

Niraj H Tolia

List of Publications by Year in descending order

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63
papers

5,234
citations

136950

32
h-index

114465

63
g-index

72
all docs

72
docs citations

72
times ranked

6154
citing authors

#	ARTICLE	IF	CITATIONS
1	Purified Argonaute2 and an siRNA form recombinant human RISC. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 340-349.	8.2	658
2	Analysis of the <i>C. elegans</i> Argonaute Family Reveals that Distinct Argonautes Act Sequentially during RNAi. <i>Cell</i> , 2006, 127, 747-757.	28.9	576
3	The crystal structure of the Argonaute2 PAZ domain reveals an RNA binding motif in RNAi effector complexes. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1026-1032.	8.2	487
4	Slicer and the Argonautes. <i>Nature Chemical Biology</i> , 2007, 3, 36-43.	8.0	410
5	Structural Basis for the EBA-175 Erythrocyte Invasion Pathway of the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell</i> , 2005, 122, 183-193.	28.9	289
6	Strategies for protein coexpression in <i>Escherichia coli</i> . <i>Nature Methods</i> , 2006, 3, 55-64.	19.0	207
7	Argonaute Slicing Is Required for Heterochromatic Silencing and Spreading. <i>Science</i> , 2006, 313, 1134-1137.	12.6	182
8	Plasmepsins IX and X are essential and druggable mediators of malaria parasite egress and invasion. <i>Science</i> , 2017, 358, 518-522.	12.6	152
9	Dimerization of <i>Plasmodium vivax</i> DBP is induced upon receptor binding and drives recognition of DARC. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 908-914.	8.2	128
10	Allosteric activation of ADAMTS13 by von Willebrand factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18584-18589.	7.1	123
11	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882.	12.8	113
12	Protein-based antigen presentation platforms for nanoparticle vaccines. <i>Npj Vaccines</i> , 2021, 6, 70.	6.0	105
13	Red Blood Cell Invasion by <i>Plasmodium vivax</i> : Structural Basis for DBP Engagement of DARC. <i>PLoS Pathogens</i> , 2014, 10, e1003869.	4.7	99
14	Rhoptry Proteins ROP5 and ROP18 Are Major Murine Virulence Factors in Genetically Divergent South American Strains of <i>Toxoplasma gondii</i> . <i>PLoS Genetics</i> , 2015, 11, e1005434.	3.5	99
15	Tetracycline-inactivating enzymes from environmental, human commensal, and pathogenic bacteria cause broad-spectrum tetracycline resistance. <i>Communications Biology</i> , 2020, 3, 241.	4.4	97
16	Plasticity, dynamics, and inhibition of emerging tetracycline resistance enzymes. <i>Nature Chemical Biology</i> , 2017, 13, 730-736.	8.0	93
17	Broadly neutralizing epitopes in the <i>Plasmodium vivax</i> vaccine candidate Duffy Binding Protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6277-6282.	7.1	92
18	<i>Plasmodium falciparum</i> erythrocyte-binding antigen 175 triggers a biophysical change in the red blood cell that facilitates invasion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4225-4230.	7.1	71

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19	A sugar phosphatase regulates the methylerythritol phosphate (MEP) pathway in malaria parasites. <i>Nature Communications</i> , 2014, 5, 4467.	12.8	69
20	Molecular Basis for Sialic Acid-dependent Receptor Recognition by the Plasmodium falciparum Invasion Protein Erythrocyte-binding Antigen-140/BAEBL. <i>Journal of Biological Chemistry</i> , 2013, 288, 12406-12415.	3.4	57
21	Plasmodium falciparum ligand binding to erythrocytes induce alterations in deformability essential for invasion. <i>ELife</i> , 2017, 6, .	6.0	57
22	Structural and Functional Basis for Inhibition of Erythrocyte Invasion by Antibodies that Target Plasmodium falciparum EBA-175. <i>PLoS Pathogens</i> , 2013, 9, e1003390.	4.7	55
23	Prediction of New Stabilizing Mutations Based on Mechanistic Insights from Markov State Models. <i>ACS Central Science</i> , 2017, 3, 1311-1321.	11.3	55
24	Malaria parasite CelTOS targets the inner leaflet of cell membranes for pore-dependent disruption. <i>ELife</i> , 2016, 5, .	6.0	54
25	Structural basis for neutralization of Plasmodium vivax by naturally acquired human antibodies that target DBP. <i>Nature Microbiology</i> , 2019, 4, 1486-1496.	13.3	52
26	Multimeric Assembly of Host-Pathogen Adhesion Complexes Involved in Apicomplexan Invasion. <i>PLoS Pathogens</i> , 2014, 10, e1004120.	4.7	51
27	Evolutionary fine-tuning of conformational ensembles in FimH during host-pathogen interactions. <i>Science Advances</i> , 2017, 3, e1601944.	10.3	50
28	Crystal and Solution Structures of Plasmodium falciparum Erythrocyte-binding Antigen 140 Reveal Determinants of Receptor Specificity during Erythrocyte Invasion. <i>Journal of Biological Chemistry</i> , 2012, 287, 36830-36836.	3.4	48
29	Structural basis for placental malaria mediated by Plasmodium falciparum VAR2CSA. <i>Nature Microbiology</i> , 2021, 6, 380-391.	13.3	47
30	Defining the interaction of the protease CpaA with its type II secretion chaperone CpaB and its contribution to virulence in Acinetobacter species. <i>Journal of Biological Chemistry</i> , 2017, 292, 19628-19638.	3.4	41
31	Structural Analysis of the Synthetic Duffy Binding Protein (DBP) Antigen DEKnull Relevant for Plasmodium vivax Malaria Vaccine Design. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003644.	3.0	40
32	A human monoclonal antibody blocks malaria transmission and defines a highly conserved neutralizing epitope on gametes. <i>Nature Communications</i> , 2021, 12, 1750.	12.8	39
33	Critical Glycosylated Residues in Exon Three of Erythrocyte Glycophorin A Engage Plasmodium falciparum EBA-175 and Define Receptor Specificity. <i>MBio</i> , 2014, 5, e01606-14.	4.1	36
34	DARC extracellular domain remodeling in maturing reticulocytes explains Plasmodium vivax tropism. <i>Blood</i> , 2017, 130, 1441-1444.	1.4	35
35	Red cell receptors as access points for malaria infection. <i>Current Opinion in Hematology</i> , 2016, 23, 215-223.	2.5	34
36	An engineered vaccine of the Plasmodium vivax Duffy binding protein enhances induction of broadly neutralizing antibodies. <i>Scientific Reports</i> , 2017, 7, 13779.	3.3	33

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37	Malaria adhesins: structure and function. <i>Cellular Microbiology</i> , 2014, 16, 621-631.	2.1	31
38	Getting in: The structural biology of malaria invasion. <i>PLoS Pathogens</i> , 2019, 15, e1007943.	4.7	30
39	Liposome Disruption Assay to Examine Lytic Properties of Biomolecules. <i>Bio-protocol</i> , 2017, 7, .	0.4	29
40	malERA: An updated research agenda for basic science and enabling technologies in malaria elimination and eradication. <i>PLoS Medicine</i> , 2017, 14, e1002451.	8.4	29
41	Identification and Characterization of Functional Human Monoclonal Antibodies to <i>Plasmodium vivax</i> Duffy-Binding Protein. <i>Journal of Immunology</i> , 2019, 202, 2648-2660.	0.8	26
42	Semisynthetic Analogues of Anhydrotetracycline as Inhibitors of Tetracycline Destructase Enzymes. <i>ACS Infectious Diseases</i> , 2019, 5, 618-633.	3.8	24
43	Exploring the minimal structure of a functional ADAMTS13 by mutagenesis and small-angle X-ray scattering. <i>Blood</i> , 2019, 133, 1909-1918.	1.4	23
44	A quantitative assay for binding and inhibition of <i>Plasmodium falciparum</i> Erythrocyte Binding Antigen 175 reveals high affinity binding depends on both DBL domains. <i>Protein Expression and Purification</i> , 2014, 95, 188-194.	1.3	20
45	Blood-Stage Malaria Parasite Antigens: Structure, Function, and Vaccine Potential. <i>Journal of Molecular Biology</i> , 2019, 431, 4259-4280.	4.2	20
46	Native Mass Spectrometry, Ion mobility, and Collision-Induced Unfolding Categorize Malaria Antigen/Antibody Binding. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2515-2518.	2.8	17
47	Shed EBA-175 mediates red blood cell clustering that enhances malaria parasite growth and enables immune evasion. <i>ELife</i> , 2018, 7, .	6.0	16
48	Inhibitory Humoral Responses to the <i>Plasmodium falciparum</i> Vaccine Candidate EBA-175 Are Independent of the Erythrocyte Invasion Pathway. <i>Vaccine Journal</i> , 2013, 20, 1238-1245.	3.1	15
49	Cap-domain closure enables diverse substrate recognition by the C2-type haloacid dehalogenase-like sugar phosphatase <i>Plasmodium falciparum</i> HAD1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1824-1834.	2.5	14
50	Molecular Mechanism of Action of Antimalarial Benzoisothiazolones: Species-Selective Inhibitors of the <i>Plasmodium</i> spp. MEP Pathway enzyme, IspD. <i>Scientific Reports</i> , 2016, 6, 36777.	3.3	13
51	The structure of <i>Acinetobacter</i> -secreted protease CpaA complexed with its chaperone CpaB reveals a novel mode of a T2SS chaperone-substrate interaction. <i>Journal of Biological Chemistry</i> , 2019, 294, 13344-13354.	3.4	13
52	A function of profilin in force generation during malaria parasite motility independent of actin binding. <i>Journal of Cell Science</i> , 2020, 134, .	2.0	11
53	Allelic variants of full-length VAR2CSA, the placental malaria vaccine candidate, differ in antigenicity and receptor binding affinity. <i>Communications Biology</i> , 2021, 4, 1309.	4.4	11
54	Moderately Neutralizing Epitopes in Nonfunctional Regions Dominate the Antibody Response to <i>Plasmodium falciparum</i> EBA-140. <i>Infection and Immunity</i> , 2019, 87, .	2.2	8

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55	Comparison of Type 1 D-3-phosphoglycerate dehydrogenases reveals unique regulation in pathogenic Mycobacteria. Archives of Biochemistry and Biophysics, 2015, 570, 32-39.	3.0	7
56	Naturally Acquired Antibody Response to Malaria Transmission Blocking Vaccine Candidate Pvs230 Domain 1. Frontiers in Immunology, 2019, 10, 2295.	4.8	6
57	Membrane Lipid Screen to Identify Molecular Targets of Biomolecules. Bio-protocol, 2017, 7, .	0.4	5
58	Implications of conformational flexibility, lipid binding, and regulatory domains in cell-traversal protein CelTOS for apicomplexan migration. Journal of Biological Chemistry, 2022, 298, 102241.	3.4	4
59	Crystal structure of P. falciparum Cpn60 bound to ATP reveals an open dynamic conformation before substrate binding. Scientific Reports, 2021, 11, 5930.	3.3	2
60	Structural Basis for the EBA-175 Erythrocyte Invasion Pathway of the Malaria Parasite Plasmodium falciparum. Cell, 2005, 122, 485.	28.9	1
61	A Folded ADAMTS13 Conformation Identified By Small-Angle X-Ray Scattering Can Account for Allosteric Regulation By Distal Thrombospondin-1 and CUB Domains. Blood, 2014, 124, 107-107.	1.4	1
62	Small-Angle X-Ray Scattering Studies of ADAMTS13 Demonstrate a Conformational Response to Substrate Binding in Solution. Blood, 2011, 118, 1191-1191.	1.4	0
63	The Hunt for the "Minimal" Structure of a Functional ADAMTS13: Study of Deletion Mutations of ADAMTS13 By Small-Angle X-Ray Scattering. Blood, 2016, 128, 254-254.	1.4	0