

# Ian A Wilson

## List of Publications by Year in descending order

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353  
papers

57,976  
citations

733

120  
h-index

1421

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.	13.7	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.	6.0	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.	6.0	1,287
4	Antibody Recognition of a Highly Conserved Influenza Virus Epitope. <i>Science</i> , 2009, 324, 246-251.	6.0	1,220
5	New World Bats Harbor Diverse Influenza A Viruses. <i>PLoS Pathogens</i> , 2013, 9, e1003657.	2.1	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.	3.3	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.	6.0	870
8	Structure and Receptor Specificity of the Hemagglutinin from an H5N1 Influenza Virus. <i>Science</i> , 2006, 312, 404-410.	6.0	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.	2.1	835
10	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011, 480, 336-343.	13.7	794
11	Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1477-1483.	6.0	793
12	A Highly Conserved Neutralizing Epitope on Group 2 Influenza A Viruses. <i>Science</i> , 2011, 333, 843-850.	6.0	772
13	Antibody Domain Exchange Is an Immunological Solution to Carbohydrate Cluster Recognition. <i>Science</i> , 2003, 300, 2065-2071.	6.0	736
14	HIV vaccine design and the neutralizing antibody problem. <i>Nature Immunology</i> , 2004, 5, 233-236.	7.0	721
15	Highly Conserved Protective Epitopes on Influenza B Viruses. <i>Science</i> , 2012, 337, 1343-1348.	6.0	705
16	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. <i>Nature</i> , 2014, 509, 55-62.	13.7	681
17	Rational HIV Immunogen Design to Target Specific Germline B Cell Receptors. <i>Science</i> , 2013, 340, 711-716.	6.0	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.	1.5	664

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19	Cryo-EM Structure of a Fully Glycosylated Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1484-1490.	6.0	662
20	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. <i>Science</i> , 2011, 334, 1097-1103.	6.0	644
21	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
22	A structural analysis of M protein in coronavirus assembly and morphology. <i>Journal of Structural Biology</i> , 2011, 174, 11-22.	1.3	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.	2.0	570
24	Crystal Structure of Human Toll-Like Receptor 3 (TLR3) Ectodomain. <i>Science</i> , 2005, 309, 581-585.	6.0	545
25	Structural basis of a shared antibody response to SARS-CoV-2. <i>Science</i> , 2020, 369, 1119-1123.	6.0	536
26	Computational Design of Proteins Targeting the Conserved Stem Region of Influenza Hemagglutinin. <i>Science</i> , 2011, 332, 816-821.	6.0	527
27	Structural Basis of Preexisting Immunity to the 2009 H1N1 Pandemic Influenza Virus. <i>Science</i> , 2010, 328, 357-360.	6.0	521
28	Antibody-antigen interactions: new structures and new conformational changes. <i>Current Opinion in Structural Biology</i> , 1994, 4, 857-867.	2.6	505
29	STRUCTURAL BASIS OF T CELL RECOGNITION. <i>Annual Review of Immunology</i> , 1999, 17, 369-397.	9.5	488
30	HIV-1 neutralizing antibodies induced by native-like envelope trimers. <i>Science</i> , 2015, 349, aac4223.	6.0	482
31	A stable trimeric influenza hemagglutinin stem as a broadly protective immunogen. <i>Science</i> , 2015, 349, 1301-1306.	6.0	480
32	Structural Basis of TLR5-Flagellin Recognition and Signaling. <i>Science</i> , 2012, 335, 859-864.	6.0	454
33	Structure of the Uncleaved Human H1 Hemagglutinin from the Extinct 1918 Influenza Virus. <i>Science</i> , 2004, 303, 1866-1870.	6.0	440
34	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012, 489, 526-532.	13.7	434
35	A Dynamic Knockout Reveals That Conformational Fluctuations Influence the Chemical Step of Enzyme Catalysis. <i>Science</i> , 2011, 332, 234-238.	6.0	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.	6.6	410

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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.	3.3	397
38	Broadly Neutralizing Antibodies Present New Prospects to Counter Highly Antigenically Diverse Viruses. <i>Science</i> , 2012, 337, 183-186.	6.0	394
39	A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. <i>Science Advances</i> , 2019, 5, eaav4580.	4.7	393
40	Exploitation of glycosylation in enveloped virus pathobiology. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1480-1497.	1.1	383
41	HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. <i>Science</i> , 2016, 351, 1458-1463.	6.0	382
42	Hepatitis C Virus E2 Envelope Glycoprotein Core Structure. <i>Science</i> , 2013, 342, 1090-1094.	6.0	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.	1.5	356
44	Massively parallel de novo protein design for targeted therapeutics. <i>Nature</i> , 2017, 550, 74-79.	13.7	354
45	Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. <i>Cell Reports</i> , 2020, 31, 107725.	2.9	353
46	A Blueprint for HIV Vaccine Discovery. <i>Cell Host and Microbe</i> , 2012, 12, 396-407.	5.1	348
47	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. <i>Nature Biotechnology</i> , 2012, 30, 543-548.	9.4	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.	6.6	342
49	Immunogenicity of Stabilized HIV-1 Envelope Trimers with Reduced Exposure of Non-neutralizing Epitopes. <i>Cell</i> , 2015, 163, 1702-1715.	13.5	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.	3.3	340
51	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. <i>Immunity</i> , 2016, 45, 483-496.	6.6	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.	3.3	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.	6.6	323
54	Glycan microarray technologies: tools to survey host specificity of influenza viruses. <i>Nature Reviews Microbiology</i> , 2006, 4, 857-864.	13.6	319

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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.	3.6	314
56	Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	309
57	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. <i>Science</i> , 2021, 373, 818-823.	6.0	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.	13.5	305
59	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020, 11, 2688.	5.8	304
60	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. <i>Science</i> , 2021, 371, .	6.0	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.	3.3	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.	6.6	286
63	Crystal Structure of a Shark Single-Domain Antibody V Region in Complex with Lysozyme. <i>Science</i> , 2004, 305, 1770-1773.	6.0	282
64	Antibody-antigen interactions. <i>Current Opinion in Structural Biology</i> , 1993, 3, 113-118.	2.6	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.	3.3	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.	2.1	267
67	The HIV-1 envelope glycoprotein structure: nailing down a moving target. <i>Immunological Reviews</i> , 2017, 275, 21-32.	2.8	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.	2.9	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.	1.5	247
70	Structural Characterization of the 1918 Influenza Virus H1N1 Neuraminidase. <i>Journal of Virology</i> , 2008, 82, 10493-10501.	1.5	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.	1.5	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.	3.3	236

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73	Tailored Immunogens Direct Affinity Maturation toward HIV Neutralizing Antibodies. <i>Cell</i> , 2016, 166, 1459-1470.e11.	13.5	230
74	Antibody Elbow Angles are Influenced by their Light Chain Class. <i>Journal of Molecular Biology</i> , 2006, 357, 1566-1574.	2.0	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.	3.3	225
76	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017, 547, 360-363.	13.7	217
77	Major antigen-induced domain rearrangements in an antibody. <i>Structure</i> , 1993, 1, 83-93.	1.6	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.	2.9	216
79	A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic $\beta^2$ -Hairpin Structure. <i>Immunity</i> , 2017, 46, 690-702.	6.6	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.	6.6	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.	6.6	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.	6.6	200
83	Global Efforts in Structural Genomics. <i>Science</i> , 2001, 294, 89-92.	6.0	195
84	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
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.	3.3	188
86	A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. <i>PLoS Pathogens</i> , 2017, 13, e1006682.	2.1	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.	3.3	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.	6.6	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.	15.2	183
90	Reshaping Antibody Diversity. <i>Cell</i> , 2013, 153, 1379-1393.	13.5	179

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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	Receptor mimicry by antibody F045â€“092 facilitates universal binding to the H3 subtype of influenza virus. <i>Nature Communications</i> , 2014, 5, 3614.	5.8	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.	6.6	175
94	A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. <i>Science</i> , 2019, 366, .	6.0	172
95	Improving the Immunogenicity of Native-like HIV-1 Envelope Trimers by Hyperstabilization. <i>Cell Reports</i> , 2017, 20, 1805-1817.	2.9	171
96	Universal protection against influenza infection by a multidomain antibody to influenza hemagglutinin. <i>Science</i> , 2018, 362, 598-602.	6.0	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.	1.0	165
98	Design of protein-binding proteins from the target structure alone. <i>Nature</i> , 2022, 605, 551-560.	13.7	164
99	Antigen Recognition by Variable Lymphocyte Receptors. <i>Science</i> , 2008, 321, 1834-1837.	6.0	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.	5.1	163
101	Broadly protective human antibodies that target the active site of influenza virus neuraminidase. <i>Science</i> , 2019, 366, 499-504.	6.0	162
102	Structural Evolution of Glycan Recognition by a Family of Potent HIV Antibodies. <i>Cell</i> , 2014, 159, 69-79.	13.5	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.	5.8	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.	3.3	159
105	Antibody responses to viral infections: a structural perspective across three different enveloped viruses. <i>Nature Microbiology</i> , 2019, 4, 734-747.	5.9	158
106	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
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.	2.0	154
108	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. <i>Nature</i> , 2017, 548, 108-111.	13.7	154

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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.	6.6	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.	2.9	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.	4.2	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.	2.3	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.	3.3	149
114	Applications of the streak seeding technique in protein crystallization. <i>Journal of Crystal Growth</i> , 1991, 110, 270-282.	0.7	147
115	Presenting native-like trimeric HIV-1 antigens with self-assembling nanoparticles. <i>Nature Communications</i> , 2016, 7, 12041.	5.8	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.	5.9	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.	3.6	141
118	Antibody Recognition of the Pandemic H1N1 Influenza Virus Hemagglutinin Receptor Binding Site. <i>Journal of Virology</i> , 2013, 87, 12471-12480.	1.5	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.	0.9	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.	6.6	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.	2.1	138
122	Broadly neutralizing antibodies against influenza viruses. <i>Antiviral Research</i> , 2013, 98, 476-483.	1.9	136
123	The challenge of protein structure determination—lessons from structural genomics. <i>Protein Science</i> , 2007, 16, 2472-2482.	3.1	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.	3.3	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.	3.3	135
126	Structural Constraints Determine the Glycosylation of HIV-1 Envelope Trimers. <i>Cell Reports</i> , 2015, 11, 1604-1613.	2.9	135



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127	Potent peptidic fusion inhibitors of influenza virus. <i>Science</i> , 2017, 358, 496-502.	6.0	135
128	Uncleaved prefusion-optimized gp140 trimers derived from analysis of HIV-1 envelope metastability. <i>Nature Communications</i> , 2016, 7, 12040.	5.8	134
129	Preferential Recognition of Avian-Like Receptors in Human Influenza A H7N9 Viruses. <i>Science</i> , 2013, 342, 1230-1235.	6.0	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.	2.0	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.	5.8	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.	6.6	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.	3.3	127
134	HMGB1 Activates Proinflammatory Signaling via TLR5 Leading to Allodynia. <i>Cell Reports</i> , 2016, 17, 1128-1140.	2.9	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.	5.8	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.	2.0	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.	3.3	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.	5.8	116
139	Structure and Immune Recognition of the HIV Glycan Shield. <i>Annual Review of Biophysics</i> , 2018, 47, 499-523.	4.5	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.	1.5	114
141	Structural Characterization of an Early Fusion Intermediate of Influenza Virus Hemagglutinin. <i>Journal of Virology</i> , 2011, 85, 5172-5182.	1.5	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, .	5.8	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.	1.5	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.	2.1	111

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145	Broadly neutralizing antibodies target the coronavirus fusion peptide. <i>Science</i> , 2022, 377, 728-735.	6.0	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.	1.5	110
147	CD4-Induced Activation in a Soluble HIV-1 Env Trimer. <i>Structure</i> , 2014, 22, 974-984.	1.6	108
148	Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. <i>Nature Biotechnology</i> , 2017, 35, 667-671.	9.4	108
149	Genetically encoding phosphotyrosine and its nonhydrolyzable analog in bacteria. <i>Nature Chemical Biology</i> , 2017, 13, 845-849.	3.9	105
150	Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. <i>PLoS Pathogens</i> , 2016, 12, e1005815.	2.1	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.	2.9	103
152	Comprehensive Antigenic Map of a Cleaved Soluble HIV-1 Envelope Trimer. <i>PLoS Pathogens</i> , 2015, 11, e1004767.	2.1	100
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