

Ian A Wilson

List of Publications by Year in descending order

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Version: 2024-02-01

353
papers

57,976
citations

867

120
h-index

1631

221
g-index

406
all docs

406
docs citations

406
times ranked

41549
citing authors

#	ARTICLE	IF	CITATIONS
1	Neutralizing Antibodies to SARS-CoV-2 Selected from a Human Antibody Library Constructed Decades Ago. <i>Advanced Science</i> , 2022, 9, e2102181.	5.6	14
2	N-Glycolylneuraminic Acid Binding of Avian and Equine H7 Influenza A Viruses. <i>Journal of Virology</i> , 2022, 96, jvi0212021.	1.5	14
3	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.	1.0	5
4	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.	5.8	123
5	SARS-CoV-2 Beta variant infection elicits potent lineage-specific and cross-reactive antibodies. <i>Science</i> , 2022, 375, 782-787.	6.0	60
6	A novel CSP C-terminal epitope targeted by an antibody with protective activity against <i>Plasmodium falciparum</i> . <i>PLoS Pathogens</i> , 2022, 18, e1010409.	2.1	14
7	A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2. <i>Immunity</i> , 2022, 55, 1105-1117.e4.	6.6	44
8	Design of protein-binding proteins from the target structure alone. <i>Nature</i> , 2022, 605, 551-560.	13.7	164
9	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.	3.3	27
10	Influenza chimeric hemagglutinin structures in complex with broadly protective antibodies to the stem and trimer interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	10
11	Protective neutralizing epitopes in SARS-CoV-2. <i>Immunological Reviews</i> , 2022, 310, 76-92.	2.8	23
12	Targeted isolation of diverse human protective broadly neutralizing antibodies against SARS-like viruses. <i>Nature Immunology</i> , 2022, 23, 960-970.	7.0	39
13	Superimmunity by pan-sarbecovirus nanobodies. <i>Cell Reports</i> , 2022, 39, 111004.	2.9	13
14	Neutralizing Antibody Response to Sarbecovirus Is Delayed in Sequential Heterologous Immunization. <i>Viruses</i> , 2022, 14, 1382.	1.5	2
15	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, .	3.3	34
16	Antigenic imprinting in SARS-CoV-2. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	6
17	Broadly neutralizing antibodies target the coronavirus fusion peptide. <i>Science</i> , 2022, 377, 728-735.	6.0	111
18	Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 192-203.	1.0	165

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19	50 Years of structural immunology. <i>Journal of Biological Chemistry</i> , 2021, 296, 100745.	1.6	15
20	Structural and biophysical correlation of anti-NANP antibodies with in vivo protection against <i>P. falciparum</i> . <i>Nature Communications</i> , 2021, 12, 1063.	5.8	30
21	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. <i>Science</i> , 2021, 371, .	6.0	304
22	Structural basis for differential recognition of phosphohistidine-containing peptides by 1-pHis and 3-pHis monoclonal antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
23	A cross-neutralizing antibody between HIV-1 and influenza virus. <i>PLoS Pathogens</i> , 2021, 17, e1009407.	2.1	23
24	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, .	4.7	80
25	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.	6.6	23
26	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.	2.9	46
27	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. <i>Science</i> , 2021, 373, 818-823.	6.0	309
28	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.	5.1	49
29	Selection of a picomolar antibody that targets CXCR2-mediated neutrophil activation and alleviates EAE symptoms. <i>Nature Communications</i> , 2021, 12, 2547.	5.8	11
30	Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. <i>Nature Communications</i> , 2021, 12, 2633.	5.8	25
31	NMR Based SARS-CoV-2 Antibody Screening. <i>Journal of the American Chemical Society</i> , 2021, 143, 7930-7934.	6.6	10
32	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.	2.9	16
33	Diverse immunoglobulin gene usage and convergent epitope targeting in neutralizing antibody responses to SARS-CoV-2. <i>Cell Reports</i> , 2021, 35, 109109.	2.9	21
34	Sequence signatures of two public antibody clonotypes that bind SARS-CoV-2 receptor binding domain. <i>Nature Communications</i> , 2021, 12, 3815.	5.8	44
35	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.	1.6	7
36	Neutralizing Antibodies Induced by First-Generation gp41-Stabilized HIV-1 Envelope Trimers and Nanoparticles. <i>MBio</i> , 2021, 12, e0042921.	1.8	6

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37	Functional human IgA targets a conserved site on malaria sporozoites. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	21
38	Novel lamprey antibody recognizes terminal sulfated galactose epitopes on mammalian glycoproteins. <i>Communications Biology</i> , 2021, 4, 674.	2.0	13
39	Bispecific antibodies targeting distinct regions of the spike protein potentially neutralize SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2021, 13, eabj5413.	5.8	79
40	COVA1-18 neutralizing antibody protects against SARS-CoV-2 in three preclinical models. <i>Nature Communications</i> , 2021, 12, 6097.	5.8	38
41	Structural and Biochemical Characterization of Cysteinylation in Broadly Neutralizing Antibodies to HIV-1. <i>Journal of Molecular Biology</i> , 2021, 433, 167303.	2.0	1
42	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.	5.3	20
43	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.	1.8	21
44	Vaccine innovations for emerging infectious diseases—a symposium report. <i>Annals of the New York Academy of Sciences</i> , 2020, 1462, 14-26.	1.8	15
45	Influenza Hemagglutinin Structures and Antibody Recognition. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020, 10, a038778.	2.9	79
46	Diverse Antibody Responses to Conserved Structural Motifs in <i>Plasmodium falciparum</i> Circumsporozoite Protein. <i>Journal of Molecular Biology</i> , 2020, 432, 1048-1063.	2.0	28
47	Structural Biology of Influenza Hemagglutinin: An Amaranthine Adventure. <i>Viruses</i> , 2020, 12, 1053.	1.5	35
48	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.	13.5	305
49	An Alternative Binding Mode of IGHV3-53 Antibodies to the SARS-CoV-2 Receptor Binding Domain. <i>Cell Reports</i> , 2020, 33, 108274.	2.9	152
50	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.	3.3	25
51	Structural basis of a shared antibody response to SARS-CoV-2. <i>Science</i> , 2020, 369, 1119-1123.	6.0	536
52	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.	6.6	185
53	An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. <i>Science Advances</i> , 2020, 6, eabb5642.	4.7	26
54	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, .	4.2	21

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55	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. <i>PLoS Pathogens</i> , 2020, 16, e1008753.	2.1	61
56	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, .	4.7	19
57	Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	309
58	Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. <i>Cell Reports</i> , 2020, 31, 107725.	2.9	353
59	Innovations in structure-based antigen design and immune monitoring for next generation vaccines. <i>Current Opinion in Immunology</i> , 2020, 65, 50-56.	2.4	43
60	HIV-1 Envelope and MPER Antibody Structures in Lipid Assemblies. <i>Cell Reports</i> , 2020, 31, 107583.	2.9	60
61	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.	3.3	7
62	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020, 11, 2688.	5.8	304
63	Structural basis of broad HIV neutralization by a vaccine-induced cow antibody. <i>Science Advances</i> , 2020, 6, eaba0468.	4.7	31
64	Isolation of potent SARS-CoV-2 neutralizing antibodies and protection from disease in a small animal model. <i>Science</i> , 2020, 369, 956-963.	6.0	1,287
65	Different genetic barriers for resistance to HA stem antibodies in influenza H3 and H1 viruses. <i>Science</i> , 2020, 368, 1335-1340.	6.0	51
66	Structure and mechanism of monoclonal antibody binding to the junctional epitope of <i>Plasmodium falciparum</i> circumsporozoite protein. <i>PLoS Pathogens</i> , 2020, 16, e1008373.	2.1	30
67	Major antigenic site B of human influenza H3N2 viruses has an evolving local fitness landscape. <i>Nature Communications</i> , 2020, 11, 1233.	5.8	40
68	A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. <i>Science</i> , 2020, 368, 630-633.	6.0	1,379
69	Structural basis for the stabilization of amyloidogenic immunoglobulin light chains by hydantoins. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2020, 30, 127356.	1.0	15
70	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.	5.1	16
71	The Impact of Sustained Immunization Regimens on the Antibody Response to Oligomannose Glycans. <i>ACS Chemical Biology</i> , 2020, 15, 789-798.	1.6	9
72	Autologous Antibody Responses to an HIV Envelope Glycan Hole Are Not Easily Broadened in Rabbits. <i>Journal of Virology</i> , 2020, 94, .	1.5	57

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73	Proof of concept for rational design of hepatitis C virus E2 core nanoparticle vaccines. <i>Science Advances</i> , 2020, 6, eaaz6225.	4.7	44
74	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, .	1.5	29
75	A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody. <i>PLoS Pathogens</i> , 2020, 16, e1009089.	2.1	55
76	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
77	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
78	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
79	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. , 2020, 16, e1008753.		0
80	Structures of single-layer β -sheet proteins evolved from hairpin repeats. <i>Protein Science</i> , 2019, 28, 1676-1689.	3.1	4
81	A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. <i>Science</i> , 2019, 366, .	6.0	172
82	Broadly protective human antibodies that target the active site of influenza virus neuraminidase. <i>Science</i> , 2019, 366, 499-504.	6.0	162
83	Potent anti-influenza H7 human monoclonal antibody induces separation of hemagglutinin receptor-binding head domains. <i>PLoS Biology</i> , 2019, 17, e3000139.	2.6	37
84	Exploitation of glycosylation in enveloped virus pathobiology. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1480-1497.	1.1	383
85	Structural Insights into the Lipid A Transport Pathway in MsbA. <i>Structure</i> , 2019, 27, 1114-1123.e3.	1.6	41
86	Structure and immunogenicity of a stabilized HIV-1 envelope trimer based on a group-M consensus sequence. <i>Nature Communications</i> , 2019, 10, 2355.	5.8	116
87	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.	5.1	45
88	N-Glycolylneuraminic Acid as a Receptor for Influenza A Viruses. <i>Cell Reports</i> , 2019, 27, 3284-3294.e6.	2.9	78
89	Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. <i>Cell Host and Microbe</i> , 2019, 25, 873-883.e5.	5.1	42
90	The Chimpanzee SIV Envelope Trimer: Structure and Deployment as an HIV Vaccine Template. <i>Cell Reports</i> , 2019, 27, 2426-2441.e6.	2.9	35

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91	A Site of Vulnerability on the Influenza Virus Hemagglutinin Head Domain Trimer Interface. <i>Cell</i> , 2019, 177, 1136-1152.e18.	13.5	177
92	Bacterial glycosyltransferase-mediated cell-surface chemoenzymatic glycan modification. <i>Nature Communications</i> , 2019, 10, 1799.	5.8	46
93	VH1-69 antiviral broadly neutralizing antibodies: genetics, structures, and relevance to rational vaccine design. <i>Current Opinion in Virology</i> , 2019, 34, 149-159.	2.6	92
94	Antibody responses to viral infections: a structural perspective across three different enveloped viruses. <i>Nature Microbiology</i> , 2019, 4, 734-747.	5.9	158
95	A small-molecule fusion inhibitor of influenza virus is orally active in mice. <i>Science</i> , 2019, 363, .	6.0	98
96	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.	1.6	16
97	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.	3.3	52
98	A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. <i>Science Advances</i> , 2019, 5, eaav4580.	4.7	393
99	Oligomannose Glycopeptide Conjugates Elicit Antibodies Targeting the Glycan Core Rather than Its Extremities. <i>ACS Central Science</i> , 2019, 5, 237-249.	5.3	33
100	Capturing the inherent structural dynamics of the HIV-1 envelope glycoprotein fusion peptide. <i>Nature Communications</i> , 2019, 10, 763.	5.8	30
101	Identification of Antibodies Targeting the H3N2 Hemagglutinin Receptor Binding Site following Vaccination of Humans. <i>Cell Reports</i> , 2019, 29, 4460-4470.e8.	2.9	22
102	An MPER antibody neutralizes HIV-1 using germline features shared among donors. <i>Nature Communications</i> , 2019, 10, 5389.	5.8	44
103	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.	5.1	51
104	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.	5.1	49
105	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.	1.2	7
106	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.	6.6	153
107	Immunodominance and Antigenic Variation of Influenza Virus Hemagglutinin: Implications for Design of Universal Vaccine Immunogens. <i>Journal of Infectious Diseases</i> , 2019, 219, S38-S45.	1.9	67
108	Genetic and structural insights into broad neutralization of hepatitis C virus by human V_H-1-69 antibodies. <i>Science Advances</i> , 2019, 5, eaav1882.	4.7	77

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109	Multistate design of influenza antibodies improves affinity and breadth against seasonal viruses. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1597-1602.	3.3	23
110	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, .	1.5	66
111	Novel Rigid Glycomimetics to Inhibit Influenza Infection. FASEB Journal, 2019, 33, .	0.2	0
112	Structural insights into the design of novel anti-influenza therapies. Nature Structural and Molecular Biology, 2018, 25, 115-121.	3.6	81
113	Integrity of Glycosylation Processing of a Glycan-Depleted Trimeric HIV-1 Immunogen Targeting Key B-Cell Lineages. Journal of Proteome Research, 2018, 17, 987-999.	1.8	23
114	â€œInverse Drug Discoveryâ€•Strategy To Identify Proteins That Are Targeted by Latent Electrophiles As Exemplified by Aryl Fluorosulfates. Journal of the American Chemical Society, 2018, 140, 200-210.	6.6	206
115	Structure and Immune Recognition of the HIV Glycan Shield. Annual Review of Biophysics, 2018, 47, 499-523.	4.5	115
116	A complex epistatic network limits the mutational reversibility in the influenza hemagglutinin receptor-binding site. Nature Communications, 2018, 9, 1264.	5.8	58
117	A small-molecule fragment that emulates binding of receptor and broadly neutralizing antibodies to influenza A hemagglutinin. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4240-4245.	3.3	25
118	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.	2.0	12
119	A public antibody lineage that potently inhibits malaria infection through dual binding to the circumsporozoite protein. Nature Medicine, 2018, 24, 401-407.	15.2	183
120	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.	1.6	40
121	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.	1.7	75
122	HIV-1 vaccine design through minimizing envelope metastability. Science Advances, 2018, 4, eaau6769.	4.7	75
123	Recurring and Adaptable Binding Motifs in Broadly Neutralizing Antibodies to Influenza Virus Are Encoded on the D3-9 Segment of the Ig Gene. Cell Host and Microbe, 2018, 24, 569-578.e4.	5.1	32
124	Cryo-EM structure of <i>P. falciparum</i> circumsporozoite protein with a vaccine-elicited antibody is stabilized by somatically mutated inter-Fab contacts. Science Advances, 2018, 4, eaau8529.	4.7	70
125	Structural Basis for Recognition of a Unique Epitope by a Human Anti-tau Antibody. Structure, 2018, 26, 1626-1634.e4.	1.6	9
126	Universal protection against influenza infection by a multidomain antibody to influenza hemagglutinin. Science, 2018, 362, 598-602.	6.0	170

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127	Structure-Activity Relationships in Metal-Binding Pharmacophores for Influenza Endonuclease. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10206-10217.	2.9	42
128	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.	1.1	18
129	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.	3.3	18
130	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. <i>Nature Communications</i> , 2018, 9, 1956.	5.8	50
131	The Unusual Genetics and Biochemistry of Bovine Immunoglobulins. <i>Advances in Immunology</i> , 2018, 137, 135-164.	1.1	36
132	Immunogenetic and structural analysis of a class of HCV broadly neutralizing antibodies and their precursors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7569-7574.	3.3	14
133	The human naive B cell repertoire contains distinct subclasses for a germline-targeting HIV-1 vaccine immunogen. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	113
134	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.	6.6	175
135	The Neutralizing Face of Hepatitis C Virus E2 Envelope Glycoprotein. <i>Frontiers in Immunology</i> , 2018, 9, 1315.	2.2	56
136	A multifunctional human monoclonal neutralizing antibody that targets a unique conserved epitope on influenza HA. <i>Nature Communications</i> , 2018, 9, 2669.	5.8	67
137	A common antigenic motif recognized by naturally occurring human VH5 ₁ /VL4 ₁ anti-tau antibodies with distinct functionalities. <i>Acta Neuropathologica Communications</i> , 2018, 6, 43.	2.4	15
138	Co-evolution of HIV Envelope and Apex-Targeting Neutralizing Antibody Lineage Provides Benchmarks for Vaccine Design. <i>Cell Reports</i> , 2018, 23, 3249-3261.	2.9	52
139	Epitopes for neutralizing antibodies induced by HIV-1 envelope glycoprotein BG505 SOSIP trimers in rabbits and macaques. <i>PLoS Pathogens</i> , 2018, 14, e1006913.	2.1	111
140	The HIV-1 envelope glycoprotein structure: nailing down a moving target. <i>Immunological Reviews</i> , 2017, 275, 21-32.	2.8	251
141	Unique Structural Features of Influenza Virus H15 Hemagglutinin. <i>Journal of Virology</i> , 2017, 91, .	1.5	12
142	The 150-Loop Restricts the Host Specificity of Human H10N8 Influenza Virus. <i>Cell Reports</i> , 2017, 19, 235-245.	2.9	35
143	A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic I ² -Hairpin Structure. <i>Immunity</i> , 2017, 46, 690-702.	6.6	216
144	In vitro evolution of an influenza broadly neutralizing antibody is modulated by hemagglutinin receptor specificity. <i>Nature Communications</i> , 2017, 8, 15371.	5.8	55

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145	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.	6.6	96
146	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.	6.6	286
147	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.	3.3	56
148	Reducing V3 Antigenicity and Immunogenicity on Soluble, Native-Like HIV-1 Env SOSIP Trimers. <i>Journal of Virology</i> , 2017, 91, .	1.5	57
149	Semi-quantitative models for identifying potent and selective transthyretin amyloidogenesis inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017, 27, 3441-3449.	1.0	8
150	Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. <i>Nature Biotechnology</i> , 2017, 35, 667-671.	9.4	108
151	Genetically encoding phosphotyrosine and its nonhydrolyzable analog in bacteria. <i>Nature Chemical Biology</i> , 2017, 13, 845-849.	3.9	105
152	Diversity of Functionally Permissive Sequences in the Receptor-Binding Site of Influenza Hemagglutinin. <i>Cell Host and Microbe</i> , 2017, 21, 742-753.e8.	5.1	59
153	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, .	1.5	27
154	Immunological memory to hyperphosphorylated tau in asymptomatic individuals. <i>Acta Neuropathologica</i> , 2017, 133, 767-783.	3.9	43
155	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.	5.1	163
156	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.	3.3	340
157	Structural Insights into VLR Fine Specificity for Blood Group Carbohydrates. <i>Structure</i> , 2017, 25, 1667-1678.e4.	1.6	27
158	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.	2.9	58
159	Massively parallel de novo protein design for targeted therapeutics. <i>Nature</i> , 2017, 550, 74-79.	13.7	354
160	Potent peptidic fusion inhibitors of influenza virus. <i>Science</i> , 2017, 358, 496-502.	6.0	135
161	Improving the Immunogenicity of Native-like HIV-1 Envelope Trimers by Hyperstabilization. <i>Cell Reports</i> , 2017, 20, 1805-1817.	2.9	171
162	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.	4.2	151

#	ARTICLE	IF	CITATIONS
163	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.	2.9	103
164	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.	1.6	31
165	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.	6.6	27
166	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. <i>Nature</i> , 2017, 548, 108-111.	13.7	154
167	A single mutation in Taiwanese H6N1 influenza hemagglutinin switches binding to human α 2-6 sialic acid receptors. <i>EMBO Molecular Medicine</i> , 2017, 9, 1314-1325.	3.3	44
168	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.	6.6	90
169	Crystal structure of an anti-idiotypic variable lymphocyte receptor. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 682-687.	0.4	3
170	Bacterially derived synthetic mimetics of mammalian oligomannose prime antibody responses that neutralize HIV infectivity. <i>Nature Communications</i> , 2017, 8, 1601.	5.8	33
171	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.	3.3	116
172	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.	2.0	133
173	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017, 547, 360-363.	13.7	217
174	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.	1.0	48
175	An HIV-1 antibody from an elite neutralizer implicates the fusion peptide as a site of vulnerability. <i>Nature Microbiology</i> , 2017, 2, 16199.	5.9	144
176	Three mutations switch H7N9 influenza to human-type receptor specificity. <i>PLoS Pathogens</i> , 2017, 13, e1006390.	2.1	83
177	A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. <i>PLoS Pathogens</i> , 2017, 13, e1006682.	2.1	188
178	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.	2.1	58
179	Probing the antigenicity of hepatitis C virus envelope glycoprotein complex by high-throughput mutagenesis. <i>PLoS Pathogens</i> , 2017, 13, e1006735.	2.1	66
180	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.	2.1	49

#	ARTICLE	IF	CITATIONS
181	Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. PLoS Pathogens, 2016, 12, e1005815.	2.1	104
182	Uncleaved prefusion-optimized gp140 trimers derived from analysis of HIV-1 envelope metastability. Nature Communications, 2016, 7, 12040.	5.8	134
183	Presenting native-like trimeric HIV-1 antigens with self-assembling nanoparticles. Nature Communications, 2016, 7, 12041.	5.8	146
184	UHMâ€“ULM interactions in the RBM39â€“U2AF65 splicing-factor complex. Acta Crystallographica Section D: Structural Biology, 2016, 72, 497-511.	1.1	36
185	HIV's Achilles' Heel. Scientific American, 2016, 315, 50-55.	1.0	6
186	Key gp120 Glycans Pose Roadblocks to the Rapid Development of VRC01-Class Antibodies in an HIV-1-Infected Chinese Donor. Immunity, 2016, 44, 939-950.	6.6	85
187	Early Antibody Lineage Diversification and Independent Limb Maturation Lead to Broad HIV-1 Neutralization Targeting the Env High-Mannose Patch. Immunity, 2016, 44, 1215-1226.	6.6	138
188	Arylfluorosulfates Inactivate Intracellular Lipid Binding Protein(s) through Chemoselective SuFEx Reaction with a Binding Site Tyr Residue. Journal of the American Chemical Society, 2016, 138, 7353-7364.	6.6	212
189	A Distinct Type of Pilus from the Human Microbiome. Cell, 2016, 165, 690-703.	13.5	78
190	Stabilizing the C_H2 Domain of an Antibody by Engineering in an Enhanced Aromatic Sequon. ACS Chemical Biology, 2016, 11, 1852-1861.	1.6	40
191	Tailored Immunogens Direct Affinity Maturation toward HIV Neutralizing Antibodies. Cell, 2016, 166, 1459-1470.e11.	13.5	230
192	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. Immunity, 2016, 45, 483-496.	6.6	335
193	Holes in the Glycan Shield of the Native HIV Envelope Are a Target of Trimer-Elicited Neutralizing Antibodies. Cell Reports, 2016, 16, 2327-2338.	2.9	216
194	Dynamic Local Polymorphisms in the Gbx1 Homeodomain Induced by DNA Binding. Structure, 2016, 24, 1372-1379.	1.6	2
195	A Prominent Site of Antibody Vulnerability on HIV Envelope Incorporates a Motif Associated with CCR5 Binding and Its Camouflaging Glycans. Immunity, 2016, 45, 31-45.	6.6	129
196	HMGB1 Activates Proinflammatory Signaling via TLR5 Leading to Allodynia. Cell Reports, 2016, 17, 1128-1140.	2.9	125
197	Structural flexibility at a major conserved antibody target on hepatitis C virus E2 antigen. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12768-12773.	3.3	78
198	Conservation and diversity in the ultralong third heavy-chain complementarity-determining region of bovine antibodies. Science Immunology, 2016, 1, .	5.6	52

#	ARTICLE	IF	CITATIONS
199	HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. <i>Science</i> , 2016, 351, 1458-1463.	6.0	382
200	Dlx5 Homeodomain:DNA Complex: Structure, Binding and Effect of Mutations Related to Split Hand and Foot Malformation Syndrome. <i>Journal of Molecular Biology</i> , 2016, 428, 1130-1141.	2.0	10
201	Composition and Antigenic Effects of Individual Glycan Sites of a Trimeric HIV-1 Envelope Glycoprotein. <i>Cell Reports</i> , 2016, 14, 2695-2706.	2.9	250
202	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.	1.6	15
203	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. <i>Immunity</i> , 2016, 44, 21-31.	6.6	87
204	H7N9 influenza virus neutralizing antibodies that possess few somatic mutations. <i>Journal of Clinical Investigation</i> , 2016, 126, 1482-1494.	3.9	62
205	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.	2.1	138
206	Approaching rational epitope vaccine design for hepatitis C virus with meta-server and multivalent scaffolding. <i>Scientific Reports</i> , 2015, 5, 12501.	1.6	68
207	Structural Basis for a Switch in Receptor Binding Specificity of Two H5N1 Hemagglutinin Mutants. <i>Cell Reports</i> , 2015, 13, 1683-1691.	2.9	18
208	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.	6.6	86
209	Immunogenicity of Stabilized HIV-1 Envelope Trimers with Reduced Exposure of Non-neutralizing Epitopes. <i>Cell</i> , 2015, 163, 1702-1715.	13.5	341
210	Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. <i>Immunity</i> , 2015, 43, 1053-1063.	6.6	200
211	Structural Constraints Determine the Glycosylation of HIV-1 Envelope Trimers. <i>Cell Reports</i> , 2015, 11, 1604-1613.	2.9	135
212	Antibody potency relates to the ability to recognize the closed, pre-fusion form of HIV Env. <i>Nature Communications</i> , 2015, 6, 6144.	5.8	130
213	Insights into the trimeric HIV-1 envelope glycoprotein structure. <i>Trends in Biochemical Sciences</i> , 2015, 40, 101-107.	3.7	95
214	HIV-1 neutralizing antibodies induced by native-like envelope trimers. <i>Science</i> , 2015, 349, aac4223.	6.0	482
215	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.	2.0	44
216	Comprehensive Antigenic Map of a Cleaved Soluble HIV-1 Envelope Trimer. <i>PLoS Pathogens</i> , 2015, 11, e1004767.	2.1	100

#	ARTICLE	IF	CITATIONS
217	Capitalizing on knowledge of hepatitis C virus neutralizing epitopes for rational vaccine design. <i>Current Opinion in Virology</i> , 2015, 11, 148-157.	2.6	54
218	Structure of the apo anti-influenza CH65 Fab. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 145-148.	0.4	5
219	Structure-based discovery of NANOG variant with enhanced properties to promote self-renewal and reprogramming of pluripotent stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4666-4671.	3.3	43
220	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.	1.5	247
221	A Human-Infecting H10N8 Influenza Virus Retains a Strong Preference for Avian-type Receptors. <i>Cell Host and Microbe</i> , 2015, 17, 377-384.	5.1	54
222	Structure and Receptor Binding of the Hemagglutinin from a Human H6N1 Influenza Virus. <i>Cell Host and Microbe</i> , 2015, 17, 369-376.	5.1	44
223	Design and Structure of an Engineered Disulfide-Stabilized Influenza Virus Hemagglutinin Trimer. <i>Journal of Virology</i> , 2015, 89, 7417-7420.	1.5	32
224	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. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2099-2108.	2.5	69
225	Insights into Substrate Specificity of NlpC/P60 Cell Wall Hydrolases Containing Bacterial SH3 Domains. <i>MBio</i> , 2015, 6, e02327-14.	1.8	46
226	Antibodies to a conformational epitope on gp41 neutralize HIV-1 by destabilizing the Env spike. <i>Nature Communications</i> , 2015, 6, 8167.	5.8	87
227	A stable trimeric influenza hemagglutinin stem as a broadly protective immunogen. <i>Science</i> , 2015, 349, 1301-1306.	6.0	480
228	A General Method for Insertion of Functional Proteins within Proteins via Combinatorial Selection of Permissive Junctions. <i>Chemistry and Biology</i> , 2015, 22, 1134-1143.	6.2	9
229	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.	3.3	127
230	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.	1.5	88
231	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.	1.5	80
232	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.	1.3	27
233	Soluble human TLR2 ectodomain binds diacylglycerol from microbial lipopeptides and glycolipids. <i>Innate Immunity</i> , 2015, 21, 175-193.	1.1	25
234	Redesigned HIV antibodies exhibit enhanced neutralizing potency and breadth. <i>Journal of Clinical Investigation</i> , 2015, 125, 2523-2531.	3.9	31

#	ARTICLE	IF	CITATIONS
235	Crystal Structure of a Two-Subunit TrkA Octameric Gating Ring Assembly. PLoS ONE, 2015, 10, e0122512.	1.1	2
236	Structural Insights into the Recognition of Phosphopeptide by the FHA Domain of Kanadaplin. PLoS ONE, 2014, 9, e107309.	1.1	6
237	Promiscuous Glycan Site Recognition by Antibodies to the High-Mannose Patch of gp120 Broadens Neutralization of HIV. Science Translational Medicine, 2014, 6, 236ra63.	5.8	160
238	Receptor mimicry by antibody F045â€“092 facilitates universal binding to the H3 subtype of influenza virus. Nature Communications, 2014, 5, 3614.	5.8	175
239	Recombinant HIV envelope trimer selects for quaternary-dependent antibodies targeting the trimer apex. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17624-17629.	3.3	324
240	STRUCTURAL BASIS FOR HOST/COMMENSAL-MICROBE INTERACTIONS IN THE HUMAN DISTAL GUT MICROBIOME. , 2014, , .		0
241	Stapled HIV-1 peptides recapitulate antigenic structures and engage broadly neutralizing antibodies. Nature Structural and Molecular Biology, 2014, 21, 1058-1067.	3.6	69
242	Structure-Guided Functional Characterization of DUF1460 Reveals a Highly Specific NlpC/P60 Amidase Family. Structure, 2014, 22, 1799-1809.	1.6	10
243	Stable 293ÂT and CHO cell lines expressing cleaved, stable HIV-1 envelope glycoprotein trimers for structural and vaccine studies. Retrovirology, 2014, 11, 33.	0.9	46
244	Structure of 2G12 Fab ₂ in Complex with Soluble and Fully Glycosylated HIV-1 Env by Negative-Stain Single-Particle Electron Microscopy. Journal of Virology, 2014, 88, 10177-10188.	1.5	67
245	Structures of a Bifunctional Cell Wall Hydrolase CwlT Containing a Novel Bacterial Lysozyme and an NlpC/P60 dl-Endopeptidase. Journal of Molecular Biology, 2014, 426, 169-184.	2.0	25
246	Broadly Neutralizing HIV Antibodies Define a Glycan-Dependent Epitope on the Prefusion Conformation of gp41 on Cleaved Envelope Trimers. Immunity, 2014, 40, 657-668.	6.6	342
247	A Structurally Distinct Human Mycoplasma Protein that Generically Blocks Antigen-Antibody Union. Science, 2014, 343, 656-661.	6.0	85
248	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. Nature, 2014, 509, 55-62.	13.7	681
249	Structural Delineation of a Quaternary, Cleavage-Dependent Epitope at the gp41-gp120 Interface on Intact HIV-1 Env Trimers. Immunity, 2014, 40, 669-680.	6.6	323
250	Hemagglutinin Receptor Specificity and Structural Analyses of Respiratory Droplet-Transmissible H5N1 Viruses. Journal of Virology, 2014, 88, 768-773.	1.5	61
251	A common solution to group 2 influenza virus neutralization. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 445-450.	3.3	187
252	Characterization of a Broadly Neutralizing Monoclonal Antibody That Targets the Fusion Domain of Group 2 Influenza A Virus Hemagglutinin. Journal of Virology, 2014, 88, 13580-13592.	1.5	110

#	ARTICLE	IF	CITATIONS
253	Structural Evolution of Glycan Recognition by a Family of Potent HIV Antibodies. <i>Cell</i> , 2014, 159, 69-79.	13.5	161
254	Structural Characterization of Viral Epitopes Recognized by Broadly Cross-Reactive Antibodies. <i>Current Topics in Microbiology and Immunology</i> , 2014, 386, 323-341.	0.7	83
255	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.	0.9	139
256	Alternative Recognition of the Conserved Stem Epitope in Influenza A Virus Hemagglutinin by a V_H-3-30-Encoded Heterosubtypic Antibody. <i>Journal of Virology</i> , 2014, 88, 7083-7092.	1.5	62
257	CD4-Induced Activation in a Soluble HIV-1 Env Trimer. <i>Structure</i> , 2014, 22, 974-984.	1.6	108
258	Antibody Structure. <i>Microbiology Spectrum</i> , 2014, 2, .	1.2	31
259	HIV ENVELOPE AND INFLUENZA HEMAGGLUTININ FUSION GLYCOPROTEINS AND THE QUEST FOR A UNIVERSAL VACCINE. , 2014, , .		0
260	Bifunctional coumarin derivatives that inhibit transthyretin amyloidogenesis and serve as fluorescent transthyretin folding sensors. <i>Chemical Communications</i> , 2013, 49, 9188.	2.2	35
261	Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1477-1483.	6.0	793
262	Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1484-1490.	6.0	662
263	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.	1.5	51
264	Hepatitis C Virus E2 Envelope Glycoprotein Core Structure. <i>Science</i> , 2013, 342, 1090-1094.	6.0	374
265	Antibody Recognition of the Pandemic H1N1 Influenza Virus Hemagglutinin Receptor Binding Site. <i>Journal of Virology</i> , 2013, 87, 12471-12480.	1.5	139
266	Preferential Recognition of Avian-Like Receptors in Human Influenza A H7N9 Viruses. <i>Science</i> , 2013, 342, 1230-1235.	6.0	133
267	Structural Characterization of Cleaved, Soluble HIV-1 Envelope Glycoprotein Trimers. <i>Journal of Virology</i> , 2013, 87, 9865-9872.	1.5	71
268	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.	3.6	141
269	Broadly neutralizing antibodies against influenza viruses. <i>Antiviral Research</i> , 2013, 98, 476-483.	1.9	136
270	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. <i>Science</i> , 2013, 340, 711-716.	6.0	680

#	ARTICLE	IF	CITATIONS
271	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.	3.6	314
272	Reshaping Antibody Diversity. <i>Cell</i> , 2013, 153, 1379-1393.	13.5	179
273	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.	2.1	267
274	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.	2.1	835
275	New World Bats Harbor Diverse Influenza A Viruses. <i>PLoS Pathogens</i> , 2013, 9, e1003657.	2.1	1,050
276	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.	3.3	236
277	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.	3.3	188
278	Influences on Trimerization and Aggregation of Soluble, Cleaved HIV-1 SOSIP Envelope Glycoprotein. <i>Journal of Virology</i> , 2013, 87, 9873-9885.	1.5	76
279	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.	3.3	135
280	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.	1.6	7
281	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.	1.5	114
282	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.	2.1	80
283	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.	3.3	159
284	Highly Conserved Protective Epitopes on Influenza B Viruses. <i>Science</i> , 2012, 337, 1343-1348.	6.0	705
285	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.	1.5	79
286	A Blueprint for HIV Vaccine Discovery. <i>Cell Host and Microbe</i> , 2012, 12, 396-407.	5.1	348
287	Structural insights into key sites of vulnerability on HIV-1 Env and influenza HA. <i>Immunological Reviews</i> , 2012, 250, 180-198.	2.8	84
288	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012, 489, 526-532.	13.7	434

#	ARTICLE	IF	CITATIONS
289	Structural Characterization of the Hemagglutinin Receptor Specificity from the 2009 H1N1 Influenza Pandemic. <i>Journal of Virology</i> , 2012, 86, 982-990.	1.5	155
290	Structural Basis of TLR5-Flagellin Recognition and Signaling. <i>Science</i> , 2012, 335, 859-864.	6.0	454
291	Broadly Neutralizing Antibodies Present New Prospects to Counter Highly Antigenically Diverse Viruses. <i>Science</i> , 2012, 337, 183-186.	6.0	394
292	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.	3.3	135
293	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. <i>Nature Biotechnology</i> , 2012, 30, 543-548.	9.4	342
294	Variable Lymphocyte Receptor Recognition of the Immunodominant Glycoprotein of <i>Bacillus anthracis</i> Spores. <i>Structure</i> , 2012, 20, 479-486.	1.6	47
295	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. <i>Science</i> , 2011, 332, 234-238.	6.0	414
296	Broad neutralization coverage of HIV by multiple highly potent antibodies. <i>Nature</i> , 2011, 477, 466-470.	13.7	1,397
297	A structural analysis of M protein in coronavirus assembly and morphology. <i>Journal of Structural Biology</i> , 2011, 174, 11-22.	1.3	625
298	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. <i>Science</i> , 2011, 334, 1097-1103.	6.0	644
299	A Highly Conserved Neutralizing Epitope on Group 2 Influenza A Viruses. <i>Science</i> , 2011, 333, 843-850.	6.0	772
300	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. <i>Science</i> , 2011, 332, 816-821.	6.0	527
301	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011, 480, 336-343.	13.7	794
302	Structural Characterization of an Early Fusion Intermediate of Influenza Virus Hemagglutinin. <i>Journal of Virology</i> , 2011, 85, 5172-5182.	1.5	113
303	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.	3.3	149
304	Structure of the β -glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L-Ala- β -D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364.	0.7	64
305	The JCSG high-throughput structural biology pipeline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1137-1142.	0.7	99
306	Structural Basis of Preexisting Immunity to the 2009 H1N1 Pandemic Influenza Virus. <i>Science</i> , 2010, 328, 357-360.	6.0	521

#	ARTICLE	IF	CITATIONS
307	Structure, Receptor Binding, and Antigenicity of Influenza Virus Hemagglutinins from the 1957 H2N2 Pandemic. <i>Journal of Virology</i> , 2010, 84, 1715-1721.	1.5	90
308	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.	1.5	92
309	Structural Basis of Murein Peptide Specificity of a $\hat{1}^3$ -D-Glutamyl-L-Diamino Acid Endopeptidase. <i>Structure</i> , 2009, 17, 303-313.	1.6	73
310	Antibody Recognition of a Highly Conserved Influenza Virus Epitope. <i>Science</i> , 2009, 324, 246-251.	6.0	1,220
311	Recent Avian H5N1 Viruses Exhibit Increased Propensity for Acquiring Human Receptor Specificity. <i>Journal of Molecular Biology</i> , 2008, 381, 1382-1394.	2.0	192
312	Structural Characterization of the 1918 Influenza Virus H1N1 Neuraminidase. <i>Journal of Virology</i> , 2008, 82, 10493-10501.	1.5	241
313	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.	1.5	112
314	Antigen Recognition by Variable Lymphocyte Receptors. <i>Science</i> , 2008, 321, 1834-1837.	6.0	163
315	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.	2.0	121
316	The challenge of protein structure determination—lessons from structural genomics. <i>Protein Science</i> , 2007, 16, 2472-2482.	3.1	135
317	Structure and Receptor Specificity of the Hemagglutinin from an H5N1 Influenza Virus. <i>Science</i> , 2006, 312, 404-410.	6.0	865
318	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.	2.0	570
319	Antibody Elbow Angles are Influenced by their Light Chain Class. <i>Journal of Molecular Biology</i> , 2006, 357, 1566-1574.	2.0	229
320	Glycan microarray technologies: tools to survey host specificity of influenza viruses. <i>Nature Reviews Microbiology</i> , 2006, 4, 857-864.	13.6	319
321	Toward a Carbohydrate-Based HIV-1 Vaccine. <i>ACS Symposium Series</i> , 2006, , 161-185.	0.5	3
322	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.	3.3	225
323	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.	3.3	268
324	A Single Amino Acid Substitution in 1918 Influenza Virus Hemagglutinin Changes Receptor Binding Specificity. <i>Journal of Virology</i> , 2005, 79, 11533-11536.	1.5	356

#	ARTICLE	IF	CITATIONS
325	Dissection of the carbohydrate specificity of the broadly neutralizing anti-HIV-1 antibody 2G12. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13372-13377.	3.3	291
326	Crystal Structure of Human Toll-Like Receptor 3 (TLR3) Ectodomain. Science, 2005, 309, 581-585.	6.0	545
327	Broadly Neutralizing Anti-HIV Antibody 4E10 Recognizes a Helical Conformation of a Highly Conserved Fusion-Associated Motif in gp41. Immunity, 2005, 22, 163-173.	6.6	410
328	Printed covalent glycan array for ligand profiling of diverse glycan binding proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17033-17038.	3.3	1,039
329	HIV vaccine design and the neutralizing antibody problem. Nature Immunology, 2004, 5, 233-236.	7.0	721
330	Crystal Structure of a Shark Single-Domain Antibody V Region in Complex with Lysozyme. Science, 2004, 305, 1770-1773.	6.0	282
331	Monoglucosylated glycans in the secreted human complement component C3: implications for protein biosynthesis and structure. FEBS Letters, 2004, 566, 270-274.	1.3	47
332	Structure of the Uncleaved Human H1 Hemagglutinin from the Extinct 1918 Influenza Virus. Science, 2004, 303, 1866-1870.	6.0	440
333	Fine Mapping of the Interaction of Neutralizing and Nonneutralizing Monoclonal Antibodies with the CD4 Binding Site of Human Immunodeficiency Virus Type 1 gp120. Journal of Virology, 2003, 77, 642-658.	1.5	237
334	Antibody Domain Exchange Is an Immunological Solution to Carbohydrate Cluster Recognition. Science, 2003, 300, 2065-2071.	6.0	736
335	The Carbohydrate Epitope of the Neutralizing Anti-HIV-1 Antibody 2G12. Advances in Experimental Medicine and Biology, 2003, 535, 205-218.	0.8	65
336	Structural genomics of the Thermotoga maritima proteome implemented in a high-throughput structure determination pipeline. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11664-11669.	3.3	397
337	The Broadly Neutralizing Anti-Human Immunodeficiency Virus Type 1 Antibody 2G12 Recognizes a Cluster of 2 Mannose Residues on the Outer Face of gp120. Journal of Virology, 2002, 76, 7306-7321.	1.5	664
338	Crystal Structure of a Neutralizing Human IgG Against HIV-1: A Template for Vaccine Design. Science, 2001, 293, 1155-1159.	6.0	870
339	Global Efforts in Structural Genomics. Science, 2001, 294, 89-92.	6.0	195
340	Crystal structure of Sar1-GDP at 1.7 Å resolution and the role of the NH2 terminus in ER export. Journal of Cell Biology, 2001, 155, 937-948.	2.3	149
341	A New Functional Domain of Guanine Nucleotide Dissociation Inhibitor (GDI) Involved in Rab Recycling. Traffic, 2000, 1, 270-281.	1.3	37
342	STRUCTURAL BASIS OF T CELL RECOGNITION. Annual Review of Immunology, 1999, 17, 369-397.	9.5	488

#	ARTICLE	IF	CITATIONS
343	Engineering protein for X-ray crystallography: The murine major histocompatibility complex class II molecule. <i>Protein Science</i> , 1998, 7, 413-418.	3.1	18
344	Structural Basis of Plasticity in T Cell Receptor Recognition of a Self Peptide-MHC Antigen. <i>Science</i> , 1998, 279, 1166-1172.	6.0	641
345	Antibody-antigen interactions: new structures and new conformational changes. <i>Current Opinion in Structural Biology</i> , 1994, 4, 857-867.	2.6	505
346	Major antigen-induced domain rearrangements in an antibody. <i>Structure</i> , 1993, 1, 83-93.	1.6	216
347	Three-dimensional Structure of an Anti-steroid Fab ² and Progesterone-Fab ² Complex. <i>Journal of Molecular Biology</i> , 1993, 231, 103-118.	2.0	154
348	X-Ray Crystallographic Studies of Antibody-Peptide Complexes. <i>ImmunoMethods</i> , 1993, 3, 211-221.	0.8	24
349	Antibody-antigen interactions. <i>Current Opinion in Structural Biology</i> , 1993, 3, 113-118.	2.6	279
350	Applications of the streak seeding technique in protein crystallization. <i>Journal of Crystal Growth</i> , 1991, 110, 270-282.	0.7	147
351	Analytical and production seeding techniques. <i>Methods</i> , 1990, 1, 38-49.	1.9	98
352	Antibody Structure. , 0, , 49-62.		1
353	Dynamics of B-Cell Repertoires and Emergence of Cross-Reactive Responses in COVID-19 Patients with Different Disease Severity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2