

Hideo Imamura

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

2,621
citations

304743

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| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Transcriptional Shift and Metabolic Adaptations during <i>Leishmania</i> Quiescence Using Stationary Phase and Drug Pressure as Models. <i>Microorganisms</i> , 2022, 10, 97. | 3.6 | 7 |
| 2 | Genomic and Phenotypic Characterization of Experimentally Selected Resistant <i>Leishmania donovani</i> Reveals a Role for Dynamin-1-Like Protein in the Mechanism of Resistance to a Novel Antileishmanial Compound. <i>MBio</i> , 2022, 13, e0326421. | 4.1 | 5 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | Global genome diversity of the <i>Leishmania donovani</i> complex. <i>ELife</i> , 2020, 9, . | 6.0 | 90 |
| 7 | 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 |
| 8 | Meiotic sex in Chagas disease parasite <i>Trypanosoma cruzi</i> . <i>Nature Communications</i> , 2019, 10, 3972. | 12.8 | 58 |
| 9 | 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 |
| 10 | A Guide to Next Generation Sequence Analysis of <i>Leishmania</i> Genomes. <i>Methods in Molecular Biology</i> , 2019, 1971, 69-94. | 0.9 | 7 |
| 11 | 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 |
| 12 | Genomes of <i>Leishmania</i> parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007900. | 3.0 | 48 |
| 13 | 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 |
| 14 | 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 |
| 15 | Genomic Analysis of Colombian <i>Leishmania panamensis</i> strains with different level of virulence. <i>Scientific Reports</i> , 2018, 8, 17336. | 3.3 | 25 |
| 16 | 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 |
| 17 | Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in <i>Trypanosomatids</i> . <i>Scientific Reports</i> , 2017, 7, 3725. | 3.3 | 24 |
| 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 | 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 |
| 20 | 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 |
| 21 | Evidence for viable and stable triploid <i>Trypanosoma congolense</i> parasites. <i>Parasites and Vectors</i> , 2017, 10, 468. | 2.5 | 10 |
| 22 | 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 |
| 23 | 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 |
| 24 | <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 |
| 25 | Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. <i>MBio</i> , 2016, 7, e02198-15. | 4.1 | 18 |
| 26 | 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 |
| 27 | Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, . | 6.0 | 147 |
| 28 | 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 |
| 29 | 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 |
| 30 | Adaptive mechanisms in pathogens: universal aneuploidy in <i>Leishmania</i> . <i>Trends in Parasitology</i> , 2012, 28, 370-376. | 3.3 | 120 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | Weak preservation of local neutral substitution rates across mammalian genomes. BMC Evolutionary Biology, 2009, 9, 89. | 3.2 | 8 |
| 38 | Minimum model for the $\hat{1}\pm$ -helix- $\hat{1}^2$ -hairpin transition in proteins. Proteins: Structure, Function and Bioinformatics, 2007, 67, 459-468. | 2.6 | 4 |
| 39 | Sequences conserved by selection across mouse and human malaria species. BMC Genomics, 2007, 8, 372. | 2.8 | 9 |
| 40 | Dependence of folding dynamics and structural stability on the location of a hydrophobic pair in $\hat{1}^2$ -hairpins. Proteins: Structure, Function and Bioinformatics, 2006, 63, 555-570. | 2.6 | 21 |
| 41 | Self-Assembly of the Ionic Peptide EAK16: The Effect of Charge Distributions on Self-Assembly. Biophysical Journal, 2004, 87, 1249-1259. | 0.5 | 103 |
| 42 | Conformational conversion of proteins due to mutation. Europhysics Letters, 2004, 67, 491-497. | 2.0 | 6 |
| 43 | Universal model for $\hat{1}\pm$ -helix and $\hat{1}^2$ -sheet structures in protein. Physica A: Statistical Mechanics and Its Applications, 2003, 321, 181-188. | 2.6 | 13 |