

Hideo Imamura

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

2,621
citations

304743

22
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254184

43
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53
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docs citations

53
times ranked

2409
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing of multiple <i>Leishmania donovani</i> clinical isolates provides insights into population structure and mechanisms of drug resistance. <i>Genome Research</i> , 2011, 21, 2143-2156.	5.5	381
2	Chromosome and gene copy number variation allow major structural change between species and strains of <i>Leishmania</i> . <i>Genome Research</i> , 2011, 21, 2129-2142.	5.5	380
3	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	6.0	147
4	Genomic Confirmation of Hybridisation and Recent Inbreeding in a Vector-Isolated <i>Leishmania</i> Population. <i>PLoS Genetics</i> , 2014, 10, e1004092.	3.5	142
5	Genome and Phylogenetic Analyses of <i>Trypanosoma evansi</i> Reveal Extensive Similarity to <i>T. brucei</i> and Multiple Independent Origins for Dyskinetoplasty. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3404.	3.0	124
6	Adaptive mechanisms in pathogens: universal aneuploidy in <i>Leishmania</i> . <i>Trends in Parasitology</i> , 2012, 28, 370-376.	3.3	120
7	Self-Assembly of the Ionic Peptide EAK16: The Effect of Charge Distributions on Self-Assembly. <i>Biophysical Journal</i> , 2004, 87, 1249-1259.	0.5	103
8	Haplotype selection as an adaptive mechanism in the protozoan pathogen <i>Leishmania donovani</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1961-1969.	7.8	95
9	Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, .	6.0	90
10	Genomic and Molecular Characterization of Miltefosine Resistance in <i>Leishmania infantum</i> Strains with Either Natural or Acquired Resistance through Experimental Selection of Intracellular Amastigotes. <i>PLoS ONE</i> , 2016, 11, e0154101.	2.5	80
11	Molecular Mechanisms of Drug Resistance in Natural <i>Leishmania</i> Populations Vary with Genetic Background. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1514.	3.0	79
12	<i>In vitro</i> selection of miltefosine resistance in promastigotes of <i>Leishmania donovani</i> from Nepal: genomic and metabolomic characterization. <i>Molecular Microbiology</i> , 2016, 99, 1134-1148.	2.5	67
13	Ecological divergence and hybridization of Neotropical <i>Leishmania</i> parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25159-25168.	7.1	60
14	Meiotic sex in Chagas disease parasite <i>Trypanosoma cruzi</i> . <i>Nature Communications</i> , 2019, 10, 3972.	12.8	58
15	Genome-wide SNP and microsatellite variation illuminate population-level epidemiology in the <i>Leishmania donovani</i> species complex. <i>Infection, Genetics and Evolution</i> , 2012, 12, 149-159.	2.3	50
16	Discovery and genomic analyses of hybridization between divergent lineages of <i>Trypanosoma congolense</i> , causative agent of Animal African Trypanosomiasis. <i>Molecular Ecology</i> , 2017, 26, 6524-6538.	3.9	50
17	Genomic and transcriptomic alterations in <i>Leishmania donovani</i> lines experimentally resistant to antileishmanial drugs. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 246-264.	3.4	49
18	Genomic analysis of Isometamidium Chloride resistance in <i>Trypanosoma congolense</i> . <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2017, 7, 350-361.	3.4	48

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19	Genomes of Leishmania parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007900.	3.0	48
20	Major changes in chromosomal copy, gene expression and gene dosage driven by SbIII in <i>Leishmania braziliensis</i> and <i>Leishmania panamensis</i> . <i>Scientific Reports</i> , 2019, 9, 9485.	3.3	42
21	Genomic insights into virulence mechanisms of <i>Leishmania donovani</i> : evidence from an atypical strain. <i>BMC Genomics</i> , 2018, 19, 843.	2.8	33
22	Integrated genomic and metabolomic profiling of ISC1, an emerging <i>Leishmania donovani</i> population in the Indian subcontinent. <i>Infection, Genetics and Evolution</i> , 2018, 62, 170-178.	2.3	32
23	Genomic Analysis of Colombian <i>Leishmania panamensis</i> strains with different level of virulence. <i>Scientific Reports</i> , 2018, 8, 17336.	3.3	25
24	Tracking of quiescence in <i>Leishmania</i> by quantifying the expression of GFP in the ribosomal DNA locus. <i>Scientific Reports</i> , 2019, 9, 18951.	3.3	25
25	The effect of <i>Plasmodium falciparum</i> Sir2a histone deacetylase on clonal and longitudinal variation in expression of the var family of virulence genes. <i>International Journal for Parasitology</i> , 2010, 40, 35-43.	3.1	24
26	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017, 7, 3725.	3.3	24
27	Genetic Markers for SSG Resistance in <i>Leishmania donovani</i> and SSG Treatment Failure in Visceral Leishmaniasis Patients of the Indian Subcontinent. <i>Journal of Infectious Diseases</i> , 2012, 206, 752-755.	4.0	23
28	Dependence of folding dynamics and structural stability on the location of a hydrophobic pair in β^2 -hairpins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 555-570.	2.6	21
29	Species- and Strain-Specific Adaptation of the HSP70 Super Family in Pathogenic Trypanosomatids. <i>Genome Biology and Evolution</i> , 2016, 8, 1980-1995.	2.5	20
30	Evaluation of whole genome amplification and bioinformatic methods for the characterization of <i>Leishmania</i> genomes at a single cell level. <i>Scientific Reports</i> , 2020, 10, 15043.	3.3	20
31	Single locus genotyping to track <i>Leishmania donovani</i> in the Indian subcontinent: Application in Nepal. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005420.	3.0	19
32	Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. <i>MBio</i> , 2016, 7, e02198-15.	4.1	18
33	Refining wet lab experiments with in silico searches: A rational quest for diagnostic peptides in visceral leishmaniasis. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007353.	3.0	16
34	High throughput single-cell genome sequencing gives insights into the generation and evolution of mosaic aneuploidy in <i>Leishmania donovani</i> . <i>Nucleic Acids Research</i> , 2022, 50, 293-305.	14.5	14
35	Universal model for β^1 -helix and β^2 -sheet structures in protein. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2003, 321, 181-188.	2.6	13
36	Evidence for viable and stable triploid <i>Trypanosoma congolense</i> parasites. <i>Parasites and Vectors</i> , 2017, 10, 468.	2.5	10

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37	Sequences conserved by selection across mouse and human malaria species. BMC Genomics, 2007, 8, 372.	2.8	9
38	Weak preservation of local neutral substitution rates across mammalian genomes. BMC Evolutionary Biology, 2009, 9, 89.	3.2	8
39	A Guide to Next Generation Sequence Analysis of Leishmania Genomes. Methods in Molecular Biology, 2019, 1971, 69-94.	0.9	7
40	Transcriptional Shift and Metabolic Adaptations during Leishmania Quiescence Using Stationary Phase and Drug Pressure as Models. Microorganisms, 2022, 10, 97.	3.6	7
41	Conformational conversion of proteins due to mutation. Europhysics Letters, 2004, 67, 491-497.	2.0	6
42	Genomic and Phenotypic Characterization of Experimentally Selected Resistant Leishmania donovani Reveals a Role for Dynamin-1-Like Protein in the Mechanism of Resistance to a Novel Antileishmanial Compound. MBio, 2022, 13, e0326421.	4.1	5
43	Minimum model for the α -helix- β -hairpin transition in proteins. Proteins: Structure, Function and Bioinformatics, 2007, 67, 459-468.	2.6	4