Richard D Pearson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Malaria protection due to sickle haemoglobin depends on parasite genotype. Nature, 2022, 602, 106-111.	27.8	36
2	Geographical distribution and genetic diversity of Plasmodium vivax reticulocyte binding protein 1a correlates with patient antigenicity. PLoS Neglected Tropical Diseases, 2022, 16, e0010492.	3.0	2
3	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	97
4	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	1.8	51
5	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. ELife, 2021, 10, .	6.0	53
6	Whole genome sequencing of Plasmodium vivax isolates reveals frequent sequence and structural polymorphisms in erythrocyte binding genes. PLoS Neglected Tropical Diseases, 2020, 14, e0008234.	3.0	25
7	Intrinsic multiplication rate variation and plasticity of human blood stage malaria parasites. Communications Biology, 2020, 3, 624.	4.4	16
8	Transmission of Artemisinin-Resistant Malaria Parasites to Mosquitoes under Antimalarial Drug Pressure. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	29
9	Triple artemisinin-based combination therapies versus artemisinin-based combination therapies for uncomplicated Plasmodium falciparum malaria: a multicentre, open-label, randomised clinical trial. Lancet, The, 2020, 395, 1345-1360.	13.7	182
10	Genetic diversity and neutral selection in Plasmodium vivax erythrocyte binding protein correlates with patient antigenicity. PLoS Neglected Tropical Diseases, 2020, 14, e0008202.	3.0	5
11	Emergence of artemisinin-resistant Plasmodium falciparum with kelch13 C580Y mutations on the island of New Guinea. PLoS Pathogens, 2020, 16, e1009133.	4.7	81
12	Title is missing!. , 2020, 14, e0008234.		0
13	Title is missing!. , 2020, 14, e0008234.		0
14	Title is missing!. , 2020, 14, e0008234.		0
15	Title is missing!. , 2020, 14, e0008234.		0
16	Title is missing!. , 2020, 16, e1009133.		0
17	Title is missing!. , 2020, 16, e1009133.		0

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19	Title is missing!. , 2020, 16, e1009133.		0
20	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. Lancet Infectious Diseases, The, 2019, 19, 943-951.	9.1	219
21	Determinants of dihydroartemisinin-piperaquine treatment failure in Plasmodium falciparum malaria in Cambodia, Thailand, and Vietnam: a prospective clinical, pharmacological, and genetic study. Lancet Infectious Diseases, The, 2019, 19, 952-961.	9.1	252
22	Frequent expansion of Plasmodium vivax Duffy Binding Protein in Ethiopia and its epidemiological significance. PLoS Neglected Tropical Diseases, 2019, 13, e0007222.	3.0	25
23	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. Journal of Infectious Diseases, 2019, 220, 1738-1749.	4.0	50
24	The origins and relatedness structure of mixed infections vary with local prevalence of P. falciparum malaria. ELife, 2019, 8, .	6.0	52
25	Origins of the current outbreak of multidrug-resistant malaria in southeast Asia: a retrospective genetic study. Lancet Infectious Diseases, The, 2018, 18, 337-345.	9.1	161
26	Transferrin receptor 1 is a reticulocyte-specific receptor for <i>Plasmodium vivax</i> . Science, 2018, 359, 48-55.	12.6	158
27	Cryo-EM structure of an essential Plasmodium vivax invasion complex. Nature, 2018, 559, 135-139.	27.8	43
28	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. Nature Communications, 2018, 9, 2585.	12.8	59
29	Long read assemblies of geographically dispersed Plasmodium falciparum isolates reveal highly structured subtelomeres. Wellcome Open Research, 2018, 3, 52.	1.8	114
30	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
31	Genetic markers associated with dihydroartemisinin–piperaquine failure in Plasmodium falciparum malaria in Cambodia: a genotype–phenotype association study. Lancet Infectious Diseases, The, 2017, 17, 164-173.	9.1	301
32	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
33	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
34	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	5.5	180
35	Genomic Analysis Reveals a Common Breakpoint in Amplifications of the <i>Plasmodium vivax</i> Multidrug Resistance 1 Locus in Thailand. Journal of Infectious Diseases, 2016, 214, 1235-1242.	4.0	29
36	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	21.4	169

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37	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. American Journal of Human Genetics, 2016, 98, 1092-1100.	6.2	39
38	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	2.9	8
39	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. Human Molecular Genetics, 2014, 23, 3316-3326.	2.9	37
40	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	12.8	72
41	The South Asian Genome. PLoS ONE, 2014, 9, e102645.	2.5	43
42	Spatio-temporal distribution of antimalarial drug resistant gene mutations in a Plasmodium falciparum parasite population from Kilifi, Kenya: A 25-year retrospective study. Wellcome Open Research, 0, 7, 45.	1.8	8
43	An open dataset of Plasmodium vivax genome variation in 1,895 worldwide samples. Wellcome Open Research, 0, 7, 136.	1.8	16