Kathryn E Tiedje

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An accurate method for identifying recent recombinants from unaligned sequences. Bioinformatics, 2022, 38, 1823-1829.	4.1	3
2	Age-specific patterns of DBLα var diversity can explain why residents of high malaria transmission areas remain susceptible to Plasmodium falciparum blood stage infection throughout life. International Journal for Parasitology, 2022, 52, 721-731.	3.1	15
3	Indoor residual spraying with a non-pyrethroid insecticide reduces the reservoir of Plasmodium falciparum in a high-transmission area in northern Ghana. PLOS Global Public Health, 2022, 2, e0000285.	1.6	11
4	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of Plasmodium falciparum within and between continents. PLoS Genetics, 2021, 17, e1009269.	3.5	20
5	Frequency-Dependent Competition Between Strains Imparts Persistence to Perturbations in a Model of Plasmodium falciparum Malaria Transmission. Frontiers in Ecology and Evolution, 2021, 9, .	2.2	13
6	The impact of indoor residual spraying on <i>Plasmodium falciparum</i> microsatellite variation in an area of high seasonal malaria transmission in Ghana, West Africa. Molecular Ecology, 2021, 30, 3974-3992.	3.9	6
7	Evolution of Antimalarial Drug Resistance Markers in the Reservoir of <i>Plasmodium falciparum</i> Infections in the Upper East Region of Ghana. Journal of Infectious Diseases, 2020, 222, 1692-1701.	4.0	8
8	Competition for hosts modulates vast antigenic diversity to generate persistent strain structure in Plasmodium falciparum. PLoS Biology, 2019, 17, e3000336.	5.6	40
9	Signatures of competition and strain structure within the major bloodâ€stage antigen of <i>Plasmodium falciparum</i> in a local community in Ghana. Ecology and Evolution, 2018, 8, 3574-3588.	1.9	10
10	Networks of genetic similarity reveal non-neutral processes shape strain structure in Plasmodium falciparum. Nature Communications, 2018, 9, 1817.	12.8	39
11	Evidence of strain structure in <i>Plasmodium falciparum var</i> gene repertoires in children from Gabon, West Africa. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4103-E4111.	7.1	53
12	Population genomics of virulence genes of Plasmodium falciparum in clinical isolates from Uganda. Scientific Reports, 2017, 7, 11810.	3.3	31
13	Evolutionary structure of <i>Plasmodium falciparum</i> major variant surface antigen genes in South America: Implications for epidemic transmission and surveillance. Ecology and Evolution, 2017, 7, 9376-9390.	1.9	16
14	Seasonal Variation in the Epidemiology of Asymptomatic Plasmodium falciparum Infections across Two Catchment Areas in Bongo District, Ghana. American Journal of Tropical Medicine and Hygiene, 2017, 97, 199-212.	1.4	38
15	Lack of Geospatial Population Structure Yet Significant Linkage Disequilibrium in the Reservoir of Plasmodium falciparum in Bongo District, Ghana. American Journal of Tropical Medicine and Hygiene, 2017, 97, 1180-1189.	1.4	12