

Dominic P Kwiatkowski

List of Publications by Year in descending order

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Version: 2024-02-01

142
papers

18,498
citations

29994

54
h-index

16605

123
g-index

170
all docs

170
docs citations

170
times ranked

19763
citing authors

#	ARTICLE	IF	CITATIONS
1	Detecting recent positive selection in the human genome from haplotype structure. <i>Nature</i> , 2002, 419, 832-837.	13.7	1,881
2	Spread of Artemisinin Resistance in <i>Plasmodium falciparum</i> Malaria. <i>New England Journal of Medicine</i> , 2014, 371, 411-423.	13.9	1,753
3	Common West African HLA antigens are associated with protection from severe malaria. <i>Nature</i> , 1991, 352, 595-600.	13.7	1,494
4	Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. <i>Nature</i> , 2021, 593, 266-269.	13.7	1,001
5	Genetic architecture of artemisinin-resistant <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2015, 47, 226-234.	9.4	515
6	The African Genome Variation Project shapes medical genetics in Africa. <i>Nature</i> , 2015, 517, 327-332.	13.7	473
7	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	13.7	450
8	A transcriptional switch underlies commitment to sexual development in malaria parasites. <i>Nature</i> , 2014, 507, 248-252.	13.7	430
9	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
10	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	2.9	375
11	Independent Emergence of Artemisinin Resistance Mutations Among <i>Plasmodium falciparum</i> in Southeast Asia. <i>Journal of Infectious Diseases</i> , 2015, 211, 670-679.	1.9	368
12	Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. <i>Science</i> , 2015, 347, 431-435.	6.0	362
13	Natural selection and infectious disease in human populations. <i>Nature Reviews Genetics</i> , 2014, 15, 379-393.	7.7	353
14	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
15	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. <i>Nature Genetics</i> , 2010, 42, 739-741.	9.4	332
16	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.	4.6	301
17	Association of Malaria Parasite Population Structure, HLA, and Immunological Antagonism. <i>Science</i> , 1998, 279, 1173-1177.	6.0	278
18	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.	4.6	252

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19	Genetic loci associated with delayed clearance of <i>Plasmodium falciparum</i> following artemisinin treatment in Southeast Asia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 240-245.	3.3	242
20	Severe Malarial Anemia and Cerebral Malaria Are Associated with Different Tumor Necrosis Factor Promoter Alleles. Journal of Infectious Diseases, 1999, 179, 287-290.	1.9	231
21	Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. Lancet Infectious Diseases, The, 2019, 19, 943-951.	4.6	219
22	K13-Propeller Polymorphisms in Plasmodium falciparum Parasites From Sub-Saharan Africa. Journal of Infectious Diseases, 2015, 211, 1352-5.	1.9	203
23	A novel locus of resistance to severe malaria in a region of ancient balancing selection. Nature, 2015, 526, 253-257.	13.7	182
24	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.	6.3	182
25	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . Genome Research, 2016, 26, 1288-1299.	2.4	180
26	Generation of Antigenic Diversity in Plasmodium falciparum by Structured Rearrangement of Var Genes During Mitosis. PLoS Genetics, 2014, 10, e1004812.	1.5	171
27	Genomic analysis of local variation and recent evolution in Plasmodium vivax. Nature Genetics, 2016, 48, 959-964.	9.4	169
28	Population Genomic Scan for Candidate Signatures of Balancing Selection to Guide Antigen Characterization in Malaria Parasites. PLoS Genetics, 2012, 8, e1002992.	1.5	167
29	Origins of the current outbreak of multidrug-resistant malaria in southeast Asia: a retrospective genetic study. Lancet Infectious Diseases, The, 2018, 18, 337-345.	4.6	161
30	Adaptive introgression between Anopheles sibling species eliminates a major genomic island but not reproductive isolation. Nature Communications, 2014, 5, 4248.	5.8	143
31	Resistance to malaria through structural variation of red blood cell invasion receptors. Science, 2017, 356, .	6.0	135
32	Whole genome sequencing of Plasmodium falciparum from dried blood spots using selective whole genome amplification. Malaria Journal, 2016, 15, 597.	0.8	129
33	Admixture into and within sub-Saharan Africa. ELife, 2016, 5, .	2.8	120
34	Enhancing Blockade of Plasmodium falciparum Erythrocyte Invasion: Assessing Combinations of Antibodies against PfRH5 and Other Merozoite Antigens. PLoS Pathogens, 2012, 8, e1002991.	2.1	114
35	Genome-Wide Analysis of Selection on the Malaria Parasite Plasmodium falciparum in West African Populations of Differing Infection Endemicity. Molecular Biology and Evolution, 2014, 31, 1490-1499.	3.5	107
36	Major subpopulations of <i>Plasmodium falciparum</i> in sub-Saharan Africa. Science, 2019, 365, 813-816.	6.0	105

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37	Inherited Variability of Tumor Necrosis Factor Production and Susceptibility to Infectious Disease. <i>Proceedings of the Association of American Physicians</i> , 1999, 111, 290-298.	2.1	105
38	Characterization of Within-Host <i>Plasmodium falciparum</i> Diversity Using Next-Generation Sequence Data. <i>PLoS ONE</i> , 2012, 7, e32891.	1.1	102
39	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	0.9	97
40	Molecular epidemiology of resistance to antimalarial drugs in the Greater Mekong subregion: an observational study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1470-1480.	4.6	94
41	THE REAL McCOIL: A method for the concurrent estimation of the complexity of infection and SNP allele frequency for malaria parasites. <i>PLoS Computational Biology</i> , 2017, 13, e1005348.	1.5	93
42	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> ,the, 2018, 5, e333-e345.	2.2	90
43	Extreme mutation bias and high AT content in <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2017, 45, gkw1259.	6.5	89
44	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.	2.1	81
45	Genomic reconstruction of the SARS-CoV-2 epidemic in England. <i>Nature</i> , 2021, 600, 506-511.	13.7	80
46	Using CF11 cellulose columns to inexpensively and effectively remove human DNA from <i>Plasmodium falciparum</i> -infected whole blood samples. <i>Malaria Journal</i> , 2012, 11, 41.	0.8	79
47	Whole-genome sequencing reveals high complexity of copy number variation at insecticide resistance loci in malaria mosquitoes. <i>Genome Research</i> , 2019, 29, 1250-1261.	2.4	79
48	Mapping imported malaria in Bangladesh using parasite genetic and human mobility data. <i>ELife</i> , 2019, 8, .	2.8	78
49	Genome-wide screen identifies new candidate genes associated with artemisinin susceptibility in <i>Plasmodium falciparum</i> in Kenya. <i>Scientific Reports</i> , 2013, 3, 3318.	1.6	75
50	Glucose-6-phosphate dehydrogenase deficiency and the risk of malaria and other diseases in children in Kenya: a case-control and a cohort study. <i>Lancet Haematology</i> ,the, 2015, 2, e437-e444.	2.2	74
51	Ethical Data Release in Genome-Wide Association Studies in Developing Countries. <i>PLoS Medicine</i> , 2009, 6, e1000143.	3.9	68
52	An Effective Method to Purify <i>Plasmodium falciparum</i> DNA Directly from Clinical Blood Samples for Whole Genome High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e22213.	1.1	68
53	Early cytokine induction by <i>Plasmodium falciparum</i> is not a classical endotoxin-like process. <i>European Journal of Immunology</i> , 1999, 29, 2636-2644.	1.6	65
54	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017, 6, .	2.8	64

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55	Evolutionary analysis of the most polymorphic gene family in falciparum malaria. Wellcome Open Research, 2019, 4, 193.	0.9	64
56	Population Genetic Analysis of Plasmodium falciparum Parasites Using a Customized Illumina GoldenGate Genotyping Assay. PLoS ONE, 2011, 6, e20251.	1.1	63
57	Association of hepatitis B surface antigen carriage with severe malaria in Gambian children. Nature Medicine, 1995, 1, 374-375.	15.2	62
58	Whole-Genome Scans Provide Evidence of Adaptive Evolution in Malawian Plasmodium falciparum Isolates. Journal of Infectious Diseases, 2014, 210, 1991-2000.	1.9	62
59	Culture adaptation of malaria parasites selects for convergent loss-of-function mutants. Scientific Reports, 2017, 7, 41303.	1.6	62
60	Seasonal Childhood Anaemia in West Africa Is Associated with the Haptoglobin 2-2 Genotype. PLoS Medicine, 2006, 3, e172.	3.9	60
61	Genomic analysis of a pre-elimination Malaysian Plasmodium vivax population reveals selective pressures and changing transmission dynamics. Nature Communications, 2018, 9, 2585.	5.8	59
62	Data sharing and intellectual property in a genomic epidemiology network: policies for large-scale research collaboration. Bulletin of the World Health Organization, 2006, 84, 382-387.	1.5	58
63	Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. ELife, 2021, 10, .	2.8	53
64	The origins and relatedness structure of mixed infections vary with local prevalence of P. falciparum malaria. ELife, 2019, 8, .	2.8	52
65	An open dataset of Plasmodium falciparum genome variation in 7,000 worldwide samples. Wellcome Open Research, 2021, 6, 42.	0.9	51
66	Clinical Features of Severe Malaria Associated with Death: A 13-Year Observational Study in The Gambia. PLoS ONE, 2012, 7, e45645.	1.1	50
67	Discovery and Validation of Biomarkers to Guide Clinical Management of Pneumonia in African Children. Clinical Infectious Diseases, 2014, 58, 1707-1715.	2.9	50
68	Genomic Analysis of Plasmodium vivax in Southern Ethiopia Reveals Selective Pressures in Multiple Parasite Mechanisms. Journal of Infectious Diseases, 2019, 220, 1738-1749.	1.9	50
69	Changes in Malaria Parasite Drug Resistance in an Endemic Population Over a 25-Year Period With Resulting Genomic Evidence of Selection. Journal of Infectious Diseases, 2014, 209, 1126-1135.	1.9	49
70	Independent Origin and Global Distribution of Distinct Plasmodium vivax Duffy Binding Protein Gene Duplications. PLoS Neglected Tropical Diseases, 2016, 10, e0005091.	1.3	48
71	Drug-Resistant Genotypes and Multi-Clonality in Plasmodium falciparum Analysed by Direct Genome Sequencing from Peripheral Blood of Malaria Patients. PLoS ONE, 2011, 6, e23204.	1.1	41
72	The origins of malaria artemisinin resistance defined by a genetic and transcriptomic background. Nature Communications, 2018, 9, 5158.	5.8	41

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73	A high throughput multi-locus insecticide resistance marker panel for tracking resistance emergence and spread in <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2019, 9, 13335.	1.6	41
74	Multi-population genomic analysis of malaria parasites indicates local selection and differentiation at the <i>gdv1</i> locus regulating sexual development. <i>Scientific Reports</i> , 2018, 8, 15763.	1.6	40
75	Monitoring parasite diversity for malaria elimination in sub-Saharan Africa. <i>Science</i> , 2014, 345, 1297-1298.	6.0	39
76	Malaria protection due to sickle haemoglobin depends on parasite genotype. <i>Nature</i> , 2022, 602, 106-111.	13.7	36
77	Malaria is a cause of iron deficiency in African children. <i>Nature Medicine</i> , 2021, 27, 653-658.	15.2	35
78	Comparison of genomic signatures of selection on <i>Plasmodium falciparum</i> between different regions of a country with high malaria endemicity. <i>BMC Genomics</i> , 2015, 16, 527.	1.2	34
79	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the <i>Plasmodium falciparum</i> population in Malawi. <i>Malaria Journal</i> , 2016, 15, 575.	0.8	34
80	Consistent signatures of selection from genomic analysis of pairs of temporal and spatial <i>Plasmodium falciparum</i> populations from The Gambia. <i>Scientific Reports</i> , 2018, 8, 9687.	1.6	33
81	Resistance to pirimiphos-methyl in West African <i>Anopheles</i> is spreading via duplication and introgression of the <i>Ace1</i> locus. <i>PLoS Genetics</i> , 2021, 17, e1009253.	1.5	33
82	Population genetic structure and adaptation of malaria parasites on the edge of endemic distribution. <i>Molecular Ecology</i> , 2017, 26, 2880-2894.	2.0	32
83	Molecular markers for artemisinin and partner drug resistance in natural <i>Plasmodium falciparum</i> populations following increased insecticide treated net coverage along the slope of mount Cameroon: cross-sectional study. <i>Infectious Diseases of Poverty</i> , 2017, 6, 136.	1.5	32
84	Evolution of the Insecticide Target <i>Rdl</i> in African <i>Anopheles</i> Is Driven by Interspecific and Interkaryotypic Introgression. <i>Molecular Biology and Evolution</i> , 2020, 37, 2900-2917.	3.5	31
85	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.	1.9	29
86	Massive introgression drives species radiation at the range limit of <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2017, 7, 46451.	1.6	28
87	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	1.5	27
88	Binding of <i>Plasmodium falciparum</i> Merozoite Surface Proteins DBLMSP and DBLMSP2 to Human Immunoglobulin M Is Conserved among Broadly Diverged Sequence Variants. <i>Journal of Biological Chemistry</i> , 2016, 291, 14285-14299.	1.6	27
89	Micro-epidemiological structuring of <i>Plasmodium falciparum</i> parasite populations in regions with varying transmission intensities in Africa. <i>Wellcome Open Research</i> , 2017, 2, 10.	0.9	27
90	A Genome Wide Association Study of <i>Plasmodium falciparum</i> Susceptibility to 22 Antimalarial Drugs in Kenya. <i>PLoS ONE</i> , 2014, 9, e96486.	1.1	27

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91	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	5.8	27
92	Effective Preparation of <i>Plasmodium vivax</i> Field Isolates for High-Throughput Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e53160.	1.1	26
93	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	0.8	26
94	Heterogeneous alleles comprising G6PD deficiency trait in West Africa exert contrasting effects on two major clinical presentations of severe malaria. <i>Malaria Journal</i> , 2016, 15, 13.	0.8	25
95	Two complement receptor one alleles have opposing associations with cerebral malaria and interact with α -thalassaemia. <i>ELife</i> , 2018, 7, .	2.8	25
96	Understandings of genomic research in developing countries: a qualitative study of the views of MalariaGEN participants in Mali. <i>BMC Medical Ethics</i> , 2015, 16, 42.	1.0	23
97	Environmental Correlation Analysis for Genes Associated with Protection against Malaria. <i>Molecular Biology and Evolution</i> , 2016, 33, 1188-1204.	3.5	21
98	Microsatellite genotyping and genome-wide single nucleotide polymorphism-based indices of <i>Plasmodium falciparum</i> diversity within clinical infections. <i>Malaria Journal</i> , 2016, 15, 275.	0.8	20
99	The ferroportin Q248H mutation protects from anemia, but not malaria or bacteremia. <i>Science Advances</i> , 2019, 5, eaaw0109.	4.7	20
100	Severe anemia in Malawian children. <i>Malawi Medical Journal</i> , 2016, 28, 99-107.	0.2	19
101	Malaria genomics: tracking a diverse and evolving parasite population. <i>International Health</i> , 2015, 7, 82-84.	0.8	18
102	Genomic variation in two gametocyte non-producing <i>Plasmodium falciparum</i> clonal lines. <i>Malaria Journal</i> , 2016, 15, 229.	0.8	18
103	Development of copy number assays for detection and surveillance of piperazine resistance associated plasmepsin 2/3 copy number variation in <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2020, 19, 181.	0.8	18
104	A targeted amplicon sequencing panel to simultaneously identify mosquito species and <i>Plasmodium</i> presence across the entire <i>Anopheles</i> genus. <i>Molecular Ecology Resources</i> , 2022, 22, 28-44.	2.2	18
105	The ethics of sustainable genomic research in Africa. <i>Genome Biology</i> , 2016, 17, 44.	3.8	17
106	Proteomic profiling of the plasma of Gambian children with cerebral malaria. <i>Malaria Journal</i> , 2018, 17, 337.	0.8	16
107	Intrinsic multiplication rate variation and plasticity of human blood stage malaria parasites. <i>Communications Biology</i> , 2020, 3, 624.	2.0	16
108	An open dataset of <i>Plasmodium vivax</i> genome variation in 1,895 worldwide samples. <i>Wellcome Open Research</i> , 0, 7, 136.	0.9	16

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109	Maintenance of MHC polymorphism. <i>Nature</i> , 1992, 355, 403-403.	13.7	15
110	A forward genetic screen reveals a primary role for <i>Plasmodium falciparum</i> Reticulocyte Binding Protein Homologue 2a and 2b in determining alternative erythrocyte invasion pathways. <i>PLoS Pathogens</i> , 2018, 14, e1007436.	2.1	15
111	Elucidating relationships between <i>P.falciparum</i> prevalence and measures of genetic diversity with a combined genetic-epidemiological model of malaria. <i>PLoS Computational Biology</i> , 2021, 17, e1009287.	1.5	14
112	Geographic-genetic analysis of <i>Plasmodium falciparum</i> parasite populations from surveys of primary school children in Western Kenya. <i>Wellcome Open Research</i> , 2017, 2, 29.	0.9	14
113	Global diversity and balancing selection of 23 leading <i>Plasmodium falciparum</i> candidate vaccine antigens. <i>PLoS Computational Biology</i> , 2022, 18, e1009801.	1.5	14
114	Mapping the travel patterns of people with malaria in Bangladesh. <i>BMC Medicine</i> , 2020, 18, 45.	2.3	11
115	The complexity of genetic variation in a simple immune system. <i>Trends in Genetics</i> , 2005, 21, 197-199.	2.9	10
116	Geographic-genetic analysis of <i>Plasmodium falciparum</i> parasite populations from surveys of primary school children in Western Kenya. <i>Wellcome Open Research</i> , 0, 2, 29.	0.9	10
117	Host Genetic Factors in Resistance and Susceptibility to Malaria. , 0, , 462-479.		10
118	G6PD gene variants and its association with malaria in a Sri Lankan population. <i>Malaria Journal</i> , 2015, 14, 93.	0.8	9
119	The genome sequence of the bootlace worm, <i>Lineus longissimus</i> (Gunnerus, 1770). <i>Wellcome Open Research</i> , 2021, 6, 272.	0.9	8
120	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.	0.9	8
121	Multi-locus genotyping reveals established endemicity of a geographically distinct <i>Plasmodium vivax</i> population in Mauritania, West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008945.	1.3	7
122	Panoptes: web-based exploration of large scale genome variation data. <i>Bioinformatics</i> , 2017, 33, 3243-3249.	1.8	6
123	Identification of a Novel Clinical Phenotype of Severe Malaria using a Network-Based Clustering Approach. <i>Scientific Reports</i> , 2018, 8, 12849.	1.6	4
124	Interferon-gamma polymorphisms and risk of iron deficiency and anaemia in Gambian children. <i>Wellcome Open Research</i> , 2020, 5, 40.	0.9	4
125	Host genetic polymorphisms and serological response against malaria in a selected population in Sri Lanka. <i>Malaria Journal</i> , 2018, 17, 473.	0.8	3
126	The Duffy T-33C is an insightful marker of human history and admixture. <i>Meta Gene</i> , 2020, 26, 100782.	0.3	3

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127	Early cytokine induction by Plasmodium falciparum is not a classical endotoxin-like process. , 1999, 29, 2636.		3
128	Investigating the drivers of the spatio-temporal patterns of genetic differences between Plasmodium falciparum malaria infections in Kilifi County, Kenya. Scientific Reports, 2019, 9, 19018.	1.6	2
129	High-throughput genotyping assays for identification of glycoprotein B deletion variants in population studies. Experimental Biology and Medicine, 2021, 246, 916-928.	1.1	2
130	Cooperation in Countering Artemisinin Resistance in Africa: Learning from COVID-19. American Journal of Tropical Medicine and Hygiene, 2022, , .	0.6	2
131	EXACT AND HEURISTIC APPROACHES FOR IDENTIFYING DISEASE-ASSOCIATED SNP MOTIFS. , 2007, , .		1
132	Functional Implications of Genetic Variation in Non-Coding DNA for Disease Susceptibility and Gene Regulation. Clinical Science, 2002, 103, 1P-2P.	0.0	0
133	A haptoglobin gene promoter polymorphism (Aâ€61C) protects from anaemia in pregnant Zanzibari women. FASEB Journal, 2007, 21, A1119.	0.2	0
134	A61â€™ haptoglobin gene promoter polymorphism and protection from malaria in Gambian children.. FASEB Journal, 2007, 21, A164.	0.2	0
135	Title is missing!. , 2020, 14, e0008945.		0
136	Title is missing!. , 2020, 14, e0008945.		0
137	Title is missing!. , 2020, 14, e0008945.		0
138	Title is missing!. , 2020, 14, e0008945.		0
139	Title is missing!. , 2020, 16, e1009133.		0
140	Title is missing!. , 2020, 16, e1009133.		0
141	Title is missing!. , 2020, 16, e1009133.		0
142	Title is missing!. , 2020, 16, e1009133.		0