Amanda K Lukens

List of Publications by Year
in descending order

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36 papers	2,447 citations	236833 25 h-index	345118 36 g-index
39 all docs	39 docs citations	39 times ranked	3702 citing authors

#	Article	IF	Citations
1	A genome-wide map of diversity in Plasmodium falciparum. Nature Genetics, 2007, 39, 113-119.	9.4	320
2	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. Cell, 2015, 162, 738-750.	13.5	230
3	Diversity-oriented synthesis yields novel multistage antimalarial inhibitors. Nature, 2016, 538, 344-349.	13.7	214
4	Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. Science, 2018, 359, 191-199.	6.0	194
5	Genome-wide SNP genotyping highlights the role of natural selection in Plasmodium falciparumpopulation divergence. Genome Biology, 2008, 9, R171.	3.8	119
6	Sequence-based association and selection scans identify drug resistance loci in the Plasmodium falciparum malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13052-13057.	3.3	99
7	Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. Science, 2018, 362, .	6.0	99
8	A broad analysis of resistance development in the malaria parasite. Nature Communications, 2016, 7, 11901.	5.8	94
9	In Vivo Transcriptome ofPlasmodium falciparumReveals Overexpression of Transcripts That Encode Surface Proteins. Journal of Infectious Diseases, 2005, 191, 1196-1203.	1.9	92
10	Genetic Surveillance Detects Both Clonal and Epidemic Transmission of Malaria following Enhanced Intervention in Senegal. PLoS ONE, 2013, 8, e60780.	1.1	87
11	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	1.5	85
12	The cytoplasmic prolyl-tRNA synthetase of the malaria parasite is a dual-stage target of febrifugine and its analogs. Science Translational Medicine, 2015, 7, 288ra77.	5.8	82
13	Triaminopyrimidine is a fast-killing and long-acting antimalarial clinical candidate. Nature Communications, 2015, 6, 6715.	5.8	55
14	Harnessing evolutionary fitness in Plasmodium falciparum for drug discovery and suppressing resistance. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 799-804.	3.3	54
15	Diversity-Oriented Synthesis Yields a Novel Lead for the Treatment of Malaria. ACS Medicinal Chemistry Letters, 2012, 3, 112-117.	1.3	52
16	MalDA, Accelerating Malaria Drug Discovery. Trends in Parasitology, 2021, 37, 493-507.	1.5	51
17	SNP Genotyping Identifies New Signatures of Selection in a Deep Sample of West African Plasmodium falciparum Malaria Parasites. Molecular Biology and Evolution, 2012, 29, 3249-3253.	3.5	41
18	New paradigms for understanding and step changes in treating active and chronic, persistent apicomplexan infections. Scientific Reports, 2016, 6, 29179.	1.6	40

#	Article	IF	Citations
19	Chemogenomics identifies acetyl-coenzyme A synthetase as a target for malaria treatment and prevention. Cell Chemical Biology, 2022, 29, 191-201.e8.	2.5	39
20	Prioritization of Molecular Targets for Antimalarial Drug Discovery. ACS Infectious Diseases, 2021, 7, 2764-2776.	1.8	35
21	Plasmodium falciparum Cyclic Amine Resistance Locus (PfCARL), a Resistance Mechanism for Two Distinct Compound Classes. ACS Infectious Diseases, 2016, 2, 816-826.	1.8	34
22	Diversity-Oriented Synthesis-Facilitated Medicinal Chemistry: Toward the Development of Novel Antimalarial Agents. Journal of Medicinal Chemistry, 2014, 57, 8496-8502.	2.9	33
23	Exploring the 3-piperidin-4-yl-1H-indole scaffold as a novel antimalarial chemotype. European Journal of Medicinal Chemistry, 2015, 102, 320-333.	2.6	31
24	In vitro selection predicts malaria parasite resistance to dihydroorotate dehydrogenase inhibitors in a mouse infection model. Science Translational Medicine, 2019, 11, .	5.8	30
25	Intrinsic susceptibility of mouse trophoblasts to natural killer cell-mediated attack in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16940-16945.	3.3	29
26	Diversity-Oriented Synthesis Probe TargetsPlasmodium falciparumCytochrome b Ubiquinone Reduction Site and Synergizes With Oxidation Site Inhibitors. Journal of Infectious Diseases, 2015, 211, 1097-1103.	1.9	29
27	Quantitative Proteomic Profiling Reveals Novel Plasmodium falciparum Surface Antigens and Possible Vaccine Candidates. Molecular and Cellular Proteomics, 2018, 17, 43-60.	2.5	29
28	Polymorphism in dhfr/dhps genes, parasite density and ex vivo response to pyrimethamine in Plasmodium falciparum malaria parasites in Thies, Senegal. International Journal for Parasitology: Drugs and Drug Resistance, 2013, 3, 135-142.	1.4	27
29	Aminoazabenzimidazoles, a Novel Class of Orally Active Antimalarial Agents. Journal of Medicinal Chemistry, 2014, 57, 5702-5713.	2.9	24
30	Probing the Azaaurone Scaffold against the Hepatic and Erythrocytic Stages of Malaria Parasites. ChemMedChem, 2016, 11, 2194-2204.	1.6	23
31	Genome-Wide Association Studies of Drug-Resistance Determinants. Trends in Parasitology, 2017, 33, 214-230.	1.5	16
32	Intramolecular Diazaâ€Dielsâ€“Alder Protocol: A New Diastereoselective and Modular Oneâ€Step Synthesis of Constrained Polycyclic Frameworks. Chemistry - A European Journal, 2017, 23, 4137-4148.	1.7	15
33	Identification of Collateral Sensitivity to Dihydroorotate Dehydrogenase Inhibitors in Plasmodium falciparum. ACS Infectious Diseases, 2018, 4, 508-515.	1.8	15
34	The Plasmodium falciparum ABC transporter ABCI3 confers parasite strain-dependent pleiotropic antimalarial drug resistance. Cell Chemical Biology, 2022, 29, 824-839.e6.	2.5	14
35	Adaptive laboratory evolution in S. cerevisiae highlights role of transcription factors in fungal xenobiotic resistance. Communications Biology, 2022, 5, 128.	2.0	8
36	The Adaptive Proline Response in P. falciparum Is Independent of PfeIK1 and eIF2Î± Signaling. ACS Infectious Diseases, 2019, 5, 515-520.	1.8	5