

Sandra Regina Maruyama

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

2,012
citations

516561

16
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713332

21
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docs citations

23
times ranked

3694
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
2	CEMiTool: a Bioconductor package for performing comprehensive modular co-expression analyses. <i>BMC Bioinformatics</i> , 2018, 19, 56.	1.2	215
3	An insight into the sialotranscriptome of the brown dog tick, <i>Rhipicephalus sanguineus</i> . <i>BMC Genomics</i> , 2010, 11, 450.	1.2	91
4	Analysis of the Salivary Gland Transcriptome of Unfed and Partially Fed <i>Amblyomma sculptum</i> Ticks and Descriptive Proteome of the Saliva. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 476.	1.8	79
5	The sialotranscriptome of <i>Amblyomma triste</i> , <i>Amblyomma parvum</i> and <i>Amblyomma cajennense</i> ticks, uncovered by 454-based RNA-seq. <i>Parasites and Vectors</i> , 2014, 7, 430.	1.0	75
6	The expression of genes coding for distinct types of glycine-rich proteins varies according to the biology of three metastriate ticks, <i>Rhipicephalus (Boophilus) microplus</i> , <i>Rhipicephalus sanguineus</i> and <i>Amblyomma cajennense</i> . <i>BMC Genomics</i> , 2010, 11, 363.	1.2	60
7	Characterisation of divergent flavivirus NS3 and NS5 protein sequences detected in <i>Rhipicephalus microplus</i> ticks from Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2014, 109, 38-50.	0.8	59
8	The sialotranscriptome of <i>Antricola delacruzi</i> female ticks is compatible with non-hematophagous behavior and an alternative source of food. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 332-342.	1.2	52
9	Mining a differential sialotranscriptome of <i>Rhipicephalus microplus</i> guides antigen discovery to formulate a vaccine that reduces tick infestations. <i>Parasites and Vectors</i> , 2017, 10, 206.	1.0	46
10	Immune and biochemical responses in skin differ between bovine hosts genetically susceptible and resistant to the cattle tick <i>Rhipicephalus microplus</i> . <i>Parasites and Vectors</i> , 2017, 10, 51.	1.0	38
11	Complete Coding Genome Sequence for Mogiana Tick Virus, a Jingmenvirus Isolated from Ticks in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	30
12	<i>Rhipicephalus (Boophilus) microplus</i> : Clotting time in tick-infested skin varies according to local inflammation and gene expression patterns in tick salivary glands. <i>Experimental Parasitology</i> , 2010, 124, 428-435.	0.5	29
13	Immune recognition of salivary proteins from the cattle tick <i>Rhipicephalus microplus</i> differs according to the genotype of the bovine host. <i>Parasites and Vectors</i> , 2017, 10, 144.	1.0	22
14	NOD2-RIP2-mediated Signaling Helps Shape Adaptive Immunity in Visceral Leishmaniasis. <i>Journal of Infectious Diseases</i> , 2016, 214, 1647-1657.	1.9	20
15	From Chromosomes to Genome: Insights into the Evolutionary Relationships and Biogeography of Old World Knifefishes (Notopteridae; Osteoglossiformes). <i>Genes</i> , 2018, 9, 306.	1.0	17
16	TLR4 abrogates the Th1 immune response through IRF1 and IFN- γ to prevent immunopathology during <i>L. infantum</i> infection. <i>PLoS Pathogens</i> , 2020, 16, e1008435.	2.1	16
17	Meiosis, spermatogenesis and nucleolar behavior in the seminiferous tubules of Alydidae, Coreidae and Rhopalidae (Heteroptera) species. <i>Genetics and Molecular Research</i> , 2009, 8, 1383-1396.	0.3	13
18	Haplotypes of the bovine IgG2 heavy gamma chain in tick-resistant and tick-susceptible breeds of cattle. <i>Immunogenetics</i> , 2011, 63, 319-324.	1.2	10

#	ARTICLE	IF	CITATIONS
19	Blood transcriptome profile induced by an efficacious vaccine formulated with salivary antigens from cattle ticks. <i>Npj Vaccines</i> , 2019, 4, 53.	2.9	8
20	Total Ortholog Median Matrix as an alternative unsupervised approach for phylogenomics based on evolutionary distance between protein coding genes. <i>Scientific Reports</i> , 2021, 11, 3791.	1.6	2