Parallel Hash Function. BioMed Research International, 2015, 2015, 1-9.	0.9	11
56	Comparative genomic analysis of Leishmania (Viannia) peruviana and Leishmania (Viannia) braziliensis. BMC Genomics, 2015, 16, 715.	1.2	54
57	Phenotypic profiling of CD8+ T cells during Plasmodium vivax blood-stage infection. BMC Infectious Diseases, 2015, 15, 35.	1.3	13
58	Improving Serodiagnosis of Human and Canine Leishmaniasis with Recombinant Leishmania braziliensis Cathepsin L-like Protein and a Synthetic Peptide Containing Its Linear B-cell Epitope. PLoS Neglected Tropical Diseases, 2015, 9, e3426.	1.3	21
59	CD4+ T cells apoptosis in Plasmodium vivax infection is mediated by activation of both intrinsic and extrinsic pathways. Malaria Journal, 2015, 14, 5.	0.8	17
60	Use of Phage Display technology in development of canine visceral leishmaniasis vaccine using synthetic peptide trapped in sphingomyelin/cholesterol liposomes. Parasites and Vectors, 2015, 8, 133.	1.0	21
61	Proteins Selected in Leishmania (Viannia) braziliensis by an Immunoproteomic Approach with Potential Serodiagnosis Applications for Tegumentary Leishmaniasis. Vaccine Journal, 2015, 22, 1187-1196.	3.2	54
62	Chromosomal copy number variation reveals differential levels of genomic plasticity in distinct Trypanosoma cruzi strains. BMC Genomics, 2015, 16, 499.	1.2	68
63	Vaccination using live attenuated Leishmania donovani centrin deleted parasites induces protection in dogs against Leishmania infantum. Vaccine, 2015, 33, 280-288.	1.7	85
64	Linear B-cell epitope mapping of MAPK3 and MAPK4 from Leishmania braziliensis: implications for the serodiagnosis of human and canine leishmaniasis. Applied Microbiology and Biotechnology, 2015, 99, 1323-1336.	1.7	32
65	Design, structural and spectroscopic elucidation of new nitroaromatic carboxylic acids and semicarbazones for the in vitro screening of anti-leishmanial activity. Journal of Molecular Structure, 2015, 1079, 298-306.	1.8	11
66	Evasion of the Immune Response by Trypanosoma cruzi during Acute Infection. Frontiers in Immunology, 2015, 6, 659.	2.2	128
67	Genome-Wide Screening and Identification of New Trypanosoma cruzi Antigens with Potential Application for Chronic Chagas Disease Diagnosis. PLoS ONE, 2014, 9, e106304.	1.1	15
68	Genome of the Avirulent Human-Infective Trypanosomeâ€”Trypanosoma rangeli. PLoS Neglected Tropical Diseases, 2014, 8, e3176.	1.3	72
69	Unveiling the Intracellular Survival Gene Kit of Trypanosomatid Parasites. PLoS Pathogens, 2014, 10, e1004399.	2.1	29
70	Evaluation of three recombinant Leishmania infantum antigens in human and canine visceral leishmaniasis diagnosis. Acta Tropica, 2014, 137, 25-30.	0.9	33
71	Epitope Mapping of the HSP83.1 Protein of Leishmania braziliensis Discloses Novel Targets for Immunodiagnosis of Tegumentary and Visceral Clinical Forms of Leishmaniasis. Vaccine Journal, 2014, 21, 949-959.	3.2	20
72	Mapping B-Cell Epitopes for the Peroxidoxin of Leishmania (Viannia) braziliensis and Its Potential for the Clinical Diagnosis of Tegumentary and Visceral Leishmaniasis. PLoS ONE, 2014, 9, e99216.	1.1	34

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73	Expression of IL-4, IL-10 and IFN-Î³ in the liver tissue of cattle that are naturally infected with Fasciola hepatica. Veterinary Parasitology, 2013, 195, 177-182.	0.7	27
74	Distinct genomic organization, mRNA expression and cellular localization of members of two amastin sub-families present in Trypanosoma cruzi. BMC Microbiology, 2013, 13, 10.	1.3	25
75	Parasitological and immunological aspects of early Ascaris spp. infection in mice. International Journal for Parasitology, 2013, 43, 697-706.	1.3	53
76	Induction of immunogenicity by live attenuated Leishmania donovani centrin deleted parasites in dogs. Vaccine, 2013, 31, 1785-1792.	1.7	60
77	Combined Action of Nucleic Acid-Sensing Toll-like Receptors and TLR11/TLR12 Heterodimers Imparts Resistance to Toxoplasma gondii in Mice. Cell Host and Microbe, 2013, 13, 42-53.	5.1	166
78	Identification of Strain-Specific B-cell Epitopes in Trypanosoma cruzi Using Genome-Scale Epitope Prediction and High-Throughput Immunoscreening with Peptide Arrays. PLoS Neglected Tropical Diseases, 2013, 7, e2524.	1.3	45
79	Repeat-Enriched Proteins Are Related to Host Cell Invasion and Immune Evasion in Parasitic Protozoa. Molecular Biology and Evolution, 2013, 30, 951-963.	3.5	38
80	Predicting the Proteins of Angomonas deanei, Strigomonas culicis and Their Respective Endosymbionts Reveals New Aspects of the Trypanosomatidae Family. PLoS ONE, 2013, 8, e60209.	1.1	55
81	The MASP Family of Trypanosoma cruzi: Changes in Gene Expression and Antigenic Profile during the Acute Phase of Experimental Infection. PLoS Neglected Tropical Diseases, 2012, 6, e1779.	1.3	62
82	Anatomy and evolution of telomeric and subtelomeric regions in the human protozoan parasite Trypanosoma cruzi. BMC Genomics, 2012, 13, 229.	1.2	43
83	Trypanosoma cruzi Gene Expression in Response to Gamma Radiation. PLoS ONE, 2012, 7, e29596.	1.1	13
84	Development of a dual reporter system to identify regulatory cis-acting elements in untranslated regions of Trypanosoma cruzi mRNAs. Parasitology International, 2011, 60, 161-169.	0.6	16
85	Analysis of Leishmania chagasi by 2-D Difference Gel Eletrophoresis (2-D DIGE) and Immunoproteomic: Identification of Novel Candidate Antigens for Diagnostic Tests and Vaccine. Journal of Proteome Research, 2011, 10, 2172-2184.	1.8	60
86	Innate Immune Recognition of an AT-Rich Stem-Loop DNA Motif in the Plasmodium falciparum Genome. Immunity, 2011, 35, 194-207.	6.6	234
87	Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two Corynebacterium pseudotuberculosis Strains. PLoS ONE, 2011, 6, e18551.	1.1	75
88	Identification of a Highly Antigenic Linear B Cell Epitope within Plasmodium vivax Apical Membrane Antigen 1 (AMA-1). PLoS ONE, 2011, 6, e21289.	1.1	40
89	Genomic Analyses, Gene Expression and Antigenic Profile of the Trans-Sialidase Superfamily of Trypanosoma cruzi Reveal an Undetected Level of Complexity. PLoS ONE, 2011, 6, e25914.	1.1	87
90	Hookworm products ameliorate dextran sodium sulfate-induced colitis in BALB/c mice. Inflammatory Bowel Diseases, 2011, 17, 2275-2286.	0.9	91

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91	Requirement of UNC93B1 Reveals a Critical Role for TLR7 in Host Resistance to Primary Infection with Trypanosoma cruzi. Journal of Immunology, 2011, 187, 1903-1911.	0.4	67
92	Induction of CD4+CD25+FOXP3+ Regulatory T Cells during Human Hookworm Infection Modulates Antigen-Mediated Lymphocyte Proliferation. PLoS Neglected Tropical Diseases, 2011, 5, e1383.	1.3	55
93	Identification of genes encoding hypothetical proteins in open-reading frame expressed sequence tags from mammalian stages of Trypanosoma cruzi. Genetics and Molecular Research, 2011, 10, 1589-1630.	0.3	4
94	Epidemiologic aspects of an outbreak of Trypanosoma vivax in a dairy cattle herd in Minas Gerais state, Brazil. Veterinary Parasitology, 2010, 169, 320-326.	0.7	34
95	The endless race betweenTrypanosoma cruziand host immunity: lessons for and beyond Chagas disease. Expert Reviews in Molecular Medicine, 2010, 12, e29.	1.6	158
96	Genomic organization and expression profile of the mucin-associated surface protein (masp) family of the human pathogen Trypanosoma cruzi. Nucleic Acids Research, 2009, 37, 3407-3417.	6.5	111
97	The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358.	13.7	945
98	Molecular characterization of ribonucleoproteic antigens containing repeated amino acid sequences from Trypanosoma cruzi. Microbes and Infection, 2008, 10, 716-725.	1.0	14
99	Genetic profiling of Trypanosoma cruzi directly in infected tissues using nested PCR of polymorphic microsatellites. International Journal for Parasitology, 2008, 38, 839-850.	1.3	51
100	Sequences involved in mRNA processing in Trypanosoma cruzi. International Journal for Parasitology, 2008, 38, 1383-1389.	1.3	26
101	Sequence diversity and evolution of multigene families in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 2008, 157, 65-72.	0.5	47
102	Genomic organization and transcription analysis of the 195-bp satellite DNA in Trypanosoma cruzi. Molecular and Biochemical Parasitology, 2008, 160, 60-64.	0.5	30
103	Recruitment and Endo-Lysosomal Activation of TLR9 in Dendritic Cells Infected withTrypanosoma cruzi. Journal of Immunology, 2008, 181, 1333-1344.	0.4	74
104	Toll-Like Receptor 9-Dependent Immune Activation by Unmethylated CpG Motifs in Aspergillus fumigatus DNA. Infection and Immunity, 2008, 76, 2123-2129.	1.0	143
105	Malaria hemozoin is immunologically inert but radically enhances innate responses by presenting malaria DNA to Toll-like receptor 9. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1919-1924.	3.3	468
106	Cofactor-independent phosphoglycerate mutase is an essential gene in procyclic form Trypanosoma brucei. Parasitology Research, 2007, 100, 887-892.	0.6	11
107	Control mechanisms of tubulin gene expression in Trypanosoma cruzi. International Journal for Parasitology, 2006, 36, 87-96.	1.3	24
108	Evolution of non-LTR retrotransposons in the trypanosomatid genomes: Leishmania major has lost the active elements. Molecular and Biochemical Parasitology, 2006, 145, 158-170.	0.5	31

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109	The Trypanosoma cruzi L1Tc and NARTc Non-LTR Retrotransposons Show Relative Site Specificity for Insertion. Molecular Biology and Evolution, 2006, 23, 411-420.	3.5	25
110	The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas Disease. Science, 2005, 309, 409-415.	6.0	1,273
111	Comparative Genomics of Trypanosomatid Parasitic Protozoa. Science, 2005, 309, 404-409.	6.0	713
112	The Genome of the African Trypanosome Trypanosoma brucei. Science, 2005, 309, 416-422.	6.0	1,496
113	Advances in schistosome genomics. Trends in Parasitology, 2004, 20, 154-157.	1.5	61
114	Expression of exogenous genes in Trypanosoma cruzi : improving vectors and electroporation protocols. Parasitology Research, 2004, 92, 113-120.	0.6	91
115	The sequence and analysis of Trypanosoma brucei chromosome II. Nucleic Acids Research, 2003, 31, 4856-4863.	6.5	59
116	Trypanosoma cruzi: RNA structure and post-transcriptional control of tubulin gene expression. Experimental Parasitology, 2002, 102, 123-133.	0.5	34
117	Characterization of cDNA clones encoding ribonucleoprotein antigens expressed in Trypanosoma cruzi amastigotes. Parasitology Research, 2002, 88, 292-300.	0.6	25
118	Molecular cloning and characterization of the DNA mismatch repair gene class 2 from the Trypanosoma cruzi. Gene, 2001, 272, 323-333.	1.0	30
119	Molecular cloning and characterization of a gene encoding the 29-kDa proteasome subunit from Trypanosoma cruzi. Molecular Genetics and Genomics, 2001, 265, 986-992.	1.0	10
120	Replacement of Leishmania (Leishmania) infantum Populations in an Endemic Focus of Visceral Leishmaniasis in Brazil. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	0