

Harry A Noyes

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,562
citations

159585

30
h-index

206112

48
g-index

75
all docs

75
docs citations

75
times ranked

3215
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetics of Human Schistosomiasis Infection Intensity and Liver Disease: A Review. <i>Frontiers in Immunology</i> , 2021, 12, 613468.	4.8	11
2	Unmapped exome reads implicate a role for Anelloviridae in childhood HIV-1 long-term non-progression. <i>Npj Genomic Medicine</i> , 2021, 6, 24.	3.8	3
3	Candidate gene family-based and case-control studies of susceptibility to high <i>Schistosoma mansoni</i> worm burden in African children: a protocol. <i>AAS Open Research</i> , 2021, 4, 36.	1.5	0
4	Field assessment in Cameroon of a reader of POC-CCA lateral flow strips for the quantification of <i>Schistosoma mansoni</i> circulating cathodic antigen in urine. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009569.	3.0	15
5	High Levels of Genetic Diversity within Nilo-Saharan Populations: Implications for Human Adaptation. <i>American Journal of Human Genetics</i> , 2020, 107, 473-486.	6.2	12
6	Variant antigen diversity in <i>Trypanosoma vivax</i> is not driven by recombination. <i>Nature Communications</i> , 2020, 11, 844.	12.8	22
7	Copy number variation in human genomes from three major ethno-linguistic groups in Africa. <i>BMC Genomics</i> , 2020, 21, 289.	2.8	7
8	SNPs in IL4 and IFNG show no protective associations with human African trypanosomiasis in the Democratic Republic of the Congo: a case-control study. <i>AAS Open Research</i> , 2020, 3, 35.	1.5	0
9	Association of APOL1 renal disease risk alleles with <i>Trypanosoma brucei rhodesiense</i> infection outcomes in the northern part of Malawi. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007603.	3.0	13
10	Association between IL1 gene polymorphism and human African trypanosomiasis in populations of sleeping sickness foci of southern Cameroon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007283.	3.0	2
11	Macrophage migrating inhibitory factor expression is associated with <i>Trypanosoma brucei gambiense</i> infection and is controlled by trans-acting expression quantitative trait loci in the Guinean population. <i>Infection, Genetics and Evolution</i> , 2019, 71, 108-115.	2.3	3
12	Do Cryptic Reservoirs Threaten Gambiense-Sleeping Sickness Elimination?. <i>Trends in Parasitology</i> , 2018, 34, 197-207.	3.3	139
13	Variant antigen repertoires in <i>Trypanosoma congolense</i> populations and experimental infections can be profiled from deep sequence data using universal protein motifs. <i>Genome Research</i> , 2018, 28, 1383-1394.	5.5	15
14	No evidence for association between APOL1 kidney disease risk alleles and Human African Trypanosomiasis in two Ugandan populations. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006300.	3.0	12
15	Candidate genes-based investigation of susceptibility to Human African Trypanosomiasis in CÔte d'Ivoire. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005992.	3.0	14
16	Introducing the TrypanoGEN biobank: A valuable resource for the elimination of human African trypanosomiasis. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005438.	3.0	27
17	Candidate gene polymorphisms study between human African trypanosomiasis clinical phenotypes in Guinea. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005833.	3.0	21
18	A polymorphism in the haptoglobin, haptoglobin related protein locus is associated with risk of human sleeping sickness within Cameroonian populations. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005979.	3.0	14

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19	APOL1 renal risk variants have contrasting resistance and susceptibility associations with African trypanosomiasis. <i>ELife</i> , 2017, 6, .	6.0	95
20	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
21	Evidence for genes controlling resistance to <i>Heligmosomoides bakeri</i> on mouse chromosome 1. <i>Parasitology</i> , 2015, 142, 566-575.	1.5	0
22	A simple procedure for directly obtaining haplotype sequences of diploid genomes. <i>BMC Genomics</i> , 2015, 16, 642.	2.8	2
23	The Quality of Methods Reporting in Parasitology Experiments. <i>PLoS ONE</i> , 2014, 9, e101131.	2.5	12
24	Whole-Genome Sequencing of <i>Trypanosoma brucei</i> Reveals Introgression between Subspecies That Is Associated with Virulence. <i>MBio</i> , 2013, 4, .	4.1	42
25	Novel SNP Discovery in African Buffalo, <i>Syncerus caffer</i> , Using High-Throughput Sequencing. <i>PLoS ONE</i> , 2012, 7, e48792.	2.5	15
26	Multiorgan Dysfunction Caused by Travel-associated African Trypanosomiasis. <i>Emerging Infectious Diseases</i> , 2012, 18, 287-289.	4.3	15
27	Genetic and expression analysis of cattle identifies candidate genes in pathways responding to <i>Trypanosoma congolense</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9304-9309.	7.1	92
28	Quantitative trait loci for resistance to <i>Heligmosomoides bakeri</i> and associated immunological and pathological traits in mice: comparison of loci on chromosomes 5, 8 and 11 in F2 and F6/7 inter-cross lines of mice. <i>Parasitology</i> , 2010, 137, 311-320.	1.5	8
29	Genotype and expression analysis of two inbred mouse strains and two derived congenic strains suggest that most gene expression is trans regulated and sensitive to genetic background. <i>BMC Genomics</i> , 2010, 11, 361.	2.8	10
30	A Comprehensive Genetic Analysis of Candidate Genes Regulating Response to <i>Trypanosoma congolense</i> Infection in Mice. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e880.	3.0	14
31	Claudin 13, a Member of the Claudin Family Regulated in Mouse Stress Induced Erythropoiesis. <i>PLoS ONE</i> , 2010, 5, e12667.	2.5	18
32	Clinical Chemistry of Congenic Mice with Quantitative Trait Loci for Predicted Responses to <i>Trypanosoma congolense</i> Infection. <i>Infection and Immunity</i> , 2009, 77, 3948-3957.	2.2	7
33	Development of a Multilocus Microsatellite Typing Approach for Discriminating Strains of <i>Leishmania</i> (<i>Viannia</i>) Species. <i>Journal of Clinical Microbiology</i> , 2009, 47, 2818-2825.	3.9	50
34	<i>Heligmosomoides bakeri</i> : a model for exploring the biology and genetics of resistance to chronic gastrointestinal nematode infections. <i>Parasitology</i> , 2009, 136, 1565-1580.	1.5	55
35	A Systematic Strategy for the Discovery of Candidate Genes Responsible for Phenotypic Variation. <i>Methods in Molecular Biology</i> , 2009, 573, 329-345.	0.9	6
36	Mechanisms Controlling Anaemia in <i>Trypanosoma congolense</i> Infected Mice. <i>PLoS ONE</i> , 2009, 4, e5170.	2.5	49

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37	Strong position-dependent effects of sequence mismatches on signal ratios measured using long oligonucleotide microarrays. <i>BMC Genomics</i> , 2008, 9, 317.	2.8	27
38	An integrated pipeline for the development of novel panels of mapped microsatellite markers for <i>Leishmania donovani</i> complex, <i>Leishmania braziliensis</i> and <i>Leishmania major</i> . <i>Parasitology</i> , 2008, 135, 567-574.	1.5	15
39	A systematic strategy for large-scale analysis of genotype-phenotype correlations: identification of candidate genes involved in African trypanosomiasis. <i>Nucleic Acids Research</i> , 2007, 35, 5625-5633.	14.5	51
40	Trypanosomes, After the Genome (ed. D. Barry, R. McCulloch, J. Mottram and A. Acosta-Serrano), pp. 423. Horizon Bioscience, Wymondham, Norfolk, UK. ISBN 13:978-1-904933-27-4. Â£140. <i>Parasitology</i> , 2007, 134, 2081-2082.	1.5	0
41	<i>Leishmania donovani</i> and Cutaneous Leishmaniasis, Sri Lanka. <i>Emerging Infectious Diseases</i> , 2007, 13, 476-478.	4.3	86
42	A molecular phylogeny of the nightjars (Aves: Caprimulgidae) suggests extensive conservation of primitive morphological traits across multiple lineages. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 789-796.	2.7	19
43	A systematic strategy for the discovery of candidate genes responsible for phenotypic variation. <i>BMC Bioinformatics</i> , 2007, 8, .	2.6	2
44	Phylogeny of <i>Trypanosoma (Megatrypanum) theileri</i> and related trypanosomes reveals lineages of isolates associated with artiodactyl hosts diverging on SSU and ITS ribosomal sequences. <i>Parasitology</i> , 2006, 132, 215.	1.5	68
45	Gene expression profiling in a mouse model for African trypanosomiasis. <i>Genes and Immunity</i> , 2006, 7, 667-679.	4.1	35
46	A Gambian Infant with Fever and an Unexpected Blood Film. <i>PLoS Medicine</i> , 2006, 3, e355.	8.4	41
47	MALE SEX PHEROMONES AND THE PHYLOGEOGRAPHIC STRUCTURE OF THE LUTZOMYIA LONGIPALPIS SPECIES COMPLEX (DIPTERA: PSYCHODIDAE) FROM BRAZIL AND VENEZUELA. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 73, 734-743.	1.4	50
48	Male sex pheromones and the phylogeographic structure of the <i>Lutzomyia longipalpis</i> species complex (Diptera: Psychodidae) from Brazil and Venezuela. <i>American Journal of Tropical Medicine and Hygiene</i> , 2005, 73, 734-43.	1.4	25
49	<i>Leishmania donovani</i> is the only cause of visceral leishmaniasis in East Africa; previous descriptions of <i>L. infantum</i> and <i>L. archibaldi</i> from this region are a consequence of convergent evolution in the isoenzyme data. <i>Parasitology</i> , 2004, 129, 399-409.	1.5	91
50	Phylogeny, taxonomy and grouping of <i>Trypanosoma rangeli</i> isolates from man, triatomines and sylvatic mammals from widespread geographical origin based on SSU and ITS ribosomal sequences. <i>Parasitology</i> , 2004, 129, 549-561.	1.5	111
51	Genetic identification of two sibling species of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) that produce distinct male sex pheromones in Sobral, Cear� State, Brazil. <i>Molecular Ecology</i> , 2003, 12, 1879-1894.	3.9	55
52	Host specificity of <i>Trypanosoma (Herpetosoma)</i> species: evidence that bank voles (<i>Clethrionomys</i>) carry at least two polyphyletic parasites. <i>Parasitology</i> , 2002, 124, 185-190.	1.5	42
53	A previously unclassified trypanosomatid responsible for human cutaneous lesions in Martinique (French West Indies) is the most divergent member of the genus <i>Leishmania</i> ss. <i>Parasitology</i> , 2002, 124, 17-24.	1.5	58
54	Towards a standard battery of microsatellite markers for the analysis of the <i>Leishmania donovani</i> complex. <i>Annals of Tropical Medicine and Parasitology</i> , 2002, 96, 265-270.	1.6	50

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55	DNA extraction and amplification of <i>Leishmania</i> from archived, Giemsa-stained slides, for the diagnosis of cutaneous leishmaniasis by PCR. <i>Annals of Tropical Medicine and Parasitology</i> , 2002, 96, 31-34.	1.6	84
56	Polymorphic microsatellite repeats are not conserved between <i>Leishmania donovani</i> and <i>Leishmania major</i> . <i>Molecular Ecology Notes</i> , 2002, 2, 104-106.	1.7	20
57	Corrigendum to "A nested PCR for the <i>ssrRNA</i> gene detects <i>Trypanosoma binneyi</i> in the platypus and <i>Trypanosoma</i> sp. in wombats and kangaroos in Australia" [<i>International Journal for Parasitology</i> 29 (2) (1999) 331-339]. <i>International Journal for Parasitology</i> , 2000, 30, 228.	3.1	10
58	Evidence for a neotropical origin of <i>Leishmania</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2000, 95, 575-578.	1.6	29
59	An outbreak of cutaneous leishmaniasis in an Afghan refugee settlement in north-west Pakistan. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 1999, 93, 133-136.	1.8	74
60	<i>Leishmania</i> (<i>Sauroleishmania</i>): A Comment on Classification. <i>Parasitology Today</i> , 1998, 14, 167.	3.0	17
61	Reply. <i>Parasitology Today</i> , 1998, 14, 335.	3.0	6
62	The Evolution of <i>Trypanosomes</i> Infecting Humans and Primates. <i>Memorias Do Instituto Oswaldo Cruz</i> , 1998, 93, 669-676.	1.6	60
63	A Nested-PCR-Based Schizodeme Method for Identifying <i>Leishmania</i> Kinetoplast Minicircle Classes Directly from Clinical Samples and Its Application to the Study of the Epidemiology of <i>Leishmania tropica</i> in Pakistan. <i>Journal of Clinical Microbiology</i> , 1998, 36, 2877-2881.	3.9	226
64	Implications of a Neotropical Origin of the Genus <i>Leishmania</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 1998, 93, 657-662.	1.6	35
65	The <i>Leishmania hertigi</i> (Kinetoplastida; Trypanosomatidae) Complex and the Lizard <i>Leishmania</i> : Their Classification and Evidence for a Neotropical Origin of the <i>Leishmania-Endotrypanum</i> Clade. <i>Journal of Eukaryotic Microbiology</i> , 1997, 44, 511-517.	1.7	54
66	<i>Leishmania chagasi</i> : Genotypically Similar Parasites from Honduras Cause both Visceral and Cutaneous Leishmaniasis in Humans. <i>Experimental Parasitology</i> , 1997, 85, 264-273.	1.2	58
67	Comparison of the sex-pheromone components of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) from areas of visceral and atypical cutaneous leishmaniasis in Honduras and Costa Rica. <i>Annals of Tropical Medicine and Parasitology</i> , 1996, 90, 533-541.	1.6	33
68	<i>Leishmania herreri</i> (Kinetoplastida; Trypanosomatidae) is more closely related to <i>Endotrypanum</i> (Kinetoplastida; Trypanosomatidae) than to <i>Leishmania</i> . <i>Molecular and Biochemical Parasitology</i> , 1996, 80, 119-123.	1.1	29
69	<i>Leishmania</i> and <i>Sauroleishmania</i> : The Use of Random Amplified Polymorphic DNA for the Identification of Parasites from Vertebrates and Invertebrates. <i>Experimental Parasitology</i> , 1996, 83, 150-154.	1.2	32
70	Appraisal of Various Random Amplified Polymorphic DNA-Polymerase Chain Reaction Primers for <i>Leishmania</i> Identification. <i>American Journal of Tropical Medicine and Hygiene</i> , 1996, 55, 98-105.	1.4	46
71	Gene expression changes in mammalian hosts during schistosomiasis: a review. <i>AAS Open Research</i> , 0, 4, 54.	1.5	1
72	Candidate gene family-based and case-control studies of susceptibility to high <i>Schistosoma mansoni</i> worm burden in African children: a protocol. <i>AAS Open Research</i> , 0, 4, 36.	1.5	2