Matthew Higgins

List of Publications by Year in descending order

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79 5,093 papers citations

36 68
h-index g-index

95266

87 87 all docs citations

87 times ranked 5805 citing authors

#	Article	IF	CITATIONS
1	Heterotypic interactions drive antibody synergy against a malaria vaccine candidate. Nature Communications, 2022, 13, 933.	12.8	23
2	Why it might be bad for brain cells to eat malaria parasites. Journal of Experimental Medicine, 2021, 218, .	8.5	0
3	Structure-Guided Design of a Synthetic Mimic of an Endothelial Protein C Receptor-Binding PfEMP1 Protein. MSphere, 2021, 6, .	2.9	3
4	Can We AlphaFold Our Way Out of the Next Pandemic?. Journal of Molecular Biology, 2021, 433, 167093.	4.2	20
5	High-throughput hit-squad tackles trypanosomes. Trends in Parasitology, 2021, 37, 772-774.	3. 3	1
6	Design of a basiginâ€mimicking inhibitor targeting the malaria invasion protein RH5. Proteins: Structure, Function and Bioinformatics, 2020, 88, 187-195.	2.6	6
7	Staging an Antibody Contest to Fight Malaria. Immunity, 2020, 53, 697-699.	14.3	0
8	Structural basis for RIFIN-mediated activation of LILRB1 in malaria. Nature, 2020, 587, 309-312.	27.8	30
9	Structure of the Inhibited State of the Sec Translocon. Molecular Cell, 2020, 79, 406-415.e7.	9.7	44
10	Structure of the <i>Plasmodium</i> -interspersed repeat proteins of the malaria parasite. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32098-32104.	7.1	10
11	The Structure of the Cysteine-Rich Domain of Plasmodium falciparum P113 Identifies the Location of the RH5 Binding Site. MBio, 2020, $11,\ldots$	4.1	7
12	A spike with which to beat COVID-19?. Nature Reviews Microbiology, 2020, 18, 414-414.	28.6	5
13	The RH5-CyRPA-Ripr Complex as a Malaria Vaccine Target. Trends in Parasitology, 2020, 36, 545-559.	3.3	47
14	A receptor for the complement regulator factor H increases transmission of trypanosomes to tsetse flies. Nature Communications, 2020, 11, 1326.	12.8	23
15	Analysis of Plasmodium falciparum Rh2b deletion polymorphism across different transmission areas. Scientific Reports, 2020, 10, 1498.	3.3	3
16	A helminth-derived suppressor of ST2 blocks allergic responses. ELife, 2020, 9, .	6.0	39
17	Structure of the trypanosome transferrin receptor reveals mechanisms of ligand recognition and immune evasion. Nature Microbiology, 2019, 4, 2074-2081.	13.3	20
18	A single dose of antibody-drug conjugate cures a stage 1 model of African trypanosomiasis. PLoS Neglected Tropical Diseases, 2019, 13, e0007373.	3.0	11

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19	Structural basis for inhibition of Plasmodium vivax invasion by a broadly neutralizing vaccine-induced human antibody. Nature Microbiology, 2019, 4, 1497-1507.	13.3	48
20	Functional Comparison of Blood-Stage Plasmodium falciparum Malaria Vaccine Candidate Antigens. Frontiers in Immunology, 2019, 10, 1254.	4.8	31
21	Human Antibodies that Slow Erythrocyte Invasion Potentiate Malaria-Neutralizing Antibodies. Cell, 2019, 178, 216-228.e21.	28.9	107
22	Divergent roles for the RH5 complex components, CyRPA and RIPR in human-infective malaria parasites. PLoS Pathogens, 2019, 15, e1007809.	4.7	29
23	Structural insights into diverse modes of ICAM-1 binding by <i>Plasmodium falciparum</i> -infected erythrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20124-20134.	7.1	24
24	In silico guided reconstruction and analysis of ICAM-1-binding var genes from Plasmodium falciparum. Scientific Reports, 2018, 8, 3282.	3.3	4
25	A new site of attack for a malaria vaccine. Nature Medicine, 2018, 24, 382-383.	30.7	5
26	The structure of serum resistance-associated protein and its implications for human African trypanosomiasis. Nature Microbiology, 2018, 3, 295-301.	13.3	21
27	Structural basis for recognition of the malaria vaccine candidate Pfs48/45 by a transmission blocking antibody. Nature Communications, 2018, 9, 3822.	12.8	39
28	O-h what a surprise. Nature Microbiology, 2018, 3, 856-857.	13.3	2
29	Malaria Vaccines: Recent Advances and New Horizons. Cell Host and Microbe, 2018, 24, 43-56.	11.0	234
30	Production, quality control, stability, and potency of cGMP-produced Plasmodium falciparum RH5.1 protein vaccine expressed in Drosophila S2 cells. Npj Vaccines, 2018, 3, 32.	6.0	53
31	One-step design of a stable variant of the malaria invasion protein RH5 for use as a vaccine immunogen. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 998-1002.	7.1	7 5
32	Accelerating the clinical development of protein-based vaccines for malaria by efficient purification using a four amino acid C-terminal ‰C-tag'. International Journal for Parasitology, 2017, 47, 435-446.	3.1	55
33	Structure-Guided Identification of a Family of Dual Receptor-Binding PfEMP1 that Is Associated with Cerebral Malaria. Cell Host and Microbe, 2017, 21, 403-414.	11.0	140
34	On the state of crystallography at the dawn of the electron microscopy revolution. Current Opinion in Structural Biology, 2017, 46, 95-101.	5.7	11
35	Towards an anti-disease malaria vaccine. Emerging Topics in Life Sciences, 2017, 1, 539-545.	2.6	5
36	Human vaccination against Plasmodium vivax Duffy-binding protein induces strain-transcending antibodies. JCI Insight, 2017, 2, .	5.0	78

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37	A Receptor's Tale: An Eon in the Life of a Trypanosome Receptor. PLoS Pathogens, 2017, 13, e1006055.	4.7	27
38	The structure of a LAIR1-containing human antibody reveals a novel mechanism of antigen recognition. ELife, $2017, 6, .$	6.0	11
39	The structural basis for CD36 binding by the malaria parasite. Nature Communications, 2016, 7, 12837.	12.8	160
40	Production of full-length soluble Plasmodium falciparum RH5 protein vaccine using a Drosophila melanogaster Schneider 2 stable cell line system. Scientific Reports, 2016, 6, 30357.	3.3	54
41	Conformational Selection in a Protein-Protein Interaction Revealed by Dynamic Pathway Analysis. Cell Reports, 2016, 14, 32-42.	6.4	52
42	Evolutionary diversification of the trypanosome haptoglobin-haemoglobin receptor from an ancestral haemoglobin receptor. ELife, 2016, 5, .	6.0	28
43	Structural Conservation Despite Huge Sequence Diversity Allows EPCR Binding by the PfEMP1 Family Implicated in Severe Childhood Malaria. Cell Host and Microbe, 2015, 17, 118-129.	11.0	141
44	Mapping the Binding Site of a Cross-Reactive <i>Plasmodium falciparum</i> PfEMP1 Monoclonal Antibody Inhibitory of ICAM-1 Binding. Journal of Immunology, 2015, 195, 3273-3283.	0.8	25
45	Fragments of Bacterial Endoglycosidase S and Immunoglobulin G Reveal Subdomains of Each That Contribute to Deglycosylation. Journal of Biological Chemistry, 2014, 289, 13876-13889.	3.4	27
46	Evolution of the primate trypanolytic factor APOL1. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2130-9.	7.1	183
47	Sequence variation and structural conservation allows development of novel function and immune evasion in parasite surface protein families. Protein Science, 2014, 23, 354-365.	7.6	36
48	From (+)-epigallocatechin gallate to a simplified synthetic analogue as a cytoadherence inhibitor for P. falciparum. RSC Advances, 2014, 4, 4769-4781.	3.6	13
49	Structure of malaria invasion protein RH5 with erythrocyte basigin and blocking antibodies. Nature, 2014, 515, 427-430.	27.8	180
50	Rosetting Plasmodium falciparum-Infected Erythrocytes Bind to Human Brain Microvascular Endothelial Cells $\langle i \rangle$ In Vitro $\langle i \rangle$, Demonstrating a Dual Adhesion Phenotype Mediated by Distinct P. falciparum Erythrocyte Membrane Protein 1 Domains. Infection and Immunity, 2014, 82, 949-959.	2.2	51
51	Structural basis for ligand and innate immunity factor uptake by the trypanosome haptoglobin-haemoglobin receptor. ELife, 2014, 3, e05553.	6.0	49
52	Malaria's deadly grip: cytoadhesion of <i>Plasmodium falciparum</i> -infected erythrocytes. Cellular Microbiology, 2013, 15, 1976-1983.	2.1	177
53	Engineering Hydrophobic Protein–Carbohydrate Interactions to Fine-Tune Monoclonal Antibodies. Journal of the American Chemical Society, 2013, 135, 9723-9732.	13.7	78
54	Severe malaria is associated with parasite binding to endothelial protein C receptor. Nature, 2013, 498, 502-505.	27.8	460

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55	A Novel Domain Cassette Identifies <i>Plasmodium falciparum</i> PfEMP1 Proteins Binding ICAM-1 and Is a Target of Cross-Reactive, Adhesion-Inhibitory Antibodies. Journal of Immunology, 2013, 190, 240-249.	0.8	101
56	Molecular Architecture of a Complex between an Adhesion Protein from the Malaria Parasite and Intracellular Adhesion Molecule 1. Journal of Biological Chemistry, 2013, 288, 5992-6003.	3.4	37
57	Structure of the trypanosome haptoglobin–hemoglobin receptor and implications for nutrient uptake and innate immunity. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1905-1910.	7.1	81
58	Tic22 Is an Essential Chaperone Required for Protein Import into the Apicoplast*. Journal of Biological Chemistry, 2012, 287, 39505-39512.	3.4	54
59	Overproduction, purification and crystallization of PfTic22, a component of the import apparatus from the apicoplast ofPlasmodium falciparum. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 351-354.	0.7	2
60	Immunisation with Recombinant PfEMP1 Domains Elicits Functional Rosette-Inhibiting and Phagocytosis-Inducing Antibodies to Plasmodium falciparum. PLoS ONE, 2011, 6, e16414.	2.5	41
61	Structural insights into chondroitin sulfate binding in pregnancy-associated malaria. Biochemical Society Transactions, 2010, 38, 1337-1341.	3.4	12
62	Carbohydrate binding molecules in malaria pathology. Current Opinion in Structural Biology, 2010, 20, 560-566.	5.7	17
63	Chondroitin Sulfate A-Adhering <i>Plasmodium falciparum</i> I>-Infected Erythrocytes Express Functionally Important Antibody Epitopes Shared by Multiple Variants. Journal of Immunology, 2010, 185, 7553-7561.	0.8	56
64	Full-Length Recombinant Plasmodium falciparum VAR2CSA Binds Specifically to CSPG and Induces Potent Parasite Adhesion-Blocking Antibodies. Journal of Molecular Biology, 2010, 397, 826-834.	4.2	106
65	Structural Comparison of Two CSPG-Binding DBL Domains from the VAR2CSA Protein Important in Malaria during Pregnancy. Journal of Molecular Biology, 2009, 393, 202-213.	4.2	59
66	Overproduction, purification and crystallization of a chondroitin sulfate A-binding DBL domain from aPlasmodium falciparum var2csa-encoded PfEMP1 protein. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 221-223.	0.7	12
67	The Structure of a Chondroitin Sulfate-binding Domain Important in Placental Malaria. Journal of Biological Chemistry, 2008, 283, 21842-21846.	3.4	92
68	In Vitro Techniques. , 2006, , 201-378.		2
69	Recoverin Binds Exclusively to an Amphipathic Peptide at the N Terminus of Rhodopsin Kinase, Inhibiting Rhodopsin Phosphorylation without Affecting Catalytic Activity of the Kinase. Journal of Biological Chemistry, 2006, 281, 19426-19432.	3.4	53
70	In Vitro Reconstitution of Discrete Stages of Dynaminâ€dependent Endocytosis. Methods in Enzymology, 2005, 404, 597-611.	1.0	4
71	Structure of the periplasmic component of a bacterial drug efflux pump. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9994-9999.	7.1	243
72	Three's company: component structures bring a closer view of tripartite drug efflux pumps. Current Opinion in Structural Biology, 2004, 14, 741-747.	5.7	132

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73	Structure of the Ligand-blocked Periplasmic Entrance of the Bacterial Multidrug Efflux Protein TolC. Journal of Molecular Biology, 2004, 342, 697-702.	4.2	53
74	Oligomerization and activation of the Flil ATPase central to bacterial flagellum assembly. Molecular Microbiology, 2003, 48, 1349-1355.	2.5	100
75	Calnexin co-expression and the use of weaker promoters increase the expression of correctly assembled Shaker potassium channel in insect cells. Biochimica Et Biophysica Acta - Biomembranes, 2003, 1610, 124-132.	2.6	39
76	Snap-shots of clathrin-mediated endocytosis. Trends in Biochemical Sciences, 2002, 27, 257-263.	7.5	78
77	Molecular architecture of a retinal cGMP-gated channel: the arrangement of the cytoplasmic domains. EMBO Journal, 2002, 21, 2087-2094.	7.8	39
78	Simultaneous Binding of PtdIns(4,5)P2 and Clathrin by AP180 in the Nucleation of Clathrin Lattices on Membranes. Science, 2001, 291, 1051-1055.	12.6	667
79	Differential Trafficking and Expression of PIR Proteins in Acute and Chronic Plasmodium Infections. Frontiers in Cellular and Infection Microbiology, 0, 12, .	3.9	3