

Zbynek Bozdech

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73
papers

7,151
citations

38
h-index

84
g-index

91
ext. papers

8,483
ext. citations

10
avg, IF

5.25
L-index

#	Paper	IF	Citations
73	Spread of artemisinin resistance in <i>Plasmodium falciparum</i> malaria. <i>New England Journal of Medicine</i> , 2014 , 371, 411-23	59.2	1366
72	The transcriptome of the intraerythrocytic developmental cycle of <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2003 , 1, E5	9.7	1175
71	Expression profiling of the schizont and trophozoite stages of <i>Plasmodium falciparum</i> with a long-oligonucleotide microarray. <i>Genome Biology</i> , 2003 , 4, R9	18.3	277
70	Drug resistance. Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. <i>Science</i> , 2015 , 347, 431-5	33.3	258
69	A role for the protease falcipain 1 in host cell invasion by the human malaria parasite. <i>Science</i> , 2002 , 298, 2002-6	33.3	247
68	Comparative whole genome transcriptome analysis of three <i>Plasmodium falciparum</i> strains. <i>Nucleic Acids Research</i> , 2006 , 34, 1166-73	20.1	239
67	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, 16290-5	11.5	197
66	Targeting the cell stress response of <i>Plasmodium falciparum</i> to overcome artemisinin resistance. <i>PLoS Biology</i> , 2015 , 13, e1002132	9.7	193
65	<i>Plasmodium falciparum</i> heterochromatin protein 1 marks genomic loci linked to phenotypic variation of exported virulence factors. <i>PLoS Pathogens</i> , 2009 , 5, e1000569	7.6	192
64	Heterochromatin protein 1 secures survival and transmission of malaria parasites. <i>Cell Host and Microbe</i> , 2014 , 16, 165-176	23.4	168
63	A subset of group A-like var genes encodes the malaria parasite ligands for binding to human brain endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E1772-81	11.5	158
62	Transcriptional variation in the malaria parasite <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2012 , 22, 925-38	9.7	157
61	Transcriptional profiling of growth perturbations of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature Biotechnology</i> , 2010 , 28, 91-8	44.5	155
60	Declining Efficacy of Artemisinin Combination Therapy Against <i>P. Falciparum</i> Malaria on the Thai-Myanmar Border (2003-2013): The Role of Parasite Genetic Factors. <i>Clinical Infectious Diseases</i> , 2016 , 63, 784-791	11.6	130
59	A major role for the <i>Plasmodium falciparum</i> ApiAP2 protein PfsIP2 in chromosome end biology. <i>PLoS Pathogens</i> , 2010 , 6, e1000784	7.6	125
58	Genome-wide identification of genes upregulated at the onset of gametocytogenesis in <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2005 , 143, 100-10	1.9	119
57	Artemisinin resistance in <i>Plasmodium falciparum</i> is associated with an altered temporal pattern of transcription. <i>BMC Genomics</i> , 2011 , 12, 391	4.5	107

56	Histone deacetylases play a major role in the transcriptional regulation of the Plasmodium falciparum life cycle. <i>PLoS Pathogens</i> , 2010 , 6, e1000737	7.6	106
55	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	18.3	97
54	Quantitative time-course profiling of parasite and host cell proteins in the human malaria parasite Plasmodium falciparum. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006411	7.6	95
53	Identifying purine nucleoside phosphorylase as the target of quinine using cellular thermal shift assay. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	81
52	Oxidative stress and protein damage responses mediate artemisinin resistance in malaria parasites. <i>PLoS Pathogens</i> , 2018 , 14, e1006930	7.6	78
51	Mechanistic insights into non-immunosuppressive immunophilin ligands as potential antimalarial therapeutics. <i>Malaria Journal</i> , 2010 , 9,	3.6	78
50	A Plasmodium Falciparum Bromodomain Protein Regulates Invasion Gene Expression. <i>Cell Host and Microbe</i> , 2015 , 17, 741-51	23.4	74
49	Dynamic epigenetic regulation of gene expression during the life cycle of malaria parasite Plasmodium falciparum. <i>PLoS Pathogens</i> , 2013 , 9, e1003170	7.6	67
48	Comparative transcriptional and genomic analysis of Plasmodium falciparum field isolates. <i>PLoS Pathogens</i> , 2009 , 5, e1000644	7.6	64
47	Antibodies targeting the PFRH1 binding domain inhibit invasion of Plasmodium falciparum merozoites. <i>PLoS Pathogens</i> , 2008 , 4, e1000104	7.6	59
46	Comparative Heterochromatin Profiling Reveals Conserved and Unique Epigenome Signatures Linked to Adaptation and Development of Malaria Parasites. <i>Cell Host and Microbe</i> , 2018 , 23, 407-420.e8 ²³⁻⁴	7.6	57
45	Plasmodium falciparum 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, 3329-36	3.7	56
44	Antioxidant defense in Plasmodium falciparum--data mining of the transcriptome. <i>Malaria Journal</i> , 2004 , 3, 23	3.6	54
43	Data mining of the transcriptome of Plasmodium falciparum: the pentose phosphate pathway and ancillary processes. <i>Malaria Journal</i> , 2005 , 4, 17	3.6	51
42	Comparative gene expression profiling of P. falciparum malaria parasites exposed to three different histone deacetylase inhibitors. <i>PLoS ONE</i> , 2012 , 7, e31847	3.7	51
41	DNA microarrays for malaria. <i>Trends in Parasitology</i> , 2002 , 18, 39-45	6.4	50
40	Epigenetic memory takes center stage in the survival strategy of malaria parasites. <i>Current Opinion in Microbiology</i> , 2014 , 20, 88-95	7.9	49
39	H2A.Z and H2B.Z double-variant nucleosomes define intergenic regions and dynamically occupy var gene promoters in the malaria parasite Plasmodium falciparum. <i>Molecular Microbiology</i> , 2013 , 87, 1167-82 ⁴¹	4.1	49

38	Selection of long oligonucleotides for gene expression microarrays using weighted rank-sum strategy. <i>BMC Bioinformatics</i> , 2007 , 8, 350	3.6	46
37	New insights into the Plasmodium vivax transcriptome using RNA-Seq. <i>Scientific Reports</i> , 2016 , 6, 20498	4.9	46
36	Adaptation of Plasmodium falciparum to its transmission environment. <i>Nature Ecology and Evolution</i> , 2018 , 2, 377-387	12.3	42
35	Biochemical analysis of the 20 S proteasome of Trypanosoma brucei. <i>Journal of Biological Chemistry</i> , 2003 , 278, 15800-8	5.4	36
34	Integrated analysis of the Plasmodium species transcriptome. <i>EBioMedicine</i> , 2016 , 7, 255-66	8.8	34
33	The human malaria parasite Plasmodium falciparum exports the ATP-binding cassette protein PFGCN20 to membrane structures in the host red blood cell. <i>Molecular and Biochemical Parasitology</i> , 1998 , 97, 81-95	1.9	33
32	Analysis of subtelomeric virulence gene families in Plasmodium falciparum by comparative transcriptional profiling. <i>Molecular Microbiology</i> , 2012 , 84, 243-59	4.1	31
31	DNA damage regulation and its role in drug-related phenotypes in the malaria parasites. <i>Scientific Reports</i> , 2016 , 6, 23603	4.9	31
30	Crystal structure of the FK506 binding domain of Plasmodium falciparum FKBP35 in complex with FK506. <i>Biochemistry</i> , 2008 , 47, 5951-61	3.2	28
29	Cellular thermal shift assay for the identification of drug-target interactions in the Plasmodium falciparum proteome. <i>Nature Protocols</i> , 2020 , 15, 1881-1921	18.8	27
28	Identification of a new chemical class of antimalarials. <i>Journal of Infectious Diseases</i> , 2012 , 206, 735-43	7	23
27	Structural polymorphism in the promoter of pfmrp2 confers Plasmodium falciparum tolerance to quinoline drugs. <i>Molecular Microbiology</i> , 2014 , 91, 918-34	4.1	22
26	Cloning and sequence analysis of a novel member of the ATP-binding cassette (ABC) protein gene family from Plasmodium falciparum. <i>Molecular and Biochemical Parasitology</i> , 1996 , 81, 41-51	1.9	22
25	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. <i>Malaria Journal</i> , 2015 , 14, 110	3.6	21
24	The origins of malaria artemisinin resistance defined by a genetic and transcriptomic background. <i>Nature Communications</i> , 2018 , 9, 5158	17.4	21
23	A whole cell pathway screen reveals seven novel chemosensitizers to combat chloroquine resistant malaria. <i>Scientific Reports</i> , 2013 , 3, 1734	4.9	19
22	Quantitative proteomics reveals new insights into erythrocyte invasion by Plasmodium falciparum. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M1111.010645	7.6	18
21	Artemisinin-resistant K13 mutations rewire Plasmodium falciparum's intra-erythrocytic metabolic program to enhance survival. <i>Nature Communications</i> , 2021 , 12, 530	17.4	18

20	Epigenetic landscapes underlining global patterns of gene expression in the human malaria parasite, <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology</i> , 2017 , 47, 399-407	4.3	17
19	Histone 4 lysine 8 acetylation regulates proliferation and host-pathogen interaction in <i>Plasmodium falciparum</i> . <i>Epigenetics and Chromatin</i> , 2017 , 10, 40	5.8	15
18	Genome-wide analysis in <i>Plasmodium falciparum</i> reveals early and late phases of RNA polymerase II occupancy during the infectious cycle. <i>BMC Genomics</i> , 2014 , 15, 959	4.5	14
17	DNA microarray-based genome-wide analyses of <i>Plasmodium</i> parasites. <i>Methods in Molecular Biology</i> , 2013 , 923, 189-211	1.4	13
16	Design of a variant surface antigen-supplemented microarray chip for whole transcriptome analysis of multiple <i>Plasmodium falciparum</i> cytoadherent strains, and identification of strain-transcendent rif and stevor genes. <i>Malaria Journal</i> , 2011 , 10, 180	3.6	12
15	A moonlighting function of <i>Plasmodium falciparum</i> histone 3, mono-methylated at lysine 9?. <i>PLoS ONE</i> , 2010 , 5, e10252	3.7	12
14	Defining species specific genome differences in malaria parasites. <i>BMC Genomics</i> , 2010 , 11, 128	4.5	11
13	Gene copy number variation in natural populations of <i>Plasmodium falciparum</i> in Eastern Africa. <i>BMC Genomics</i> , 2018 , 19, 372	4.5	10
12	Transcriptome profiling reveals functional variation in <i>Plasmodium falciparum</i> parasites from controlled human malaria infection studies. <i>EBioMedicine</i> , 2019 , 48, 442-452	8.8	9
11	Role of calcium signaling in the transcriptional regulation of the apicoplast genome of <i>Plasmodium falciparum</i> . <i>BioMed Research International</i> , 2014 , 2014, 869401	3	8
10	The genomics of malaria infection. <i>Trends in Parasitology</i> , 2004 , 20, 553-7	6.4	8
9	A crucial piece in the puzzle of the artemisinin resistance mechanism in <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2015 , 31, 345-6	6.4	5
8	A heat-shock response regulated by the PfAP2-HS transcription factor protects human malaria parasites from febrile temperatures. <i>Nature Microbiology</i> , 2021 , 6, 1163-1174	26.6	5
7	The parasitophorous vacuole nutrient channel is critical for drug access in malaria parasites and modulates the artemisinin resistance fitness cost. <i>Cell Host and Microbe</i> , 2021 , 29, 1774-1787.e9	23.4	4
6	Protein transport in the host cell cytoplasm and ATP-binding cassette proteins in <i>Plasmodium falciparum</i> -infected erythrocytes. <i>Novartis Foundation Symposium</i> , 1999 , 226, 231-41; discussion 241-5		4
5	A comprehensive RNA handling and transcriptomics guide for high-throughput processing of <i>Plasmodium</i> blood-stage samples. <i>Malaria Journal</i> , 2020 , 19, 363	3.6	3
4	Reticulocyte Infection Leads to Altered Behaviour, Drug Sensitivity and Host Cell Remodelling by <i>Plasmodium falciparum</i>		1
3	Transcriptomics and proteomics 2016 , 197-217		1

2	Artemisinin resistance in the malaria parasite, Plasmodium falciparum, originates from its initial transcriptional response.. <i>Communications Biology</i> , 2022 , 5, 274	6.7	1
1	Mediator Complex of the Malaria Parasite Associates with Evolutionarily Novel Subunits.. <i>ACS Omega</i> , 2022 , 7, 14867-14874	3.9	