

Peter Preiser

List of Publications by Year in descending order

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125
papers

6,606
citations

87401

40
h-index

84171

75
g-index

132
all docs

132
docs citations

132
times ranked

6590
citing authors

#	ARTICLE	IF	CITATIONS
1	Laser-Induced Surface Acoustic Wave Sensing-Based Malaria Parasite Detection and Analysis. IEEE Transactions on Instrumentation and Measurement, 2022, 71, 1-9.	2.4	12
2	Finger stick blood test to assess postvaccination <sc>SARS-CoV</sc>-2 neutralizing antibody response against variants. Bioengineering and Translational Medicine, 2022, 7, .	3.9	7
3	Selective expression of variant surface antigens enables Plasmodium falciparum to evade immune clearance in vivo. Nature Communications, 2022, 13, .	5.8	5
4	<sc>Plasmodium falciparum</sc> replication factor C subunit 1 is involved in genotoxic stress response. Cellular Microbiology, 2021, 23, e13277.	1.1	2
5	Functional Characterization of the m⁶-A-Dependent Translational Modulator PfYTH.2 in the Human Malaria Parasite. MBio, 2021, 12, .	1.8	11
6	Malaria Parasite Stress Tolerance Is Regulated by DNMT2-Mediated tRNA Cytosine Methylation. MBio, 2021, 12, e0255821.	1.8	18
7	A rapid simple point-of-care assay for the detection of SARS-CoV-2 neutralizing antibodies. Communications Medicine, 2021, 1, .	1.9	23
8	Discovery of a new predominant cytosine DNA modification that is linked to gene expression in malaria parasites. Nucleic Acids Research, 2020, 48, 184-199.	6.5	24
9	Microfluidic label-free bioprocessing of human reticulocytes from erythroid culture. Lab on A Chip, 2020, 20, 3445-3460.	3.1	15
10	Exploring the virulence gene interactome with<sc>CRISPR</sc>/<sc>dC</sc>as9 in the human malaria parasite. Molecular Systems Biology, 2020, 16, e9569.	3.2	32
11	Whole-Cell Phenotypic Screening of Medicines for Malaria Venture Pathogen Box Identifies Specific Inhibitors of <sc>Plasmodium falciparum</sc> Late-Stage Development and Egress. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	10
12	A Photoacoustic-Surface-Acoustic-Wave Sensor for Ring-Stage Malaria Parasite Detection. IEEE Transactions on Circuits and Systems II: Express Briefs, 2020, 67, 881-885.	2.2	11
13	A processing product of the Plasmodium falciparum reticulocyte binding protein RH1 shows a close association with AMA1 during junction formation. Cellular Microbiology, 2020, 22, e13232.	1.1	3
14	Transcriptome-wide dynamics of extensive m6A mRNA methylation during Plasmodium falciparum blood-stage development. Nature Microbiology, 2019, 4, 2246-2259.	5.9	66
15	Transcriptome profiling reveals functional variation in Plasmodium falciparum parasites from controlled human malaria infection studies. EBioMedicine, 2019, 48, 442-452.	2.7	19
16	Enhancing the sensitivity of micro magnetic resonance relaxometry detection of low parasitemia Plasmodium falciparum in human blood. Scientific Reports, 2019, 9, 2555.	1.6	10
17	Immunomic Identification of Malaria Antigens Associated With Protection in Mice. Molecular and Cellular Proteomics, 2019, 18, 837-853.	2.5	1
18	Comparative Heterochromatin Profiling Reveals Conserved and Unique Epigenome Signatures Linked to Adaptation and Development of Malaria Parasites. Cell Host and Microbe, 2018, 23, 407-420.e8.	5.1	99

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19	Targeted Phenotypic Screening in <i>Plasmodium falciparum</i> and <i>Toxoplasma gondii</i> Reveals Novel Modes of Action of Medicines for Malaria Venture Malaria Box Molecules. <i>MSphere</i> , 2018, 3, .	1.3	30
20	Chemogenomic Profiling of Human and Microbial FK506-Binding Proteins. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 3660-3673.	2.9	42
21	Microvesicles from malaria-infected red blood cells activate natural killer cells via MDA5 pathway. <i>PLoS Pathogens</i> , 2018, 14, e1007298.	2.1	54
22	tRNA epitranscriptomics and biased codon use are linked to proteome expression in <i>Plasmodium falciparum</i> . <i>Molecular Systems Biology</i> , 2018, 14, e8009.	3.2	34
23	One-step solid-oil-water emulsion for sustained bioactive ranibizumab release. <i>Expert Opinion on Drug Delivery</i> , 2018, 15, 1143-1156.	2.4	5
24	Surface enhanced Raman spectroscopy for malaria diagnosis and intradermal measurements. , 2018, , .		0
25	Three Is a Crowd – New Insights into Rosetting in <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2017, 33, 309-320.	1.5	37
26	<i>P. falciparum</i> RH5-Basigin interaction induces changes in the cytoskeleton of the host RBC. <i>Cellular Microbiology</i> , 2017, 19, e12747.	1.1	36
27	Expression dynamics and physiologically relevant functional study of STEVOR in asexual stages of <i>Plasmodium falciparum</i> infection. <i>Cellular Microbiology</i> , 2017, 19, e12715.	1.1	11
28	Host immune evasion strategies of malaria blood stage parasite. <i>Molecular BioSystems</i> , 2017, 13, 2498-2508.	2.9	18
29	An ApiAP2 member regulates expression of clonally variant genes of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Scientific Reports</i> , 2017, 7, 14042.	1.6	42
30	Dengue Virus-Infected Dendritic Cells, but Not Monocytes, Activate Natural Killer Cells through a Contact-Dependent Mechanism Involving Adhesion Molecules. <i>MBio</i> , 2017, 8, .	1.8	50
31	New insights into the <i>Plasmodium vivax</i> transcriptome using RNA-Seq. <i>Scientific Reports</i> , 2016, 6, 20498.	1.6	65
32	Towards ultrasensitive malaria diagnosis using surface enhanced Raman spectroscopy. <i>Scientific Reports</i> , 2016, 6, 20177.	1.6	48
33	Towards field malaria diagnosis using surface enhanced Raman spectroscopy. , 2016, , .		1
34	PfRH2b specific monoclonal antibodies inhibit merozoite invasion. <i>Molecular Microbiology</i> , 2016, 102, 386-404.	1.2	18
35	Proteome mapping of <i>Plasmodium</i> : identification of the <i>P. yoelii</i> remodelome. <i>Scientific Reports</i> , 2016, 6, 31055.	1.6	9
36	Characterization of the <i>Plasmodium</i> Interspersed Repeats (PIR) proteins of <i>Plasmodium chabaudi</i> indicates functional diversity. <i>Scientific Reports</i> , 2016, 6, 23449.	1.6	34

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37	Breadth of humoral response and antigenic targets of sporozoite-inhibitory antibodies associated with sterile protection induced by controlled human malaria infection. <i>Cellular Microbiology</i> , 2016, 18, 1739-1750.	1.1	33
38	Integrated analysis of the Plasmodium species transcriptome. <i>EBioMedicine</i> , 2016, 7, 255-266.	2.7	55
39	Review of Surface Enhanced Raman Spectroscopy for Malaria Diagnosis and a New Approach for the Detection of Single Parasites in the Ring Stage. <i>IEEE Journal of Selected Topics in Quantum Electronics</i> , 2016, 22, 179-187.	1.9	13
40	Investigation of surface enhanced Raman spectroscopy for hemozoin detection in malaria diagnosis. , 2016, , .		1
41	Differential Spleen Remodeling Associated with Different Levels of Parasite Virulence Controls Disease Outcome in Malaria Parasite Infections. <i>MSphere</i> , 2016, 1, .	1.3	7
42	Neutralizing Antibodies against Plasmodium falciparum Associated with Successful Cure after Drug Therapy. <i>PLoS ONE</i> , 2016, 11, e0159347.	1.1	8
43	Delineation of Natural Killer Cell Differentiation from Myeloid Progenitors in Human. <i>Scientific Reports</i> , 2015, 5, 15118.	1.6	24
44	De Novo Generated Human Red Blood Cells in Humanized Mice Support Plasmodium falciparum Infection. <i>PLoS ONE</i> , 2015, 10, e0129825.	1.1	27
45	Enhancing malaria diagnosis through microfluidic cell enrichment and magnetic resonance relaxometry detection. <i>Scientific Reports</i> , 2015, 5, 11425.	1.6	63
46	Basigin is a druggable target for host-oriented antimalarial interventions. <i>Journal of Experimental Medicine</i> , 2015, 212, 1145-1151.	4.2	62
47	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , 2015, 14, 110.	0.8	31
48	Synthesis, characterization and in vitro evaluation of novel enantiomerically-pure sulphonamide antimalarials. <i>Organic and Biomolecular Chemistry</i> , 2015, 13, 10681-10690.	1.5	9
49	Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. <i>Science</i> , 2015, 347, 431-435.	6.0	362
50	A High-Content Phenotypic Screen Reveals the Disruptive Potency of Quinacrine and 3- <i>nitro</i> -4-chlorobenzamide on the Digestive Vacuole of Plasmodium falciparum. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 550-558.	1.4	23
51	Human natural killer cells control <i>Plasmodium falciparum</i> infection by eliminating infected red blood cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1479-1484.	3.3	67
52	Structural polymorphism in the promoter of <i>pfmrp2</i> confers <i>Plasmodium falciparum</i> tolerance to quinoline drugs. <i>Molecular Microbiology</i> , 2014, 91, 918-934.	1.2	28
53	Identification of a new export signal in <i>Plasmodium yoelii</i> : identification of a new exportome. <i>Cellular Microbiology</i> , 2014, 16, 673-686.	1.1	14
54	STEVOR Is a Plasmodium falciparum Erythrocyte Binding Protein that Mediates Merozoite Invasion and Rosetting. <i>Cell Host and Microbe</i> , 2014, 16, 81-93.	5.1	148

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55	Micromagnetic resonance relaxometry for rapid label-free malaria diagnosis. <i>Nature Medicine</i> , 2014, 20, 1069-1073.	15.2	111
56	Small Molecule Targeting Malaria Merozoite Surface Protein-1 (MSP-1) Prevents Host Invasion of Divergent Plasmodial Species. <i>Journal of Infectious Diseases</i> , 2014, 210, 1616-1626.	1.9	36
57	In Vivo Splenic Clearance Correlates with In Vitro Deformability of Red Blood Cells from Plasmodium yoelii-Infected Mice. <i>Infection and Immunity</i> , 2014, 82, 2532-2541.	1.0	38
58	Glycophorin C (CD236R) mediates vivax malaria parasite rosetting to normocytes. <i>Blood</i> , 2014, 123, e100-e109.	0.6	44
59	A multidimensional platform for the purification of non-coding RNA species. <i>Nucleic Acids Research</i> , 2013, 41, e168-e168.	6.5	40
60	Adamantyl Derivative As a Potent Inhibitor of Plasmodium FK506 Binding Protein 35. <i>ACS Medicinal Chemistry Letters</i> , 2013, 4, 1097-1101.	1.3	21
61	The role of the reticulocyte-binding-like protein homologues of Plasmodium in erythrocyte sensing and invasion. <i>Cellular Microbiology</i> , 2013, 15, 35-44.	1.1	31
62	Triggers of key calcium signals during erythrocyte invasion by Plasmodium falciparum. <i>Nature Communications</i> , 2013, 4, 2862.	5.8	60
63	Small molecule Plasmodium FKBP35 inhibitor as a potential antimalaria agent. <i>Scientific Reports</i> , 2013, 3, 2501.	1.6	29
64	The Role of Serine-Type Serine Repeat Antigen in Plasmodium yoelii Blood Stage Development. <i>PLoS ONE</i> , 2013, 8, e60723.	1.1	10
65	A switch in infected erythrocyte deformability at the maturation and blood circulation of Plasmodium falciparum transmission stages. <i>Blood</i> , 2012, 119, e172-e180.	0.6	130
66	Structural architecture and interplay of the nucleotide- and erythrocyte binding domain of the reticulocyte binding protein Py235 from Plasmodium yoelii. <i>International Journal for Parasitology</i> , 2012, 42, 1083-1089.	1.3	4
67	Editorial "Singapore Malaria Network Meeting (SingMalNet) 2012. <i>International Journal for Parasitology</i> , 2012, 42, 1047.	1.3	0
68	Quantitative Proteomics Reveals New Insights into Erythrocyte Invasion by Plasmodium falciparum. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.010645.	2.5	20
69	Transcriptional variation in the malaria parasite Plasmodium falciparum. <i>Genome Research</i> , 2012, 22, 925-938.	2.4	194
70	Characterization and gene expression analysis of the cir multi-gene family of plasmodium chabaudi chabaudi (AS). <i>BMC Genomics</i> , 2012, 13, 125.	1.2	26
71	Analysis of subtelomeric virulence gene families in Plasmodium falciparum by comparative transcriptional profiling. <i>Molecular Microbiology</i> , 2012, 84, 243-259.	1.2	38
72	Red blood cell rheology using single controlled laser-induced cavitation bubbles. <i>Lab on A Chip</i> , 2011, 11, 672-678.	3.1	36

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73	Effect of cell-seeding density on the proliferation and gene expression profile of human umbilical vein endothelial cells within ex vivo culture. <i>Cytotherapy</i> , 2011, 13, 606-617.	0.3	32
74	Changes in Parasite Virulence Induced by the Disruption of a Single Member of the 235 kDa Rhoptry Protein Multigene Family of <i>Plasmodium yoelii</i> . <i>PLoS ONE</i> , 2011, 6, e20170.	1.1	12
75	NMR solution structure of NBD94483-502 of the nucleotide-binding domain of the <i>Plasmodium yoelii</i> reticulocyte-binding protein Py235. <i>FEMS Microbiology Letters</i> , 2011, 318, 152-158.	0.7	3
76	Quantitative Time-course Profiling of Parasite and Host Cell Proteins in the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006411.	2.5	145
77	Comparison of the adhesion and proliferation characteristics of HUVEC and two endothelial cell lines (CRL 2922 and CRL 2873) on various substrata. <i>Biotechnology and Bioprocess Engineering</i> , 2011, 16, 127-135.	1.4	5
78	Artemisinin resistance in <i>Plasmodium falciparum</i> is associated with an altered temporal pattern of transcription. <i>BMC Genomics</i> , 2011, 12, 391.	1.2	135
79	Structural Characterization of the Erythrocyte Binding Domain of the Reticulocyte Binding Protein Homologue Family of <i>Plasmodium yoelii</i> . <i>Infection and Immunity</i> , 2011, 79, 2880-2888.	1.0	11
80	Differences in Erythrocyte Receptor Specificity of Different Parts of the <i>Plasmodium falciparum</i> Reticulocyte Binding Protein Homologue 2a. <i>Infection and Immunity</i> , 2011, 79, 3421-3430.	1.0	35
81	Biophysics of Malarial Parasite Exit from Infected Erythrocytes. <i>PLoS ONE</i> , 2011, 6, e20869.	1.1	84
82	The pir multigene family of <i>Plasmodium</i> : Antigenic variation and beyond. <i>Molecular and Biochemical Parasitology</i> , 2010, 170, 65-73.	0.5	79
83	Crystallographic studies of the coupling segment NBD94674â€“781 of the nucleotide-binding domain of the <i>Plasmodium yoelii</i> reticulocyte-binding protein Py235. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1631-1634.	0.7	0
84	Transcriptional profiling of growth perturbations of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Biotechnology</i> , 2010, 28, 91-98.	9.4	196
85	Structural Determination of Functional Units of the Nucleotide Binding Domain (NBD94) of the Reticulocyte Binding Protein Py235 of <i>Plasmodium yoelii</i> . <i>PLoS ONE</i> , 2010, 5, e9146.	1.1	9
86	Adhesion, proliferation, and gene expression profile of human umbilical vein endothelial cells cultured on bilayered polyelectrolyte coatings composed of glycosaminoglycans. <i>Biointerphases</i> , 2010, 5, FA53-FA62.	0.6	17
87	Immobilization of Recombinant Vault Nanoparticles on Solid Substrates. <i>ACS Nano</i> , 2010, 4, 1417-1424.	7.3	16
88	Small variant surface antigens and <i>Plasmodium</i> evasion of immunity. <i>Future Microbiology</i> , 2010, 5, 663-682.	1.0	34
89	Rapid Changes in Transcription Profiles of the <i>Plasmodium yoelii</i> yir Multigene Family in Clonal Populations: Lack of Epigenetic Memory?. <i>PLoS ONE</i> , 2009, 4, e4285.	1.1	25
90	The <i>Plasmodium falciparum</i> STEVOR Multigene Family Mediates Antigenic Variation of the Infected Erythrocyte. <i>PLoS Pathogens</i> , 2009, 5, e1000307.	2.1	98

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91	Comparative Transcriptional and Genomic Analysis of <i>Plasmodium falciparum</i> Field Isolates. <i>PLoS Pathogens</i> , 2009, 5, e1000644.	2.1	76
92	Characterization of the repertoire diversity of the <i>Plasmodium falciparum</i> <i>stevor</i> multigene family in laboratory and field isolates. <i>Malaria Journal</i> , 2009, 8, 140.	0.8	9
93	A novel semi-automatic image processing approach to determine <i>Plasmodium falciparum</i> parasitemia in Giemsa-stained thin blood smears. <i>BMC Cell Biology</i> , 2008, 9, 15.	3.0	63
94	Crystal Structure of the FK506 Binding Domain of <i>Plasmodium falciparum</i> FKBP35 in Complex with FK506. <i>Biochemistry</i> , 2008, 47, 5951-5961.	1.2	35
95	Quantitative protein expression profiling reveals extensive post-transcriptional regulation and post-translational modifications in schizont-stage malaria parasites. <i>Genome Biology</i> , 2008, 9, R177.	13.9	107
96	The C-Terminal Segment of the Cysteine-Rich Interdomain of <i>Plasmodium falciparum</i> Erythrocyte Membrane Protein 1 Determines CD36 Binding and Elicits Antibodies That Inhibit Adhesion of Parasite-Infected Erythrocytes. <i>Infection and Immunity</i> , 2008, 76, 1837-1847.	1.0	16
97	The transcriptome of <i>Plasmodium vivax</i> reveals divergence and diversity of transcriptional regulation in malaria parasites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16290-16295.	3.3	234
98	ATP/ADP Binding to a Novel Nucleotide Binding Domain of the Reticulocyte-binding Protein Py235 of <i>Plasmodium yoelii</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 36386-36396.	1.6	12
99	Antibodies Targeting the PfRH1 Binding Domain Inhibit Invasion of <i>Plasmodium falciparum</i> Merozoites. <i>PLoS Pathogens</i> , 2008, 4, e1000104.	2.1	65
100	<i>Plasmodium falciparum</i> STEVOR Proteins Are Highly Expressed in Patient Isolates and Located in the Surface Membranes of Infected Red Blood Cells and the Apical Tips of Merozoites. <i>Infection and Immunity</i> , 2008, 76, 3329-3336.	1.0	63
101	Variable expression of the 235 kDa rhoptry protein of <i>Plasmodium yoelii</i> mediate host cell adaptation and immune evasion. <i>Molecular Microbiology</i> , 2007, 65, 333-346.	1.2	41
102	Invasion of host cells by malaria parasites: a tale of two protein families. <i>Molecular Microbiology</i> , 2007, 65, 231-249.	1.2	122
103	Variable expression of the 235 kDa rhoptry protein of <i>Plasmodium yoelii</i> mediate host cell adaptation and immune evasion. <i>Molecular Microbiology</i> , 2007, 65, 1596-1596.	1.2	3
104	Selection of long oligonucleotides for gene expression microarrays using weighted rank-sum strategy. <i>BMC Bioinformatics</i> , 2007, 8, 350.	1.2	50
105	Transcription and alternative splicing in the <i>yir</i> multigene family of the malaria parasite <i>Plasmodium yoelii</i> : Identification of motifs suggesting epigenetic and post-transcriptional control of RNA expression. <i>Molecular and Biochemical Parasitology</i> , 2007, 156, 1-11.	0.5	23
106	Automatic Analysis of Cos-7 Binding Assay Imagery for Malaria Vaccination Experiments. , 2006, , .		1
107	Estimating Malaria Parasitaemia from Blood Smear Images. , 2006, , .		43
108	Differences in the copy number of the <i>py235</i> gene family in virulent and avirulent lines of <i>Plasmodium yoelii</i> . <i>Molecular and Biochemical Parasitology</i> , 2006, 150, 186-191.	0.5	11

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109	Host immunity modulates transcriptional changes in a multigene family (yir) of rodent malaria. <i>Molecular Microbiology</i> , 2005, 58, 636-647.	1.2	41
110	Antibodies against MAEBL Ligand Domains M1 and M2 Inhibit Sporozoite Development In Vitro. <i>Infection and Immunity</i> , 2004, 72, 3604-3608.	1.0	46
111	Distinct Trafficking and Localization of STEVOR Proteins in Three Stages of the Plasmodium falciparum Life Cycle. <i>Infection and Immunity</i> , 2004, 72, 6597-6602.	1.0	76
112	The Py235 proteins: glimpses into the versatility of a malaria multigene family. <i>Microbes and Infection</i> , 2004, 6, 864-873.	1.0	27
113	Conservation and Developmental Control of Alternative Splicing in maebl Among Malaria Parasites. <i>Journal of Molecular Biology</i> , 2004, 343, 589-599.	2.0	41
114	Antigenic Variation in Plasmodium falciparum and Other Plasmodium Species. , 2003, , 291-318.		6
115	Analysis of Gene Expression by RT-PCR. , 2002, 72, 213-224.		1
116	Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii. <i>Nature</i> , 2002, 419, 512-519.	13.7	666
117	Parasite packs a punch. <i>Nature Medicine</i> , 2002, 8, 1198-1199.	15.2	0
118	A genetic screen for improved plasmid segregation reveals a role for Rep20 in the interaction of Plasmodium falciparum chromosomes. <i>EMBO Journal</i> , 2002, 21, 1231-1239.	3.5	106
119	Distribution and characterisation of the 235 kDa rhostry multigene family within the genomes of virulent and avirulent lines of Plasmodium yoelii. <i>Molecular and Biochemical Parasitology</i> , 2001, 114, 197-208.	0.5	21
120	The apical organelles of malaria merozoites: host cell selection, invasion, host immunity and immune evasion. <i>Microbes and Infection</i> , 2000, 2, 1461-1477.	1.0	101
121	Plasmodium yoelii:Differences in the Transcription of the 235-kDa Rhostry Protein Multigene Family in Lethal and Nonlethal Lines. <i>Experimental Parasitology</i> , 1998, 89, 50-57.	0.5	27
122	Evidence for a Single Origin of the 35 kb Plastid DNA in Apicomplexans. <i>Protist</i> , 1998, 149, 51-59.	0.6	56
123	Thiostrepton binds to malarial plastid rRNA. <i>FEBS Letters</i> , 1997, 406, 123-125.	1.3	83
124	Complete Gene Map of the Plastid-like DNA of the Malaria Parasite Plasmodium falciparum. <i>Journal of Molecular Biology</i> , 1996, 261, 155-172.	2.0	535
125	The evolutionary origin of the 35 kb circular DNA of Plasmodium falciparum: new evidence supports a possible rhodophyte ancestry. <i>Molecular Genetics and Genomics</i> , 1994, 243, 249-252.	2.4	113