

Jesse D Bloom

List of Publications by Year in Descending Order

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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.

177
papers

12,415
citations

55
h-index

109
g-index

230
ext. papers

17,474
ext. citations

14.3
avg, IF

7.37
L-index

#	Paper	IF	Citations
177	Structural changes in the SARS-CoV-2 spike E406W mutant escaping a clinical monoclonal antibody cocktail. 2022,		2
176	Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. 2022,		8
175	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry.. <i>Science</i> , 2022 , 375, eabm8143	33.3	23
174	Dynamics of infection-elicited SARS-CoV-2 antibodies in children over time. 2022,		1
173	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses.. <i>Nature</i> , 2022,	50.4	19
172	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy.. <i>PLoS Pathogens</i> , 2022 , 18, e1010248	7.6	7
171	Defining the risk of SARS-CoV-2 variants on immune protection.. <i>Nature</i> , 2022,	50.4	7
170	An antibody-escape estimator for mutations to the SARS-CoV-2 receptor-binding domain.. <i>Virus Evolution</i> , 2022 , 8, veac021	3.7	3
169	Selection analysis identifies clusters of unusual mutational changes in Omicron lineage BA.1 that likely impact Spike function.. <i>Molecular Biology and Evolution</i> , 2022,	8.3	10
168	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice.. <i>Science Translational Medicine</i> , 2022 , 14, eabn1252	17.5	3
167	Broadly neutralizing antibodies target a hemagglutinin anchor epitope.. <i>Nature</i> , 2021,	50.4	7
166	An antibody-escape calculator for mutations to the SARS-CoV-2 receptor-binding domain. 2021,		10
165	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry 2021,		7
164	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy 2021 ,		5
163	Humoral immunogenicity of the seasonal influenza vaccine before and after CAR-T-cell therapy: a prospective observational study 2021 , 9,		1
162	Emergence and spread of a SARS-CoV-2 variant through Europe in the summer of 2020 2021,		142
161	Comprehensive mapping of mutations in the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human plasma antibodies. <i>Cell Host and Microbe</i> , 2021 , 29, 463-476.e6	23.4	569

160	Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines 2021 ,		12
159	Mutational escape from the polyclonal antibody response to SARS-CoV-2 infection is largely shaped by a single class of antibodies 2021 ,		27
158	Cell-Culture Adaptation of H3N2 Influenza Virus Impacts Acid Stability and Reduces Airborne Transmission in Ferret Model. <i>Viruses</i> , 2021 , 13,	6.2	4
157	A human coronavirus evolves antigenically to escape antibody immunity. <i>PLoS Pathogens</i> , 2021 , 17, e1009453	9.5	93
156	The SARS-CoV-2 mRNA-1273 vaccine elicits more RBD-focused neutralization, but with broader antibody binding within the RBD 2021 ,		11
155	Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016. <i>Cell Reports Medicine</i> , 2021 , 2, 100255	18	205
154	Structural basis for broad sarbecovirus neutralization by a human monoclonal antibody 2021 ,		14
153	Antibodies to the SARS-CoV-2 receptor-binding domain that maximize breadth and resistance to viral escape 2021 ,		12
152	Investigate the origins of COVID-19. <i>Science</i> , 2021 , 372, 694	33.3	39
151	Humoral immunogenicity of the seasonal influenza vaccine before and after CAR-T-cell therapy 2021 ,		3
150	Antibodies elicited by mRNA-1273 vaccination bind more broadly to the receptor binding domain than do those from SARS-CoV-2 infection. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	74
149	Stabilization of the SARS-CoV-2 Spike Receptor-Binding Domain Using Deep Mutational Scanning and Structure-Based Design. <i>Frontiers in Immunology</i> , 2021 , 12, 710263	8.4	7
148	Comprehensive Profiling of Mutations to Influenza Virus PB2 That Confer Resistance to the Cap-Binding Inhibitor Pimodivir. <i>Viruses</i> , 2021 , 13,	6.2	2
147	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021 , 595, 707-712	50.4	168
146	Functional development of a V3/glycan-specific broadly neutralizing antibody isolated from a case of HIV superinfection. <i>ELife</i> , 2021 , 10,	8.9	2
145	Mapping mutations to the SARS-CoV-2 RBD that escape binding by different classes of antibodies. <i>Nature Communications</i> , 2021 , 12, 4196	17.4	106
144	Dynamics of Neutralizing Antibody Titers in the Months After Severe Acute Respiratory Syndrome Coronavirus 2 Infection. <i>Journal of Infectious Diseases</i> , 2021 , 223, 197-205	7	119
143	Complete Mapping of Mutations to the SARS-CoV-2 Spike Receptor-Binding Domain that Escape Antibody Recognition. <i>Cell Host and Microbe</i> , 2021 , 29, 44-57.e9	23.4	525

142	Genetic and structural basis for recognition of SARS-CoV-2 spike protein by a two-antibody cocktail 2021 ,		28
141	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19. <i>Science</i> , 2021 , 371, 850-854	33.3	395
140	Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016 2021 ,		28
139	Broad sarbecovirus neutralization by a human monoclonal antibody. <i>Nature</i> , 2021 , 597, 103-108	50.4	94
138	Multivalent designed proteins protect against SARS-CoV-2 variants of concern 2021 ,		4
137	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021 , 597, 97-102	50.4	118
136	Recovery of Deleted Deep Sequencing Data Sheds More Light on the Early Wuhan SARS-CoV-2 Epidemic. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5211-5224	8.3	6
135	Genetic and structural basis for SARS-CoV-2 variant neutralization by a two-antibody cocktail. <i>Nature Microbiology</i> , 2021 , 6, 1233-1244	26.6	72
134	Neutralizing Monoclonal Antibodies That Target the Spike Receptor Binding Domain Confer Fc Receptor-Independent Protection against SARS-CoV-2 Infection in Syrian Hamsters. <i>MBio</i> , 2021 , 12, e0239521	7.8	5
133	Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines. <i>Cell</i> , 2021 , 184, 5432-5447.e16	56.2	34
132	High-resolution mapping of the neutralizing and binding specificities of polyclonal sera post-HIV Env trimer vaccination. <i>ELife</i> , 2021 , 10,	8.9	3
131	When two are better than one: Modeling the mechanisms of antibody mixtures. <i>PLoS Computational Biology</i> , 2020 , 16, e1007830	5	4
130	Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. <i>Viruses</i> , 2020 , 12,	6.2	360
129	Antibody Neutralization of an Influenza Virus that Uses Neuraminidase for Receptor Binding. <i>Viruses</i> , 2020 , 12,	6.2	4
128	Different genetic barriers for resistance to HA stem antibodies in influenza H3 and H1 viruses. <i>Science</i> , 2020 , 368, 1335-1340	33.3	22
127	APOBEC3C Tandem Domain Proteins Create Super Restriction Factors against HIV-1. <i>MBio</i> , 2020 , 11,	7.8	3
126	Deep Mutational Scanning to Map How Zika Envelope Protein Mutations Affect Viral Growth and Antibody Escape. <i>Proceedings (mdpi)</i> , 2020 , 50, 93	0.3	
125	Restriction of HIV-1 Escape by a Highly Broad and Potent Neutralizing Antibody. <i>Cell</i> , 2020 , 180, 471-489.e22	62.2	47

124	Linking influenza virus evolution within and between human hosts. <i>Virus Evolution</i> , 2020 , 6, veaa010	3.7	29
123	: Interactive visualization tool for deep mutational scanning data. <i>Journal of Open Source Software</i> , 2020 , 5,	5.2	24
122	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak 2020 ,		9
121	Deep mutational scanning of SARS-CoV-2 receptor binding domain reveals constraints on folding and ACE2 binding 2020 ,		33
120	Attenuated influenza virions expressing the SARS-CoV-2 receptor-binding domain induce neutralizing antibodies in mice 2020 ,		2
119	Neutralizing antibodies correlate with protection from SARS-CoV-2 in humans during a fishery vessel outbreak with high attack rate 2020 ,		26
118	Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition 2020 ,		32
117	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19 2020 ,		34
116	Phage-DMS: A Comprehensive Method for Fine Mapping of Antibody Epitopes. <i>IScience</i> , 2020 , 23, 101628.1		6
115	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. <i>Cell</i> , 2020 , 182, 1295-1310.e20	56.2	935
114	Neutralizing Antibodies Correlate with Protection from SARS-CoV-2 in Humans during a Fishery Vessel Outbreak with a High Attack Rate. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	320
113	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak. <i>Nature Communications</i> , 2020 , 11, 4378	17.4	45
112	Attenuated Influenza Virions Expressing the SARS-CoV-2 Receptor-Binding Domain Induce Neutralizing Antibodies in Mice. <i>Viruses</i> , 2020 , 12,	6.2	9
111	When two are better than one: Modeling the mechanisms of antibody mixtures 2020 , 16, e1007830		
110	When two are better than one: Modeling the mechanisms of antibody mixtures 2020 , 16, e1007830		
109	When two are better than one: Modeling the mechanisms of antibody mixtures 2020 , 16, e1007830		
108	When two are better than one: Modeling the mechanisms of antibody mixtures 2020 , 16, e1007830		
107	Deep Mutational Scanning Comprehensively Maps How Zika Envelope Protein Mutations Affect Viral Growth and Antibody Escape. <i>Journal of Virology</i> , 2019 , 93,	6.6	12

106	An Antigenic Atlas of HIV-1 Escape from Broadly Neutralizing Antibodies Distinguishes Functional and Structural Epitopes. <i>Immunity</i> , 2019 , 50, 520-532.e3	32.3	42
105	Comprehensive profiling of translation initiation in influenza virus infected cells. <i>PLoS Pathogens</i> , 2019 , 15, e1007518	7.6	16
104	Massively Parallel Profiling of HIV-1 Resistance to the Fusion Inhibitor Enfuvirtide. <i>Viruses</i> , 2019 , 11,	6.2	7
103	Single-Cell Virus Sequencing of Influenza Infections That Trigger Innate Immunity. <i>Journal of Virology</i> , 2019 , 93,	6.6	51
102	Deep Mutational Scan of the Highly Conserved Influenza A Virus M1 Matrix Protein Reveals Substantial Intrinsic Mutational Tolerance. <i>Journal of Virology</i> , 2019 , 93,	6.6	11
101	Determinants of Zika virus host tropism uncovered by deep mutational scanning. <i>Nature Microbiology</i> , 2019 , 4, 876-887	26.6	29
100	Reconciling disparate estimates of viral genetic diversity during human influenza infections. <i>Nature Genetics</i> , 2019 , 51, 1298-1301	36.3	22
99	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. <i>Cell</i> , 2019 , 178, 567-584.e19	56.2	64
98	alignparse: A Python package for parsing complex features from high-throughput long-read sequencing. <i>Journal of Open Source Software</i> , 2019 , 4,	5.2	6
97	Comprehensive mapping of adaptation of the avian influenza polymerase protein PB2 to humans. <i>ELife</i> , 2019 , 8,	8.9	24
96	Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin. <i>ELife</i> , 2019 , 8,	8.9	47
95	Author response: Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin 2019 ,		7
94	Identification of Antibodies Targeting the H3N2 Hemagglutinin Receptor Binding Site following Vaccination of Humans. <i>Cell Reports</i> , 2019 , 29, 4460-4470.e8	10.6	10
93	Within-Host Evolution of Human Influenza Virus. <i>Trends in Microbiology</i> , 2018 , 26, 781-793	12.4	55
92	How single mutations affect viral escape from broad and narrow antibodies to H1 influenza hemagglutinin. <i>Nature Communications</i> , 2018 , 9, 1386	17.4	74
91	Sera from Individuals with Narrowly Focused Influenza Virus Antibodies Rapidly Select Viral Escape Mutations. <i>Journal of Virology</i> , 2018 , 92,	6.6	15
90	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV. <i>PLoS Pathogens</i> , 2018 , 14, e1007159	7.6	27
89	Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8276-E8285	11.5	79

88	Author response: Extreme heterogeneity of influenza virus infection in single cells 2018 ,		5
87	Enhanced ER proteostasis and temperature differentially impact the mutational tolerance of influenza hemagglutinin. <i>ELife</i> , 2018 , 7,	8.9	11
86	Estimating the frequency of multiplets in single-cell RNA sequencing from cell-mixing experiments. <i>PeerJ</i> , 2018 , 6, e5578	3.1	17
85	Modeling site-specific amino-acid preferences deepens phylogenetic estimates of viral sequence divergence. <i>Virus Evolution</i> , 2018 , 4, vey033	3.7	10
84	613. Transmission of Influenza Virus in Mother and Infant Transmission Events in Nepal. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S223-S224	1	1
83	Cooperating H3N2 Influenza Virus Variants Are Not Detectable in Primary Clinical Samples. <i>MSphere</i> , 2018 , 3,	5	21
82	Destabilized adaptive influenza variants critical for innate immune system escape are potentiated by host chaperones. <i>PLoS Biology</i> , 2018 , 16, e3000008	9.7	14
81	Extreme heterogeneity of influenza virus infection in single cells. <i>ELife</i> , 2018 , 7,	8.9	122
80	Mapping mutational effects along the evolutionary landscape of HIV envelope. <i>ELife</i> , 2018 , 7,	8.9	50
79	Comprehensive Mapping of HIV-1 Escape from a Broadly Neutralizing Antibody. <i>Cell Host and Microbe</i> , 2017 , 21, 777-787.e4	23.4	51
78	Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. <i>Nature Biotechnology</i> , 2017 , 35, 667-671	44.5	84
77	Identification of positive selection in genes is greatly improved by using experimentally informed site-specific models. <i>Biology Direct</i> , 2017 , 12, 1	7.2	40
76	A framework for exhaustively mapping functional missense variants. <i>Molecular Systems Biology</i> , 2017 , 13, 957	12.2	69
75	Complete mapping of viral escape from neutralizing antibodies. <i>PLoS Pathogens</i> , 2017 , 13, e1006271	7.6	80
74	Deep mutational scanning identifies sites in influenza nucleoprotein that affect viral inhibition by MxA. <i>PLoS Pathogens</i> , 2017 , 13, e1006288	7.6	38
73	Parallel evolution of influenza across multiple spatiotemporal scales. <i>ELife</i> , 2017 , 6,	8.9	89
72	phydms: software for phylogenetic analyses informed by deep mutational scanning. <i>PeerJ</i> , 2017 , 5, e36571	3.1	14
71	Experimental Estimation of the Effects of All Amino-Acid Mutations to HIV ₁ Envelope Protein on Viral Replication in Cell Culture. <i>PLoS Pathogens</i> , 2016 , 12, e1006114	7.6	57

70	Cooperation between distinct viral variants promotes growth of H3N2 influenza in cell culture. <i>ELife</i> , 2016 , 5, e13974	8.9	51
69	Accurate Measurement of the Effects of All Amino-Acid Mutations on Influenza Hemagglutinin. <i>Viruses</i> , 2016 , 8,	6.2	122
68	Software for the analysis and visualization of deep mutational scanning data. <i>BMC Bioinformatics</i> , 2015 , 16, 168	3.6	72
67	Positive Selection in CD8+ T-Cell Epitopes of Influenza Virus Nucleoprotein Revealed by a Comparative Analysis of Human and Swine Viral Lineages. <i>Journal of Virology</i> , 2015 , 89, 11275-83	6.6	30
66	Site-Specific Amino Acid Preferences Are Mostly Conserved in Two Closely Related Protein Homologs. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2944-60	8.3	60
65	Influenza viruses with receptor-binding N1 neuraminidases occur sporadically in several lineages and show no attenuation in cell culture or mice. <i>Journal of Virology</i> , 2015 , 89, 3737-45	6.6	13
64	Potential antigenic explanation for atypical H1N1 infections among middle-aged adults during the 2013-2014 influenza season. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15798-803	11.5	159
63	Improving pandemic influenza risk assessment. <i>ELife</i> , 2014 , 3, e03883	8.9	45
62	Epistatically interacting substitutions are enriched during adaptive protein evolution. <i>PLoS Genetics</i> , 2014 , 10, e1004328	6	46
61	An experimentally informed evolutionary model improves phylogenetic fit to divergent lactamase homologs. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2753-69	8.3	24
60	An experimentally determined evolutionary model dramatically improves phylogenetic fit. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1956-78	8.3	116
59	Estimating the fitness advantage conferred by permissive neuraminidase mutations in recent oseltamivir-resistant A(H1N1)pdm09 influenza viruses. <i>PLoS Pathogens</i> , 2014 , 10, e1004065	7.6	97
58	The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin. <i>ELife</i> , 2014 , 3,	8.9	132
57	Author response: The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin 2014 ,		2
56	Author response: Improving pandemic influenza risk assessment 2014 ,		2
55	A mutant influenza virus that uses an N1 neuraminidase as the receptor-binding protein. <i>Journal of Virology</i> , 2013 , 87, 12531-40	6.6	55
54	Broad protection against influenza infection by vectored immunoprophylaxis in mice. <i>Nature Biotechnology</i> , 2013 , 31, 647-52	44.5	88
53	Mutational effects on stability are largely conserved during protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 21071-6	11.5	90

52	Stability-mediated epistasis constrains the evolution of an influenza protein. <i>ELife</i> , 2013 , 2, e00631	8.9	220
51	Author response: Stability-mediated epistasis constrains the evolution of an influenza protein 2013		2
50	Mucin biopolymers as broad-spectrum antiviral agents. <i>Biomacromolecules</i> , 2012 , 13, 1724-32	6.9	104
49	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012 , 21, 769-85	6.3	136
48	The global spread of drug-resistant influenza. <i>Journal of the Royal Society Interface</i> , 2012 , 9, 648-56	4.1	34
47	A computational-experimental approach identifies mutations that enhance surface expression of an oseltamivir-resistant influenza neuraminidase. <i>PLoS ONE</i> , 2011 , 6, e22201	3.7	38
46	Permissive secondary mutations enable the evolution of influenza oseltamivir resistance. <i>Science</i> , 2010 , 328, 1272-5	33.3	478
45	Consensus protein design without phylogenetic bias. <i>Journal of Molecular Biology</i> , 2010 , 399, 541-6	6.5	62
44	Inferring stabilizing mutations from protein phylogenies: application to influenza hemagglutinin. <i>PLoS Computational Biology</i> , 2009 , 5, e1000349	5	50
43	In the light of directed evolution: pathways of adaptive protein evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106 Suppl 1, 9995-10000	11.5	315
42	Neutral genetic drift can alter promiscuous protein functions, potentially aiding functional evolution. <i>Biology Direct</i> , 2007 , 2, 17	7.2	125
41	Evolution favors protein mutational robustness in sufficiently large populations. <i>BMC Biology</i> , 2007 , 5, 29	7.3	79
40	A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments. <i>Nature Biotechnology</i> , 2007 , 25, 1051-6	44.5	124
39	Probing the role of PrP repeats in conformational conversion and amyloid assembly of chimeric yeast prions. <i>Journal of Biological Chemistry</i> , 2007 , 282, 34204-12	5.4	27
38	Thermodynamics of neutral protein evolution. <i>Genetics</i> , 2007 , 175, 255-66	4	120
37	Structural determinants of the rate of protein evolution in yeast. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1751-61	8.3	138
36	Structure-guided recombination creates an artificial family of cytochromes P450. <i>PLoS Biology</i> , 2006 , 4, e112	9.7	116
35	Protein stability promotes evolvability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 5869-74	11.5	812

34	Predicting the tolerance of proteins to random amino acid substitution. <i>Biophysical Journal</i> , 2005 , 89, 3714-20	2.9	36
33	Evolving strategies for enzyme engineering. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 447-52	8.1	273
32	Why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 14338-43	11.5	590
31	Thermodynamic prediction of protein neutrality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 606-11	11.5	272
30	The elongation of yeast prion fibers involves separable steps of association and conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 2287-92	11.5	81
29	Evolutionary rate depends on number of protein-protein interactions independently of gene expression level: response. <i>BMC Evolutionary Biology</i> , 2004 , 4, 14	3	38
28	Stability and the evolvability of function in a model protein. <i>Biophysical Journal</i> , 2004 , 86, 2758-64	2.9	80
27	Apparent dependence of protein evolutionary rate on number of interactions is linked to biases in protein-protein interactions data sets. <i>BMC Evolutionary Biology</i> , 2003 , 3, 21	3	104
26	Bidirectional amyloid fiber growth for a yeast prion determinant. <i>Current Biology</i> , 2001 , 11, 366-9	6.3	80
25	Structure, receptor recognition and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein		
24	Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin		5
23	Influenza H3 and H1 hemagglutinins have different genetic barriers for resistance to broadly neutralizing stem antibodies		1
22	Identification of positive selection in genes is greatly improved by using experimentally informed site-specific models		5
21	Accurate measurement of the effects of all amino-acid mutations to influenza hemagglutinin		7
20	Expanding the Atlas of Functional Missense Variation for Human Genes		2
19	Protocol and reagents for pseudotyping lentiviral particles with SARS-CoV-2 Spike protein for neutralization assays		45
18	dms-view: Interactive visualization tool for deep mutational scanning data		2
17	Dynamics of neutralizing antibody titers in the months after SARS-CoV-2 infection		38

16	A human coronavirus evolves antigenically to escape antibody immunity	17
15	Quantifying the effects of single mutations on viral escape from broad and narrow antibodies to an H1 influenza hemagglutinin	2
14	Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants	4
13	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV	1
12	Sera from individuals with narrowly focused influenza virus antibodies rapidly select viral escape mutations in ovo	1
11	Reconciling disparate estimates of viral genetic diversity during human influenza infections	3
10	Single-cell virus sequencing of influenza infections that trigger innate immunity	6
9	Deep mutational scanning comprehensively maps how Zika envelope protein mutations affect viral growth and antibody escape	1
8	Linking influenza virus evolution within and between human hosts	1
7	alignparse: A Python package for parsing complex features from high-throughput long-read sequencing	1
6	The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin	1
5	Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic	2
4	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses	10
3	Comprehensive mapping of mutations to the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human serum antibodies	97
2	A public broadly neutralizing antibody class targets a membrane-proximal anchor epitope of influenza virus hemagglutinin	1
1	Shifting mutational constraints in the SARS-CoV-2 receptor-binding domain during viral evolution	6