

# Chris I Newbold

## List of Publications by Year in descending order

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85  
papers

14,155  
citations

41258

49  
h-index

62479

80  
g-index

95  
all docs

95  
docs citations

95  
times ranked

11933  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
2	Switches in expression of <i>plasmodium falciparum</i> var genes correlate with changes in antigenic and cytoadherent phenotypes of infected erythrocytes. <i>Cell</i> , 1995, 82, 101-110.	13.5	938
3	Relation between severe malaria morbidity in children and level of <i>Plasmodium falciparum</i> transmission in Africa. <i>Lancet</i> , The, 1997, 349, 1650-1654.	6.3	561
4	Exported Proteins Required for Virulence and Rigidity of <i>Plasmodium falciparum</i> -Infected Human Erythrocytes. <i>Cell</i> , 2008, 134, 48-61.	13.5	450
5	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. <i>Nature</i> , 2012, 487, 375-379.	13.7	450
6	Immunity to non-cerebral severe malaria is acquired after one or two infections. <i>Nature Medicine</i> , 1999, 5, 340-343.	15.2	433
7	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
8	ABACAS: algorithm-based automatic contiguation of assembled sequences. <i>Bioinformatics</i> , 2009, 25, 1968-1969.	1.8	406
9	REAPR: a universal tool for genome assembly evaluation. <i>Genome Biology</i> , 2013, 14, R47.	13.9	395
10	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-seq. <i>Molecular Microbiology</i> , 2010, 76, 12-24.	1.2	374
11	Antigenic Variation at the Infected Red Cell Surface in Malaria. <i>Annual Review of Microbiology</i> , 2001, 55, 673-707.	2.9	323
12	Receptor-Specific Adhesion and Clinical Disease in <i>Plasmodium falciparum</i> . <i>American Journal of Tropical Medicine and Hygiene</i> , 1997, 57, 389-398.	0.6	308
13	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	1.7	251
14	A simple RNA analysis method shows var and rif multigene family expression patterns in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2000, 105, 311-315.	0.5	245
15	Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. <i>Bioinformatics</i> , 2010, 26, 1704-1707.	1.8	212
16	Host-mediated regulation of superinfection in malaria. <i>Nature Medicine</i> , 2011, 17, 732-737.	15.2	212
17	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	9.4	184
18	A post-assembly genome-improvement toolkit (PAGIT) to obtain annotated genomes from contigs. <i>Nature Protocols</i> , 2012, 7, 1260-1284.	5.5	167

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19	Characterization of the pathway for transport of the cytoadherence-mediating protein, PfEMP1, to the host cell surface in malaria parasite-infected erythrocytes. <i>Molecular Microbiology</i> , 2003, 50, 1215-1227.	1.2	159
20	<i>Plasmodium falciparum</i> Variant Surface Antigen Expression Patterns during Malaria. <i>PLoS Pathogens</i> , 2005, 1, e26.	2.1	158
21	A comprehensive evaluation of assembly scaffolding tools. <i>Genome Biology</i> , 2014, 15, R42.	13.9	153
22	Transient cross-reactive immune responses can orchestrate antigenic variation in malaria. <i>Nature</i> , 2004, 429, 555-558.	13.7	150
23	<i>Plasmodium malariae</i> and <i>P. ovale</i> genomes provide insights into malaria parasite evolution. <i>Nature</i> , 2017, 542, 101-104.	13.7	150
24	Cytoadherence, pathogenesis and the infected red cell surface in <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology</i> , 1999, 29, 927-937.	1.3	141
25	Whole genome sequencing of <i>Plasmodium falciparum</i> from dried blood spots using selective whole genome amplification. <i>Malaria Journal</i> , 2016, 15, 597.	0.8	129
26	Genomes of all known members of a <i>Plasmodium</i> subgenus reveal paths to virulent human malaria. <i>Nature Microbiology</i> , 2018, 3, 687-697.	5.9	129
27	<i>Plasmodium falciparum</i> var gene expression is developmentally controlled at the level of RNA polymerase II-mediated transcription initiation. <i>Molecular Microbiology</i> , 2007, 63, 1237-1247.	1.2	128
28	Variable var transition rates underlie antigenic variation in malaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11129-11134.	3.3	127
29	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. <i>Nature Communications</i> , 2014, 5, 4754.	5.8	124
30	Relationships between sequestration, antigenic variation and chronic parasitism in <i>Plasmodium chabaudi chabaudi</i> —a rodent malaria model. <i>Parasite Immunology</i> , 1990, 12, 45-64.	0.7	118
31	A new <i>Plasmodium vivax</i> reference sequence with improved assembly of the subtelomeres reveals an abundance of pir genes. <i>Wellcome Open Research</i> , 2016, 1, 4.	0.9	118
32	Long read assemblies of geographically dispersed <i>Plasmodium falciparum</i> isolates reveal highly structured subtelomeres. <i>Wellcome Open Research</i> , 2018, 3, 52.	0.9	114
33	Antigenic Variation in <i>Plasmodium falciparum</i> Malaria Involves a Highly Structured Switching Pattern. <i>PLoS Pathogens</i> , 2011, 7, e1001306.	2.1	114
34	A well-conserved <i>Plasmodium falciparum</i> var gene shows an unusual stage-specific transcript pattern. <i>Molecular Microbiology</i> , 2003, 48, 1339-1348.	1.2	110
35	A potential novel mechanism for the insertion of a membrane protein revealed by a biochemical analysis of the <i>Plasmodium falciparum</i> cytoadherence molecule PfEMP-1. <i>Molecular Microbiology</i> , 2004, 55, 1272-1284.	1.2	99
36	<i>Plasmodium falciparum</i> antigenic variation. Mapping mosaic var gene sequences onto a network of shared, highly polymorphic sequence blocks. <i>Molecular Microbiology</i> , 2008, 68, 1519-1534.	1.2	91

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37	Statistical estimation of cell-cycle progression and lineage commitment in <i>Plasmodium falciparum</i> reveals a homogeneous pattern of transcription in ex vivo culture. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7559-7564.	3.3	84
38	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . Genome Research, 2008, 18, 281-292.	2.4	81
39	Complete avian malaria parasite genomes reveal features associated with lineage-specific evolution in birds and mammals. Genome Research, 2018, 28, 547-560.	2.4	78
40	PfEMP1 expression is reduced on the surface of knobless <i>Plasmodium falciparum</i> infected erythrocytes. Journal of Cell Science, 2005, 118, 2507-2518.	1.2	74
41	Evolutionary analysis of the most polymorphic gene family in falciparum malaria. Wellcome Open Research, 2019, 4, 193.	0.9	64
42	Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing. Journal of Clinical Microbiology, 2013, 51, 745-751.	1.8	63
43	Genomic representation of var gene sequences in <i>Plasmodium falciparum</i> field isolates from different geographic regions1Note: Nucleotide sequences for data reported in this paper are in the EMBL, GenBank, and DDJB databases under the accession numbers Z94724–Z94751.1. Molecular and Biochemical Parasitology, 1997, 87, 235-238.	0.5	60
44	Delivery of the Malaria Virulence Protein PfEMP1 to the Erythrocyte Surface Requires Cholesterol-Rich Domains. Eukaryotic Cell, 2006, 5, 849-860.	3.4	60
45	Functional Identification of the <i>Plasmodium</i> Centromere and Generation of a <i>Plasmodium</i> Artificial Chromosome. Cell Host and Microbe, 2010, 7, 245-255.	5.1	58
46	Antigenic variation in <i>Plasmodium falciparum</i> : mechanisms and consequences. Current Opinion in Microbiology, 1999, 2, 420-425.	2.3	56
47	Current status of the <i>Plasmodium falciparum</i> genome project. Molecular and Biochemical Parasitology, 1996, 79, 1-12.	0.5	55
48	An approach to classifying sequence tags sampled from <i>Plasmodium falciparum</i> var genes. Molecular and Biochemical Parasitology, 2007, 154, 98-102.	0.5	55
49	Limited Spatial Clustering of Individual <i>Plasmodium falciparum</i> Alleles in Field Isolates from Coastal Kenya. American Journal of Tropical Medicine and Hygiene, 1997, 57, 205-215.	0.6	53
50	Microarray-based comparative genomic analyses of the human malaria parasite <i>Plasmodium falciparum</i> using Affymetrix arrays. Molecular and Biochemical Parasitology, 2005, 144, 177-186.	0.5	52
51	Progression of the canonical reference malaria parasite genome from 2002–2019. Wellcome Open Research, 2019, 4, 58.	0.9	51
52	Antibody-independent mechanisms regulate the establishment of chronic <i>Plasmodium</i> infection. Nature Microbiology, 2017, 2, 16276.	5.9	50
53	Genome-wide profiling of chromosome interactions in <i>Plasmodium falciparum</i> characterizes nuclear architecture and reconfigurations associated with antigenic variation. Molecular Microbiology, 2013, 90, 519-537.	1.2	48
54	Progression of the canonical reference malaria parasite genome from 2002–2019. Wellcome Open Research, 2019, 4, 58.	0.9	47

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55	Serological cross-reaction between high molecular weight proteins synthesized in blood schizonts of <i>Plasmodium yoelii</i> , <i>Plasmodium chabaudi</i> and <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 1983, 9, 191-196.	0.5	45
56	Acquired immunity and postnatal clinical protection in childhood cerebral malaria. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 33-38.	1.2	40
57	Intraerythrocytic polyubiquitin expression in <i>Plasmodium falciparum</i> is subjected to developmental and heat-shock control. <i>Molecular and Biochemical Parasitology</i> , 2000, 105, 115-125.	0.5	37
58	Repeated clinical malaria episodes are associated with modification of the immune system in children. <i>BMC Medicine</i> , 2019, 17, 60.	2.3	37
59	A possible molecular basis for strain specific immunity to malaria. <i>Molecular and Biochemical Parasitology</i> , 1984, 11, 337-347.	0.5	29
60	Stage-specific merozoite surface protein 2 antisense transcripts in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 123, 79-83.	0.5	29
61	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. <i>DNA Research</i> , 2014, 21, 661-671.	1.5	27
62	The antigenic switching network of <i>Plasmodium falciparum</i> and its implications for the immuno-epidemiology of malaria. <i>ELife</i> , 2013, 2, e01074.	2.8	27
63	<i>Plasmodium falciparum</i> infected erythrocytes induce hepcidin ( <i>HAMP</i> ) mRNA synthesis by peripheral blood mononuclear cells. <i>British Journal of Haematology</i> , 2009, 147, 769-771.	1.2	26
64	Effect of <i>var</i> gene disruption on switching in <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2002, 45, 1131-1141.	1.2	24
65	Genome Wide Adaptations of <i>Plasmodium falciparum</i> in Response to Lumefantrine Selective Drug Pressure. <i>PLoS ONE</i> , 2012, 7, e31623.	1.1	22
66	Intraerythrocytic development and antigenicity of asexual malaria parasites. <i>Molecular and Biochemical Parasitology</i> , 1984, 11, 1-22.	0.5	20
67	The path of drug resistance. <i>Nature</i> , 1990, 345, 202-203.	13.7	20
68	CD4 T Cell Responses to a Variant Antigen of the Malaria Parasite <i>Plasmodium falciparum</i> , Erythrocyte Membrane Protein 1, in Individuals Living in Malaria-Endemic Areas. <i>Journal of Infectious Diseases</i> , 2002, 185, 812-819.	1.9	19
69	Transcription of a subtelomericly located <i>var</i> gene variant in <i>Plasmodium falciparum</i> appears to require the truncation of an adjacent <i>var</i> gene. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 193-199.	0.5	19
70	Genomic and transcriptomic evidence for descent from <i>Plasmodium</i> and loss of blood schizogony in <i>Hepaticystis</i> parasites from naturally infected red colobus monkeys. <i>PLoS Pathogens</i> , 2020, 16, e1008717.	2.1	18
71	Stage-specific promoter activity from stably maintained episomes in <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology</i> , 2002, 32, 1203-1206.	1.3	15
72	Pre-clinical evaluation of a <i>P. berghei</i> -based whole-sporozoite malaria vaccine candidate. <i>Npj Vaccines</i> , 2018, 3, 54.	2.9	15

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73	Intraerythrocytic development and antigenicity of <i>Plasmodium falciparum</i> and comparison with simian and rodent malaria parasites. <i>Molecular and Biochemical Parasitology</i> , 1983, 9, 227-240.	0.5	13
74	Parasite polypeptides lost during schizogony and erythrocyte invasion by the malaria parasites, <i>Plasmodium chabaudi</i> and <i>Plasmodium knowlesi</i> . <i>Molecular and Biochemical Parasitology</i> , 1983, 7, 9-18.	0.5	13
75	Cellular responses to <i>Plasmodium falciparum</i> erythrocyte membrane protein-1: use of relatively conserved synthetic peptide pools to determine CD4 T cell responses in malaria-exposed individuals in Benin, West Africa. <i>Malaria Journal</i> , 2002, 1, 7.	0.8	10
76	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 2021, 6, 22.	0.9	6
77	In silico guided reconstruction and analysis of ICAM-1-binding var genes from <i>Plasmodium falciparum</i> . <i>Scientific Reports</i> , 2018, 8, 3282.	1.6	4
78	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 0, 6, 22.	0.9	4
79	Reply to: Hepcidin in malaria superinfection: can findings be translated to humans?. <i>Nature Medicine</i> , 2011, 17, 1341-1342.	15.2	3
80	Title to be confirmed. <i>Biochemical Society Transactions</i> , 2000, 28, A474-A474.	1.6	0
81	Functional Identification of the <i>Plasmodium</i> Centromere and Generation of a <i>Plasmodium</i> Artificial Chromosome. <i>Cell Host and Microbe</i> , 2010, 7, 420.	5.1	0
82	Title is missing!. , 2020, 16, e1008717.		0
83	Title is missing!. , 2020, 16, e1008717.		0
84	Title is missing!. , 2020, 16, e1008717.		0
85	Title is missing!. , 2020, 16, e1008717.		0