

# 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	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 2021, 6, 22.	0.9	6
2	Genomic and transcriptomic evidence for descent from Plasmodium and loss of blood schizogony in Hepatocystis parasites from naturally infected red colobus monkeys. PLoS Pathogens, 2020, 16, e1008717.	2.1	18
3	Title is missing!. , 2020, 16, e1008717.		0
4	Title is missing!. , 2020, 16, e1008717.		0
5	Title is missing!. , 2020, 16, e1008717.		0
6	Title is missing!. , 2020, 16, e1008717.		0
7	Repeated clinical malaria episodes are associated with modification of the immune system in children. BMC Medicine, 2019, 17, 60.	2.3	37
8	Progression of the canonical reference malaria parasite genome from 2002â€“2019. Wellcome Open Research, 2019, 4, 58.	0.9	51
9	Progression of the canonical reference malaria parasite genome from 2002â€“2019. Wellcome Open Research, 2019, 4, 58.	0.9	47
10	Evolutionary analysis of the most polymorphic gene family in falciparum malaria. Wellcome Open Research, 2019, 4, 193.	0.9	64
11	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
12	In silico guided reconstruction and analysis of ICAM-1-binding var genes from Plasmodium falciparum. Scientific Reports, 2018, 8, 3282.	1.6	4
13	Pre-clinical evaluation of a P. berghei-based whole-sporozoite malaria vaccine candidate. Npj Vaccines, 2018, 3, 54.	2.9	15
14	Genomes of all known members of a Plasmodium subgenus reveal paths to virulent human malaria. Nature Microbiology, 2018, 3, 687-697.	5.9	129
15	Long read assemblies of geographically dispersed Plasmodium falciparum isolates reveal highly structured subtelomeres. Wellcome Open Research, 2018, 3, 52.	0.9	114
16	Plasmodium malariae and P. ovale genomes provide insights into malaria parasite evolution. Nature, 2017, 542, 101-104.	13.7	150
17	Antibody-independent mechanisms regulate the establishment of chronic Plasmodium infection. Nature Microbiology, 2017, 2, 16276.	5.9	50
18	Whole genome sequencing of Plasmodium falciparum from dried blood spots using selective whole genome amplification. Malaria Journal, 2016, 15, 597.	0.8	129

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19	A new <i>Plasmodium vivax</i> reference sequence with improved assembly of the subtelomeres reveals an abundance of <i>pir</i> genes. Wellcome Open Research, 2016, 1, 4.	0.9	118
20	Optimized Whole-Genome Amplification Strategy for Extremely AT-Biased Template. DNA Research, 2014, 21, 661-671.	1.5	27
21	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. BMC Biology, 2014, 12, 86.	1.7	251
22	Genome sequencing of chimpanzee malaria parasites reveals possible pathways of adaptation to human hosts. Nature Communications, 2014, 5, 4754.	5.8	124
23	A comprehensive evaluation of assembly scaffolding tools. Genome Biology, 2014, 15, R42.	13.9	153
24	REAPR: a universal tool for genome assembly evaluation. Genome Biology, 2013, 14, R47.	13.9	395
25	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. Nature Genetics, 2013, 45, 648-655.	9.4	424
26	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
27	Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing. Journal of Clinical Microbiology, 2013, 51, 745-751.	1.8	63
28	The antigenic switching network of <i>Plasmodium falciparum</i> and its implications for the immuno-epidemiology of malaria. ELife, 2013, 2, e01074.	2.8	27
29	Genome Wide Adaptations of <i>Plasmodium falciparum</i> in Response to Lumefantrine Selective Drug Pressure. PLoS ONE, 2012, 7, e31623.	1.1	22
30	Analysis of <i>Plasmodium falciparum</i> diversity in natural infections by deep sequencing. Nature, 2012, 487, 375-379.	13.7	450
31	A post-assembly genome-improvement toolkit (PAGIT) to obtain annotated genomes from contigs. Nature Protocols, 2012, 7, 1260-1284.	5.5	167
32	Host-mediated regulation of superinfection in malaria. Nature Medicine, 2011, 17, 732-737.	15.2	212
33	Reply to: Hepcidin in malaria superinfection: can findings be translated to humans?. Nature Medicine, 2011, 17, 1341-1342.	15.2	3
34	Antigenic Variation in <i>Plasmodium falciparum</i> Malaria Involves a Highly Structured Switching Pattern. PLoS Pathogens, 2011, 7, e1001306.	2.1	114
35	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-Seq. Molecular Microbiology, 2010, 76, 12-24.	1.2	374
36	Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. Bioinformatics, 2010, 26, 1704-1707.	1.8	212

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37	Functional Identification of the Plasmodium Centromere and Generation of a Plasmodium Artificial Chromosome. <i>Cell Host and Microbe</i> , 2010, 7, 245-255.	5.1	58
38	Functional Identification of the Plasmodium Centromere and Generation of a Plasmodium Artificial Chromosome. <i>Cell Host and Microbe</i> , 2010, 7, 420.	5.1	0
39	Statistical estimation of cell-cycle progression and lineage commitment in <i>Plasmodium falciparum</i> reveals a homogeneous pattern of transcription in <i>ex vivo</i> culture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7559-7564.	3.3	84
40	ABACAS: algorithm-based automatic contiguation of assembled sequences. <i>Bioinformatics</i> , 2009, 25, 1968-1969.	1.8	406
41	<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
42	<i>Plasmodium falciparum</i> antigenic variation. Mapping mosaic <i>var</i> gene sequences onto a network of shared, highly polymorphic sequence blocks. <i>Molecular Microbiology</i> , 2008, 68, 1519-1534.	1.2	91
43	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
44	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292.	2.4	81
45	Genome variation and evolution of the malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Genetics</i> , 2007, 39, 120-125.	9.4	184
46	<i>Plasmodium falciparum var</i> 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
47	An approach to classifying sequence tags sampled from <i>Plasmodium falciparum var</i> genes. <i>Molecular and Biochemical Parasitology</i> , 2007, 154, 98-102.	0.5	55
48	Delivery of the Malaria Virulence Protein PfEMP1 to the Erythrocyte Surface Requires Cholesterol-Rich Domains. <i>Eukaryotic Cell</i> , 2006, 5, 849-860.	3.4	60
49	Microarray-based comparative genomic analyses of the human malaria parasite <i>Plasmodium falciparum</i> using Affymetrix arrays. <i>Molecular and Biochemical Parasitology</i> , 2005, 144, 177-186.	0.5	52
50	<i>Plasmodium falciparum</i> Variant Surface Antigen Expression Patterns during Malaria. <i>PLoS Pathogens</i> , 2005, 1, e26.	2.1	158
51	PfEMP1 expression is reduced on the surface of knobless <i>Plasmodium falciparum</i> infected erythrocytes. <i>Journal of Cell Science</i> , 2005, 118, 2507-2518.	1.2	74
52	Variable <i>var</i> 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
53	Transient cross-reactive immune responses can orchestrate antigenic variation in malaria. <i>Nature</i> , 2004, 429, 555-558.	13.7	150
54	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

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55	Transcription of a subtelomerically located var gene variant in <i>Plasmodium falciparum</i> appears to require the truncation of an adjacent var gene. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 193-199.	0.5	19
56	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
57	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
58	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
59	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
60	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
61	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
62	Effect of var gene disruption on switching in <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2002, 45, 1131-1141.	1.2	24
63	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
64	Antigenic Variation at the Infected Red Cell Surface in Malaria. <i>Annual Review of Microbiology</i> , 2001, 55, 673-707.	2.9	323
65	Title to be confirmed. <i>Biochemical Society Transactions</i> , 2000, 28, A474-A474.	1.6	0
66	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
67	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
68	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
69	Immunity to non-cerebral severe malaria is acquired after one or two infections. <i>Nature Medicine</i> , 1999, 5, 340-343.	15.2	433
70	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
71	Antigenic variation in <i>Plasmodium falciparum</i> : mechanisms and consequences. <i>Current Opinion in Microbiology</i> , 1999, 2, 420-425.	2.3	56
72	Relation between severe malaria morbidity in children and level of <i>Plasmodium falciparum</i> transmission in Africa. <i>Lancet</i> , 1997, 349, 1650-1654.	6.3	561

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73	Genomic representation of var gene sequences in Plasmodium falciparum 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 to Z94751.1. Molecular and Biochemical Parasitology, 1997, 87, 235-238.	0.5	60
74	Limited Spatial Clustering of Individual Plasmodium falciparum Alleles in Field Isolates from Coastal Kenya. American Journal of Tropical Medicine and Hygiene, 1997, 57, 205-215.	0.6	53
75	Receptor-Specific Adhesion and Clinical Disease in Plasmodium falciparum. American Journal of Tropical Medicine and Hygiene, 1997, 57, 389-398.	0.6	308
76	Current status of the Plasmodium falciparum genome project. Molecular and Biochemical Parasitology, 1996, 79, 1-12.	0.5	55
77	Switches in expression of plasmodium falciparum var genes correlate with changes in antigenic and cytoadherent phenotypes of infected erythrocytes. Cell, 1995, 82, 101-110.	13.5	938
78	Relationships between sequestration, antigenic variation and chronic parasitism in Plasmodium chabaudi chabaudi a rodent malaria model. Parasite Immunology, 1990, 12, 45-64.	0.7	118
79	The path of drug resistance. Nature, 1990, 345, 202-203.	13.7	20
80	Intraerythrocytic development and antigenicity of asexual malaria parasites. Molecular and Biochemical Parasitology, 1984, 11, 1-22.	0.5	20
81	A possible molecular basis for strain specific immunity to malaria. Molecular and Biochemical Parasitology, 1984, 11, 337-347.	0.5	29
82	Serological cross-reaction between high molecular weight proteins synthesized in blood schizonts of Plasmodium yoelii, Plasmodium chabaudi and Plasmodium falciparum. Molecular and Biochemical Parasitology, 1983, 9, 191-196.	0.5	45
83	Intraerythrocytic development and antigenicity of Plasmodium falciparum and comparison with simian and rodent malaria parasites. Molecular and Biochemical Parasitology, 1983, 9, 227-240.	0.5	13
84	Parasite polypeptides lost during schizogony and erythrocyte invasion by the malaria parasites, Plasmodium chabaudi and Plasmodium knowlesi. Molecular and Biochemical Parasitology, 1983, 7, 9-18.	0.5	13
85	Individual-level variations in malaria susceptibility and acquisition of clinical protection. Wellcome Open Research, 0, 6, 22.	0.9	4