

Richard D Pearson

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,700
citations

257450

24
h-index

395702

33
g-index

54
all docs

54
docs citations

54
times ranked

6964
citing authors

#	ARTICLE	IF	CITATIONS
1	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
2	Genetic markers associated with dihydroartemisinin-piperazine failure in <i>Plasmodium falciparum</i> malaria in Cambodia: a genotype-phenotype association study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 164-173.	9.1	301
3	Determinants of dihydroartemisinin-piperazine treatment failure in <i>Plasmodium falciparum</i> malaria in Cambodia, Thailand, and Vietnam: a prospective clinical, pharmacological, and genetic study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 952-961.	9.1	252
4	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 943-951.	9.1	219
5	Triple artemisinin-based combination therapies versus artemisinin-based combination therapies for uncomplicated <i>Plasmodium falciparum</i> malaria: a multicentre, open-label, randomised clinical trial. <i>Lancet</i> , The, 2020, 395, 1345-1360.	13.7	182
6	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2016, 26, 1288-1299.	5.5	180
7	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	21.4	169
8	Origins of the current outbreak of multidrug-resistant malaria in southeast Asia: a retrospective genetic study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 337-345.	9.1	161
9	Transferrin receptor 1 is a reticulocyte-specific receptor for <i>Plasmodium vivax</i> . <i>Science</i> , 2018, 359, 48-55.	12.6	158
10	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018, 3, 52.	1.8	114
11	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	97
12	Emergence of artemisinin-resistant <i>Plasmodium falciparum</i> with kelch13 C580Y mutations on the island of New Guinea. <i>PLoS Pathogens</i> , 2020, 16, e1009133.	4.7	81
13	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014, 5, 4204.	12.8	72
14	Genomic analysis of a pre-elimination Malaysian <i>Plasmodium vivax</i> population reveals selective pressures and changing transmission dynamics. <i>Nature Communications</i> , 2018, 9, 2585.	12.8	59
15	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. <i>ELife</i> , 2021, 10, .	6.0	53
16	The origins and relatedness structure of mixed infections vary with local prevalence of <i>P. falciparum</i> malaria. <i>ELife</i> , 2019, 8, .	6.0	52
17	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	1.8	51
18	Genomic Analysis of <i>Plasmodium vivax</i> in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. <i>Journal of Infectious Diseases</i> , 2019, 220, 1738-1749.	4.0	50

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19	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
20	Cryo-EM structure of an essential <i>Plasmodium vivax</i> invasion complex. <i>Nature</i> , 2018, 559, 135-139.	27.8	43
21	The South Asian Genome. <i>PLoS ONE</i> , 2014, 9, e102645.	2.5	43
22	Polymorphism in a lincRNA Associates with a Doubled Risk of Pneumococcal Bacteremia in Kenyan Children. <i>American Journal of Human Genetics</i> , 2016, 98, 1092-1100.	6.2	39
23	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. <i>Human Molecular Genetics</i> , 2014, 23, 3316-3326.	2.9	37
24	Malaria protection due to sickle haemoglobin depends on parasite genotype. <i>Nature</i> , 2022, 602, 106-111.	27.8	36
25	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
26	Genomic Analysis Reveals a Common Breakpoint in Amplifications of the <i>Plasmodium vivax</i> Multidrug Resistance 1 Locus in Thailand. <i>Journal of Infectious Diseases</i> , 2016, 214, 1235-1242.	4.0	29
27	Transmission of Artemisinin-Resistant Malaria Parasites to Mosquitoes under Antimalarial Drug Pressure. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	3.2	29
28	Frequent expansion of <i>Plasmodium vivax</i> Duffy Binding Protein in Ethiopia and its epidemiological significance. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007222.	3.0	25
29	Whole genome sequencing of <i>Plasmodium vivax</i> isolates reveals frequent sequence and structural polymorphisms in erythrocyte binding genes. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008234.	3.0	25
30	Intrinsic multiplication rate variation and plasticity of human blood stage malaria parasites. <i>Communications Biology</i> , 2020, 3, 624.	4.4	16
31	An open dataset of <i>Plasmodium vivax</i> genome variation in 1,895 worldwide samples. <i>Wellcome Open Research</i> , 0, 7, 136.	1.8	16
32	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. <i>Human Molecular Genetics</i> , 2015, 24, 1504-1512.	2.9	8
33	Spatio-temporal distribution of antimalarial drug resistant gene mutations in a <i>Plasmodium falciparum</i> parasite population from Kilifi, Kenya: A 25-year retrospective study. <i>Wellcome Open Research</i> , 0, 7, 45.	1.8	8
34	Genetic diversity and neutral selection in <i>Plasmodium vivax</i> erythrocyte binding protein correlates with patient antigenicity. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008202.	3.0	5
35	Geographical distribution and genetic diversity of <i>Plasmodium vivax</i> reticulocyte binding protein 1a correlates with patient antigenicity. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010492.	3.0	2
36	Title is missing!. , 2020, 14, e0008234.		0

#	ARTICLE	IF	CITATIONS
37	Title is missing!. , 2020, 14, e0008234.		0
38	Title is missing!. , 2020, 14, e0008234.		0
39	Title is missing!. , 2020, 14, e0008234.		0
40	Title is missing!. , 2020, 16, e1009133.		0
41	Title is missing!. , 2020, 16, e1009133.		0
42	Title is missing!. , 2020, 16, e1009133.		0
43	Title is missing!. , 2020, 16, e1009133.		0