Jude M Przyborski

List of Publications by Year
in descending order

76	2,995	172457	182427
papers	citations	29 h-index	51 g-index

78	78	78	2468
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A single member of the Plasmodium falciparum var multigene family determines cytoadhesion to the placental receptor chondroitin sulphate A. EMBO Reports, 2005, 6, 775-781.	4.5	187
2	Der1-mediated Preprotein Import into the Periplastid Compartment of Chromalveolates?. Molecular Biology and Evolution, 2007, 24, 918-928.	8.9	142
3	Compartmentation of Redox Metabolism in Malaria Parasites. PLoS Pathogens, 2010, 6, e1001242.	4.7	139
4	Plasmodium falciparum-encoded exported hsp70/hsp40 chaperone/co-chaperone complexes within the host erythrocyte. Cellular Microbiology, 2012, 14, 1784-1795.	2.1	137
5	An Unusual ERAD-Like Complex Is Targeted to the Apicoplast ofPlasmodium falciparum. Eukaryotic Cell, 2009, 8, 1134-1145.	3.4	136
6	Protein unfolding is an essential requirement for transport across the parasitophorous vacuolar membrane of Plasmodium falciparum. Molecular Microbiology, 2009, 71, 613-628.	2.5	126
7	Trafficking of STEVOR to the Maurer's clefts in Plasmodium falciparum-infected erythrocytes. EMBO Journal, 2005, 24, 2306-2317.	7.8	125
8	Parasite-encoded Hsp40 proteins define novel mobile structures in the cytosol of the P. falciparum-infected erythrocyte. Cellular Microbiology, 2010, 12, 1398-1420.	2.1	117
9	Intracellular Protozoan Parasites of Humans: The Role of Molecular Chaperones in Development and Pathogenesis. Protein and Peptide Letters, 2011, 18, 143-157.	0.9	115
10	Uncovering Common Principles in Protein Export of Malaria Parasites. Cell Host and Microbe, 2012, 12, 717-729.	11.0	115
11	Spatial association with PTEX complexes defines regions for effector export into Plasmodium falciparum-infected erythrocytes. Nature Communications, 2013, 4, 1415.	12.8	79
12	Export of malaria proteins requires co-translational processing of the PEXEL motif independent of phosphatidylinositol-3-phosphate binding. Nature Communications, 2016, 7, 10470.	12.8	65
13	Maurerâ€™s cleftsâ€”a novel secretory organelle?. Molecular and Biochemical Parasitology, 2003, 132, 17-26.	1.1	64
14	Malaria proteases mediate inside-out egress of gametocytes from red blood cells following parasite transmission to the mosquito. Cellular Microbiology, 2011, 13, 897-912.	2.1	63
15	Characterisation of the Plasmodium falciparum Hsp70â€“Hsp90 organising protein (PfHop). Cell Stress and Chaperones, 2012, 17, 191-202.	2.9	63
16	Distribution of the SELMA Translocon in Secondary Plastids of Red Algal Origin and Predicted Uncoupling of Ubiquitin-Dependent Translocation from Degradation. Eukaryotic Cell, 2012, 11, 1472-1481.	3.4	58
17	Wherever I may roam: Protein and membrane trafficking in P. falciparum-infected red blood cells. Molecular and Biochemical Parasitology, 2012, 186, 95-116.	1.1	56
18	Plasmodium falciparum encodes a single cytosolic type I Hsp40 that functionally interacts with Hsp70 and is upregulated by heat shock. Cell Stress and Chaperones, 2011, 16, 389-401.	2.9	54

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19	The long and winding road: Protein trafficking mechanisms in the Plasmodium falciparum infected erythrocyte. Molecular and Biochemical Parasitology, 2006, 147, 1-8.	1.1	47
20	Protein Transport Across the Parasitophorous Vacuole of Plasmodium falciparum: Into the Great Wide Open. Traffic, 2008, 9, 157-165.	2.7	47
21	Plasmodial HSP70s are functionally adapted to the malaria parasite life cycle. Frontiers in Molecular Biosciences, 2015, 2, 34.	3.5	45
22	The exported chaperone Hsp70-x supports virulence functions for Plasmodium falciparum blood stage parasites. PLoS ONE, 2017, 12, e0181656.	2.5	45
23	Two nucleusâ€localized CDKâ€like kinases with crucial roles for malaria parasite erythrocytic replication are involved in phosphorylation of splicing factor. Journal of Cellular Biochemistry, 2011, 112, 1295-1310.	2.6	44
24	Transport of nuclear-encoded proteins into secondarily evolved plastids. Biological Chemistry, 2007, 388, 899-906.	2.5	40
25	Plasmodium falciparum Hop (PfHop) Interacts with the Hsp70 Chaperone in a Nucleotide-Dependent Fashion and Exhibits Ligand Selectivity. PLoS ONE, 2015, 10, e0135326.	2.5	40
26	Proteomic analysis of exported chaperone/co-chaperone complexes of P. falciparum reveals an array of complex protein-protein interactions. Scientific Reports, 2017, 7, 42188.	3.3	38
27	Protein Traffic to the Plasmodium falciparum Apicoplast: Evidence for a Sorting Branch Point at the Golgi. Traffic, 2014, 15, 1290-1304.	2.7	36
28	Toxoplasma gondii Toc75 Functions in Import of Stromal but not Peripheral Apicoplast Proteins. Traffic, 2015, 16, 1254-1269.	2.7	36
29	Willingness to pay for hypothetical malaria vaccines in rural Burkina Faso. Scandinavian Journal of Public Health, 2005, 33, 146-150.	2.3	33
30	Distinct subcellular localization in the cytosol and apicoplast, unexpected dimerization and inhibition of Plasmodium falciparum glyoxalases. Molecular Microbiology, 2010, 76, 92-103.	2.5	32
31	Determination of glutathione redox potential and pH value in subcellular compartments of malaria parasites. Free Radical Biology and Medicine, 2017, 104, 104-117.	2.9	32
32	Partners in Mischief: Functional Networks of Heat Shock Proteins of Plasmodium falciparum and Their Influence on Parasite Virulence. Biomolecules, 2019, 9, 295.	4.0	31
33	J-dot targeting of an exported HSP40 in Plasmodium falciparum-infected erythrocytes. International Journal for Parasitology, 2016, 46, 519-525.	3.1	29
34	Recovery of adhesion to chondroitin-4-sulphate in Plasmodium falciparum var CSA disruption mutants by antigenically similar PfEMP1 variants. Molecular Microbiology, 2004, 49, 655-669.	2.5	28
35	Recruitment of human aquaporin 3 to internal membranes in the Plasmodium falciparum infected erythrocyte. Molecular and Biochemical Parasitology, 2009, 167, 48-53.	1.1	27
36	A Plasmodium falciparum copper-binding membrane protein with copper transport motifs. Malaria Journal, 2012, 11, 397.	2.3	25

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37	Plasmodium glyceraldehyde-3-phosphate dehydrogenase: A potential malaria diagnostic target. Experimental Parasitology, 2017, 179, 7-19.	1.2	25
38	Hydrogen peroxide dynamics in subcellular compartments of malaria parasites using genetically encoded redox probes. Scientific Reports, 2017, 7, 10449.	3.3	24
39	PARASITOLOGY: The Malarial Secretome. Science, 2004, 306, 1897-1898.	12.6	23
40	Trafficking of the exported P. falciparum chaperone PfHsp70x. Scientific Reports, 2016, 6, 36174.	3.3	23
41	Genetic Evidence Strongly Support an Essential Role for PfPV1 in Intra-Erythrocytic Growth of P. falciparum. PLoS ONE, 2011, 6, e18396.	2.5	23
42	A seven-helix protein constitutes stress granules crucial for regulating translation during human-to-mosquito transmission of Plasmodium falciparum. PLoS Pathogens, 2018, 14, e1007249.	4.7	22
43	The apicomplexan parasiteBabesia divergensinternalizes band 3, glycophorin A and spectrin during invasion of human red blood cells. Cellular Microbiology, 2015, 17, 1052-1068.	2.1	21
44	Ticket to ride: export of proteins to the Plasmodium falciparumâ€infected erythrocyte. Molecular Microbiology, 2016, 101, 1-11.	2.5	21
45	Genomic and Proteomic Evidence for the Presence of a Peroxisome in the Apicomplexan Parasite Toxoplasma gondii and Other Coccidia. Genome Biology and Evolution, 2017, 9, 3108-3121.	2.5	21
46	A patatinâ€like phospholipase functions during gametocyte induction in the malaria parasite Plasmodium falciparum. Cellular Microbiology, 2020, 22, e13146.	2.1	21
47	Alternative Protein Secretion in the Malaria Parasite Plasmodium falciparum. PLoS ONE, 2015, 10, e0125191.	2.5	19
48	Characterization of Tt ALV2, an Essential Charged Repeat Motif Protein of the Tetrahymena thermophila Membrane Skeleton. Eukaryotic Cell, 2013, 12, 932-940.	3.4	17
49	PFB0595w is a Plasmodium falciparum J protein that co-localizes with PfHsp70-1 and can stimulate its in vitro ATP hydrolysis activity. International Journal of Biochemistry and Cell Biology, 2015, 62, 47-53.	2.8	17
50	The malaria parasite Plasmodium falciparum: cell biological peculiarities and nutritional consequences. Protoplasma, 2010, 240, 3-12.	2.1	16
51	Subcellular localization of adenylate kinases in Plasmodium falciparum. FEBS Letters, 2012, 586, 3037-3043.	2.8	16
52	Functional relevance of in vivo half antibody exchange of an IgG4 therapeutic antibody-drug conjugate. PLoS ONE, 2018, 13, e0195823.	2.5	16
53	Return to sender: use of Plasmodium ER retrieval sequences to study protein transport in the infected erythrocyte and predict putative ER protein families. Parasitology Research, 2009, 104, 1535-1541.	1.6	15
54	Insight into the Selenoproteome of the Malaria ParasitePlasmodium falciparum. Antioxidants and Redox Signaling, 2012, 17, 534-543.	5.4	15

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55	A WD40-repeat protein unique to malaria parasites associates with adhesion protein complexes and is crucial for blood stage progeny. Malaria Journal, 2015, 14, 435.	2.3	14
56	Use of self-assembling GFP to determine protein topology and compartmentalisation in the Plasmodium falciparum-infected erythrocyte. Molecular and Biochemical Parasitology, 2013, 187, 87-90.	1.1	13
57	Trafficking of PfExp1 to the parasitophorous vacuolar membrane ofPlasmodium falciparumis independent of protein folding and the PTEX translocon. Cellular Microbiology, 2017, 19, e12710.	2.1	11
58	Identification and initial characterisation of a Plasmodium falciparum Cox17 copper metallochaperone. Experimental Parasitology, 2015, 148, 30-39.	1.2	10
59	A nuclear protein, PfMORC confers melatonin dependent synchrony of the human malaria parasite P. falciparum in the asexual stage. Scientific Reports, 2021, 11, 2057.	3.3	10
60	Fractionation of Plasmodium-Infected Human Red Blood Cells to Study Protein Trafficking. Methods in Molecular Biology, 2015, 1270, 71-80.	0.9	10
61	Prokaryotic ancestry and gene fusion of a dual localized peroxiredoxin in malaria parasites. Microbial Cell, 2015, 2, 5-13.	3.2	9
62	Co-chaperone involvement in knob biogenesis implicates host-derived chaperones in malaria virulence. PLoS Pathogens, 2021, 17, e1009969.	4.7	9
63	The histone H4 gene of Plasmodium falciparum is developmentally transcribed in asexual parasites. Parasitology Research, 2003, 90, 387-389.	1.6	8
64	The Maurer's clefts of Plasmodium falciparum: parasite-induced islands within an intracellular ocean. Trends in Parasitology, 2008, 24, 285-288.	3.3	8
65	Proteomic analysis of Plasmodium falciparum histone deacetylase 1 complex proteins. Experimental Parasitology, 2019, 198, 7-16.	1.2	8
66	A Putative Non-Canonical Ras-Like GTPase from P. falciparum: Chemical Properties and Characterization of the Protein. PLoS ONE, 2015, 10, e0140994.	2.5	6
67	Identification of sulfenylation patterns in trophozoite stage Plasmodium falciparum using a non-dimedone based probe. Molecular and Biochemical Parasitology, 2021, 242, 111362.	1.1	6
68	TLR8 is activated by 5Ê¹-methylthioinosine, a Plasmodium falciparum-derived intermediate of the purine salvage pathway. Cell Reports, 2022, 39, 110691.	6.4	6
69	The N-terminal extension of the P. falciparum GBP130 signal peptide is irrelevant for signal sequence function. International Journal of Medical Microbiology, 2018, 308, 3-12.	3.6	5
70	Structure and Function of Redox-Sensitive Superfolder Green Fluorescent Protein Variant. Antioxidants and Redox Signaling, 2022, 37, 1-18.	5.4	5
71	Protein biochemistry: Don't forget the cell biology. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 456.	2.3	3
72	Introductory Chapter: The Importance of Heat Shock Proteins in Survival and Pathogenesis of the Malaria Parasite Plasmodium falciparum. Advances in Experimental Medicine and Biology, 2021, 1340, 1-9.	1.6	1

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73	Babesia divergens-infected red blood cells take up glutamate via an EAAT3 independent mechanism. International Journal of Medical Microbiology, 2018, 308, 148-154.	3.6	0
74	Detection of the in vitro modulation of Plasmodium falciparum Arf1 by Sec7 and ArfGAP domains using a colorimetric plate-based assay. Scientific Reports, 2020, 10, 4193.	3.3	0
75	Protein Traffic. , 2013, , 1-12.		0
76	Characterization of Plasmodium falciparum macrophage migration inhibitory factor homologue and its cysteine deficient mutants. Parasitology International, 2022, 87, 102513.	1.3	0