

Ian A Wilson

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

379
papers

44,686
citations

108
h-index

205
g-index

406
ext. papers

52,899
ext. citations

16
avg, IF

7.54
L-index

#	Paper	IF	Citations
379	Broad neutralization coverage of HIV by multiple highly potent antibodies. <i>Nature</i> , 2011 , 477, 466-70	50.4	1164
378	Antibody recognition of a highly conserved influenza virus epitope. <i>Science</i> , 2009 , 324, 246-51	33.3	1031
377	A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. <i>Science</i> , 2020 , 368, 630-633	33.3	954
376	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, 17033-8	11.5	949
375	Isolation of potent SARS-CoV-2 neutralizing antibodies and protection from disease in a small animal model. <i>Science</i> , 2020 , 369, 956-963	33.3	906
374	New world bats harbor diverse influenza A viruses. <i>PLoS Pathogens</i> , 2013 , 9, e1003657	7.6	825
373	Structure and receptor specificity of the hemagglutinin from an H5N1 influenza virus. <i>Science</i> , 2006 , 312, 404-10	33.3	786
372	Crystal structure of a neutralizing human IGG against HIV-1: a template for vaccine design. <i>Science</i> , 2001 , 293, 1155-9	33.3	764
371	Crystal structure of a soluble cleaved HIV-1 envelope trimer. <i>Science</i> , 2013 , 342, 1477-83	33.3	687
370	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011 , 480, 336-43	50.4	682
369	Antibody domain exchange is an immunological solution to carbohydrate cluster recognition. <i>Science</i> , 2003 , 300, 2065-71	33.3	674
368	HIV vaccine design and the neutralizing antibody problem. <i>Nature Immunology</i> , 2004 , 5, 233-6	19.1	659
367	A highly conserved neutralizing epitope on group 2 influenza A viruses. <i>Science</i> , 2011 , 333, 843-50	33.3	645
366	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	7.6	644
365	The broadly neutralizing anti-human immunodeficiency virus type 1 antibody 2G12 recognizes a cluster of alpha1->2 mannose residues on the outer face of gp120. <i>Journal of Virology</i> , 2002 , 76, 7306-21	6.6	617
364	Structural basis of plasticity in T cell receptor recognition of a self peptide-MHC antigen. <i>Science</i> , 1998 , 279, 1166-72	33.3	595
363	A potent and broad neutralizing antibody recognizes and penetrates the HIV glycan shield. <i>Science</i> , 2011 , 334, 1097-103	33.3	576

362	Cryo-EM structure of a fully glycosylated soluble cleaved HIV-1 envelope trimer. <i>Science</i> , 2013 , 342, 1484-90	33.3	573
361	Highly conserved protective epitopes on influenza B viruses. <i>Science</i> , 2012 , 337, 1343-8	33.3	543
360	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. <i>Nature</i> , 2014 , 509, 55-62	50.4	537
359	Rational HIV immunogen design to target specific germline B cell receptors. <i>Science</i> , 2013 , 340, 711-6	33.3	519
358	Glycan microarray analysis of the hemagglutinins from modern and pandemic influenza viruses reveals different receptor specificities. <i>Journal of Molecular Biology</i> , 2006 , 355, 1143-55	6.5	519
357	Crystal structure of human toll-like receptor 3 (TLR3) ectodomain. <i>Science</i> , 2005 , 309, 581-5	33.3	483
356	Structural basis of preexisting immunity to the 2009 H1N1 pandemic influenza virus. <i>Science</i> , 2010 , 328, 357-60	33.3	459
355	A structural analysis of M protein in coronavirus assembly and morphology. <i>Journal of Structural Biology</i> , 2011 , 174, 11-22	3.4	449
354	Antibody-antigen interactions: new structures and new conformational changes. <i>Current Opinion in Structural Biology</i> , 1994 , 4, 857-67	8.1	447
353	Computational design of proteins targeting the conserved stem region of influenza hemagglutinin. <i>Science</i> , 2011 , 332, 816-21	33.3	441
352	Structural basis of T cell recognition. <i>Annual Review of Immunology</i> , 1999 , 17, 369-97	34.7	427
351	Structure of the uncleaved human H1 hemagglutinin from the extinct 1918 influenza virus. <i>Science</i> , 2004 , 303, 1866-70	33.3	411
350	HIV-1 VACCINES. HIV-1 neutralizing antibodies induced by native-like envelope trimers. <i>Science</i> , 2015 , 349, aac4223	33.3	394
349	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, 11664-9	11.5	381
348	Broadly neutralizing anti-HIV antibody 4E10 recognizes a helical conformation of a highly conserved fusion-associated motif in gp41. <i>Immunity</i> , 2005 , 22, 163-73	32.3	379
347	A stable trimeric influenza hemagglutinin stem as a broadly protective immunogen. <i>Science</i> , 2015 , 349, 1301-6	33.3	364
346	Structural basis of TLR5-flagellin recognition and signaling. <i>Science</i> , 2012 , 335, 859-64	33.3	356
345	A dynamic knockout reveals that conformational fluctuations influence the chemical step of enzyme catalysis. <i>Science</i> , 2011 , 332, 234-8	33.3	350

344	Cross-neutralization of influenza A viruses mediated by a single antibody loop. <i>Nature</i> , 2012 , 489, 526-32	50.4	344
343	Structural basis of a shared antibody response to SARS-CoV-2. <i>Science</i> , 2020 , 369, 1119-1123	33.3	338
342	Broadly neutralizing antibodies present new prospects to counter highly antigenically diverse viruses. <i>Science</i> , 2012 , 337, 183-6	33.3	334
341	A single amino acid substitution in 1918 influenza virus hemagglutinin changes receptor binding specificity. <i>Journal of Virology</i> , 2005 , 79, 11533-6	6.6	327
340	A Blueprint for HIV Vaccine Discovery. <i>Cell Host and Microbe</i> , 2012 , 12, 396-407	23.4	302
339	Hepatitis C virus E2 envelope glycoprotein core structure. <i>Science</i> , 2013 , 342, 1090-4	33.3	300
338	Broadly neutralizing HIV antibodies define a glycan-dependent epitope on the prefusion conformation of gp41 on cleaved envelope trimers. <i>Immunity</i> , 2014 , 40, 657-68	32.3	286
337	Glycan microarray technologies: tools to survey host specificity of influenza viruses. <i>Nature Reviews Microbiology</i> , 2006 , 4, 857-64	22.2	286
336	Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing. <i>Nature Biotechnology</i> , 2012 , 30, 543-8	44.5	279
335	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	17.6	274
334	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, 13372-7	11.5	270
333	A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. <i>Science Advances</i> , 2019 , 5, eaav4580	14.3	268
332	Structural delineation of a quaternary, cleavage-dependent epitope at the gp41-gp120 interface on intact HIV-1 Env trimers. <i>Immunity</i> , 2014 , 40, 669-80	32.3	267
331	HIV-1 broadly neutralizing antibody precursor B cells revealed by germline-targeting immunogen. <i>Science</i> , 2016 , 351, 1458-63	33.3	266
330	Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. <i>Cell Reports</i> , 2020 , 31, 107725	10.6	263
329	Antibody-antigen interactions. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 113-118	8.1	256
328	Immunogenicity of Stabilized HIV-1 Envelope Trimers with Reduced Exposure of Non-neutralizing Epitopes. <i>Cell</i> , 2015 , 163, 1702-15	56.2	251
327	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, 14943-8	11.5	249

326	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	11.5	246
325	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, 17624-9	11.5	239
324	Massively parallel de novo protein design for targeted therapeutics. <i>Nature</i> , 2017 , 550, 74-79	50.4	235
323	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	7.6	235
322	Crystal structure of a shark single-domain antibody V region in complex with lysozyme. <i>Science</i> , 2004 , 305, 1770-3	33.3	235
321	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. <i>Immunity</i> , 2016 , 45, 483-496	32.3	232
320	Exploitation of glycosylation in enveloped virus pathobiology. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019 , 1863, 1480-1497	4	228
319	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, 642-58	6.6	225
318	Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. <i>Eurosurveillance</i> , 2020 , 25,	19.8	220
317	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, 4351-6	11.5	214
316	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	32.3	204
315	Structural characterization of the 1918 influenza virus H1N1 neuraminidase. <i>Journal of Virology</i> , 2008 , 82, 10493-501	6.6	204
314	Major antigen-induced domain rearrangements in an antibody. <i>Structure</i> , 1993 , 1, 83-93	5.2	201
313	Composition and Antigenic Effects of Individual Glycan Sites of a Trimeric HIV-1 Envelope Glycoprotein. <i>Cell Reports</i> , 2016 , 14, 2695-706	10.6	193
312	A native-like SOSIP.664 trimer based on an HIV-1 subtype B env gene. <i>Journal of Virology</i> , 2015 , 89, 3380-95	6.5	191
311	Antibody elbow angles are influenced by their light chain class. <i>Journal of Molecular Biology</i> , 2006 , 357, 1566-74	6.5	185
310	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	56.2	182
309	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, 2788-93	11.5	179

308	The HIV-1 envelope glycoprotein structure: nailing down a moving target. <i>Immunological Reviews</i> , 2017 , 275, 21-32	11.3	178
307	Tailored Immunogens Direct Affinity Maturation toward HIV Neutralizing Antibodies. <i>Cell</i> , 2016 , 166, 1459-1470.e11	56.2	178
306	Recent avian H5N1 viruses exhibit increased propensity for acquiring human receptor specificity. <i>Journal of Molecular Biology</i> , 2008 , 381, 1382-94	6.5	176
305	Global efforts in structural genomics. <i>Science</i> , 2001 , 294, 89-92	33.3	176
304	Vulnerabilities in coronavirus glycan shields despite extensive glycosylation. <i>Nature Communications</i> , 2020 , 11, 2688	17.4	174
303	Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. <i>Immunity</i> , 2015 , 43, 1053-63	32.3	170
302	Holes in the Glycan Shield of the Native HIV Envelope Are a Target of Trimer-Elicited Neutralizing Antibodies. <i>Cell Reports</i> , 2016 , 16, 2327-38	10.6	163
301	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, 445-50	11.5	161
300	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017 , 547, 360-363	50.4	155
299	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, 18256-61	11.5	151
298	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. <i>Science</i> , 2021 , 371,	33.3	149
297	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	17.5	148
296	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. <i>Science</i> , 2021 , 373, 818-823	33.3	148
295	Structural evolution of glycan recognition by a family of potent HIV antibodies. <i>Cell</i> , 2014 , 159, 69-79	56.2	147
294	A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic E-Hairpin Structure. <i>Immunity</i> , 2017 , 46, 690-702	32.3	146
293	Antigen recognition by variable lymphocyte receptors. <i>Science</i> , 2008 , 321, 1834-7	33.3	146
292	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, 7353-64	16.4	146
291	A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. <i>PLoS Pathogens</i> , 2017 , 13, e1006682	7.6	143

290	Three-dimensional structure of an anti-steroid FabSand progesterone-FabScomplex. <i>Journal of Molecular Biology</i> , 1993 , 231, 103-18	6.5	143
289	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, 11440-5	11.5	139
288	Reshaping antibody diversity. <i>Cell</i> , 2013 , 153, 1379-93	56.2	138
287	Applications of the streak seeding technique in protein crystallization. <i>Journal of Crystal Growth</i> , 1991 , 110, 270-282	1.6	135
286	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, 937-48	7.3	133
285	Structural characterization of the hemagglutinin receptor specificity from the 2009 H1N1 influenza pandemic. <i>Journal of Virology</i> , 2012 , 86, 982-90	6.6	132
284	Receptor mimicry by antibody F045-092 facilitates universal binding to the H3 subtype of influenza virus. <i>Nature Communications</i> , 2014 , 5, 3614	17.4	130
283	"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	16.4	127
282	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, 1458-63	11.5	125
281	Preferential recognition of avian-like receptors in human influenza A H7N9 viruses. <i>Science</i> , 2013 , 342, 1230-5	33.3	124
280	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	23.4	121
279	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	3.6	121
278	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, 17040-5	11.5	119
277	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, 1533-44	6.5	115
276	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, 9499-504	11.5	113
275	Improving the Immunogenicity of Native-like HIV-1 Envelope Trimers by Hyperstabilization. <i>Cell Reports</i> , 2017 , 20, 1805-1817	10.6	112
274	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	32.3	112
273	A public antibody lineage that potently inhibits malaria infection through dual binding to the circumsporozoite protein. <i>Nature Medicine</i> , 2018 , 24, 401-407	50.5	110

272	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	32.3	110
271	A Site of Vulnerability on the Influenza Virus Hemagglutinin Head Domain Trimer Interface. <i>Cell</i> , 2019 , 177, 1136-1152.e18	56.2	107
270	Antibody recognition of the pandemic H1N1 Influenza virus hemagglutinin receptor binding site. <i>Journal of Virology</i> , 2013 , 87, 12471-80	6.6	107
269	A recurring motif for antibody recognition of the receptor-binding site of influenza hemagglutinin. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 363-70	17.6	107
268	An Alternative Binding Mode of IGHV3-53 Antibodies to the SARS-CoV-2 Receptor Binding Domain. <i>Cell Reports</i> , 2020 , 33, 108274	10.6	107
267	The challenge of protein structure determination--lessons from structural genomics. <i>Protein Science</i> , 2007 , 16, 2472-82	6.3	106
266	Universal protection against influenza infection by a multidomain antibody to influenza hemagglutinin. <i>Science</i> , 2018 , 362, 598-602	33.3	106
265	An HIV-1 antibody from an elite neutralizer implicates the fusion peptide as a site of vulnerability. <i>Nature Microbiology</i> , 2016 , 2, 16199	26.6	103
264	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, 1215-26	32.3	102
263	CD4-induced activation in a soluble HIV-1 Env trimer. <i>Structure</i> , 2014 , 22, 974-84	5.2	101
262	Structural Constraints Determine the Glycosylation of HIV-1 Envelope Trimers. <i>Cell Reports</i> , 2015 , 11, 1604-13	10.6	101
261	Antibody potency relates to the ability to recognize the closed, pre-fusion form of HIV Env. <i>Nature Communications</i> , 2015 , 6, 6144	17.4	101
260	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	7.6	101
259	Presenting native-like trimeric HIV-1 antigens with self-assembling nanoparticles. <i>Nature Communications</i> , 2016 , 7, 12041	17.4	101
258	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	16.6	100
257	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. <i>Nature</i> , 2017 , 548, 108-111	50.4	99
256	Broadly neutralizing antibodies against influenza viruses. <i>Antiviral Research</i> , 2013 , 98, 476-83	10.8	99
255	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, 6359-68	6.6	99

254	Potent peptidic fusion inhibitors of influenza virus. <i>Science</i> , 2017 , 358, 496-502	33.3	98
253	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, 11947-52	11.5	97
252	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	32.3	97
251	Structural characterization of an early fusion intermediate of influenza virus hemagglutinin. <i>Journal of Virology</i> , 2011 , 85, 5172-82	6.6	96
250	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	32.3	96
249	Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 538, 192-203	3.4	93
248	Analytical and production seeding techniques. <i>Methods</i> , 1990 , 1, 38-49	4.6	92
247	Structure of a classical broadly neutralizing stem antibody in complex with a pandemic H2 influenza virus hemagglutinin. <i>Journal of Virology</i> , 2013 , 87, 7149-54	6.6	91
246	Antibody responses to viral infections: a structural perspective across three different enveloped viruses. <i>Nature Microbiology</i> , 2019 , 4, 734-747	26.6	89
245	A generalized HIV vaccine design strategy for priming of broadly neutralizing antibody responses. <i>Science</i> , 2019 , 366,	33.3	89
244	The JCSG high-throughput structural biology pipeline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1137-42		89
243	HMGB1 Activates Proinflammatory Signaling via TLR5 Leading to Allodynia. <i>Cell Reports</i> , 2016 , 17, 1128-1140	11.4	88
242	Uncleaved prefusion-optimized gp140 trimers derived from analysis of HIV-1 envelope metastability. <i>Nature Communications</i> , 2016 , 7, 12040	17.4	86
241	Comprehensive antigenic map of a cleaved soluble HIV-1 envelope trimer. <i>PLoS Pathogens</i> , 2015 , 11, e1004767	7.6	85
240	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, 13580-92	6.6	85
239	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	6.5	85
238	Structure, receptor binding, and antigenicity of influenza virus hemagglutinins from the 1957 H2N2 pandemic. <i>Journal of Virology</i> , 2010 , 84, 1715-21	6.6	85
237	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, 8451-62	6.6	85

236	Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. <i>Nature Biotechnology</i> , 2017 , 35, 667-671	44.5	84
235	Broadly protective human antibodies that target the active site of influenza virus neuraminidase. <i>Science</i> , 2019 , 366, 499-504	33.3	83
234	Structure and Immune Recognition of the HIV Glycan Shield. <i>Annual Review of Biophysics</i> , 2018 , 47, 499-521	52.1	81
233	Insights into the trimeric HIV-1 envelope glycoprotein structure. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 101-7	10.3	78
232	Epitopes for neutralizing antibodies induced by HIV-1 envelope glycoprotein BG505 SOSIP trimers in rabbits and macaques. <i>PLoS Pathogens</i> , 2018 , 14, e1006913	7.6	78
231	Structural insights into key sites of vulnerability on HIV-1 Env and influenza HA. <i>Immunological Reviews</i> , 2012 , 250, 180-98	11.3	76
230	Minimally Mutated HIV-1 Broadly Neutralizing Antibodies to Guide Reductionist Vaccine Design. <i>PLoS Pathogens</i> , 2016 , 12, e1005815	7.6	76
229	Genetically encoding phosphotyrosine and its nonhydrolyzable analog in bacteria. <i>Nature Chemical Biology</i> , 2017 , 13, 845-849	11.7	72
228	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	32.3	71
227	Influences on trimerization and aggregation of soluble, cleaved HIV-1 SOSIP envelope glycoprotein. <i>Journal of Virology</i> , 2013 , 87, 9873-85	6.6	71
226	Structural characterization of viral epitopes recognized by broadly cross-reactive antibodies. <i>Current Topics in Microbiology and Immunology</i> , 2015 , 386, 323-41	3.3	70
225	Structural basis for antibody recognition of the NANP repeats in circumsporozoite protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E10438-E10445	11.5	70
224	A small-molecule fusion inhibitor of influenza virus is orally active in mice. <i>Science</i> , 2019 , 363,	33.3	69
223	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	7.6	69
222	Structure and immunogenicity of a stabilized HIV-1 envelope trimer based on a group-M consensus sequence. <i>Nature Communications</i> , 2019 , 10, 2355	17.4	68
221	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, 1105-18	6.6	67
220	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. <i>Immunity</i> , 2016 , 44, 21-31	32.3	67
219	Structural characterization of cleaved, soluble HIV-1 envelope glycoprotein trimers. <i>Journal of Virology</i> , 2013 , 87, 9865-72	6.6	67

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3	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates 2020 , 16, e1008753		

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