Roger C Wiegand

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10427628/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A genome-wide map of diversity in Plasmodium falciparum. Nature Genetics, 2007, 39, 113-119.	21.4	320
2	A general SNP-based molecular barcode for Plasmodium falciparum identification and tracking. Malaria Journal, 2008, 7, 223.	2.3	213
3	Uptake of homologous single-stranded fragments by superhelical DNA. Journal of Molecular Biology, 1977, 116, 783-803.	4.2	143
4	Uptake of homologous single-stranded fragments by superhelical DNA. Journal of Molecular Biology, 1977, 116, 825-839.	4.2	120
5	Genome-wide SNP genotyping highlights the role of natural selection in Plasmodium falciparumpopulation divergence. Genome Biology, 2008, 9, R171.	8.8	119
6	Sequence-based association and selection scans identify drug resistance loci in the <i>Plasmodium falciparum</i> malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13052-13057.	7.1	99
7	Structural analysis of a maize gene coding for glutathione-S-transferase involved in herbicide detoxification. Plant Molecular Biology, 1986, 6, 203-211.	3.9	88
8	Human guanylin: cDNA isolation, structure, and activity. FEBS Letters, 1992, 311, 150-154.	2.8	85
9	Identification and Functional Validation of the Novel Antimalarial Resistance Locus PF10_0355 in Plasmodium falciparum. PLoS Genetics, 2011, 7, e1001383.	3.5	85
10	Messenger RNA encoding a glutathione-S-transferase responsible for herbicide tolerance in maize is induced in response to safener treatment. Plant Molecular Biology, 1986, 7, 235-243.	3.9	84
11	Rat guanylin cDNA: Characterization of the precursor of an endogenous activator of intestinal guanylate cyclase. Biochemical and Biophysical Research Communications, 1992, 185, 812-817.	2.1	84
12	Genomic Sequencing of Plasmodium falciparum Malaria Parasites from Senegal Reveals the Demographic History of the Population. Molecular Biology and Evolution, 2012, 29, 3427-3439.	8.9	58
13	Uptake of homologous single-stranded fragments by superhelical DNA. Journal of Molecular Biology, 1977, 116, 805-824.	4.2	54
14	In Vitro Resistance Selections for Plasmodium falciparum Dihydroorotate Dehydrogenase Inhibitors Give Mutants with Multiple Point Mutations in the Drug-binding Site and Altered Growth. Journal of Biological Chemistry, 2014, 289, 17980-17995.	3.4	54
15	Harnessing evolutionary fitness in <i>Plasmodium falciparum</i> for drug discovery and suppressing resistance. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 799-804.	7.1	54
16	Diversity-Oriented Synthesis Yields a Novel Lead for the Treatment of Malaria. ACS Medicinal Chemistry Letters, 2012, 3, 112-117.	2.8	52
17	Responses to Bacteria, Virus, and Malaria Distinguish the Etiology of Pediatric Clinical Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 448-459.	5.6	42
18	Diversity-Oriented Synthesis-Facilitated Medicinal Chemistry: Toward the Development of Novel Antimalarial Agents. Journal of Medicinal Chemistry, 2014, 57, 8496-8502.	6.4	33

#	Article	IF	CITATIONS
19	Diversity-Oriented Synthesis Probe TargetsPlasmodium falciparumCytochrome b Ubiquinone Reduction Site and Synergizes With Oxidation Site Inhibitors. Journal of Infectious Diseases, 2015, 211, 1097-1103.	4.0	29
20	Human cerebral malaria and Plasmodium falciparum genotypes in Malawi. Malaria Journal, 2012, 11, 35.	2.3	24
21	Transcriptional categorization of the etiology of pneumonia syndrome in pediatric patients in malaria endemic areas. Journal of Infectious Diseases, 2017, 215, jiw531.	4.0	8
22	Seeking diagnostic and prognostic biomarkers for childhood bacterial pneumonia in sub-Saharan Africa: study protocol for an observational study. BMJ Open, 2021, 11, e046590.	1.9	0