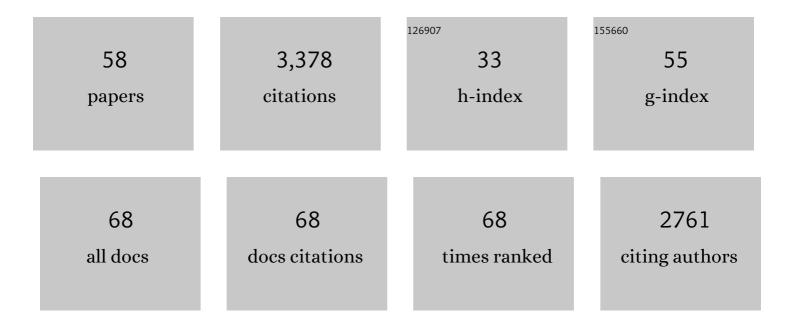
Michael D Lewis

List of Publications by Year in descending order

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MICHAEL DIEWIS

#	Article	IF	CITATIONS
1	Incomplete Recruitment of Protective T Cells Is Associated with Trypanosoma cruzi Persistence in the Mouse Colon. Infection and Immunity, 2022, 90, IAI0038221.	2.2	9
2	Microevolution of Trypanosoma cruzi reveals hybridization and clonal mechanisms driving rapid genome diversification. ELife, 2022, 11, .	6.0	9
3	Hostâ€parasite dynamics in Chagas disease from systemic to hyperâ€local scales. Parasite Immunology, 2021, 43, e12786.	1.5	19
4	Repeat-Driven Generation of Antigenic Diversity in a Major Human Pathogen,ÂTrypanosoma cruzi. Frontiers in Cellular and Infection Microbiology, 2021, 11, 614665.	3.9	25
5	Local association of Trypanosoma cruzi chronic infection foci and enteric neuropathic lesions at the tissue micro-domain scale. PLoS Pathogens, 2021, 17, e1009864.	4.7	13
6	Bioluminescent:Fluorescent Trypanosoma cruzi Reporter Strains as Tools for Exploring Chagas Disease Pathogenesis and Drug Activity. Current Pharmaceutical Design, 2021, 27, 1733-1740.	1.9	3
7	<i>In Vivo</i> Analysis of Trypanosoma cruzi Persistence Foci at Single-Cell Resolution. MBio, 2020, 11,	4.1	40
8	Challenges in Chagas Disease Drug Development. Molecules, 2020, 25, 2799.	3.8	33
9	Intracellular DNA replication and differentiation of Trypanosoma cruzi is asynchronous within individual host cells in vivo at all stages of infection. PLoS Neglected Tropical Diseases, 2020, 14, e0008007.	3.0	23
10	Fatal progression of experimental visceral leishmaniasis is associated with intestinal parasitism and secondary infection by commensal bacteria, and is delayed by antibiotic prophylaxis. PLoS Pathogens, 2020, 16, e1008456.	4.7	17
11	Drug-cured experimental Trypanosoma cruziÂinfections confer long-lasting and cross-strain protection. PLoS Neglected Tropical Diseases, 2020, 14, e0007717.	3.0	12
12	Culture-free genome-wide locus sequence typing (GLST) provides new perspectives on Trypanosoma cruzi dispersal and infection complexity. PLoS Genetics, 2020, 16, e1009170.	3.5	7
13	Exploiting Genetically Modified Dual-Reporter Strains to Monitor Experimental Trypanosoma cruzi Infections and Host-Parasite Interactions. Methods in Molecular Biology, 2019, 1955, 147-163.	0.9	15
14	Expanding the toolbox for Trypanosoma cruzi: A parasite line incorporating a bioluminescence-fluorescence dual reporter and streamlined CRISPR/Cas9 functionality for rapid in vivo localisation and phenotyping. PLoS Neglected Tropical Diseases, 2018, 12, e0006388.	3.0	79
15	Imaging the development of chronic Chagas disease after oral transmission. Scientific Reports, 2018, 8, 11292.	3.3	36
16	Development of Trypanosoma cruzi in vitro assays to identify compounds suitable for progression in Chagas' disease drug discovery. PLoS Neglected Tropical Diseases, 2018, 12, e0006612.	3.0	76
17	Assessing the Effectiveness of Curative Benznidazole Treatment in Preventing Chronic Cardiac Pathology in Experimental Models of Chagas Disease. Antimicrobial Agents and Chemotherapy, 2018, 62,	3.2	22
18	Hosts and vectors of <i>Trypanosoma cruzi</i> discrete typing units in the Chagas disease endemic region of the Paraguayan Chaco. Parasitology, 2017, 144, 884-898.	1.5	16

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19	The midgut microbiota plays an essential role in sand fly vector competence for <i>Leishmania major</i> . Cellular Microbiology, 2017, 19, e12755.	2.1	67
20	Genome-wide mutagenesis and multi-drug resistance in American trypanosomes induced by the front-line drug benznidazole. Scientific Reports, 2017, 7, 14407.	3.3	41
21	Biological factors that impinge on Chagas disease drug development. Parasitology, 2017, 144, 1871-1880.	1.5	45
22	Highly Sensitive Bioluminescence Imaging Models for Chagas Disease Drug Discovery. Proceedings (mdpi), 2017, 1, 676.	0.2	0
23	Apolipoprotein L1 Variant Associated with Increased Susceptibility to Trypanosome Infection. MBio, 2016, 7, e02198-15.	4.1	18
24	Putting Infection Dynamics at the Heart of Chagas Disease. Trends in Parasitology, 2016, 32, 899-911.	3.3	83
25	Host and parasite genetics shape a link between <i>Trypanosoma cruzi</i> infection dynamics and chronic cardiomyopathy. Cellular Microbiology, 2016, 18, 1429-1443.	2.1	78
26	Nitroheterocyclic drugs cure experimental Trypanosoma cruzi infections more effectively in the chronic stage than in the acute stage. Scientific Reports, 2016, 6, 35351.	3.3	72
27	Molecular Diversity of Trypanosoma cruzi Detected in the Vector Triatoma protracta from California, USA. PLoS Neglected Tropical Diseases, 2016, 10, e0004291.	3.0	33
28	Molecular Genotyping of Trypanosoma cruzi for Lineage Assignment and Population Genetics. Methods in Molecular Biology, 2015, 1201, 297-337.	0.9	15
29	A New Experimental Model for Assessing Drug Efficacy against Trypanosoma cruzi Infection Based on Highly Sensitive In Vivo Imaging. Journal of Biomolecular Screening, 2015, 20, 36-43.	2.6	91
30	Limited Ability of Posaconazole To Cure both Acute and Chronic Trypanosoma cruzi Infections Revealed by Highly Sensitive <i>In Vivo</i> Imaging. Antimicrobial Agents and Chemotherapy, 2015, 59, 4653-4661.	3.2	124
31	Genome and Phylogenetic Analyses of Trypanosoma evansi Reveal Extensive Similarity to T. brucei and Multiple Independent Origins for Dyskinetoplasty. PLoS Neglected Tropical Diseases, 2015, 9, e3404.	3.0	124
32	The Trypanosoma cruzi Vitamin C Dependent Peroxidase Confers Protection against Oxidative Stress but Is Not a Determinant of Virulence. PLoS Neglected Tropical Diseases, 2015, 9, e0003707.	3.0	28
33	Reply to "Drug Susceptibility of Genetically Engineered Trypanosoma cruzi Strains and Sterile Cure in Animal Models as a Criterion for Potential Clinical Efficacy of Anti-T. cruzi Drugs― Antimicrobial Agents and Chemotherapy, 2015, 59, 7925-7925.	3.2	2
34	Development of Peptide-Based Lineage-Specific Serology for Chronic Chagas Disease: Geographical and Clinical Distribution of Epitope Recognition. PLoS Neglected Tropical Diseases, 2014, 8, e2892.	3.0	37
35	Bioluminescence imaging of chronic <scp> <i>T</i> </scp> <i>rypanosoma cruzi</i> infections reveals tissueâ€specific parasite dynamics and heart disease in the absence of locally persistent infection. Cellular Microbiology, 2014, 16, 1285-1300.	2.1	210
36	Multilocus sequence and microsatellite identification of intra-specific hybrids and ancestor-like donors among natural Ethiopian isolates of Leishmania donovani. International Journal for Parasitology, 2014, 44, 751-757.	3.1	31

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37	Molecular Epidemiologic Source Tracking of Orally Transmitted Chagas Disease, Venezuela. Emerging Infectious Diseases, 2013, 19, 1098-1101.	4.3	33
38	Highly Sensitive In Vivo Imaging of Trypanosoma brucei Expressing "Red-Shifted―Luciferase. PLoS Neglected Tropical Diseases, 2013, 7, e2571.	3.0	56
39	Multiple Mitochondrial Introgression Events and Heteroplasmy in Trypanosoma cruzi Revealed by Maxicircle MLST and Next Generation Sequencing. PLoS Neglected Tropical Diseases, 2012, 6, e1584.	3.0	104
40	Comparative genomic analysis of human infective Trypanosoma cruzi lineages with the bat-restricted subspecies T. cruzi marinkellei. BMC Genomics, 2012, 13, 531.	2.8	57
41	North American import? Charting the origins of an enigmatic Trypanosoma cruzi domestic genotype. Parasites and Vectors, 2012, 5, 226.	2.5	48
42	Candidate targets for Multilocus Sequence Typing of Trypanosoma cruzi: Validation using parasite stocks from the Chaco Region and a set of reference strains. Infection, Genetics and Evolution, 2012, 12, 350-358.	2.3	54
43	Contemporary cryptic sexuality in <i>Trypanosoma cruzi</i> . Molecular Ecology, 2012, 21, 4216-4226.	3.9	96
44	Genetic Exchange in Trypanosomatids and Its Relevance to Epidemiology. , 2011, , 581-605.		1
45	Multilocus Sequence Typing (MLST) for Lineage Assignment and High Resolution Diversity Studies in Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2011, 5, e1049.	3.0	94
46	Visualisation of Leishmania donovani Fluorescent Hybrids during Early Stage Development in the Sand Fly Vector. PLoS ONE, 2011, 6, e19851.	2.5	77
47	Extraordinary Trypanosoma cruzi diversity within single mammalian reservoir hosts implies a mechanism of diversifying selection. International Journal for Parasitology, 2011, 41, 609-614.	3.1	69
48	Shotgun Sequencing Analysis of Trypanosoma cruzi I Sylvio X10/1 and Comparison with T. cruzi VI CL Brener. PLoS Neglected Tropical Diseases, 2011, 5, e984.	3.0	129
49	Recent, Independent and Anthropogenic Origins of Trypanosoma cruzi Hybrids. PLoS Neglected Tropical Diseases, 2011, 5, e1363.	3.0	117
50	Analysis of molecular diversity of the Trypanosoma cruzi trypomastigote small surface antigen reveals novel epitopes, evidence of positive selection and potential implications for lineage-specific serology. International Journal for Parasitology, 2010, 40, 921-928.	3.1	42
51	Experimental and Natural Recombination in Trypanosoma cruzi. , 2010, , 459-474.		2
52	Genotyping of Trypanosoma cruzi: Systematic Selection of Assays Allowing Rapid and Accurate Discrimination of All Known Lineages. American Journal of Tropical Medicine and Hygiene, 2009, 81, 1041-1049.	1.4	114
53	Trypanosoma cruzi IIc: Phylogenetic and Phylogeographic Insights from Sequence and Microsatellite Analysis and Potential Impact on Emergent Chagas Disease. PLoS Neglected Tropical Diseases, 2009, 3, e510.	3.0	118
54	Genome-Scale Multilocus Microsatellite Typing of Trypanosoma cruzi Discrete Typing Unit I Reveals Phylogeographic Structure and Specific Genotypes Linked to Human Infection. PLoS Pathogens, 2009, 5, e1000410.	4.7	180

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#	Article	IF	CITATIONS
55	Flow cytometric analysis and microsatellite genotyping reveal extensive DNA content variation in Trypanosoma cruzi populations and expose contrasts between natural and experimental hybrids. International Journal for Parasitology, 2009, 39, 1305-1317.	3.1	101
56	Comparative phylogeography of Trypanosoma cruzi TCIIc: New hosts, association with terrestrial ecotopes, and spatial clustering. Infection, Genetics and Evolution, 2009, 9, 1265-1274.	2.3	105
57	Resolution of multiclonal infections of Trypanosoma cruzi from naturally infected triatomine bugs and from experimentally infected mice by direct plating on a sensitive solid medium. International Journal for Parasitology, 2007, 37, 111-120.	3.1	50
58	The genotype distribution of the XRCC1gene indicates a role for base excision repair in the development of therapy-related acute myeloblastic leukemia. Blood, 2002, 100, 3761-3766.	1.4	161