

Ian A Wilson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5491764/publications.pdf>

Version: 2024-02-01

353
papers

57,976
citations

735

120
h-index

1424

221
g-index

406
all docs

406
docs citations

406
times ranked

38026
citing authors

#	ARTICLE	IF	CITATIONS
1	Broad neutralization coverage of HIV by multiple highly potent antibodies. <i>Nature</i> , 2011, 477, 466-470.	27.8	1,397
2	A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. <i>Science</i> , 2020, 368, 630-633.	12.6	1,379
3	Isolation of potent SARS-CoV-2 neutralizing antibodies and protection from disease in a small animal model. <i>Science</i> , 2020, 369, 956-963.	12.6	1,287
4	Antibody Recognition of a Highly Conserved Influenza Virus Epitope. <i>Science</i> , 2009, 324, 246-251.	12.6	1,220
5	New World Bats Harbor Diverse Influenza A Viruses. <i>PLoS Pathogens</i> , 2013, 9, e1003657.	4.7	1,050
6	Printed covalent glycan array for ligand profiling of diverse glycan binding proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17033-17038.	7.1	1,039
7	Crystal Structure of a Neutralizing Human IgG Against HIV-1: A Template for Vaccine Design. <i>Science</i> , 2001, 293, 1155-1159.	12.6	870
8	Structure and Receptor Specificity of the Hemagglutinin from an H5N1 Influenza Virus. <i>Science</i> , 2006, 312, 404-410.	12.6	865
9	A Next-Generation Cleaved, Soluble HIV-1 Env Trimer, BG505 SOSIP.664 gp140, Expresses Multiple Epitopes for Broadly Neutralizing but Not Non-Neutralizing Antibodies. <i>PLoS Pathogens</i> , 2013, 9, e1003618.	4.7	835
10	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011, 480, 336-343.	27.8	794
11	Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1477-1483.	12.6	793
12	A Highly Conserved Neutralizing Epitope on Group 2 Influenza A Viruses. <i>Science</i> , 2011, 333, 843-850.	12.6	772
13	Antibody Domain Exchange Is an Immunological Solution to Carbohydrate Cluster Recognition. <i>Science</i> , 2003, 300, 2065-2071.	12.6	736
14	HIV vaccine design and the neutralizing antibody problem. <i>Nature Immunology</i> , 2004, 5, 233-236.	14.5	721
15	Highly Conserved Protective Epitopes on Influenza B Viruses. <i>Science</i> , 2012, 337, 1343-1348.	12.6	705
16	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. <i>Nature</i> , 2014, 509, 55-62.	27.8	681
17	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. <i>Science</i> , 2013, 340, 711-716.	12.6	680
18	The Broadly Neutralizing Anti-Human Immunodeficiency Virus Type 1 Antibody 2G12 Recognizes a Cluster of 1±1â†’2 Mannose Residues on the Outer Face of gp120. <i>Journal of Virology</i> , 2002, 76, 7306-7321.	3.4	664

#	ARTICLE	IF	CITATIONS
19	Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1484-1490.	12.6	662
20	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. <i>Science</i> , 2011, 334, 1097-1103.	12.6	644
21	Structural Basis of Plasticity in T Cell Receptor Recognition of a Self Peptide-MHC Antigen. <i>Science</i> , 1998, 279, 1166-1172.	12.6	641
22	A structural analysis of M protein in coronavirus assembly and morphology. <i>Journal of Structural Biology</i> , 2011, 174, 11-22.	2.8	625
23	Glycan Microarray Analysis of the Hemagglutinins from Modern and Pandemic Influenza Viruses Reveals Different Receptor Specificities. <i>Journal of Molecular Biology</i> , 2006, 355, 1143-1155.	4.2	570
24	Crystal Structure of Human Toll-Like Receptor 3 (TLR3) Ectodomain. <i>Science</i> , 2005, 309, 581-585.	12.6	545
25	Structural basis of a shared antibody response to SARS-CoV-2. <i>Science</i> , 2020, 369, 1119-1123.	12.6	536
26	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. <i>Science</i> , 2011, 332, 816-821.	12.6	527
27	Structural Basis of Preexisting Immunity to the 2009 H1N1 Pandemic Influenza Virus. <i>Science</i> , 2010, 328, 357-360.	12.6	521
28	Antibody-antigen interactions: new structures and new conformational changes. <i>Current Opinion in Structural Biology</i> , 1994, 4, 857-867.	5.7	505
29	STRUCTURAL BASIS OF T CELL RECOGNITION. <i>Annual Review of Immunology</i> , 1999, 17, 369-397.	21.8	488
30	HIV-1 neutralizing antibodies induced by native-like envelope trimers. <i>Science</i> , 2015, 349, aac4223.	12.6	482
31	A stable trimeric influenza hemagglutinin stem as a broadly protective immunogen. <i>Science</i> , 2015, 349, 1301-1306.	12.6	480
32	Structural Basis of TLR5-Flagellin Recognition and Signaling. <i>Science</i> , 2012, 335, 859-864.	12.6	454
33	Structure of the Uncleaved Human H1 Hemagglutinin from the Extinct 1918 Influenza Virus. <i>Science</i> , 2004, 303, 1866-1870.	12.6	440
34	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012, 489, 526-532.	27.8	434
35	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. <i>Science</i> , 2011, 332, 234-238.	12.6	414
36	Broadly Neutralizing Anti-HIV Antibody 4E10 Recognizes a Helical Conformation of a Highly Conserved Fusion-Associated Motif in gp41. <i>Immunity</i> , 2005, 22, 163-173.	14.3	410

#	ARTICLE	IF	CITATIONS
37	Structural genomics of the <i>Thermotoga maritima</i> proteome implemented in a high-throughput structure determination pipeline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11664-11669.	7.1	397
38	Broadly Neutralizing Antibodies Present New Prospects to Counter Highly Antigenically Diverse Viruses. <i>Science</i> , 2012, 337, 183-186.	12.6	394
39	A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. <i>Science Advances</i> , 2019, 5, eaav4580.	10.3	393
40	Exploitation of glycosylation in enveloped virus pathobiology. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1480-1497.	2.4	383
41	HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. <i>Science</i> , 2016, 351, 1458-1463.	12.6	382
42	Hepatitis C Virus E2 Envelope Glycoprotein Core Structure. <i>Science</i> , 2013, 342, 1090-1094.	12.6	374
43	A Single Amino Acid Substitution in 1918 Influenza Virus Hemagglutinin Changes Receptor Binding Specificity. <i>Journal of Virology</i> , 2005, 79, 11533-11536.	3.4	356
44	Massively parallel de novo protein design for targeted therapeutics. <i>Nature</i> , 2017, 550, 74-79.	27.8	354
45	Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. <i>Cell Reports</i> , 2020, 31, 107725.	6.4	353
46	A Blueprint for HIV Vaccine Discovery. <i>Cell Host and Microbe</i> , 2012, 12, 396-407.	11.0	348
47	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. <i>Nature Biotechnology</i> , 2012, 30, 543-548.	17.5	342
48	Broadly Neutralizing HIV Antibodies Define a Glycan-Dependent Epitope on the Prefusion Conformation of gp41 on Cleaved Envelope Trimers. <i>Immunity</i> , 2014, 40, 657-668.	14.3	342
49	Immunogenicity of Stabilized HIV-1 Envelope Trimers with Reduced Exposure of Non-neutralizing Epitopes. <i>Cell</i> , 2015, 163, 1702-1715.	28.9	341
50	Structural basis of influenza virus fusion inhibition by the antiviral drug Arbidol. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 206-214.	7.1	340
51	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. <i>Immunity</i> , 2016, 45, 483-496.	14.3	335
52	Recombinant HIV envelope trimer selects for quaternary-dependent antibodies targeting the trimer apex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17624-17629.	7.1	324
53	Structural Delineation of a Quaternary, Cleavage-Dependent Epitope at the gp41-gp120 Interface on Intact HIV-1 Env Trimers. <i>Immunity</i> , 2014, 40, 669-680.	14.3	323
54	Glycan microarray technologies: tools to survey host specificity of influenza viruses. <i>Nature Reviews Microbiology</i> , 2006, 4, 857-864.	28.6	319

#	ARTICLE	IF	CITATIONS
55	Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 796-803.	8.2	314
56	Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. <i>Eurosurveillance</i> , 2020, 25, .	7.0	309
57	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. <i>Science</i> , 2021, 373, 818-823.	12.6	309
58	A Therapeutic Non-self-reactive SARS-CoV-2 Antibody Protects from Lung Pathology in a COVID-19 Hamster Model. <i>Cell</i> , 2020, 183, 1058-1069.e19.	28.9	305
59	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020, 11, 2688.	12.8	304
60	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. <i>Science</i> , 2021, 371, .	12.6	304
61	Dissection of the carbohydrate specificity of the broadly neutralizing anti-HIV-1 antibody 2G12. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13372-13377.	7.1	291
62	Elicitation of Robust Tier 2 Neutralizing Antibody Responses in Nonhuman Primates by HIV Envelope Trimer Immunization Using Optimized Approaches. <i>Immunity</i> , 2017, 46, 1073-1088.e6.	14.3	286
63	Crystal Structure of a Shark Single-Domain Antibody V Region in Complex with Lysozyme. <i>Science</i> , 2004, 305, 1770-1773.	12.6	282
64	Antibody-antigen interactions. <i>Current Opinion in Structural Biology</i> , 1993, 3, 113-118.	5.7	279
65	Antibody vs. HIV in a clash of evolutionary titans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14943-14948.	7.1	268
66	Broadly Neutralizing Antibody PGT121 Allosterically Modulates CD4 Binding via Recognition of the HIV-1 gp120 V3 Base and Multiple Surrounding Glycans. <i>PLoS Pathogens</i> , 2013, 9, e1003342.	4.7	267
67	The <sc>HIV</sc> envelope glycoprotein structure: nailing down a moving target. <i>Immunological Reviews</i> , 2017, 275, 21-32.	6.0	251
68	Composition and Antigenic Effects of Individual Glycan Sites of a Trimeric HIV-1 Envelope Glycoprotein. <i>Cell Reports</i> , 2016, 14, 2695-2706.	6.4	250
69	A Native-Like SOSIP.664 Trimer Based on an HIV-1 Subtype B <i>env</i> Gene. <i>Journal of Virology</i> , 2015, 89, 3380-3395.	3.4	247
70	Structural Characterization of the 1918 Influenza Virus H1N1 Neuraminidase. <i>Journal of Virology</i> , 2008, 82, 10493-10501.	3.4	241
71	Fine Mapping of the Interaction of Neutralizing and Nonneutralizing Monoclonal Antibodies with the CD4 Binding Site of Human Immunodeficiency Virus Type 1 gp120. <i>Journal of Virology</i> , 2003, 77, 642-658.	3.4	237
72	Asymmetric recognition of the HIV-1 trimer by broadly neutralizing antibody PG9. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4351-4356.	7.1	236

#	ARTICLE	IF	CITATIONS
73	Tailored Immunogens Direct Affinity Maturation toward HIV Neutralizing Antibodies. <i>Cell</i> , 2016, 166, 1459-1470.e11.	28.9	230
74	Antibody Elbow Angles are Influenced by their Light Chain Class. <i>Journal of Molecular Biology</i> , 2006, 357, 1566-1574.	4.2	229
75	Crystal structure of the IL-2 signaling complex: Paradigm for a heterotrimeric cytokine receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2788-2793.	7.1	225
76	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017, 547, 360-363.	27.8	217
77	Major antigen-induced domain rearrangements in an antibody. <i>Structure</i> , 1993, 1, 83-93.	3.3	216
78	Holes in the Glycan Shield of the Native HIV Envelope Are a Target of Trimer-Elicited Neutralizing Antibodies. <i>Cell Reports</i> , 2016, 16, 2327-2338.	6.4	216
79	A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic β^2 -Hairpin Structure. <i>Immunity</i> , 2017, 46, 690-702.	14.3	216
80	Arylfluorosulfates Inactivate Intracellular Lipid Binding Protein(s) through Chemoselective SuFEx Reaction with a Binding Site Tyr Residue. <i>Journal of the American Chemical Society</i> , 2016, 138, 7353-7364.	13.7	212
81	“Inverse Drug Discovery” Strategy To Identify Proteins That Are Targeted by Latent Electrophiles As Exemplified by Aryl Fluorosulfates. <i>Journal of the American Chemical Society</i> , 2018, 140, 200-210.	13.7	206
82	Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. <i>Immunity</i> , 2015, 43, 1053-1063.	14.3	200
83	Global Efforts in Structural Genomics. <i>Science</i> , 2001, 294, 89-92.	12.6	195
84	Recent Avian H5N1 Viruses Exhibit Increased Propensity for Acquiring Human Receptor Specificity. <i>Journal of Molecular Biology</i> , 2008, 381, 1382-1394.	4.2	192
85	Cleavage strongly influences whether soluble HIV-1 envelope glycoprotein trimers adopt a native-like conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18256-18261.	7.1	188
86	A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. <i>PLoS Pathogens</i> , 2017, 13, e1006682.	4.7	188
87	A common solution to group 2 influenza virus neutralization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 445-450.	7.1	187
88	Cross-Neutralization of a SARS-CoV-2 Antibody to a Functionally Conserved Site Is Mediated by Avidity. <i>Immunity</i> , 2020, 53, 1272-1280.e5.	14.3	185
89	A public antibody lineage that potently inhibits malaria infection through dual binding to the circumsporozoite protein. <i>Nature Medicine</i> , 2018, 24, 401-407.	30.7	183
90	Reshaping Antibody Diversity. <i>Cell</i> , 2013, 153, 1379-1393.	28.9	179

#	ARTICLE	IF	CITATIONS
91	A Site of Vulnerability on the Influenza Virus Hemagglutinin Head Domain Trimer Interface. <i>Cell</i> , 2019, 177, 1136-1152.e18.	28.9	177
92	Receptor mimicry by antibody F045â€“092 facilitates universal binding to the H3 subtype of influenza virus. <i>Nature Communications</i> , 2014, 5, 3614.	12.8	175
93	Electron-Microscopy-Based Epitope Mapping Defines Specificities of Polyclonal Antibodies Elicited during HIV-1 BG505 Envelope Trimer Immunization. <i>Immunity</i> , 2018, 49, 288-300.e8.	14.3	175
94	A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. <i>Science</i> , 2019, 366, .	12.6	172
95	Improving the Immunogenicity of Native-like HIV-1 Envelope Trimers by Hyperstabilization. <i>Cell Reports</i> , 2017, 20, 1805-1817.	6.4	171
96	Universal protection against influenza infection by a multidomain antibody to influenza hemagglutinin. <i>Science</i> , 2018, 362, 598-602.	12.6	170
97	Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 192-203.	2.1	165
98	Design of protein-binding proteins from the target structure alone. <i>Nature</i> , 2022, 605, 551-560.	27.8	164
99	Antigen Recognition by Variable Lymphocyte Receptors. <i>Science</i> , 2008, 321, 1834-1837.	12.6	163
100	Recent H3N2 Viruses Have Evolved Specificity for Extended, Branched Human-type Receptors, Conferring Potential for Increased Avidity. <i>Cell Host and Microbe</i> , 2017, 21, 23-34.	11.0	163
101	Broadly protective human antibodies that target the active site of influenza virus neuraminidase. <i>Science</i> , 2019, 366, 499-504.	12.6	162
102	Structural Evolution of Glycan Recognition by a Family of Potent HIV Antibodies. <i>Cell</i> , 2014, 159, 69-79.	28.9	161
103	Promiscuous Glycan Site Recognition by Antibodies to the High-Mannose Patch of gp120 Broadens Neutralization of HIV. <i>Science Translational Medicine</i> , 2014, 6, 236ra63.	12.4	160
104	Heterosubtypic antibody recognition of the influenza virus hemagglutinin receptor binding site enhanced by avidity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17040-17045.	7.1	159
105	Antibody responses to viral infections: a structural perspective across three different enveloped viruses. <i>Nature Microbiology</i> , 2019, 4, 734-747.	13.3	158
106	Structural Characterization of the Hemagglutinin Receptor Specificity from the 2009 H1N1 Influenza Pandemic. <i>Journal of Virology</i> , 2012, 86, 982-990.	3.4	155
107	Three-dimensional Structure of an Anti-steroid Fabâ€² and Progesterone-Fabâ€² Complex. <i>Journal of Molecular Biology</i> , 1993, 231, 103-118.	4.2	154
108	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. <i>Nature</i> , 2017, 548, 108-111.	27.8	154

#	ARTICLE	IF	CITATIONS
109	Vaccine-Induced Protection from Homologous Tier 2 SHIV Challenge in Nonhuman Primates Depends on Serum-Neutralizing Antibody Titers. <i>Immunity</i> , 2019, 50, 241-252.e6.	14.3	153
110	An Alternative Binding Mode of IGHV3-53 Antibodies to the SARS-CoV-2 Receptor Binding Domain. <i>Cell Reports</i> , 2020, 33, 108274.	6.4	152
111	Design and crystal structure of a native-like HIV-1 envelope trimer that engages multiple broadly neutralizing antibody precursors in vivo. <i>Journal of Experimental Medicine</i> , 2017, 214, 2573-2590.	8.5	151
112	Crystal structure of Sar1-GDP at 1.7 Å resolution and the role of the NH2 terminus in ER export. <i>Journal of Cell Biology</i> , 2001, 155, 937-948.	5.2	149
113	Trimeric HIV-1 glycoprotein gp140 immunogens and native HIV-1 envelope glycoproteins display the same closed and open quaternary molecular architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11440-11445.	7.1	149
114	Applications of the streak seeding technique in protein crystallization. <i>Journal of Crystal Growth</i> , 1991, 110, 270-282.	1.5	147
115	Presenting native-like trimeric HIV-1 antigens with self-assembling nanoparticles. <i>Nature Communications</i> , 2016, 7, 12041.	12.8	146
116	An HIV-1 antibody from an elite neutralizer implicates the fusion peptide as a site of vulnerability. <i>Nature Microbiology</i> , 2017, 2, 16199.	13.3	144
117	A recurring motif for antibody recognition of the receptor-binding site of influenza hemagglutinin. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 363-370.	8.2	141
118	Antibody Recognition of the Pandemic H1N1 Influenza Virus Hemagglutinin Receptor Binding Site. <i>Journal of Virology</i> , 2013, 87, 12471-12480.	3.4	139
119	Differential binding of neutralizing and non-neutralizing antibodies to native-like soluble HIV-1 Env trimers, uncleaved Env proteins, and monomeric subunits. <i>Retrovirology</i> , 2014, 11, 41.	2.0	139
120	Early Antibody Lineage Diversification and Independent Limb Maturation Lead to Broad HIV-1 Neutralization Targeting the Env High-Mannose Patch. <i>Immunity</i> , 2016, 44, 1215-1226.	14.3	138
121	Sequential and Simultaneous Immunization of Rabbits with HIV-1 Envelope Glycoprotein SOSIP.664 Trimers from Clades A, B and C. <i>PLoS Pathogens</i> , 2016, 12, e1005864.	4.7	138
122	Broadly neutralizing antibodies against influenza viruses. <i>Antiviral Research</i> , 2013, 98, 476-483.	4.1	136
123	The challenge of protein structure determination—lessons from structural genomics. <i>Protein Science</i> , 2007, 16, 2472-2482.	7.6	135
124	Structural basis of hepatitis C virus neutralization by broadly neutralizing antibody HCV1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9499-9504.	7.1	135
125	Hemagglutinin homologue from H17N10 bat influenza virus exhibits divergent receptor-binding and pH-dependent fusion activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1458-1463.	7.1	135
126	Structural Constraints Determine the Glycosylation of HIV-1 Envelope Trimers. <i>Cell Reports</i> , 2015, 11, 1604-1613.	6.4	135

#	ARTICLE	IF	CITATIONS
127	Potent peptidic fusion inhibitors of influenza virus. <i>Science</i> , 2017, 358, 496-502.	12.6	135
128	Uncleaved prefusion-optimized gp140 trimers derived from analysis of HIV-1 envelope metastability. <i>Nature Communications</i> , 2016, 7, 12040.	12.8	134
129	Preferential Recognition of Avian-Like Receptors in Human Influenza A H7N9 Viruses. <i>Science</i> , 2013, 342, 1230-1235.	12.6	133
130	A Perspective on the Structural and Functional Constraints for Immune Evasion: Insights from Influenza Virus. <i>Journal of Molecular Biology</i> , 2017, 429, 2694-2709.	4.2	133
131	Antibody potency relates to the ability to recognize the closed, pre-fusion form of HIV Env. <i>Nature Communications</i> , 2015, 6, 6144.	12.8	130
132	A Prominent Site of Antibody Vulnerability on HIV Envelope Incorporates a Motif Associated with CCR5 Binding and Its Camouflaging Glycans. <i>Immunity</i> , 2016, 45, 31-45.	14.3	129
133	Design and structure of two HIV-1 clade C SOSIP.664 trimers that increase the arsenal of native-like Env immunogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11947-11952.	7.1	127
134	HMGB1 Activates Proinflammatory Signaling via TLR5 Leading to Allodynia. <i>Cell Reports</i> , 2016, 17, 1128-1140.	6.4	125
135	A human antibody reveals a conserved site on beta-coronavirus spike proteins and confers protection against SARS-CoV-2 infection. <i>Science Translational Medicine</i> , 2022, 14, eabi9215.	12.4	123
136	Structural Basis of Enhanced Binding of Extended and Helically Constrained Peptide Epitopes of the Broadly Neutralizing HIV-1 Antibody 4E10. <i>Journal of Molecular Biology</i> , 2007, 365, 1533-1544.	4.2	121
137	Structural basis for antibody recognition of the NANP repeats in <i>Plasmodium falciparum</i> circumsporozoite protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10438-E10445.	7.1	116
138	Structure and immunogenicity of a stabilized HIV-1 envelope trimer based on a group-M consensus sequence. <i>Nature Communications</i> , 2019, 10, 2355.	12.8	116
139	Structure and Immune Recognition of the HIV Glycan Shield. <i>Annual Review of Biophysics</i> , 2018, 47, 499-523.	10.0	115
140	Structure of a Classical Broadly Neutralizing Stem Antibody in Complex with a Pandemic H2 Influenza Virus Hemagglutinin. <i>Journal of Virology</i> , 2013, 87, 7149-7154.	3.4	114
141	Structural Characterization of an Early Fusion Intermediate of Influenza Virus Hemagglutinin. <i>Journal of Virology</i> , 2011, 85, 5172-5182.	3.4	113
142	The human naive B cell repertoire contains distinct subclasses for a germline-targeting HIV-1 vaccine immunogen. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	113
143	A Glycoconjugate Antigen Based on the Recognition Motif of a Broadly Neutralizing Human Immunodeficiency Virus Antibody, 2G12, Is Immunogenic but Elicits Antibodies Unable To Bind to the Self Glycans of gp120. <i>Journal of Virology</i> , 2008, 82, 6359-6368.	3.4	112
144	Epitopes for neutralizing antibodies induced by HIV-1 envelope glycoprotein BG505 SOSIP trimers in rabbits and macaques. <i>PLoS Pathogens</i> , 2018, 14, e1006913.	4.7	111

#	ARTICLE	IF	CITATIONS
145	Broadly neutralizing antibodies target the coronavirus fusion peptide. <i>Science</i> , 2022, 377, 728-735.	12.6	111
146	Characterization of a Broadly Neutralizing Monoclonal Antibody That Targets the Fusion Domain of Group 2 Influenza A Virus Hemagglutinin. <i>Journal of Virology</i> , 2014, 88, 13580-13592.	3.4	110
147	CD4-Induced Activation in a Soluble HIV-1 Env Trimer. <i>Structure</i> , 2014, 22, 974-984.	3.3	108
148	Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. <i>Nature Biotechnology</i> , 2017, 35, 667-671.	17.5	108
149	Genetically encoding phosphotyrosine and its nonhydrolyzable analog in bacteria. <i>Nature Chemical Biology</i> , 2017, 13, 845-849.	8.0	105
150	Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. <i>PLoS Pathogens</i> , 2016, 12, e1005815.	4.7	104
151	Antibody 27F3 Broadly Targets Influenza A Group 1 and 2 Hemagglutinins through a Further Variation in VH1-69 Antibody Orientation on the HA Stem. <i>Cell Reports</i> , 2017, 20, 2935-2943.	6.4	103
152	Comprehensive Antigenic Map of a Cleaved Soluble HIV-1 Envelope Trimer. <i>PLoS Pathogens</i> , 2015, 11, e1004767.	4.7	100
153	The JCSG high-throughput structural biology pipeline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1137-1142.	0.7	99
154	Analytical and production seeding techniques. <i>Methods</i> , 1990, 1, 38-49.	3.8	98
155	A small-molecule fusion inhibitor of influenza virus is orally active in mice. <i>Science</i> , 2019, 363, .	12.6	98
156	Glycine Substitution at Helix-to-Coil Transitions Facilitates the Structural Determination of a Stabilized Subtype C HIV Envelope Glycoprotein. <i>Immunity</i> , 2017, 46, 792-803.e3.	14.3	96
157	Insights into the trimeric HIV-1 envelope glycoprotein structure. <i>Trends in Biochemical Sciences</i> , 2015, 40, 101-107.	7.5	95
158	A Conformational Switch in Human Immunodeficiency Virus gp41 Revealed by the Structures of Overlapping Epitopes Recognized by Neutralizing Antibodies. <i>Journal of Virology</i> , 2009, 83, 8451-8462.	3.4	92
159	VH1-69 antiviral broadly neutralizing antibodies: genetics, structures, and relevance to rational vaccine design. <i>Current Opinion in Virology</i> , 2019, 34, 149-159.	5.4	92
160	Structure, Receptor Binding, and Antigenicity of Influenza Virus Hemagglutinins from the 1957 H2N2 Pandemic. <i>Journal of Virology</i> , 2010, 84, 1715-1721.	3.4	90
161	HIV Envelope Glycoform Heterogeneity and Localized Diversity Govern the Initiation and Maturation of a V2 Apex Broadly Neutralizing Antibody Lineage. <i>Immunity</i> , 2017, 47, 990-1003.e9.	14.3	90
162	Influences on the Design and Purification of Soluble, Recombinant Native-Like HIV-1 Envelope Glycoprotein Trimers. <i>Journal of Virology</i> , 2015, 89, 12189-12210.	3.4	88

#	ARTICLE	IF	CITATIONS
163	Antibodies to a conformational epitope on gp41 neutralize HIV-1 by destabilizing the Env spike. <i>Nature Communications</i> , 2015, 6, 8167.	12.8	87
164	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. <i>Immunity</i> , 2016, 44, 21-31.	14.3	87
165	A Fluorogenic Aryl Fluorosulfate for Intraorganellar Transthyretin Imaging in Living Cells and in <i>Caenorhabditis elegans</i> . <i>Journal of the American Chemical Society</i> , 2015, 137, 7404-7414.	13.7	86
166	A Structurally Distinct Human Mycoplasma Protein that Generically Blocks Antigen-Antibody Union. <i>Science</i> , 2014, 343, 656-661.	12.6	85
167	Key gp120 Glycans Pose Roadblocks to the Rapid Development of VRC01-Class Antibodies in an HIV-1-Infected Chinese Donor. <i>Immunity</i> , 2016, 44, 939-950.	14.3	85
168	Structural insights into key sites of vulnerability on HIV-1 Env and influenza HA. <i>Immunological Reviews</i> , 2012, 250, 180-198.	6.0	84
169	Structural Characterization of Viral Epitopes Recognized by Broadly Cross-Reactive Antibodies. <i>Current Topics in Microbiology and Immunology</i> , 2014, 386, 323-341.	1.1	83
170	Three mutations switch H7N9 influenza to human-type receptor specificity. <i>PLoS Pathogens</i> , 2017, 13, e1006390.	4.7	83
171	Structural insights into the design of novel anti-influenza therapies. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 115-121.	8.2	81
172	Influenza Human Monoclonal Antibody 1F1 Interacts with Three Major Antigenic Sites and Residues Mediating Human Receptor Specificity in H1N1 Viruses. <i>PLoS Pathogens</i> , 2012, 8, e1003067.	4.7	80
173	Two Classes of Broadly Neutralizing Antibodies within a Single Lineage Directed to the High-Mannose Patch of HIV Envelope. <i>Journal of Virology</i> , 2015, 89, 1105-1118.	3.4	80
174	Single-component, self-assembling, protein nanoparticles presenting the receptor binding domain and stabilized spike as SARS-CoV-2 vaccine candidates. <i>Science Advances</i> , 2021, 7, .	10.3	80
175	Structure of Hepatitis C Virus Envelope Glycoprotein E2 Antigenic Site 412 to 423 in Complex with Antibody AP33. <i>Journal of Virology</i> , 2012, 86, 13085-13088.	3.4	79
176	Influenza Hemagglutinin Structures and Antibody Recognition. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020, 10, a038778.	6.2	79
177	Bispecific antibodies targeting distinct regions of the spike protein potently neutralize SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2021, 13, eabj5413.	12.4	79
178	A Distinct Type of Pilus from the Human Microbiome. <i>Cell</i> , 2016, 165, 690-703.	28.9	78
179	Structural flexibility at a major conserved antibody target on hepatitis C virus E2 antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12768-12773.	7.1	78
180	N-Glycolylneuraminic Acid as a Receptor for Influenza A Viruses. <i>Cell Reports</i> , 2019, 27, 3284-3294.e6.	6.4	78

#	ARTICLE	IF	CITATIONS
181	Genetic and structural insights into broad neutralization of hepatitis C virus by human V_H 1-69 antibodies. Science Advances, 2019, 5, eaav1882.	10.3	77
182	Influences on Trimerization and Aggregation of Soluble, Cleaved HIV-1 SOSIP Envelope Glycoprotein. Journal of Virology, 2013, 87, 9873-9885.	3.4	76
183	cGMP production and analysis of BG505 SOSIP.664, an extensively glycosylated, trimeric HIV-1 envelope glycoprotein vaccine candidate. Biotechnology and Bioengineering, 2018, 115, 885-899.	3.3	75
184	HIV-1 vaccine design through minimizing envelope metastability. Science Advances, 2018, 4, eaau6769.	10.3	75
185	Structural Basis of Murein Peptide Specificity of a Î³-D-Glutamyl-L-Diamino Acid Endopeptidase. Structure, 2009, 17, 303-313.	3.3	73
186	Structural Characterization of Cleaved, Soluble HIV-1 Envelope Glycoprotein Trimers. Journal of Virology, 2013, 87, 9865-9872.	3.4	71
187	Cryo-EM structure of P. falciparum circumsporozoite protein with a vaccine-elicited antibody is stabilized by somatically mutated inter-Fab contacts. Science Advances, 2018, 4, eaau8529.	10.3	70
188	Stapled HIV-1 peptides recapitulate antigenic structures and engage broadly neutralizing antibodies. Nature Structural and Molecular Biology, 2014, 21, 1058-1067.	8.2	69
189	Complete epitopes for vaccine design derived from a crystal structure of the broadly neutralizing antibodies PGT128 and 8ANC195 in complex with an HIV-1 Env trimer. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2099-2108.	2.5	69
190	Approaching rational epitope vaccine design for hepatitis C virus with meta-server and multivalent scaffolding. Scientific Reports, 2015, 5, 12501.	3.3	68
191	Structure of 2G12 Fab₂ in Complex with Soluble and Fully Glycosylated HIV-1 Env by Negative-Stain Single-Particle Electron Microscopy. Journal of Virology, 2014, 88, 10177-10188.	3.4	67
192	A multifunctional human monoclonal neutralizing antibody that targets a unique conserved epitope on influenza HA. Nature Communications, 2018, 9, 2669.	12.8	67
193	Immunodominance and Antigenic Variation of Influenza Virus Hemagglutinin: Implications for Design of Universal Vaccine Immunogens. Journal of Infectious Diseases, 2019, 219, S38-S45.	4.0	67
194	Closing and Opening Holes in the Glycan Shield of HIV-1 Envelope Glycoprotein SOSIP Trimers Can Redirect the Neutralizing Antibody Response to the Newly Unmasked Epitopes. Journal of Virology, 2019, 93, .	3.4	66
195	Probing the antigenicity of hepatitis C virus envelope glycoprotein complex by high-throughput mutagenesis. PLoS Pathogens, 2017, 13, e1006735.	4.7	66
196	The Carbohydrate Epitope of the Neutralizing Anti-HIV-1 Antibody 2G12. Advances in Experimental Medicine and Biology, 2003, 535, 205-218.	1.6	65
197	Structure of the Î³-D-glutamyl-L-diamino acid endopeptidase YkfC from Bacillus cereus in complex with L-Ala-Î³-D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1354-1364.	0.7	64
198	Alternative Recognition of the Conserved Stem Epitope in Influenza A Virus Hemagglutinin by a V_H 3-30-Encoded Heterosubtypic Antibody. Journal of Virology, 2014, 88, 7083-7092.	3.4	62

#	ARTICLE	IF	CITATIONS
199	H7N9 influenza virus neutralizing antibodies that possess few somatic mutations. <i>Journal of Clinical Investigation</i> , 2016, 126, 1482-1494.	8.2	62
200	Hemagglutinin Receptor Specificity and Structural Analyses of Respiratory Droplet-Transmissible H5N1 Viruses. <i>Journal of Virology</i> , 2014, 88, 768-773.	3.4	61
201	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. <i>PLoS Pathogens</i> , 2020, 16, e1008753.	4.7	61
202	HIV-1 Envelope and MPER Antibody Structures in Lipid Assemblies. <i>Cell Reports</i> , 2020, 31, 107583.	6.4	60
203	SARS-CoV-2 Beta variant infection elicits potent lineage-specific and cross-reactive antibodies. <i>Science</i> , 2022, 375, 782-787.	12.6	60
204	Diversity of Functionally Permissive Sequences in the Receptor-Binding Site of Influenza Hemagglutinin. <i>Cell Host and Microbe</i> , 2017, 21, 742-753.e8.	11.0	59
205	Elicitation of Neutralizing Antibodies Targeting the V2 Apex of the HIV Envelope Trimer in a Wild-Type Animal Model. <i>Cell Reports</i> , 2017, 21, 222-235.	6.4	58
206	A complex epistatic network limits the mutational reversibility in the influenza hemagglutinin receptor-binding site. <i>Nature Communications</i> , 2018, 9, 1264.	12.8	58
207	Lipid interactions and angle of approach to the HIV-1 viral membrane of broadly neutralizing antibody 10E8: Insights for vaccine and therapeutic design. <i>PLoS Pathogens</i> , 2017, 13, e1006212.	4.7	58
208	Reducing V3 Antigenicity and Immunogenicity on Soluble, Native-Like HIV-1 Env SOSIP Trimers. <i>Journal of Virology</i> , 2017, 91, .	3.4	57
209	Autologous Antibody Responses to an HIV Envelope Glycan Hole Are Not Easily Broadened in Rabbits. <i>Journal of Virology</i> , 2020, 94, .	3.4	57
210	Role of the CBP catalytic core in intramolecular SUMOylation and control of histone H3 acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5335-E5342.	7.1	56
211	The Neutralizing Face of Hepatitis C Virus E2 Envelope Glycoprotein. <i>Frontiers in Immunology</i> , 2018, 9, 1315.	4.8	56
212	In vitro evolution of an influenza broadly neutralizing antibody is modulated by hemagglutinin receptor specificity. <i>Nature Communications</i> , 2017, 8, 15371.	12.8	55
213	A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody. <i>PLoS Pathogens</i> , 2020, 16, e1009089.	4.7	55
214	Capitalizing on knowledge of hepatitis C virus neutralizing epitopes for rational vaccine design. <i>Current Opinion in Virology</i> , 2015, 11, 148-157.	5.4	54
215	A Human-Infecting H10N8 Influenza Virus Retains a Strong Preference for Avian-type Receptors. <i>Cell Host and Microbe</i> , 2015, 17, 377-384.	11.0	54
216	Conservation and diversity in the ultralong third heavy-chain complementarity-determining region of bovine antibodies. <i>Science Immunology</i> , 2016, 1, .	11.9	52

#	ARTICLE	IF	CITATIONS
217	Co-evolution of HIV Envelope and Apex-Targeting Neutralizing Antibody Lineage Provides Benchmarks for Vaccine Design. <i>Cell Reports</i> , 2018, 23, 3249-3261.	6.4	52
218	Stabilization of amyloidogenic immunoglobulin light chains by small molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8360-8369.	7.1	52
219	A Unique and Conserved Neutralization Epitope in H5N1 Influenza Viruses Identified by an Antibody against the A/Goose/Guangdong/1/96 Hemagglutinin. <i>Journal of Virology</i> , 2013, 87, 12619-12635.	3.4	51
220	Structural Basis of Protection against H7N9 Influenza Virus by Human Anti-N9 Neuraminidase Antibodies. <i>Cell Host and Microbe</i> , 2019, 26, 729-738.e4.	11.0	51
221	Different genetic barriers for resistance to HA stem antibodies in influenza H3 and H1 viruses. <i>Science</i> , 2020, 368, 1335-1340.	12.6	51
222	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. <i>Nature Communications</i> , 2018, 9, 1956.	12.8	50
223	A Computationally Designed Hemagglutinin Stem-Binding Protein Provides In Vivo Protection from Influenza Independent of a Host Immune Response. <i>PLoS Pathogens</i> , 2016, 12, e1005409.	4.7	49
224	Influenza H7N9 Virus Neuraminidase-Specific Human Monoclonal Antibodies Inhibit Viral Egress and Protect from Lethal Influenza Infection in Mice. <i>Cell Host and Microbe</i> , 2019, 26, 715-728.e8.	11.0	49
225	A combination of cross-neutralizing antibodies synergizes to prevent SARS-CoV-2 and SARS-CoV pseudovirus infection. <i>Cell Host and Microbe</i> , 2021, 29, 806-818.e6.	11.0	49
226	Structure-based optimization and synthesis of antiviral drug Arbidol analogues with significantly improved affinity to influenza hemagglutinin. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 3744-3748.	2.2	48
227	Monoglucosylated glycans in the secreted human complement component C3: implications for protein biosynthesis and structure. <i>FEBS Letters</i> , 2004, 566, 270-274.	2.8	47
228	Variable Lymphocyte Receptor Recognition of the Immunodominant Glycoprotein of <i>Bacillus anthracis</i> Spores. <i>Structure</i> , 2012, 20, 479-486.	3.3	47
229	Stable 293ÅT and CHO cell lines expressing cleaved, stable HIV-1 envelope glycoprotein trimers for structural and vaccine studies. <i>Retrovirology</i> , 2014, 11, 33.	2.0	46
230	Insights into Substrate Specificity of NlpC/P60 Cell Wall Hydrolases Containing Bacterial SH3 Domains. <i>MBio</i> , 2015, 6, e02327-14.	4.1	46
231	Bacterial glycosyltransferase-mediated cell-surface chemoenzymatic glycan modification. <i>Nature Communications</i> , 2019, 10, 1799.	12.8	46
232	Dynamics of B cell repertoires and emergence of cross-reactive responses in patients with different severities of COVID-19. <i>Cell Reports</i> , 2021, 35, 109173.	6.4	46
233	Preventing an Antigenically Disruptive Mutation in Egg-Based H3N2 Seasonal Influenza Vaccines by Mutational Incompatibility. <i>Cell Host and Microbe</i> , 2019, 25, 836-844.e5.	11.0	45
234	Structure of Hepatitis C Virus Envelope Glycoprotein E1 Antigenic Site 314-324 in Complex with Antibody IGH526. <i>Journal of Molecular Biology</i> , 2015, 427, 2617-2628.	4.2	44

#	ARTICLE	IF	CITATIONS
235	Structure and Receptor Binding of the Hemagglutinin from a Human H6N1 Influenza Virus. Cell Host and Microbe, 2015, 17, 369-376.	11.0	44
236	A single mutation in Taiwanese H6N1 influenza hemagglutinin switches binding to human α 2 type receptors. EMBO Molecular Medicine, 2017, 9, 1314-1325.	6.9	44
237	An MPER antibody neutralizes HIV-1 using germline features shared among donors. Nature Communications, 2019, 10, 5389.	12.8	44
238	Proof of concept for rational design of hepatitis C virus E2 core nanoparticle vaccines. Science Advances, 2020, 6, eaaz6225.	10.3	44
239	Sequence signatures of two public antibody clonotypes that bind SARS-CoV-2 receptor binding domain. Nature Communications, 2021, 12, 3815.	12.8	44
240	A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2. Immunity, 2022, 55, 1105-1117.e4.	14.3	44
241	Structure-based discovery of NANOG variant with enhanced properties to promote self-renewal and reprogramming of pluripotent stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4666-4671.	7.1	43
242	Immunological memory to hyperphosphorylated tau in asymptomatic individuals. Acta Neuropathologica, 2017, 133, 767-783.	7.7	43
243	Innovations in structure-based antigen design and immune monitoring for next generation vaccines. Current Opinion in Immunology, 2020, 65, 50-56.	5.5	43
244	Structure-Activity Relationships in Metal-Binding Pharmacophores for Influenza Endonuclease. Journal of Medicinal Chemistry, 2018, 61, 10206-10217.	6.4	42
245	Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. Cell Host and Microbe, 2019, 25, 873-883.e5.	11.0	42
246	Structural Insights into the Lipid A Transport Pathway in MsbA. Structure, 2019, 27, 1114-1123.e3.	3.3	41
247	Stabilizing the C _H 2 Domain of an Antibody by Engineering in an Enhanced Aromatic Sequon. ACS Chemical Biology, 2016, 11, 1852-1861.	3.4	40
248	Stabilization of the gp120 V3 loop through hydrophobic interactions reduces the immunodominant V3-directed non-neutralizing response to HIV-1 envelope trimers. Journal of Biological Chemistry, 2018, 293, 1688-1701.	3.4	40
249	Major antigenic site B of human influenza H3N2 viruses has an evolving local fitness landscape. Nature Communications, 2020, 11, 1233.	12.8	40
250	Targeted isolation of diverse human protective broadly neutralizing antibodies against SARS-like viruses. Nature Immunology, 2022, 23, 960-970.	14.5	39
251	COVA1-18 neutralizing antibody protects against SARS-CoV-2 in three preclinical models. Nature Communications, 2021, 12, 6097.	12.8	38
252	A New Functional Domain of Guanine Nucleotide Dissociation Inhibitor (β -GDI) Involved in Rab Recycling. Traffic, 2000, 1, 270-281.	2.7	37

#	ARTICLE	IF	CITATIONS
253	Potent anti-influenza H7 human monoclonal antibody induces separation of hemagglutinin receptor-binding head domains. <i>PLoS Biology</i> , 2019, 17, e3000139.	5.6	37
254	UHMâ€“ULM interactions in the RBM39â€“U2AF65 splicing-factor complex. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 497-511.	2.3	36
255	The Unusual Genetics and Biochemistry of Bovine Immunoglobulins. <i>Advances in Immunology</i> , 2018, 137, 135-164.	2.2	36
256	Bifunctional coumarin derivatives that inhibit transthyretin amyloidogenesis and serve as fluorescent transthyretin folding sensors. <i>Chemical Communications</i> , 2013, 49, 9188.	4.1	35
257	The 150-Loop Restricts the Host Specificity of Human H10N8 Influenza Virus. <i>Cell Reports</i> , 2017, 19, 235-245.	6.4	35
258	The Chimpanzee SIV Envelope Trimer: Structure and Deployment as an HIV Vaccine Template. <i>Cell Reports</i> , 2019, 27, 2426-2441.e6.	6.4	35
259	Structural Biology of Influenza Hemagglutinin: An Amaranthine Adventure. <i>Viruses</i> , 2020, 12, 1053.	3.3	35
260	A broad and potent neutralization epitope in SARS-related coronaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	34
261	Bacterially derived synthetic mimetics of mammalian oligomannose prime antibody responses that neutralize HIV infectivity. <i>Nature Communications</i> , 2017, 8, 1601.	12.8	33
262	Oligomannose Glycopeptide Conjugates Elicit Antibodies Targeting the Glycan Core Rather than Its Extremities. <i>ACS Central Science</i> , 2019, 5, 237-249.	11.3	33
263	Design and Structure of an Engineered Disulfide-Stabilized Influenza Virus Hemagglutinin Trimer. <i>Journal of Virology</i> , 2015, 89, 7417-7420.	3.4	32
264	Recurring and Adaptable Binding Motifs in Broadly Neutralizing Antibodies to Influenza Virus Are Encoded on the D3-9 Segment of the Ig Gene. <i>Cell Host and Microbe</i> , 2018, 24, 569-578.e4.	11.0	32
265	Antibody Structure. <i>Microbiology Spectrum</i> , 2014, 2, .	3.0	31
266	Selection of nanobodies with broad neutralizing potential against primary HIV-1 strains using soluble subtype C gp140 envelope trimers. <i>Scientific Reports</i> , 2017, 7, 8390.	3.3	31
267	Structural basis of broad HIV neutralization by a vaccine-induced cow antibody. <i>Science Advances</i> , 2020, 6, eaba0468.	10.3	31
268	Redesigned HIV antibodies exhibit enhanced neutralizing potency and breadth. <i>Journal of Clinical Investigation</i> , 2015, 125, 2523-2531.	8.2	31
269	Capturing the inherent structural dynamics of the HIV-1 envelope glycoprotein fusion peptide. <i>Nature Communications</i> , 2019, 10, 763.	12.8	30
270	Structure and mechanism of monoclonal antibody binding to theÂjunctional epitope of <i>Plasmodium falciparum</i> Âcircumsporozoite protein. <i>PLoS Pathogens</i> , 2020, 16, e1008373.	4.7	30

#	ARTICLE	IF	CITATIONS
271	Structural and biophysical correlation of anti-NANP antibodies with in vivo protection against <i>P. falciparum</i> . <i>Nature Communications</i> , 2021, 12, 1063.	12.8	30
272	Neutralizing Antibody Induction by HIV-1 Envelope Glycoprotein SOSIP Trimers on Iron Oxide Nanoparticles May Be Impaired by Mannose Binding Lectin. <i>Journal of Virology</i> , 2020, 94, .	3.4	29
273	Diverse Antibody Responses to Conserved Structural Motifs in <i>Plasmodium falciparum</i> Circumsporozoite Protein. <i>Journal of Molecular Biology</i> , 2020, 432, 1048-1063.	4.2	28
274	Crystal structure of the HIV neutralizing antibody 2G12 in complex with a bacterial oligosaccharide analog of mammalian oligomannose. <i>Glycobiology</i> , 2015, 25, 412-419.	2.5	27
275	Improving the Expression and Purification of Soluble, Recombinant Native-Like HIV-1 Envelope Glycoprotein Trimers by Targeted Sequence Changes. <i>Journal of Virology</i> , 2017, 91, .	3.4	27
276	Structural Insights into VLR Fine Specificity for Blood Group Carbohydrates. <i>Structure</i> , 2017, 25, 1667-1678.e4.	3.3	27
277	Defining the Structural Basis for Allosteric Product Release from <i>E. coli</i> Dihydrofolate Reductase Using NMR Relaxation Dispersion. <i>Journal of the American Chemical Society</i> , 2017, 139, 11233-11240.	13.7	27
278	Structural insights of a highly potent pan-neutralizing SARS-CoV-2 human monoclonal antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2120976119.	7.1	27
279	An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. <i>Science Advances</i> , 2020, 6, eabb5642.	10.3	26
280	Structures of a Bifunctional Cell Wall Hydrolase CwlT Containing a Novel Bacterial Lysozyme and an NlpC/P60 dl-Endopeptidase. <i>Journal of Molecular Biology</i> , 2014, 426, 169-184.	4.2	25
281	Soluble human TLR2 ectodomain binds diacylglycerol from microbial lipopeptides and glycolipids. <i>Innate Immunity</i> , 2015, 21, 175-193.	2.4	25
282	A small-molecule fragment that emulates binding of receptor and broadly neutralizing antibodies to influenza A hemagglutinin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4240-4245.	7.1	25
283	An influenza A hemagglutinin small-molecule fusion inhibitor identified by a new high-throughput fluorescence polarization screen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18431-18438.	7.1	25
284	Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. <i>Nature Communications</i> , 2021, 12, 2633.	12.8	25
285	X-Ray Crystallographic Studies of Antibody-Peptide Complexes. <i>ImmunoMethods</i> , 1993, 3, 211-221.	0.8	24
286	Integrity of Glycosylation Processing of a Glycan-Depleted Trimeric HIV-1 Immunogen Targeting Key B-Cell Lineages. <i>Journal of Proteome Research</i> , 2018, 17, 987-999.	3.7	23
287	Multistate design of influenza antibodies improves affinity and breadth against seasonal viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1597-1602.	7.1	23
288	A cross-neutralizing antibody between HIV-1 and influenza virus. <i>PLoS Pathogens</i> , 2021, 17, e1009407.	4.7	23

#	ARTICLE	IF	CITATIONS
289	Functional convergence of a germline-encoded neutralizing antibody response in rhesus macaques immunized with HCV envelope glycoproteins. <i>Immunity</i> , 2021, 54, 781-796.e4.	14.3	23
290	Protective neutralizing epitopes in SARS-CoV-2. <i>Immunological Reviews</i> , 2022, 310, 76-92.	6.0	23
291	Identification of Antibodies Targeting the H3N2 Hemagglutinin Receptor Binding Site following Vaccination of Humans. <i>Cell Reports</i> , 2019, 29, 4460-4470.e8.	6.4	22
292	A high-affinity antibody against the CSP N-terminal domain lacks <i>Plasmodium falciparum</i> inhibitory activity. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	21
293	Diverse immunoglobulin gene usage and convergent epitope targeting in neutralizing antibody responses to SARS-CoV-2. <i>Cell Reports</i> , 2021, 35, 109109.	6.4	21
294	Functional human IgA targets a conserved site on malaria sporozoites. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	21
295	A Novel Recombinant Influenza Virus Neuraminidase Vaccine Candidate Stabilized by a Measles Virus Phosphoprotein Tetramerization Domain Provides Robust Protection from Virus Challenge in the Mouse Model. <i>MBio</i> , 2021, 12, e0224121.	4.1	21
296	Probing Affinity, Avidity, Anticooperativity, and Competition in Antibody and Receptor Binding to the SARS-CoV-2 Spike by Single Particle Mass Analyses. <i>ACS Central Science</i> , 2021, 7, 1863-1873.	11.3	20
297	A V _H 1-69 antibody lineage from an infected Chinese donor potently neutralizes HIV-1 by targeting the V3 glycan supersite. <i>Science Advances</i> , 2020, 6, .	10.3	19
298	Engineering protein for X-ray crystallography: The murine major histocompatibility complex class II molecule I-A ^d . <i>Protein Science</i> , 1998, 7, 413-418.	7.6	18
299	Structural Basis for a Switch in Receptor Binding Specificity of Two H5N1 Hemagglutinin Mutants. <i>Cell Reports</i> , 2015, 13, 1683-1691.	6.4	18
300	Crystal structure of the post-fusion core of the Human coronavirus 229E spike protein at 1.86 Å resolution. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 841-851.	2.3	18
301	Structural basis for cooperative regulation of KIX-mediated transcription pathways by the HTLV-1 HBZ activation domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10040-10045.	7.1	18
302	Stabilization of the V2 loop improves the presentation of V2 loop-associated broadly neutralizing antibody epitopes on HIV-1 envelope trimers. <i>Journal of Biological Chemistry</i> , 2019, 294, 5616-5631.	3.4	16
303	Convergent Evolution in Breadth of Two VH6-1-Encoded Influenza Antibody Clonotypes from a Single Donor. <i>Cell Host and Microbe</i> , 2020, 28, 434-444.e4.	11.0	16
304	Discovery of Potent Coumarin-Based Kinetic Stabilizers of Amyloidogenic Immunoglobulin Light Chains Using Structure-Based Design. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 6273-6299.	6.4	16
305	Crystal Structure and Activity Studies of the C11 Cysteine Peptidase from <i>Parabacteroides merdae</i> in the Human Gut Microbiome. <i>Journal of Biological Chemistry</i> , 2016, 291, 9482-9491.	3.4	15
306	A common antigenic motif recognized by naturally occurring human VH5 ⁵¹ /VL4 ¹ anti-tau antibodies with distinct functionalities. <i>Acta Neuropathologica Communications</i> , 2018, 6, 43.	5.2	15

#	ARTICLE	IF	CITATIONS
307	Vaccine innovations for emerging infectious diseases—a symposium report. Annals of the New York Academy of Sciences, 2020, 1462, 14-26.	3.8	15
308	Structural basis for the stabilization of amyloidogenic immunoglobulin light chains by hydantoins. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 127356.	2.2	15
309	50 Years of structural immunology. Journal of Biological Chemistry, 2021, 296, 100745.	3.4	15
310	Immunogenetic and structural analysis of a class of HCV broadly neutralizing antibodies and their precursors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7569-7574.	7.1	14
311	Neutralizing Antibodies to SARS-CoV-2 Selected from a Human Antibody Library Constructed Decades Ago. Advanced Science, 2022, 9, e2102181.	11.2	14
312	<i>N</i> -Glycolylneuraminic Acid Binding of Avian and Equine H7 Influenza A Viruses. Journal of Virology, 2022, 96, jvi0212021.	3.4	14
313	A novel CSP C-terminal epitope targeted by an antibody with protective activity against Plasmodium falciparum. PLoS Pathogens, 2022, 18, e1010409.	4.7	14
314	Structural basis for differential recognition of phosphohistidine-containing peptides by 1-pHis and 3-pHis monoclonal antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	13
315	Novel lamprey antibody recognizes terminal sulfated galactose epitopes on mammalian glycoproteins. Communications Biology, 2021, 4, 674.	4.4	13
316	Superimmunity by pan-sarbecovirus nanobodies. Cell Reports, 2022, 39, 111004.	6.4	13
317	Unique Structural Features of Influenza Virus H15 Hemagglutinin. Journal of Virology, 2017, 91, .	3.4	12
318	VLR Recognition of TLR5 Expands the Molecular Characterization of Protein Antigen Binding by Non-Ig-based Antibodies. Journal of Molecular Biology, 2018, 430, 1350-1367.	4.2	12
319	Selection of a picomolar antibody that targets CXCR2-mediated neutrophil activation and alleviates EAE symptoms. Nature Communications, 2021, 12, 2547.	12.8	11
320	Structure-Guided Functional Characterization of DUF1460 Reveals a Highly Specific NlpC/P60 Amidase Family. Structure, 2014, 22, 1799-1809.	3.3	10
321	Dlx5 Homeodomain:DNA Complex: Structure, Binding and Effect of Mutations Related to Split Hand and Foot Malformation Syndrome. Journal of Molecular Biology, 2016, 428, 1130-1141.	4.2	10
322	NMR Based SARS-CoV-2 Antibody Screening. Journal of the American Chemical Society, 2021, 143, 7930-7934.	13.7	10
323	Influenza chimeric hemagglutinin structures in complex with broadly protective antibodies to the stem and trimer interface. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	10
324	A General Method for Insertion of Functional Proteins within Proteins via Combinatorial Selection of Permissive Junctions. Chemistry and Biology, 2015, 22, 1134-1143.	6.0	9

#	ARTICLE	IF	CITATIONS
325	Structural Basis for Recognition of a Unique Epitope by a Human Anti-tau Antibody. <i>Structure</i> , 2018, 26, 1626-1634.e4.	3.3	9
326	The Impact of Sustained Immunization Regimens on the Antibody Response to Oligomannose Glycans. <i>ACS Chemical Biology</i> , 2020, 15, 789-798.	3.4	9
327	Semi-quantitative models for identifying potent and selective transthyretin amyloidogenesis inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 3441-3449.	2.2	8
328	Structure and Function of the DUF2233 Domain in Bacteria and in the Human Mannose 6-Phosphate Uncovering Enzyme. <i>Journal of Biological Chemistry</i> , 2013, 288, 16789-16799.	3.4	7
329	A Dynamic Switch in Inactive p38 ^β Leads to an Excited State on the Pathway to an Active Kinase. <i>Biochemistry</i> , 2019, 58, 5160-5172.	2.5	7
330	Inhibitory antibodies identify unique sites of therapeutic vulnerability in rhinovirus and other enteroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13499-13508.	7.1	7
331	Homologous and heterologous serological response to the N-terminal domain of SARS-CoV-2 in humans and mice. <i>European Journal of Immunology</i> , 2021, 51, 2296-2305.	2.9	7
332	Structural Insights into the Recognition of Phosphopeptide by the FHA Domain of Kanadaplin. <i>PLoS ONE</i> , 2014, 9, e107309.	2.5	6
333	HIV's Achilles' Heel. <i>Scientific American</i> , 2016, 315, 50-55.	1.0	6
334	Neutralizing Antibodies Induced by First-Generation gp41-Stabilized HIV-1 Envelope Trimers and Nanoparticles. <i>MBio</i> , 2021, 12, e0042921.	4.1	6
335	Antigenic imprinting in SARS-CoV-2. <i>Clinical and Translational Medicine</i> , 2022, 12, .	4.0	6
336	Structure of the apo anti-influenza CH65 Fab. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 145-148.	0.8	5
337	Amyloidogenic immunoglobulin light chain kinetic stabilizers comprising a simple urea linker module reveal a novel binding sub-site. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2022, 60, 128571.	2.2	5
338	Structures of single-layer β -sheet proteins evolved from β -hairpin repeats. <i>Protein Science</i> , 2019, 28, 1676-1689.	7.6	4
339	Toward a Carbohydrate-Based HIV-1 Vaccine. <i>ACS Symposium Series</i> , 2006, , 161-185.	0.5	3
340	Crystal structure of an anti-idiotypic variable lymphocyte receptor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 682-687.	0.8	3
341	Dynamic Local Polymorphisms in the Cbx1 Homeodomain Induced by DNA Binding. <i>Structure</i> , 2016, 24, 1372-1379.	3.3	2
342	Crystal Structure of a Two-Subunit TrkA Octameric Gating Ring Assembly. <i>PLoS ONE</i> , 2015, 10, e0122512.	2.5	2

#	ARTICLE	IF	CITATIONS
343	Dynamics of B-Cell Repertoires and Emergence of Cross-Reactive Responses in COVID-19 Patients with Different Disease Severity. SSRN Electronic Journal, 0, , .	0.4	2
344	Neutralizing Antibody Response to Sarbecovirus Is Delayed in Sequential Heterologous Immunization. Viruses, 2022, 14, 1382.	3.3	2
345	Antibody Structure. , 0, , 49-62.		1
346	Structural and Biochemical Characterization of Cysteinylation in Broadly Neutralizing Antibodies to HIV-1. Journal of Molecular Biology, 2021, 433, 167303.	4.2	1
347	STRUCTURAL BASIS FOR HOST/COMMENSAL-MICROBE INTERACTIONS IN THE HUMAN DISTAL GUT MICROBIOME. , 2014, , .		0
348	HIV ENVELOPE AND INFLUENZA HEMAGGLUTININ FUSION GLYCOPROTEINS AND THE QUEST FOR A UNIVERSAL VACCINE. , 2014, , .		0
349	Novel Rigid Glycomimetics to Inhibit Influenza Infection. FASEB Journal, 2019, 33, .	0.5	0
350	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
351	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
352	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
353	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0