Katrin Kuhls

List of Publications by Year in descending order

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KATDIN KIIHIS

#	Article	IF	CITATIONS
1	A Historical Overview of the Classification, Evolution, and Dispersion of Leishmania Parasites and Sandflies. PLoS Neglected Tropical Diseases, 2016, 10, e0004349.	3.0	615
2	Evolutionary and geographical history of the Leishmania donovani complex with a revision of current taxonomy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9375-9380.	7.1	358
3	Leishmania infections: Molecular targets and diagnosis. Molecular Aspects of Medicine, 2017, 57, 1-29.	6.4	220
4	Comparative Microsatellite Typing of New World Leishmania infantum Reveals Low Heterogeneity among Populations and Its Recent Old World Origin. PLoS Neglected Tropical Diseases, 2011, 5, e1155.	3.0	154
5	Multilocus microsatellite typing (MLMT) reveals genetically isolated populations between and within the main endemic regions of visceral leishmaniasis. Microbes and Infection, 2007, 9, 334-343.	1.9	142
6	Molecular approaches for a better understanding of the epidemiology and population genetics of <i>Leishmania</i> . Parasitology, 2011, 138, 405-425.	1.5	142
7	Analysis of ribosomal DNA internal transcribed spacer sequences of the complex. Microbes and Infection, 2005, 7, 1224-1234.	1.9	118
8	Revision of <i>Trichoderma</i> sect. <i>Longibrachiatum</i> including related teleomorphs based on analysis of ribosomal DNA internal transcribed spacer sequences. Mycologia, 1997, 89, 442-460.	1.9	116
9	Multilocus Microsatellite Typing as a New Tool for Discrimination of Leishmania infantum MON-1 Strains. Journal of Clinical Microbiology, 2006, 44, 495-503.	3.9	98
10	Biogeography and phenotypic variation in Trichoderma sect. Longibrachiatum and associated Hypocrea species. Mycological Research, 1997, 101, 449-459.	2.5	95
11	Multilocus microsatellite typing (MLMT) reveals genetic homogeneity of Leishmania donovani strains in the Indian subcontinent. Infection, Genetics and Evolution, 2009, 9, 24-31.	2.3	81
12	Differentiation and Gene Flow among European Populations of Leishmania infantum MON-1. PLoS Neglected Tropical Diseases, 2008, 2, e261.	3.0	75
13	Population structure of Tunisian Leishmania infantum and evidence for the existence of hybrids and gene flow between genetically different populations. International Journal for Parasitology, 2009, 39, 801-811.	3.1	73
14	Comparison of molecular markers for strain typing of Leishmania infantum. Infection, Genetics and Evolution, 2006, 6, 440-446.	2.3	71
15	Inference of Population Structure of Leishmania donovani Strains Isolated from Different Ethiopian Visceral Leishmaniasis Endemic Areas. PLoS Neglected Tropical Diseases, 2010, 4, e889.	3.0	70
16	Leishmania major: Genetic heterogeneity of Iranian isolates by single-strand conformation polymorphism and sequence analysis of ribosomal DNA internal transcribed spacer. Acta Tropica, 2006, 98, 52-58.	2.0	64
17	Identification of geographically distributed sub-populations of Leishmania (Leishmania) majorby microsatellite analysis. BMC Evolutionary Biology, 2008, 8, 183.	3.2	60
18	Guns, germs and dogs: On the origin of Leishmania chagasi. Infection, Genetics and Evolution, 2011, 11, 1091-1095.	2.3	56

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19	Development of a Multilocus Microsatellite Typing Approach for Discriminating Strains of <i>Leishmania</i> (<i>Viannia</i>) Species. Journal of Clinical Microbiology, 2009, 47, 2818-2825.	3.9	50
20	Multilocus Microsatellite Typing (MLMT) of Strains from Turkey and Cyprus Reveals a Novel Monophyletic L. donovani Sensu Lato Group. PLoS Neglected Tropical Diseases, 2012, 6, e1507.	3.0	50
21	Epidemiological dynamics of antimonial resistance in Leishmania donovani: Genotyping reveals a polyclonal population structure among naturally-resistant clinical isolates from Nepal. Infection, Genetics and Evolution, 2007, 7, 206-212.	2.3	49
22	Genetic polymorphism of Algerian Leishmania infantum strains revealed by multilocus microsatellite analysis. Microbes and Infection, 2008, 10, 1309-1315.	1.9	49
23	The paraphyletic composition of Leishmania donovani zymodeme MON-37 revealed by multilocus microsatellite typing. Microbes and Infection, 2009, 11, 707-715.	1.9	44
24	PCR-fingerprinting used for comparison of ex type strains of Trichoderma species deposited in different culture collections. Microbiological Research, 1995, 150, 363-371.	5.3	40
25	Population Structure and Evidence for Both Clonality and Recombination among Brazilian Strains of the Subgenus Leishmania (Viannia). PLoS Neglected Tropical Diseases, 2013, 7, e2490.	3.0	40
26	Population genetics of Leishmania infantum in Israel and the Palestinian Authority through microsatellite analysis. Microbes and Infection, 2009, 11, 484-492.	1.9	27
27	Cellulase Formation by Species ofTrichodermasect.Longibrachiatumand ofHypocreaspp. with Anamorphs Referable toTrichodermasect.Longibrachiatum. Fungal Genetics and Biology, 1996, 20, 105-114.	2.1	25
28	Multilocus microsatellite typing shows three different genetic clusters of Leishmania major in Iran. Microbes and Infection, 2011, 13, 937-942.	1.9	25
29	Disseminated Cutaneous Leishmaniasis Resembling Post-Kala-Azar Dermal Leishmaniasis Caused by Leishmania donovani in Three Patients Co-Infected with Visceral Leishmaniasis and Human Immunodeficiency Virus/Acquired Immunodeficiency Syndrome in Ethiopia. American Journal of Tropical Medicine and Hygiene, 2011, 84, 906-912.	1.4	25
30	Heterogeneity of the internal transcribed spacer region in Leishmania tropica isolates from southern Iran. Experimental Parasitology, 2014, 144, 44-51.	1.2	25
31	PCR diagnosis of visceral leishmaniasis in an endemic region, Mymensingh district, Bangladesh. Tropical Medicine and International Health, 2009, 14, 499-503.	2.3	20
32	Phylogenetic structure of Leishmania tropica in the new endemic focus Birjand in East Iran in comparison to other Iranian endemic regions. Acta Tropica, 2016, 158, 68-76.	2.0	20
33	Atypical Lesions as a Sign of Cutaneous Dissemination of Visceral Leishmaniasis in a Human Immunodeficiency Virus–Positive Patient Simultaneously Infected by Two Viscerotropic Leishmania Species. American Journal of Tropical Medicine and Hygiene, 2011, 85, 55-59.	1.4	19
34	Identification of the agent causing visceral leishmaniasis in Uzbeki and Tajiki foci by analysing parasite DNA extracted from patients' Giemsa-stained tissue preparations. Parasitology, 2009, 136, 981-986.	1.5	17
35	A clinical isolate of <i>Leishmania donovani</i> with ITS1 sequence polymorphism as a cause of para-kala-azar dermal leishmaniasis in an Ethiopian human immunodeficiency virus-positive patient on highly active antiretroviral therapy. British Journal of Dermatology, 2010, 163, 870-874.	1.5	16
36	Multilocus genotyping reveals a polyphyletic pattern among naturally antimony-resistant Leishmania braziliensis isolates from Peru. Infection, Genetics and Evolution, 2011, 11, 1873-1880.	2.3	16

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37	Spatiotemporal and molecular epidemiology of cutaneous leishmaniasis in Libya. PLoS Neglected Tropical Diseases, 2017, 11, e0005873.	3.0	16
38	Genetic diversity evaluation on Portuguese Leishmania infantum strains by multilocus microsatellite typing. Infection, Genetics and Evolution, 2014, 26, 20-31.	2.3	15
39	A novel multilocus sequence typing scheme identifying genetic diversity amongst Leishmania donovani isolates from a genetically homogeneous population in the Indian subcontinent. International Journal for Parasitology, 2019, 49, 555-567.	3.1	15
40	Multilocus microsatellite typing revealed high genetic variability of Leishmania donovani strains isolated during and after a Kala-azar epidemic in Libo Kemkem district, Northwest Ethiopia. Microbes and Infection, 2011, 13, 595-601.	1.9	14
41	Leishmania donovani populations in Eastern Sudan: temporal structuring and a link between human and canine transmission. Parasites and Vectors, 2014, 7, 496.	2.5	14
42	A pilot study on fingerprinting Leishmania species from the Old World using Fourier transform infrared spectroscopy. Analytical and Bioanalytical Chemistry, 2017, 409, 6907-6923.	3.7	14
43	Genetic typing reveals monomorphism between antimony sensitive and resistant Leishmania donovani isolates from visceral leishmaniasis or post kala-azar dermal leishmaniasis cases in India. Parasitology Research, 2012, 111, 1559-1568.	1.6	10
44	Combined climate and regional mosquito habitat model based on machine learning. Ecological Modelling, 2021, 452, 109594.	2.5	10
45	Integrative Approach to Phlebotomus mascittii Grassi, 1908: First Record in Vienna with New Morphological and Molecular Insights. Pathogens, 2020, 9, 1032.	2.8	8
46	Epidemiological analysis of Leishmania tropica strains and giemsa-stained smears from Syrian and Turkish leishmaniasis patients using multilocus microsatellite typing (MLMT). PLoS Neglected Tropical Diseases, 2017, 11, e0005538.	3.0	6
47	Phylogenetic Studies. Methods in Molecular Biology, 2019, 1971, 9-68.	0.9	4
48	Microsatellite based molecular epidemiology of Leishmania infantum from re-emerging foci of visceral leishmaniasis in Armenia and pilot risk assessment by ecological niche modeling. PLoS Neglected Tropical Diseases, 2021, 15, e0009288.	3.0	4
49	Re-Emerging foci of visceral leishmaniasis in Armenia – first molecular diagnosis of clinical samples. Parasitology, 2019, 146, 857-864.	1.5	3
50	History of the E.I. Martsinovsky Institute of Medical Parasitology and Tropical Medicine: research on malaria and leishmaniasis. Historia, Ciencias, Saude - Manguinhos, 2020, 27, 1097-1124.	0.2	2