

Joana C Silva

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

7,002
citations

159585

30
h-index

95266

68
g-index

80
all docs

80
docs citations

80
times ranked

8682
citing authors

#	ARTICLE	IF	CITATIONS
1	STRIDE: a command-line HMM-based identifier and sub-classifier of <i>Plasmodium falciparum</i> RIFIN and STEVOR variant surface antigen families. <i>BMC Bioinformatics</i> , 2022, 23, 15.	2.6	1
2	An In Silico Analysis of Malaria Pre-Erythrocytic-Stage Antigens Interpreting Worldwide Genetic Data to Suggest Vaccine Candidate Variants and Epitopes. <i>Microorganisms</i> , 2022, 10, 1090.	3.6	2
3	<i>Plasmodium falciparum</i> 7G8 challenge provides conservative prediction of efficacy of PfNF54-based PfSPZ Vaccine in Africa. <i>Nature Communications</i> , 2022, 13, .	12.8	8
4	Comparative analysis of gene expression between <i>Babesia bovis</i> blood stages and kinetes allowed by improved genome annotation. <i>International Journal for Parasitology</i> , 2021, 51, 123-136.	3.1	23
5	Whole-genome analysis of Malawian <i>Plasmodium falciparum</i> isolates identifies possible targets of allele-specific immunity to clinical malaria. <i>PLoS Genetics</i> , 2021, 17, e1009576.	3.5	4
6	Evaluation of a high-throughput, cost-effective Illumina library preparation kit. <i>Scientific Reports</i> , 2021, 11, 15925.	3.3	6
7	Integration of population and functional genomics to understand mechanisms of artemisinin resistance in <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2021, 16, 119-128.	3.4	11
8	CD4 T Cell Responses to <i>Theileria parva</i> in Immune Cattle Recognize a Diverse Set of Parasite Antigens Presented on the Surface of Infected Lymphoblasts. <i>Journal of Immunology</i> , 2021, 207, ji2100331.	0.8	4
9	A genotyping assay to determine geographic origin and transmission potential of <i>Plasmodium falciparum</i> malaria cases. <i>Communications Biology</i> , 2021, 4, 1145.	4.4	7
10	Successful Profiling of <i>Plasmodium falciparum</i> Gene Expression in Clinical Samples via a Custom Capture Array. <i>MSystems</i> , 2021, 6, e0022621.	3.8	4
11	Strains used in whole organism <i>Plasmodium falciparum</i> vaccine trials differ in genome structure, sequence, and immunogenic potential. <i>Genome Medicine</i> , 2020, 12, 6.	8.2	61
12	Rapid evolution of genome-wide gene expression and plasticity during saline to freshwater invasions by the copepod <i>Eurytemora affinis</i> species complex. <i>Molecular Ecology</i> , 2020, 29, 4835-4856.	3.9	19
13	Epitope-based sieve analysis of <i>Plasmodium falciparum</i> sequences from a FMP2.1/AS02A vaccine trial is consistent with differential vaccine efficacy against immunologically relevant AMA1 variants. <i>Vaccine</i> , 2020, 38, 5700-5706.	3.8	5
14	Transcriptome dataset of <i>Babesia bovis</i> life stages within vertebrate and invertebrate hosts. <i>Data in Brief</i> , 2020, 33, 106533.	1.0	13
15	Comparative Transcriptomics of the Bovine Apicomplexan Parasite <i>Theileria parva</i> Developmental Stages Reveals Massive Gene Expression Variation and Potential Vaccine Antigens. <i>Frontiers in Veterinary Science</i> , 2020, 7, 287.	2.2	9
16	<i>Theileria</i> parasites subvert E2F signaling to stimulate leukocyte proliferation. <i>Scientific Reports</i> , 2020, 10, 3982.	3.3	10
17	Signature of adaptive evolution in olfactory receptor genes in Cory's Shearwater supports molecular basis for smell in procellariiform seabirds. <i>Scientific Reports</i> , 2020, 10, 543.	3.3	13
18	Re-annotation of the <i>Theileria parva</i> genome refines 53% of the proteome and uncovers essential components of N-glycosylation, a conserved pathway in many organisms. <i>BMC Genomics</i> , 2020, 21, 279.	2.8	17

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19	Optimization of parasite DNA enrichment approaches to generate whole genome sequencing data for <i>Plasmodium falciparum</i> from low parasitaemia samples. <i>Malaria Journal</i> , 2020, 19, 135.	2.3	7
20	Capture-based enrichment of <i>Theileria parva</i> DNA enables full genome assembly of first buffalo-derived strain and reveals exceptional intra-specific genetic diversity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008781.	3.0	6
21	Title is missing!. , 2020, 14, e0008781.		0
22	Title is missing!. , 2020, 14, e0008781.		0
23	Title is missing!. , 2020, 14, e0008781.		0
24	Title is missing!. , 2020, 14, e0008781.		0
25	A multiplex qPCR approach for detection of <i>pfhrp2</i> and <i>pfhrp3</i> gene deletions in multiple strain infections of <i>Plasmodium falciparum</i> . <i>Scientific Reports</i> , 2019, 9, 13107.	3.3	19
26	Genomic structure and diversity of <i>Plasmodium falciparum</i> in Southeast Asia reveal recent parasite migration patterns. <i>Nature Communications</i> , 2019, 10, 2665.	12.8	46
27	Characterization of the <i>Theileria parva</i> sporozoite proteome. <i>International Journal for Parasitology</i> , 2018, 48, 265-273.	3.1	24
28	Transcriptomics reveal potential vaccine antigens and a drastic increase of upregulated genes during <i>Theileria parva</i> development from arthropod to bovine infective stages. <i>PLoS ONE</i> , 2018, 13, e0204047.	2.5	21
29	A <i>Plasmodium berghei</i> sporozoite-based vaccination platform against human malaria. <i>Npj Vaccines</i> , 2018, 3, 33.	6.0	32
30	Discovery of a novel species, <i>Theileria haneyi</i> n. sp., infective to equids, highlights exceptional genomic diversity within the genus <i>Theileria</i> : implications for apicomplexan parasite surveillance. <i>International Journal for Parasitology</i> , 2018, 48, 679-690.	3.1	61
31	Extent and Dynamics of Polymorphism in the Malaria Vaccine Candidate <i>Plasmodium falciparum</i> Reticulocyte-binding Protein Homologue-5 in Kalifabougou, Mali. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 99, 43-50.	1.4	10
32	Evolutionary History of Chemosensory-Related Gene Families across the Arthropoda. <i>Molecular Biology and Evolution</i> , 2017, 34, 1838-1862.	8.9	157
33	Association of a Novel Mutation in the <i>Plasmodium falciparum</i> Chloroquine Resistance Transporter With Decreased Piperaquine Sensitivity. <i>Journal of Infectious Diseases</i> , 2017, 216, 468-476.	4.0	102
34	New var reconstruction algorithm exposes high var sequence diversity in a single geographic location in Mali. <i>Genome Medicine</i> , 2017, 9, 30.	8.2	13
35	A new method for sequencing the hypervariable <i>Plasmodium falciparum</i> gene <i>var2csa</i> from clinical samples. <i>Malaria Journal</i> , 2017, 16, 343.	2.3	12
36	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017, 3, e000122.	2.0	13

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37	Protection against Plasmodium falciparum malaria by PfSPZ Vaccine. JCI Insight, 2017, 2, e89154.	5.0	195
38	Absolute Quantification of the Host-To-Parasite DNA Ratio in Theileria parva-Infected Lymphocyte Cell Lines. PLoS ONE, 2016, 11, e0150401.	2.5	17
39	<i>Cryptosporidium hominis</i> gene catalog: a resource for the selection of novel <i>Cryptosporidium</i> vaccine candidates. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw137.	3.0	11
40	Annotated draft genome sequences of three species of <i>Cryptosporidium</i>: <i>Cryptosporidium meleagridis</i> isolate UKMEL1, <i>C. baileyi</i> isolate TAMU-09Q1 and <i>C. hominis</i> isolates TU502_2012 and UKH1. Pathogens and Disease, 2016, 74, ftw080.	2.0	33
41	Genome-wide diversity and gene expression profiling of Babesia microti isolates identify polymorphic genes that mediate host-pathogen interactions. Scientific Reports, 2016, 6, 35284.	3.3	74
42	Cis regulatory motifs and antisense transcriptional control in the apicomplexan Theileria parva. BMC Genomics, 2016, 17, 128.	2.8	18
43	The genomes of three stocks comprising the most widely utilized live sporozoite Theileria parva vaccine exhibit very different degrees and patterns of sequence divergence. BMC Genomics, 2015, 16, 729.	2.8	31
44	Molecular evolution of a central region containing B cell epitopes in the gene encoding the p67 sporozoite antigen within a field population of Theileria parva. Parasitology Research, 2015, 114, 1729-1737.	1.6	15
45	Plasmodium falciparum field isolates from areas of repeated emergence of drug resistant malaria show no evidence of hypermutator phenotype. Infection, Genetics and Evolution, 2015, 30, 318-322.	2.3	18
46	Theileria-transformed bovine leukocytes have cancer hallmarks. Trends in Parasitology, 2015, 31, 306-314.	3.3	97
47	A New Method for Estimating Species Age Supports the Coexistence of Malaria Parasites and Their Mammalian Hosts. Molecular Biology and Evolution, 2015, 32, 1354-1364.	8.9	39
48	Independent Emergence of Artemisinin Resistance Mutations Among Plasmodium falciparum in Southeast Asia. Journal of Infectious Diseases, 2015, 211, 670-679.	4.0	368
49	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	2.5	34
50	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 240-245.	7.1	242
51	A Novel Clade of Unique Eukaryotic Ribonucleotide Reductase R2 Subunits is Exclusive to Apicomplexan Parasites. Journal of Molecular Evolution, 2013, 77, 92-106.	1.8	7
52	Whole Genome Mapping and Re-Organization of the Nuclear and Mitochondrial Genomes of Babesia microti Isolates. PLoS ONE, 2013, 8, e72657.	2.5	39
53	Comparative genomic analysis and phylogenetic position of Theileria equi. BMC Genomics, 2012, 13, 603.	2.8	94
54	Ribonucleotide reductase as a target to control apicomplexan diseases. Current Issues in Molecular Biology, 2012, 14, 9-26.	2.4	9

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55	Two <i>Theileria parva</i> CD8 T Cell Antigen Genes Are More Variable in Buffalo than Cattle Parasites, but Differ in Pattern of Sequence Diversity. <i>PLoS ONE</i> , 2011, 6, e19015.	2.5	62
56	Genome sequences reveal divergence times of malaria parasite lineages. <i>Parasitology</i> , 2011, 138, 1737-1749.	1.5	50
57	Comparative genomics of the neglected human malaria parasite <i>Plasmodium vivax</i> . <i>Nature</i> , 2008, 455, 757-763.	27.8	756
58	IDEA: Interactive Display for Evolutionary Analyses. <i>BMC Bioinformatics</i> , 2008, 9, 524.	2.6	23
59	Properties of non-coding DNA and identification of putative cis-regulatory elements in <i>Theileria parva</i> . <i>BMC Genomics</i> , 2008, 9, 582.	2.8	13
60	Genomic Islands in the Pathogenic Filamentous Fungus <i>Aspergillus fumigatus</i> . <i>PLoS Genetics</i> , 2008, 4, e1000046.	3.5	473
61	Draft Genome Sequence of the Sexually Transmitted Pathogen <i>Trichomonas vaginalis</i> . <i>Science</i> , 2007, 315, 207-212.	12.6	731
62	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	5.6	657
63	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	12.6	713
64	Genome Sequence of <i>Theileria parva</i> , a Bovine Pathogen That Transforms Lymphocytes. <i>Science</i> , 2005, 309, 134-137.	12.6	309
65	A Potentially Functional Mariner Transposable Element in the Protist <i>Trichomonas vaginalis</i> . <i>Molecular Biology and Evolution</i> , 2004, 22, 126-134.	8.9	40
66	Evolution of P Elements in Natural Populations of <i>Drosophila willistoni</i> and <i>D. sturtevantii</i> . Sequence data from this article have been deposited with the GenBank Data Library under accession nos. AY578739, AY578740, AY578741, AY578742, AY578743, AY578744, AY578745, AY578746, AY578747, AY578748, AY578749, AY578750, AY578751, AY578752, AY578753, AY578754, AY578755, AY578756, AY578757, AY578758, AY578759, AY578760, AY578761, AY578762, AY578763, AY578764, AY578765, AY578766, AY578767, AY578768, AY578769, AY578770.	2.9	21
67	Factors that affect the horizontal transfer of transposable elements. <i>Current Issues in Molecular Biology</i> , 2004, 6, 57-71.	2.4	149
68	Patterns in spontaneous mutation revealed by human-baboon sequence comparison. <i>Trends in Genetics</i> , 2002, 18, 544-547.	6.7	56
69	Genome sequence and comparative analysis of the model rodent malaria parasite <i>Plasmodium yoelii yoelii</i> . <i>Nature</i> , 2002, 419, 512-519.	27.8	666
70	Whole-Genome Effects of Ethyl Methanesulfonate-Induced Mutation on Nine Quantitative Traits in Outbred <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001, 157, 1257-1265.	2.9	43
71	Horizontal Transfer and Selection in the Evolution of P Elements. <i>Molecular Biology and Evolution</i> , 2000, 17, 1542-1557.	8.9	111
72	Testing transposable elements as genetic drive mechanisms using <i>Drosophila</i> P element constructs as a model system. <i>Genetica</i> , 1997, 101, 13-33.	1.1	34