

# Matthew Higgins

## List of Publications by Year in descending order

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79  
papers

5,093  
citations

101384

36  
h-index

95083

68  
g-index

87  
all docs

87  
docs citations

87  
times ranked

5805  
citing authors

#	ARTICLE	IF	CITATIONS
1	Heterotypic interactions drive antibody synergy against a malaria vaccine candidate. <i>Nature Communications</i> , 2022, 13, 933.	5.8	23
2	Why it might be bad for brain cells to eat malaria parasites. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	0
3	Structure-Guided Design of a Synthetic Mimic of an Endothelial Protein C Receptor-Binding PfEMP1 Protein. <i>MSphere</i> , 2021, 6, .	1.3	3
4	Can We AlphaFold Our Way Out of the Next Pandemic?. <i>Journal of Molecular Biology</i> , 2021, 433, 167093.	2.0	20
5	High-throughput hit-squad tackles trypanosomes. <i>Trends in Parasitology</i> , 2021, 37, 772-774.	1.5	1
6	Design of a basigin-mimicking inhibitor targeting the malaria invasion protein RH5. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 187-195.	1.5	6
7	Staging an Antibody Contest to Fight Malaria. <i>Immunity</i> , 2020, 53, 697-699.	6.6	0
8	Structural basis for RIFIN-mediated activation of LILRB1 in malaria. <i>Nature</i> , 2020, 587, 309-312.	13.7	30
9	Structure of the Inhibited State of the Sec Translocon. <i>Molecular Cell</i> , 2020, 79, 406-415.e7.	4.5	44
10	Structure of the <i>Plasmodium</i> -interspersed repeat proteins of the malaria parasite. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32098-32104.	3.3	10
11	The Structure of the Cysteine-Rich Domain of <i>Plasmodium falciparum</i> P113 Identifies the Location of the RH5 Binding Site. <i>MBio</i> , 2020, 11, .	1.8	7
12	A spike with which to beat COVID-19?. <i>Nature Reviews Microbiology</i> , 2020, 18, 414-414.	13.6	5
13	The RH5-CyRPA-Ripr Complex as a Malaria Vaccine Target. <i>Trends in Parasitology</i> , 2020, 36, 545-559.	1.5	47
14	A receptor for the complement regulator factor H increases transmission of trypanosomes to tsetse flies. <i>Nature Communications</i> , 2020, 11, 1326.	5.8	23
15	Analysis of <i>Plasmodium falciparum</i> Rh2b deletion polymorphism across different transmission areas. <i>Scientific Reports</i> , 2020, 10, 1498.	1.6	3
16	A helminth-derived suppressor of ST2 blocks allergic responses. <i>ELife</i> , 2020, 9, .	2.8	39
17	Structure of the trypanosome transferrin receptor reveals mechanisms of ligand recognition and immune evasion. <i>Nature Microbiology</i> , 2019, 4, 2074-2081.	5.9	20
18	A single dose of antibody-drug conjugate cures a stage 1 model of African trypanosomiasis. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007373.	1.3	11

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19	Structural basis for inhibition of Plasmodium vivax invasion by a broadly neutralizing vaccine-induced human antibody. <i>Nature Microbiology</i> , 2019, 4, 1497-1507.	5.9	48
20	Functional Comparison of Blood-Stage Plasmodium falciparum Malaria Vaccine Candidate Antigens. <i>Frontiers in Immunology</i> , 2019, 10, 1254.	2.2	31
21	Human Antibodies that Slow Erythrocyte Invasion Potentiate Malaria-Neutralizing Antibodies. <i>Cell</i> , 2019, 178, 216-228.e21.	13.5	107
22	Divergent roles for the RH5 complex components, CyRPA and RIPR in human-infective malaria parasites. <i>PLoS Pathogens</i> , 2019, 15, e1007809.	2.1	29
23	Structural insights into diverse modes of ICAM-1 binding by <i>Plasmodium falciparum</i> -infected erythrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20124-20134.	3.3	24
24	In silico guided reconstruction and analysis of ICAM-1-binding var genes from Plasmodium falciparum. <i>Scientific Reports</i> , 2018, 8, 3282.	1.6	4
25	A new site of attack for a malaria vaccine. <i>Nature Medicine</i> , 2018, 24, 382-383.	15.2	5
26	The structure of serum resistance-associated protein and its implications for human African trypanosomiasis. <i>Nature Microbiology</i> , 2018, 3, 295-301.	5.9	21
27	Structural basis for recognition of the malaria vaccine candidate Pfs48/45 by a transmission blocking antibody. <i>Nature Communications</i> , 2018, 9, 3822.	5.8	39
28	O-h what a surprise. <i>Nature Microbiology</i> , 2018, 3, 856-857.	5.9	2
29	Malaria Vaccines: Recent Advances and New Horizons. <i>Cell Host and Microbe</i> , 2018, 24, 43-56.	5.1	234
30	Production, quality control, stability, and potency of cGMP-produced Plasmodium falciparum RH5.1 protein vaccine expressed in Drosophila S2 cells. <i>Npj Vaccines</i> , 2018, 3, 32.	2.9	53
31	One-step design of a stable variant of the malaria invasion protein RH5 for use as a vaccine immunogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 998-1002.	3.3	75
32	Accelerating the clinical development of protein-based vaccines for malaria by efficient purification using a four amino acid C-terminal $\alpha$ -C-tag <sup>TM</sup> . <i>International Journal for Parasitology</i> , 2017, 47, 435-446.	1.3	55
33	Structure-Guided Identification of a Family of Dual Receptor-Binding PfEMP1 that Is Associated with Cerebral Malaria. <i>Cell Host and Microbe</i> , 2017, 21, 403-414.	5.1	140
34	On the state of crystallography at the dawn of the electron microscopy revolution. <i>Current Opinion in Structural Biology</i> , 2017, 46, 95-101.	2.6	11
35	Towards an anti-disease malaria vaccine. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 539-545.	1.1	5
36	Human vaccination against Plasmodium vivax Duffy-binding protein induces strain-transcending antibodies. <i>JCI Insight</i> , 2017, 2, .	2.3	78

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37	A Receptor's Tale: An Eon in the Life of a Trypanosome Receptor. <i>PLoS Pathogens</i> , 2017, 13, e1006055.	2.1	27
38	The structure of a LAIR1-containing human antibody reveals a novel mechanism of antigen recognition. <i>ELife</i> , 2017, 6, .	2.8	11
39	The structural basis for CD36 binding by the malaria parasite. <i>Nature Communications</i> , 2016, 7, 12837.	5.8	160
40	Production of full-length soluble <i>Plasmodium falciparum</i> RH5 protein vaccine using a <i>Drosophila melanogaster</i> Schneider 2 stable cell line system. <i>Scientific Reports</i> , 2016, 6, 30357.	1.6	54
41	Conformational Selection in a Protein-Protein Interaction Revealed by Dynamic Pathway Analysis. <i>Cell Reports</i> , 2016, 14, 32-42.	2.9	52
42	Evolutionary diversification of the trypanosome haptoglobin-haemoglobin receptor from an ancestral haemoglobin receptor. <i>ELife</i> , 2016, 5, .	2.8	28
43	Structural Conservation Despite Huge Sequence Diversity Allows EPCR Binding by the PfEMP1 Family Implicated in Severe Childhood Malaria. <i>Cell Host and Microbe</i> , 2015, 17, 118-129.	5.1	141
44	Mapping the Binding Site of a Cross-Reactive <i>Plasmodium falciparum</i> PfEMP1 Monoclonal Antibody Inhibitory of ICAM-1 Binding. <i>Journal of Immunology</i> , 2015, 195, 3273-3283.	0.4	25
45	Fragments of Bacterial Endoglycosidase S and Immunoglobulin G Reveal Subdomains of Each That Contribute to Deglycosylation. <i>Journal of Biological Chemistry</i> , 2014, 289, 13876-13889.	1.6	27
46	Evolution of the primate trypanolytic factor APOL1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2130-9.	3.3	183
47	Sequence variation and structural conservation allows development of novel function and immune evasion in parasite surface protein families. <i>Protein Science</i> , 2014, 23, 354-365.	3.1	36
48	From (+)-epigallocatechin gallate to a simplified synthetic analogue as a cytoadherence inhibitor for <i>P. falciparum</i> . <i>RSC Advances</i> , 2014, 4, 4769-4781.	1.7	13
49	Structure of malaria invasion protein RH5 with erythrocyte basigin and blocking antibodies. <i>Nature</i> , 2014, 515, 427-430.	13.7	180
50	Rosetting <i>Plasmodium falciparum</i> -Infected Erythrocytes Bind to Human Brain Microvascular Endothelial Cells <i>In Vitro</i> , Demonstrating a Dual Adhesion Phenotype Mediated by Distinct <i>P. falciparum</i> Erythrocyte Membrane Protein 1 Domains. <i>Infection and Immunity</i> , 2014, 82, 949-959.	1.0	51
51	Structural basis for ligand and innate immunity factor uptake by the trypanosome haptoglobin-haemoglobin receptor. <i>ELife</i> , 2014, 3, e05553.	2.8	49
52	Malaria's deadly grip: cytoadhesion of <i>Plasmodium falciparum</i> -infected erythrocytes. <i>Cellular Microbiology</i> , 2013, 15, 1976-1983.	1.1	177
53	Engineering Hydrophobic Protein's Carbohydrate Interactions to Fine-Tune Monoclonal Antibodies. <i>Journal of the American Chemical Society</i> , 2013, 135, 9723-9732.	6.6	78
54	Severe malaria is associated with parasite binding to endothelial protein C receptor. <i>Nature</i> , 2013, 498, 502-505.	13.7	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. <i>Journal of Immunology</i> , 2013, 190, 240-249.	0.4	101
56	Molecular Architecture of a Complex between an Adhesion Protein from the Malaria Parasite and Intracellular Adhesion Molecule 1. <i>Journal of Biological Chemistry</i> , 2013, 288, 5992-6003.	1.6	37
57	Structure of the trypanosome haptoglobin-hemoglobin receptor and implications for nutrient uptake and innate immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1905-1910.	3.3	81
58	Tic22 Is an Essential Chaperone Required for Protein Import into the Apicoplast*. <i>Journal of Biological Chemistry</i> , 2012, 287, 39505-39512.	1.6	54
59	Overproduction, purification and crystallization of PfTic22, a component of the import apparatus from the apicoplast of <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 351-354.	0.7	2
60	Immunisation with Recombinant PfEMP1 Domains Elicits Functional Rosette-Inhibiting and Phagocytosis-Inducing Antibodies to <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2011, 6, e16414.	1.1	41
61	Structural insights into chondroitin sulfate binding in pregnancy-associated malaria. <i>Biochemical Society Transactions</i> , 2010, 38, 1337-1341.	1.6	12
62	Carbohydrate binding molecules in malaria pathology. <i>Current Opinion in Structural Biology</i> , 2010, 20, 560-566.	2.6	17
63	Chondroitin Sulfate A-Adhering <i>Plasmodium falciparum</i> -Infected Erythrocytes Express Functionally Important Antibody Epitopes Shared by Multiple Variants. <i>Journal of Immunology</i> , 2010, 185, 7553-7561.	0.4	56
64	Full-Length Recombinant <i>Plasmodium falciparum</i> VAR2CSA Binds Specifically to CSPG and Induces Potent Parasite Adhesion-Blocking Antibodies. <i>Journal of Molecular Biology</i> , 2010, 397, 826-834.	2.0	106
65	Structural Comparison of Two CSPG-Binding DBL Domains from the VAR2CSA Protein Important in Malaria during Pregnancy. <i>Journal of Molecular Biology</i> , 2009, 393, 202-213.	2.0	59
66	Overproduction, purification and crystallization of a chondroitin sulfate A-binding DBL domain from a <i>Plasmodium falciparum</i> var2csa-encoded PfEMP1 protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 221-223.	0.7	12
67	The Structure of a Chondroitin Sulfate-binding Domain Important in Placental Malaria. <i>Journal of Biological Chemistry</i> , 2008, 283, 21842-21846.	1.6	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. <i>Journal of Biological Chemistry</i> , 2006, 281, 19426-19432.	1.6	53
70	In Vitro Reconstitution of Discrete Stages of Dynamin-dependent Endocytosis. <i>Methods in Enzymology</i> , 2005, 404, 597-611.	0.4	4
71	Structure of the periplasmic component of a bacterial drug efflux pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9994-9999.	3.3	243
72	Three's company: component structures bring a closer view of tripartite drug efflux pumps. <i>Current Opinion in Structural Biology</i> , 2004, 14, 741-747.	2.6	132

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73	Structure of the Ligand-blocked Periplasmic Entrance of the Bacterial Multidrug Efflux Protein TolC. <i>Journal of Molecular Biology</i> , 2004, 342, 697-702.	2.0	53
74	Oligomerization and activation of the Flil ATPase central to bacterial flagellum assembly. <i>Molecular Microbiology</i> , 2003, 48, 1349-1355.	1.2	100
75	Calnexin co-expression and the use of weaker promoters increase the expression of correctly assembled Shaker potassium channel in insect cells. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003, 1610, 124-132.	1.4	39
76	Snap-shots of clathrin-mediated endocytosis. <i>Trends in Biochemical Sciences</i> , 2002, 27, 257-263.	3.7	78
77	Molecular architecture of a retinal cGMP-gated channel: the arrangement of the cytoplasmic domains. <i>EMBO Journal</i> , 2002, 21, 2087-2094.	3.5	39
78	Simultaneous Binding of PtdIns(4,5)P2 and Clathrin by AP180 in the Nucleation of Clathrin Lattices on Membranes. <i>Science</i> , 2001, 291, 1051-1055.	6.0	667
79	Differential Trafficking and Expression of PIR Proteins in Acute and Chronic Plasmodium Infections. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	3