

Zbynek Bozdech

List of Publications by Year in descending order

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74
papers

9,214
citations

71102

41
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76900

74
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91
all docs

91
docs citations

91
times ranked

7345
citing authors

#	ARTICLE	IF	CITATIONS
1	Artemisinin resistance in the malaria parasite, <i>Plasmodium falciparum</i> , originates from its initial transcriptional response. <i>Communications Biology</i> , 2022, 5, 274.	4.4	33
2	Mediator Complex of the Malaria Parasite <i>Plasmodium falciparum</i> Associates with Evolutionarily Novel Subunits. <i>ACS Omega</i> , 2022, 7, 14867-14874.	3.5	1
3	Stochastic expression of invasion genes in <i>Plasmodium falciparum</i> schizonts. <i>Nature Communications</i> , 2022, 13, .	12.8	9
4	Human peroxiredoxin 6 is essential for malaria parasites and provides a host-based drug target. <i>Cell Reports</i> , 2022, 39, 110923.	6.4	10
5	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.	13.3	30
6	Artemisinin-resistant K13 mutations rewire <i>Plasmodium falciparum</i> 's intra-erythrocytic metabolic program to enhance survival. <i>Nature Communications</i> , 2021, 12, 530.	12.8	82
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.	11.0	21
8	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.	2.3	19
9	Cellular thermal shift assay for the identification of drug-target interactions in the <i>Plasmodium falciparum</i> proteome. <i>Nature Protocols</i> , 2020, 15, 1881-1921.	12.0	79
10	Transcriptome profiling reveals functional variation in <i>Plasmodium falciparum</i> parasites from controlled human malaria infection studies. <i>EBioMedicine</i> , 2019, 48, 442-452.	6.1	19
11	Identifying purine nucleoside phosphorylase as the target of quinine using cellular thermal shift assay. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	153
12	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.	11.0	99
13	Adaptation of <i>Plasmodium falciparum</i> to its transmission environment. <i>Nature Ecology and Evolution</i> , 2018, 2, 377-387.	7.8	65
14	The origins of malaria artemisinin resistance defined by a genetic and transcriptomic background. <i>Nature Communications</i> , 2018, 9, 5158.	12.8	41
15	Gene copy number variation in natural populations of <i>Plasmodium falciparum</i> in Eastern Africa. <i>BMC Genomics</i> , 2018, 19, 372.	2.8	12
16	Oxidative stress and protein damage responses mediate artemisinin resistance in malaria parasites. <i>PLoS Pathogens</i> , 2018, 14, e1006930.	4.7	129
17	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.	3.1	26
18	Histone 4 lysine 8 acetylation regulates proliferation and host-pathogen interaction in <i>Plasmodium falciparum</i> . <i>Epigenetics and Chromatin</i> , 2017, 10, 40.	3.9	28

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19	New insights into the Plasmodium vivax transcriptome using RNA-Seq. Scientific Reports, 2016, 6, 20498.	3.3	65
20	DNA damage regulation and its role in drug-related phenotypes in the malaria parasites. Scientific Reports, 2016, 6, 23603.	3.3	54
21	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. Clinical Infectious Diseases, 2016, 63, 784-791.	5.8	178
22	Integrated analysis of the Plasmodium species transcriptome. EBioMedicine, 2016, 7, 255-266.	6.1	55
23	A Plasmodium Falciparum Bromodomain Protein Regulates Invasion Gene Expression. Cell Host and Microbe, 2015, 17, 741-751.	11.0	96
24	A crucial piece in the puzzle of the artemisinin resistance mechanism in Plasmodium falciparum. Trends in Parasitology, 2015, 31, 345-346.	3.3	6
25	Targeting the Cell Stress Response of Plasmodium falciparum to Overcome Artemisinin Resistance. PLoS Biology, 2015, 13, e1002132.	5.6	254
26	Plasmodium knowlesi gene expression differs in ex vivo compared to in vitro blood-stage cultures. Malaria Journal, 2015, 14, 110.	2.3	31
27	Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. Science, 2015, 347, 431-435.	12.6	362
28	Spread of Artemisinin Resistance in <i>Plasmodium falciparum</i> Malaria. New England Journal of Medicine, 2014, 371, 411-423.	27.0	1,753
29	Role of Calcium Signaling in the Transcriptional Regulation of the Apicoplast Genome of <i>Plasmodium falciparum</i> . BioMed Research International, 2014, 2014, 1-12.	1.9	12
30	Structural polymorphism in the promoter of <i>pfmrp2</i> confers <i>Plasmodium falciparum</i> tolerance to quinoline drugs. Molecular Microbiology, 2014, 91, 918-934.	2.5	28
31	Genome-wide analysis in Plasmodium falciparum reveals early and late phases of RNA polymerase II occupancy during the infectious cycle. BMC Genomics, 2014, 15, 959.	2.8	24
32	Epigenetic memory takes center stage in the survival strategy of malaria parasites. Current Opinion in Microbiology, 2014, 20, 88-95.	5.1	67
33	Heterochromatin Protein 1 Secures Survival and Transmission of Malaria Parasites. Cell Host and Microbe, 2014, 16, 165-176.	11.0	225
34	Dynamic Epigenetic Regulation of Gene Expression during the Life Cycle of Malaria Parasite Plasmodium falciparum. PLoS Pathogens, 2013, 9, e1003170.	4.7	90
35	A Whole Cell Pathway Screen Reveals Seven Novel Chemosensitizers to Combat Chloroquine Resistant Malaria. Scientific Reports, 2013, 3, 1734.	3.3	23
36	<i>H2A.Z</i> and <i>H2B.Z</i> double variant nucleosomes define intergenic regions and dynamically occupy <i>Pf</i> gene promoters in the malaria parasite <i>Plasmodium falciparum</i> . Molecular Microbiology, 2013, 87, 1167-1182.	2.5	67

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37	A subset of group A-like <i>var</i> genes encodes the malaria parasite ligands for binding to human brain endothelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1772-81.	7.1	183
38	Identification of a New Chemical Class of Antimalarials. Journal of Infectious Diseases, 2012, 206, 735-743.	4.0	28
39	Quantitative Proteomics Reveals New Insights into Erythrocyte Invasion by Plasmodium falciparum. Molecular and Cellular Proteomics, 2012, 11, M111.010645.	3.8	20
40	Transcriptional variation in the malaria parasite <i>Plasmodium falciparum</i> . Genome Research, 2012, 22, 925-938.	5.5	194
41	Analysis of subtelomeric virulence gene families in <i>Plasmodium falciparum</i> by comparative transcriptional profiling. Molecular Microbiology, 2012, 84, 243-259.	2.5	38
42	DNA Microarray-Based Genome-Wide Analyses of Plasmodium Parasites. Methods in Molecular Biology, 2012, 923, 189-211.	0.9	21
43	Comparative Gene Expression Profiling of <i>P. falciparum</i> Malaria Parasites Exposed to Three Different Histone Deacetylase Inhibitors. PLoS ONE, 2012, 7, e31847.	2.5	63
44	Quantitative Time-course Profiling of Parasite and Host Cell Proteins in the Human Malaria Parasite <i>Plasmodium falciparum</i> . Molecular and Cellular Proteomics, 2011, 10, M110.006411.	3.8	145
45	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. Malaria Journal, 2011, 10, 180.	2.3	13
46	Artemisinin resistance in <i>Plasmodium falciparum</i> is associated with an altered temporal pattern of transcription. BMC Genomics, 2011, 12, 391.	2.8	135
47	Defining species specific genome differences in malaria parasites. BMC Genomics, 2010, 11, 128.	2.8	12
48	Transcriptional profiling of growth perturbations of the human malaria parasite <i>Plasmodium falciparum</i> . Nature Biotechnology, 2010, 28, 91-98.	17.5	196
49	A Major Role for the <i>Plasmodium falciparum</i> ApiAP2 Protein PfSIP2 in Chromosome End Biology. PLoS Pathogens, 2010, 6, e1000784.	4.7	150
50	Histone Deacetylases Play a Major Role in the Transcriptional Regulation of the <i>Plasmodium falciparum</i> Life Cycle. PLoS Pathogens, 2010, 6, e1000737.	4.7	135
51	Mechanistic insights into non-immunosuppressive immunophilin ligands as potential antimalarial therapeutics. Malaria Journal, 2010, 9, .	2.3	0
52	It is all in your head: a model for cerebral malaria. Malaria Journal, 2010, 9, .	2.3	0
53	A Moonlighting Function of <i>Plasmodium falciparum</i> Histone 3, Mono-Methylated at Lysine 9?. PLoS ONE, 2010, 5, e10252.	2.5	14
54	<i>Plasmodium falciparum</i> Heterochromatin Protein 1 Marks Genomic Loci Linked to Phenotypic Variation of Exported Virulence Factors. PLoS Pathogens, 2009, 5, e1000569.	4.7	243

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55	Comparative Transcriptional and Genomic Analysis of Plasmodium falciparum Field Isolates. PLoS Pathogens, 2009, 5, e1000644.	4.7	76
56	Crystal Structure of the FK506 Binding Domain of <i>Plasmodium falciparum</i> FKBP35 in Complex with FK506. Biochemistry, 2008, 47, 5951-5961.	2.5	35
57	Quantitative protein expression profiling reveals extensive post-transcriptional regulation and post-translational modifications in schizont-stage malaria parasites. Genome Biology, 2008, 9, R177.	9.6	107
58	The transcriptome of <i>Plasmodium vivax</i> reveals divergence and diversity of transcriptional regulation in malaria parasites. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16290-16295.	7.1	234
59	Antibodies Targeting the PfRH1 Binding Domain Inhibit Invasion of Plasmodium falciparum Merozoites. PLoS Pathogens, 2008, 4, e1000104.	4.7	65
60	<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. Infection and Immunity, 2008, 76, 3329-3336.	2.2	63
61	Selection of long oligonucleotides for gene expression microarrays using weighted rank-sum strategy. BMC Bioinformatics, 2007, 8, 350.	2.6	50
62	Comparative whole genome transcriptome analysis of three Plasmodium falciparum strains. Nucleic Acids Research, 2006, 34, 1166-1173.	14.5	289
63	Genome-wide identification of genes upregulated at the onset of gametocytogenesis in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2005, 143, 100-110.	1.1	135
64	Data mining of the transcriptome of Plasmodium falciparum: the pentose phosphate pathway and ancillary processes. Malaria Journal, 2005, 4, 17.	2.3	59
65	The genomics of malaria infection. Trends in Parasitology, 2004, 20, 553-557.	3.3	9
66	Antioxidant defense in Plasmodium falciparum—data mining of the transcriptome. Malaria Journal, 2004, 3, 23.	2.3	70
67	Expression profiling of the schizont and trophozoite stages of Plasmodium falciparum with a long-oligonucleotide microarray. Genome Biology, 2003, 4, R9.	9.6	317
68	Biochemical Analysis of the 20 S Proteasome of Trypanosoma brucei. Journal of Biological Chemistry, 2003, 278, 15800-15808.	3.4	40
69	The Transcriptome of the Intraerythrocytic Developmental Cycle of Plasmodium falciparum. PLoS Biology, 2003, 1, e5.	5.6	1,433
70	A Role for the Protease Falcipain 1 in Host Cell Invasion by the Human Malaria Parasite. Science, 2002, 298, 2002-2006.	12.6	265
71	DNA microarrays for malaria. Trends in Parasitology, 2002, 18, 39-45.	3.3	58
72	Protein Transport in the Host Cell Cytoplasm and ATP-binding Cassette Proteins in <i>Plasmodium falciparum</i> Infected Erythrocytes. Novartis Foundation Symposium, 1999, 226, 231-251.	1.1	4

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73	The human malaria parasite <i>Plasmodium falciparum</i> 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.	1.1	33
74	Cloning and sequence analysis of a novel member of the ATP-binding cassette (ABC) protein gene family from <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 1996, 81, 41-51.	1.1	23