

Harry A Noyes

List of Publications by Year in descending order

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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	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
2	Do Cryptic Reservoirs Threaten Gambiense-Sleeping Sickness Elimination?. <i>Trends in Parasitology</i> , 2018, 34, 197-207.	3.3	139
3	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
4	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
5	APOL1 renal risk variants have contrasting resistance and susceptibility associations with African trypanosomiasis. <i>ELife</i> , 2017, 6, .	6.0	95
6	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
7	<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
8	<i>Leishmania donovani</i> and Cutaneous Leishmaniasis, Sri Lanka. <i>Emerging Infectious Diseases</i> , 2007, 13, 476-478.	4.3	86
9	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
10	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
11	Phylogeny of <i>Trypanosoma</i> (Megatrypanum) theileri 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
12	The Evolution of Trypanosomes Infecting Humans and Primates. <i>Memorias Do Instituto Oswaldo Cruz</i> , 1998, 93, 669-676.	1.6	60
13	<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
14	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
15	Genetic identification of two sibling species of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) that produce distinct male sex pheromones in Sobral, CearA; State, Brazil. <i>Molecular Ecology</i> , 2003, 12, 1879-1894.	3.9	55
16	<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
17	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
18	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

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19	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
20	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
21	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, 734-743.	1.4	50
22	Mechanisms Controlling Anaemia in <i>Trypanosoma congolense</i> Infected Mice. <i>PLoS ONE</i> , 2009, 4, e5170.	2.5	49
23	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
24	Host specificity of <i>Trypanosoma</i> (<i>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
25	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
26	A Gambian Infant with Fever and an Unexpected Blood Film. <i>PLoS Medicine</i> , 2006, 3, e355.	8.4	41
27	Gene expression profiling in a mouse model for African trypanosomiasis. <i>Genes and Immunity</i> , 2006, 7, 667-679.	4.1	35
28	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
29	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
30	<i>Leishmania</i> and <i>Saurolishmania</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
31	<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
32	Evidence for a neotropical origin of <i>Leishmania</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2000, 95, 575-578.	1.6	29
33	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
34	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
35	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
36	Variant antigen diversity in <i>Trypanosoma vivax</i> is not driven by recombination. <i>Nature Communications</i> , 2020, 11, 844.	12.8	22

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37	Candidate gene polymorphisms study between human African trypanosomiasis clinical phenotypes in Guinea. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005833.	3.0	21
38	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
39	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
40	Claudin 13, a Member of the Claudin Family Regulated in Mouse Stress Induced Erythropoiesis. <i>PLoS ONE</i> , 2010, 5, e12667.	2.5	18
41	<i>Leishmania</i> (<i>Sauroleishmania</i>): A Comment on Classification. <i>Parasitology Today</i> , 1998, 14, 167.	3.0	17
42	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
43	Novel SNP Discovery in African Buffalo, <i>Syncerus caffer</i> , Using High-Throughput Sequencing. <i>PLoS ONE</i> , 2012, 7, e48792.	2.5	15
44	Multiorgan Dysfunction Caused by Travel-associated African Trypanosomiasis. <i>Emerging Infectious Diseases</i> , 2012, 18, 287-289.	4.3	15
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	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
53	The Quality of Methods Reporting in Parasitology Experiments. <i>PLoS ONE</i> , 2014, 9, e101131.	2.5	12
54	The Genetics of Human Schistosomiasis Infection Intensity and Liver Disease: A Review. <i>Frontiers in Immunology</i> , 2021, 12, 613468.	4.8	11

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55	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” [International Journal for Parasitology 29 (2) (1999) 331–339]. International Journal for Parasitology, 2000, 30, 228.	3.1	10
56	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. BMC Genomics, 2010, 11, 361.	2.8	10
57	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. Parasitology, 2010, 137, 311-320.	1.5	8
58	Clinical Chemistry of Congenic Mice with Quantitative Trait Loci for Predicted Responses to <i>Trypanosoma congolense</i> Infection. Infection and Immunity, 2009, 77, 3948-3957.	2.2	7
59	Copy number variation in human genomes from three major ethno-linguistic groups in Africa. BMC Genomics, 2020, 21, 289.	2.8	7
60	Reply. Parasitology Today, 1998, 14, 335.	3.0	6
61	A Systematic Strategy for the Discovery of Candidate Genes Responsible for Phenotypic Variation. Methods in Molecular Biology, 2009, 573, 329-345.	0.9	6
62	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. Infection, Genetics and Evolution, 2019, 71, 108-115.	2.3	3
63	Unmapped exome reads implicate a role for Anelloviridae in childhood HIV-1 long-term non-progression. Npj Genomic Medicine, 2021, 6, 24.	3.8	3
64	A systematic strategy for the discovery of candidate genes responsible for phenotypic variation. BMC Bioinformatics, 2007, 8, .	2.6	2
65	A simple procedure for directly obtaining haplotype sequences of diploid genomes. BMC Genomics, 2015, 16, 642.	2.8	2
66	Association between IL1 gene polymorphism and human African trypanosomiasis in populations of sleeping sickness foci of southern Cameroon. PLoS Neglected Tropical Diseases, 2019, 13, e0007283.	3.0	2
67	Candidate gene family-based and case-control studies of susceptibility to high <i>Schistosoma mansoni</i> worm burden in African children: a protocol. AAS Open Research, 0, 4, 36.	1.5	2
68	Gene expression changes in mammalian hosts during schistosomiasis: a review. AAS Open Research, 0, 4, 54.	1.5	1
69	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. £140. Parasitology, 2007, 134, 2081-2082.	1.5	0
70	Evidence for genes controlling resistance to <i>Heligmosomoides bakeri</i> on mouse chromosome 1. Parasitology, 2015, 142, 566-575.	1.5	0
71	Candidate gene family-based and case-control studies of susceptibility to high <i>Schistosoma mansoni</i> worm burden in African children: a protocol. AAS Open Research, 2021, 4, 36.	1.5	0
72	SNPs in IL4 and IFNG show no protective associations with human African trypanosomiasis in the Democratic Republic of the Congo: a case-control study. AAS Open Research, 2020, 3, 35.	1.5	0