

Tongqing Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

140
papers

22,631
citations

22548

61
h-index

13274

135
g-index

166
all docs

166
docs citations

166
times ranked

18943
citing authors

#	ARTICLE	IF	CITATIONS
1	A broadly cross-reactive antibody neutralizes and protects against sarbecovirus challenge in mice. <i>Science Translational Medicine</i> , 2022, 14, eabj7125.	5.8	93
2	SARS-CoV-2 Omicron Variant Neutralization after mRNA-1273 Booster Vaccination. <i>New England Journal of Medicine</i> , 2022, 386, 1088-1091.	13.9	338
3	Potent anti-viral activity of a trispecific HIV neutralizing antibody in SHIV-infected monkeys. <i>Cell Reports</i> , 2022, 38, 110199.	2.9	19
4	A single residue in influenza virus H2 hemagglutinin enhances the breadth of the B cell response elicited by H2 vaccination. <i>Nature Medicine</i> , 2022, 28, 373-382.	15.2	16
5	SARS-CoV-2 Variants Increase Kinetic Stability of Open Spike Conformations as an Evolutionary Strategy. <i>MBio</i> , 2022, 13, e0322721.	1.8	48
6	Structural basis for potent antibody neutralization of SARS-CoV-2 variants including B.1.1.529. <i>Science</i> , 2022, 376, eabn8897.	6.0	119
7	Development of Neutralization Breadth against Diverse HIV-1 by Increasing Ab-Ag Interface on V2. <i>Advanced Science</i> , 2022, , 2200063.	5.6	3
8	Antigenic analysis of the HIV-1 envelope trimer implies small differences between structural states 1 and 2. <i>Journal of Biological Chemistry</i> , 2022, 298, 101819.	1.6	9
9	Structural basis for llama nanobody recognition and neutralization of HIV-1 at the CD4-binding site. <i>Structure</i> , 2022, 30, 862-875.e4.	1.6	4
10	Structure of an influenza group 2-neutralizing antibody targeting the hemagglutinin stem supersite. <i>Structure</i> , 2022, , .	1.6	1
11	LY-CoV1404 (bebtelovimab) potently neutralizes SARS-CoV-2 variants. <i>Cell Reports</i> , 2022, 39, 110812.	2.9	287
12	Molecular probes of spike ectodomain and its subdomains for SARS-CoV-2 variants, Alpha through Omicron. <i>PLoS ONE</i> , 2022, 17, e0268767.	1.1	18
13	Safety and immunogenicity of an HIV-1 prefusion-stabilized envelope trimer (Trimer 4571) vaccine in healthy adults: A first-in-human open-label, randomized, dose-escalation, phase 1 clinical trial. <i>EClinicalMedicine</i> , 2022, 48, 101477.	3.2	13
14	Broad coverage of neutralization-resistant SIV strains by second-generation SIV-specific antibodies targeting the region involved in binding CD4. <i>PLoS Pathogens</i> , 2022, 18, e1010574.	2.1	6
15	Vaccine-elicited murine antibody WS6 neutralizes diverse beta-coronaviruses by recognizing a helical stem supersite of vulnerability. <i>Structure</i> , 2022, 30, 1233-1244.e7.	1.6	13
16	Newcastle Disease Virus-Like Particles Displaying Prefusion-Stabilized SARS-CoV-2 Spikes Elicit Potent Neutralizing Responses. <i>Vaccines</i> , 2021, 9, 73.	2.1	24
17	Vaccination induces maturation in a mouse model of diverse unmutated VRC01-class precursors to HIV-neutralizing antibodies with >50% breadth. <i>Immunity</i> , 2021, 54, 324-339.e8.	6.6	36
18	Mutational fitness landscapes reveal genetic and structural improvement pathways for a vaccine-elicited HIV-1 broadly neutralizing antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21

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19	Fusion peptide priming reduces immune responses to HIV-1 envelope trimer base. <i>Cell Reports</i> , 2021, 35, 108937.	2.9	12
20	High-throughput, single-copy sequencing reveals SARS-CoV-2 spike variants coincident with mounting humoral immunity during acute COVID-19. <i>PLoS Pathogens</i> , 2021, 17, e1009431.	2.1	34
21	Potent SARS-CoV-2 neutralizing antibodies directed against spike N-terminal domain target a single supersite. <i>Cell Host and Microbe</i> , 2021, 29, 819-833.e7.	5.1	444
22	Sequence-Signature Optimization Enables Improved Identification of Human HV6-1-Derived Class Antibodies That Neutralize Diverse Influenza A Viruses. <i>Frontiers in Immunology</i> , 2021, 12, 662909.	2.2	0
23	Nanobodies from camelid mice and llamas neutralize SARS-CoV-2 variants. <i>Nature</i> , 2021, 595, 278-282.	13.7	154
24	Ultrapotent antibodies against diverse and highly transmissible SARS-CoV-2 variants. <i>Science</i> , 2021, 373, .	6.0	174
25	Structural basis of LAIR1 targeting by polymorphic Plasmodium RIFINs. <i>Nature Communications</i> , 2021, 12, 4226.	5.8	1
26	Protective antibodies elicited by SARS-CoV-2 spike protein vaccination are boosted in the lung after challenge in nonhuman primates. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	56
27	InÂvitro and inÂvivo functions of SARS-CoV-2 infection-enhancing and neutralizing antibodies. <i>Cell</i> , 2021, 184, 4203-4219.e32.	13.5	228
28	Blocking $\alpha 4 \beta 7$ integrin delays viral rebound in SHIV $SF162P3$ -infected macaques treated with anti-HIV broadly neutralizing antibodies. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	11
29	Antibody screening at reduced pH enables preferential selection of potently neutralizing antibodies targeting SARS-CoV-2. <i>AIChE Journal</i> , 2021, 67, e17440.	1.8	4
30	Paired heavy- and light-chain signatures contribute to potent SARS-CoV-2 neutralization in public antibody responses. <i>Cell Reports</i> , 2021, 37, 109771.	2.9	38
31	SARS-CoV-2 S2P spike ages through distinct states with altered immunogenicity. <i>Journal of Biological Chemistry</i> , 2021, 297, 101127.	1.6	9
32	Low-dose in vivo protection and neutralization across SARS-CoV-2 variants by monoclonal antibody combinations. <i>Nature Immunology</i> , 2021, 22, 1503-1514.	7.0	40
33	Structural basis of glycan276-dependent recognition by HIV-1 broadly neutralizing antibodies. <i>Cell Reports</i> , 2021, 37, 109922.	2.9	5
34	Structure-Based Design with Tag-Based Purification and In-Process Biotinylation Enable Streamlined Development of SARS-CoV-2 Spike Molecular Probes. <i>Cell Reports</i> , 2020, 33, 108322.	2.9	59
35	Removal of variable domain N-linked glycosylation as a means to improve the homogeneity of HIV-1 broadly neutralizing antibodies. <i>MAbs</i> , 2020, 12, 1836719.	2.6	4
36	Cryo-EM Structures of SARS-CoV-2 Spike without and with ACE2 Reveal a pH-Dependent Switch to Mediate Endosomal Positioning of Receptor-Binding Domains. <i>Cell Host and Microbe</i> , 2020, 28, 867-879.e5.	5.1	316

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37	Real-Time Conformational Dynamics of SARS-CoV-2 Spikes on Virus Particles. <i>Cell Host and Microbe</i> , 2020, 28, 880-891.e8.	5.1	153
38	Automated Design by Structure-Based Stabilization and Consensus Repair to Achieve Prefusion-Closed Envelope Trimers in a Wide Variety of HIV Strains. <i>Cell Reports</i> , 2020, 33, 108432.	2.9	32
39	Evaluation of the mRNA-1273 Vaccine against SARS-CoV-2 in Nonhuman Primates. <i>New England Journal of Medicine</i> , 2020, 383, 1544-1555.	13.9	936
40	Potent neutralizing antibodies against multiple epitopes on SARS-CoV-2 spike. <i>Nature</i> , 2020, 584, 450-456.	13.7	1,337
41	Immune Monitoring Reveals Fusion Peptide Priming to Imprint Cross-Clade HIV-Neutralizing Responses with a Characteristic Early B Cell Signature. <i>Cell Reports</i> , 2020, 32, 107981.	2.9	15
42	A platform incorporating trimeric antigens into self-assembling nanoparticles reveals SARS-CoV-2-spike nanoparticles to elicit substantially higher neutralizing responses than spike alone. <i>Scientific Reports</i> , 2020, 10, 18149.	1.6	90
43	Identification and Structure of a Multidonor Class of Head-Directed Influenza-Neutralizing Antibodies Reveal the Mechanism for Its Recurrent Elicitation. <i>Cell Reports</i> , 2020, 32, 108088.	2.9	13
44	VRC34-Antibody Lineage Development Reveals How a Required Rare Mutation Shapes the Maturation of a Broad HIV-Neutralizing Lineage. <i>Cell Host and Microbe</i> , 2020, 27, 531-543.e6.	5.1	23
45	Subnanometer structures of HIV-1 envelope trimers on aldrithiol-2-inactivated virus particles. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 726-734.	3.6	55
46	Preclinical Development of a Fusion Peptide Conjugate as an HIV Vaccine Immunogen. <i>Scientific Reports</i> , 2020, 10, 3032.	1.6	36
47	Structure-Based Design with Tag-Based Purification and In-Process Biotinylation Enable Streamlined Development of SARS-CoV-2 Spike Molecular Probes. <i>SSRN Electronic Journal</i> , 2020, , 3639618.	0.4	3
48	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. <i>Cell</i> , 2019, 178, 567-584.e19.	13.5	106
49	Neutralization-guided design of HIV-1 envelope trimers with high affinity for the unmutated common ancestor of CH235 lineage CD4bs broadly neutralizing antibodies. <i>PLoS Pathogens</i> , 2019, 15, e1008026.	2.1	56
50	A Single Substitution in gp41 Modulates the Neutralization Profile of SHIV during In Vivo Adaptation. <i>Cell Reports</i> , 2019, 27, 2593-2607.e5.	2.9	8
51	Broadly resistant HIV-1 against CD4-binding site neutralizing antibodies. <i>PLoS Pathogens</i> , 2019, 15, e1007819.	2.1	18
52	Prolonged evolution of the memory B cell response induced by a replicating adenovirus-influenza H5 vaccine. <i>Science Immunology</i> , 2019, 4, .	5.6	40
53	Longitudinal Analysis Reveals Early Development of Three MPER-Directed Neutralizing Antibody Lineages from an HIV-1-Infected Individual. <i>Immunity</i> , 2019, 50, 677-691.e13.	6.6	77
54	Associating HIV-1 envelope glycoprotein structures with states on the virus observed by smFRET. <i>Nature</i> , 2019, 568, 415-419.	13.7	156

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55	Structural Survey of Broadly Neutralizing Antibodies Targeting the HIV-1 Env Trimer Delineates Epitope Categories and Characteristics of Recognition. <i>Structure</i> , 2019, 27, 196-206.e6.	1.6	69
56	Importance of Neutralizing Monoclonal Antibodies Targeting Multiple Antigenic Sites on the Middle East Respiratory Syndrome Coronavirus Spike Glycoprotein To Avoid Neutralization Escape. <i>Journal of Virology</i> , 2018, 92, .	1.5	155
57	A Neutralizing Antibody Recognizing Primarily N-Linked Glycan Targets the Silent Face of the HIV Envelope. <i>Immunity</i> , 2018, 48, 500-513.e6.	6.6	66
58	Structure-based design of a quadrivalent fusion glycoprotein vaccine for human parainfluenza virus types 1-4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12265-12270.	3.3	70
59	HIV-1 envelope glycan modifications that permit neutralization by germline-reverted VRC01-class broadly neutralizing antibodies. <i>PLoS Pathogens</i> , 2018, 14, e1007431.	2.1	36
60	Structural Features of Broadly Neutralizing Antibodies and Rational Design of Vaccine. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1075, 73-95.	0.8	17
61	Epitope-based vaccine design yields fusion peptide-directed antibodies that neutralize diverse strains of HIV-1. <i>Nature Medicine</i> , 2018, 24, 857-867.	15.2	256
62	Quaternary contact in the initial interaction of CD4 with the HIV-1 envelope trimer. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 370-378.	3.6	94
63	Structure-Based Design of a Soluble Prefusion-Closed HIV-1 Env Trimer with Reduced CD4 Affinity and Improved Immunogenicity. <i>Journal of Virology</i> , 2017, 91, .	1.5	81
64	Quantification of the Impact of the HIV-1-Glycan Shield on Antibody Elicitation. <i>Cell Reports</i> , 2017, 19, 719-732.	2.9	160
65	Protection of calves by a prefusion-stabilized bovine RSV F vaccine. <i>Npj Vaccines</i> , 2017, 2, 7.	2.9	38
66	Free Energy Perturbation Calculation of Relative Binding Free Energy between Broadly Neutralizing Antibodies and the gp120 Glycoprotein of HIV-1. <i>Journal of Molecular Biology</i> , 2017, 429, 930-947.	2.0	82
67	Trispecific broadly neutralizing HIV antibodies mediate potent SHIV protection in macaques. <i>Science</i> , 2017, 358, 85-90.	6.0	225
68	Soluble Prefusion Closed DS-SOSIP.664-Env Trimers of Diverse HIV-1 Strains. <i>Cell Reports</i> , 2017, 21, 2992-3002.	2.9	69
69	Conformational Changes in HIV-1 Env Trimer Induced by a Single CD4 as Revealed by Cryo-EM. <i>Microscopy and Microanalysis</i> , 2017, 23, 1190-1191.	0.2	0
70	Structures of the Multidrug Transporter P-glycoprotein Reveal Asymmetric ATP Binding and the Mechanism of Polyspecificity. <i>Journal of Biological Chemistry</i> , 2017, 292, 446-461.	1.6	152
71	Targeted Isolation of Antibodies Directed against Major Sites of SIV Env Vulnerability. <i>PLoS Pathogens</i> , 2016, 12, e1005537.	2.1	51
72	Trimeric HIV-1-Env Structures Define Glycan Shields from Clades A, B, and G. <i>Cell</i> , 2016, 165, 813-826.	13.5	379

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73	Fusion peptide of HIV-1 as a site of vulnerability to neutralizing antibody. <i>Science</i> , 2016, 352, 828-833.	6.0	310
74	Somatic Hypermutation-Induced Changes in the Structure and Dynamics of HIV-1 Broadly Neutralizing Antibodies. <i>Structure</i> , 2016, 24, 1346-1357.	1.6	35
75	Identification of a CD4-Binding-Site Antibody to HIV that Evolved Near-Pan Neutralization Breadth. <i>Immunity</i> , 2016, 45, 1108-1121.	6.6	304
76	Platelet-derived growth factor- α receptor is the cellular receptor for human cytomegalovirus gHgLgO trimer. <i>Nature Microbiology</i> , 2016, 1, 16082.	5.9	170
77	Spatiotemporal hierarchy in antibody recognition against transmitted HIV-1 envelope glycoprotein during natural infection. <i>Retrovirology</i> , 2016, 13, 12.	0.9	7
78	Maturation Pathway from Germline to Broad HIV-1 Neutralizer of a CD4-Mimic Antibody. <i>Cell</i> , 2016, 165, 449-463.	13.5	305
79	Structures of HIV-1 Env V1V2 with broadly neutralizing antibodies reveal commonalities that enable vaccine design. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 81-90.	3.6	162
80	Structure-Based Design of Head-Only Fusion Glycoprotein Immunogens for Respiratory Syncytial Virus. <i>PLoS ONE</i> , 2016, 11, e0159709.	1.1	27
81	A Cysteine Zipper Stabilizes a Pre-Fusion F Glycoprotein Vaccine for Respiratory Syncytial Virus. <i>PLoS ONE</i> , 2015, 10, e0128779.	1.1	38
82	Structural Repertoire of HIV-1-Neutralizing Antibodies Targeting the CD4 Supersite in 14 Donors. <i>Cell</i> , 2015, 161, 1280-1292.	13.5	305
83	Evaluation of candidate vaccine approaches for MERS-CoV. <i>Nature Communications</i> , 2015, 6, 7712.	5.8	258
84	Crystal structure, conformational fixation and entry-related interactions of mature ligand-free HIV-1 Env. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 522-531.	3.6	333
85	Eliminating antibody polyreactivity through addition of <i>N-linked glycosylation</i> . <i>Protein Science</i> , 2015, 24, 1019-1030.	3.1	11
86	Maturation and Diversity of the VRC01-Antibody Lineage over 15 Years of Chronic HIV-1 Infection. <i>Cell</i> , 2015, 161, 470-485.	13.5	226
87	Activation and lysis of human CD4 cells latently infected with HIV-1. <i>Nature Communications</i> , 2015, 6, 8447.	5.8	88
88	Junctional and allele-specific residues are critical for MERS-CoV neutralization by an exceptionally potent germline-like antibody. <i>Nature Communications</i> , 2015, 6, 8223.	5.8	106
89	Transient Protein Expression Facilitates X-ray Structural Studies of HIV-1. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A148-A149.	0.5	0
90	Enhanced Potency of a Broadly Neutralizing HIV-1 Antibody <i>In Vitro</i> Improves Protection against Lentiviral Infection <i>In Vivo</i> . <i>Journal of Virology</i> , 2014, 88, 12669-12682.	1.5	248

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91	CD4-binding-Site Recognition by VH1-46 Germline-derived HIV-1 Neutralizers. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A120-A121.	0.5	1
92	Structure of BMS-806, a Small-molecule HIV-1 Entry Inhibitor, Bound to BG505 SOSIP.664 HIV-1 Env Trimer. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A151-A151.	0.5	4
93	Cooperation of B Cell Lineages in Induction of HIV-1-Broadly Neutralizing Antibodies. <i>Cell</i> , 2014, 158, 481-491.	13.5	266
94	Structure and immune recognition of trimeric pre-fusion HIV-1 Env. <i>Nature</i> , 2014, 514, 455-461.	13.7	702
95	Transplanting Supersites of HIV-1 Vulnerability. <i>PLoS ONE</i> , 2014, 9, e99881.	1.1	51
96	Multidonor Analysis Reveals Structural Elements, Genetic Determinants, and Maturation Pathway for HIV-1 Neutralization by VRC01-Class Antibodies. <i>Immunity</i> , 2013, 39, 245-258.	6.6	332
97	Structure of RSV Fusion Glycoprotein Trimer Bound to a Prefusion-Specific Neutralizing Antibody. <i>Science</i> , 2013, 340, 1113-1117.	6.0	656
98	Outer Domain of HIV-1 gp120: Antigenic Optimization, Structural Malleability, and Crystal Structure with Antibody VRC-PG04. <i>Journal of Virology</i> , 2013, 87, 2294-2306.	1.5	34
99	Structure-Based Design of a Fusion Glycoprotein Vaccine for Respiratory Syncytial Virus. <i>Science</i> , 2013, 342, 592-598.	6.0	797
100	Somatic Mutations of the Immunoglobulin Framework Are Generally Required for Broad and Potent HIV-1 Neutralization. <i>Cell</i> , 2013, 153, 126-138.	13.5	478
101	Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus. <i>Nature</i> , 2013, 496, 469-476.	13.7	961
102	Delineating Antibody Recognition in Polyclonal Sera from Patterns of HIV-1 Isolate Neutralization. <i>Science</i> , 2013, 340, 751-756.	6.0	213
103	Elicitation of HIV-1-neutralizing antibodies against the CD4-binding site. <i>Current Opinion in HIV and AIDS</i> , 2013, 8, 382-392.	1.5	27
104	De novo identification of VRC01 class HIV-1 neutralizing antibodies by next-generation sequencing of B-cell transcripts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4088-97.	3.3	105
105	Residue-Level Prediction of HIV-1 Antibody Epitopes Based on Neutralization of Diverse Viral Strains. <i>Journal of Virology</i> , 2013, 87, 10047-10058.	1.5	64
106	PGV04, an HIV-1 gp120 CD4 Binding Site Antibody, Is Broad and Potent in Neutralization but Does Not Induce Conformational Changes Characteristic of CD4. <i>Journal of Virology</i> , 2012, 86, 4394-4403.	1.5	109
107	Unliganded HIV-1 gp120 core structures assume the CD4-bound conformation with regulation by quaternary interactions and variable loops. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5663-5668.	3.3	222
108	Structural definition for a new modality of broad and potent antibody neutralization at the CD4-binding site on HIV-1 gp120. <i>Retrovirology</i> , 2012, 9, .	0.9	1

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109	Characteristics of HIV-1 gp120 molecules that bind ancestor, intermediate and mature forms of VRC01-like antibodies. <i>Retrovirology</i> , 2012, 9, .	0.9	0
110	Focused Evolution of HIV-1 Neutralizing Antibodies Revealed by Structures and Deep Sequencing. <i>Science</i> , 2011, 333, 1593-1602.	6.0	788
111	Crystal Structures of GII.10 and GII.12 Norovirus Protruding Domains in Complex with Histo-Blood Group Antigens Reveal Details for a Potential Site of Vulnerability. <i>Journal of Virology</i> , 2011, 85, 6687-6701.	1.5	113
112	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011, 480, 336-343.	13.7	794
113	Structure of HIV-1 gp120 with gp41-interactive region reveals layered envelope architecture and basis of conformational mobility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1166-1171.	3.3	304
114	Structural Basis for Broad and Potent Neutralization of HIV-1 by Antibody VRC01. <i>Science</i> , 2010, 329, 811-817.	6.0	1,050
115	Rational Design of Envelope Identifies Broadly Neutralizing Human Monoclonal Antibodies to HIV-1. <i>Science</i> , 2010, 329, 856-861.	6.0	1,600
116	Crystal Structure of PG16 and Chimeric Dissection with Somatically Related PG9: Structure-Function Analysis of Two Quaternary-Specific Antibodies That Effectively Neutralize HIV-1. <i>Journal of Virology</i> , 2010, 84, 8098-8110.	1.5	209
117	Structural Biology and the Design of Effective Vaccines for HIV-1 and Other Viruses. , 2010, , 387-402.		4
118	Mechanism of Human Immunodeficiency Virus Type 1 Resistance to Monoclonal Antibody b12 That Effectively Targets the Site of CD4 Attachment. <i>Journal of Virology</i> , 2009, 83, 10892-10907.	1.5	86
119	Structure-Based Stabilization of HIV-1 gp120 Enhances Humoral Immune Responses to the Induced Co-Receptor Binding Site. <i>PLoS Pathogens</i> , 2009, 5, e1000445.	2.1	113
120	Enhanced Exposure of the CD4-Binding Site to Neutralizing Antibodies by Structural Design of a Membrane-Anchored Human Immunodeficiency Virus Type 1 gp120 Domain. <i>Journal of Virology</i> , 2009, 83, 5077-5086.	1.5	43
121	Structural Basis of Immune Evasion at the Site of CD4 Attachment on HIV-1 gp120. <i>Science</i> , 2009, 326, 1123-1127.	6.0	271
122	P09-13. Structure of HIV-1 gp41 interactive region: layered architecture and basis of conformational mobility. <i>Retrovirology</i> , 2009, 6, .	0.9	0
123	P09-05. Mechanism of HIV-1 resistance to a monoclonal antibody that effectively targets the site of CD4 attachment. <i>Retrovirology</i> , 2009, 6, .	0.9	0
124	Structural basis of HIV-1 gp120 conformational mobility. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s24-s24.	0.3	3
125	Structural definition of a conserved neutralization epitope on HIV-1 gp120. <i>Nature</i> , 2007, 445, 732-737.	13.7	715
126	Interfacial metal and antibody recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14575-14580.	3.3	29

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127	Nonequivalence of the Nucleotide Binding Domains of the ArsA ATPase. <i>Journal of Biological Chemistry</i> , 2005, 280, 9921-9926.	1.6	10
128	Enhancing Protein Crystallization through Precipitant Synergy. <i>Structure</i> , 2003, 11, 1061-1070.	1.6	75
129	Unisite and Multisite Catalysis in the ArsA ATPase. <i>Journal of Biological Chemistry</i> , 2002, 277, 23815-23820.	1.6	13
130	A Kinetic Model for the Action of a Resistance Efflux Pump. <i>Journal of Biological Chemistry</i> , 2001, 276, 6378-6391.	1.6	16
131	Antimonite regulation of the ATPase activity of ArsA, the catalytic subunit of the arsenical pump. <i>Biochemical Journal</i> , 2001, 360, 589.	1.7	9
132	Antimonite regulation of the ATPase activity of ArsA, the catalytic subunit of the arsenical pump. <i>Biochemical Journal</i> , 2001, 360, 589-597.	1.7	10
133	Conformational Changes in Four Regions of the Escherichia coli ArsA ATPase Link ATP Hydrolysis to Ion Translocation. <i>Journal of Biological Chemistry</i> , 2001, 276, 30414-30422.	1.6	38
134	The ATPase Mechanism of ArsA, the Catalytic Subunit of the Arsenite Pump. <i>Journal of Biological Chemistry</i> , 1999, 274, 16153-16161.	1.6	26
135	Asp45 Is a Mg ²⁺ Ligand in the ArsA ATPase. <i>Journal of Biological Chemistry</i> , 1999, 274, 13854-13858.	1.6	18
136	Crystallization and preliminary X-ray analysis of the catalytic subunit of the ATP-dependent arsenite pump encoded by the Escherichia coli plasmid R773. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 921-924.	2.5	3
137	Mechanism of the ArsA ATPase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1999, 1461, 207-215.	1.4	53
138	Tryptophan Fluorescence Reports Nucleotide-induced Conformational Changes in a Domain of the ArsA ATPase. <i>Journal of Biological Chemistry</i> , 1997, 272, 19731-19737.	1.6	67
139	Interaction of substrate and effector binding sites in the ArsA ATPase. <i>Biochemistry</i> , 1995, 34, 13622-13626.	1.2	28
140	Paired Heavy and Light Chain Signatures Contribute to Potent SARS-CoV-2 Neutralization in Public Antibody Responses. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1