Jesse D Bloom

List of Publications by Citations

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	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. *Cell*, **2020**, 182, 1295-1310.e20	56.2	935
176	Protein stability promotes evolvability. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 5869-74	11.5	812
175	Why highly expressed proteins evolve slowly. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 14338-43	11.5	590
174	Comprehensive mapping of mutations in the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human plasma antibodies. *Cell Host and Microbe*, **2021**, 29, 463-476.e6	23.4	569
173	Complete Mapping of Mutations to the SARS-CoV-2 Spike Receptor-Binding Domain that Escape Antibody Recognition. *Cell Host and Microbe*, **2021**, 29, 44-57.e9	23.4	525
172	Permissive secondary mutations enable the evolution of influenza oseltamivir resistance. *Science*, **2010**, 328, 1272-5	33.3	478
171	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19. *Science*, **2021**, 371, 850-854	33.3	395
170	Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. *Viruses*, **2020**, 12,	6.2	360
169	Neutralizing Antibodies Correlate with Protection from SARS-CoV-2 in Humans during a Fishery Vessel Outbreak with a High Attack Rate. *Journal of Clinical Microbiology*, **2020**, 58,	9.7	320
168	In the light of directed evolution: pathways of adaptive protein evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106 Suppl 1, 9995-10000	11.5	315
167	Evolving strategies for enzyme engineering. *Current Opinion in Structural Biology*, **2005**, 15, 447-52	8.1	273
166	Thermodynamic prediction of protein neutrality. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 606-11	11.5	272
165	Stability-mediated epistasis constrains the evolution of an influenza protein. *ELife*, **2013**, 2, e00631	8.9	220
164	Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016. *Cell Reports Medicine*, **2021**, 2, 100255	18	205
163	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. *Nature*, **2021**, 595, 707-712	50.4	168
162	Potential antigenic explanation for atypical H1N1 infections among middle-aged adults during the 2013-2014 influenza season. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 15798-803	11.5	159
161	Emergence and spread of a SARS-CoV-2 variant through Europe in the summer of 2020 **2021**,		142

160	Structural determinants of the rate of protein evolution in yeast. *Molecular Biology and Evolution*, **2006**, 23, 1751-61	8.3	138
159	The interface of protein structure, protein biophysics, and molecular evolution. *Protein Science*, **2012**, 21, 769-85	6.3	136
158	The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin. *ELife*, **2014**, 3,	8.9	132
157	Neutral genetic drift can alter promiscuous protein functions, potentially aiding functional evolution. *Biology Direct*, **2007**, 2, 17	7.2	125
156	A diverse family of thermostable cytochrome P450s created by recombination of stabilizing fragments. *Nature Biotechnology*, **2007**, 25, 1051-6	44.5	124
155	Accurate Measurement of the Effects of All Amino-Acid Mutations on Influenza Hemagglutinin. *Viruses*, **2016**, 8,	6.2	122
154	Extreme heterogeneity of influenza virus infection in single cells. *ELife*, **2018**, 7,	8.9	122
153	Thermodynamics of neutral protein evolution. *Genetics*, **2007**, 175, 255-66	4	120
152	Dynamics of Neutralizing Antibody Titers in the Months After Severe Acute Respiratory Syndrome Coronavirus 2 Infection. *Journal of Infectious Diseases*, **2021**, 223, 197-205	7	119
151	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. *Nature*, **2021**, 597, 97-102	50.4	118
150	An experimentally determined evolutionary model dramatically improves phylogenetic fit. *Molecular Biology and Evolution*, **2014**, 31, 1956-78	8.3	116
149	Structure-guided recombination creates an artificial family of cytochromes P450. *PLoS Biology*, **2006**, 4, e112	9.7	116
148	Mapping mutations to the SARS-CoV-2 RBD that escape binding by different classes of antibodies. *Nature Communications*, **2021**, 12, 4196	17.4	106
147	Mucin biopolymers as broad-spectrum antiviral agents. *Biomacromolecules*, **2012**, 13, 1724-32	6.9	104
146	Apparent dependence of protein evolutionary rate on number of interactions is linked to biases in protein-protein interactions data sets. *BMC Evolutionary Biology*, **2003**, 3, 21	3	104
145	Estimating the fitness advantage conferred by permissive neuraminidase mutations in recent oseltamivir-resistant A(H1N1)pdm09 influenza viruses. *PLoS Pathogens*, **2014**, 10, e1004065	7.6	97
144	Comprehensive mapping of mutations to the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human serum antibodies		97
143	Broad sarbecovirus neutralization by a human monoclonal antibody. *Nature*, **2021**, 597, 103-108	50.4	94

142 A human coronavirus evolves antigenically to escape antibody immunity. *PLoS Pathogens*, **2021**, 17, e1009453   7.6   93

141 Mutational effects on stability are largely conserved during protein evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 21071-6   11.5   90

140 Parallel evolution of influenza across multiple spatiotemporal scales. *ELife*, **2017**, 6,   8.9   89

139 Broad protection against influenza infection by vectored immunoprophylaxis in mice. *Nature Biotechnology*, **2013**, 31, 647-52   44.5   88

138 Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. *Nature Biotechnology*, **2017**, 35, 667-671   44.5   84

137 The elongation of yeast prion fibers involves separable steps of association and conversion. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 2287-92   11.5   81

136 Stability and the evolvability of function in a model protein. *Biophysical Journal*, **2004**, 86, 2758-64   2.9   80

135 Bidirectional amyloid fiber growth for a yeast prion determinant. *Current Biology*, **2001**, 11, 366-9   6.3   80

134 Complete mapping of viral escape from neutralizing antibodies. *PLoS Pathogens*, **2017**, 13, e1006271   7.6   80

133 Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E8276-E8285   11.5   79

132 Evolution favors protein mutational robustness in sufficiently large populations. *BMC Biology*, **2007**, 5, 29   7.3   79

131 How single mutations affect viral escape from broad and narrow antibodies to H1 influenza hemagglutinin. *Nature Communications*, **2018**, 9, 1386   17.4   74

130 Antibodies elicited by mRNA-1273 vaccination bind more broadly to the receptor binding domain than do those from SARS-CoV-2 infection. *Science Translational Medicine*, **2021**, 13,   17.5   74

129 Software for the analysis and visualization of deep mutational scanning data. *BMC Bioinformatics*, **2015**, 16, 168   3.6   72

128 Genetic and structural basis for SARS-CoV-2 variant neutralization by a two-antibody cocktail. *Nature Microbiology*, **2021**, 6, 1233-1244   26.6   72

127 A framework for exhaustively mapping functional missense variants. *Molecular Systems Biology*, **2017**, 13, 957   12.2   69

126 Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. *Cell*, **2019**, 178, 567-584.e19   56.2   64

125 Consensus protein design without phylogenetic bias. *Journal of Molecular Biology*, **2010**, 399, 541-6   6.5   62

124	Site-Specific Amino Acid Preferences Are Mostly Conserved in Two Closely Related Protein Homologs. *Molecular Biology and Evolution*, **2015**, 32, 2944-60	8.3	60
123	Experimental Estimation of the Effects of All Amino-Acid Mutations to HIV Envelope Protein on Viral Replication in Cell Culture. *PLoS Pathogens*, **2016**, 12, e1006114	7.6	57
122	Within-Host Evolution of Human Influenza Virus. *Trends in Microbiology*, **2018**, 26, 781-793	12.4	55
121	A mutant influenza virus that uses an N1 neuraminidase as the receptor-binding protein. *Journal of Virology*, **2013**, 87, 12531-40	6.6	55
120	Comprehensive Mapping of HIV-1 Escape from a Broadly Neutralizing Antibody. *Cell Host and Microbe*, **2017**, 21, 777-787.e4	23.4	51
119	Single-Cell Virus Sequencing of Influenza Infections That Trigger Innate Immunity. *Journal of Virology*, **2019**, 93,	6.6	51
118	Cooperation between distinct viral variants promotes growth of H3N2 influenza in cell culture. *ELife*, **2016**, 5, e13974	8.9	51
117	Inferring stabilizing mutations from protein phylogenies: application to influenza hemagglutinin. *PLoS Computational Biology*, **2009**, 5, e1000349	5	50
116	Mapping mutational effects along the evolutionary landscape of HIV envelope. *ELife*, **2018**, 7,	8.9	50
115	Restriction of HIV-1 Escape by a Highly Broad and Potent Neutralizing Antibody. *Cell*, **2020**, 180, 471-489.e22	36.2	47
114	Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin. *ELife*, **2019**, 8,	8.9	47
113	Epistatically interacting substitutions are enriched during adaptive protein evolution. *PLoS Genetics*, **2014**, 10, e1004328	6	46
112	Improving pandemic influenza risk assessment. *ELife*, **2014**, 3, e03883	8.9	45
111	Protocol and reagents for pseudotyping lentiviral particles with SARS-CoV-2 Spike protein for neutralization assays		45
110	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak. *Nature Communications*, **2020**, 11, 4378	17.4	45
109	An Antigenic Atlas of HIV-1 Escape from Broadly Neutralizing Antibodies Distinguishes Functional and Structural Epitopes. *Immunity*, **2019**, 50, 520-532.e3	32.3	42
108	Identification of positive selection in genes is greatly improved by using experimentally informed site-specific models. *Biology Direct*, **2017**, 12, 1	7.2	40
107	Investigate the origins of COVID-19. *Science*, **2021**, 372, 694	33.3	39

106	Evolutionary rate depends on number of protein-protein interactions independently of gene expression level: response. *BMC Evolutionary Biology*, **2004**, 4, 14	3	38
105	A computational-experimental approach identifies mutations that enhance surface expression of an oseltamivir-resistant influenza neuraminidase. *PLoS ONE*, **2011**, 6, e22201	3.7	38
104	Deep mutational scanning identifies sites in influenza nucleoprotein that affect viral inhibition by MxA. *PLoS Pathogens*, **2017**, 13, e1006288	7.6	38
103	Dynamics of neutralizing antibody titers in the months after SARS-CoV-2 infection		38
102	Predicting the tolerance of proteins to random amino acid substitution. *Biophysical Journal*, **2005**, 89, 3714-20	2.9	36
101	The global spread of drug-resistant influenza. *Journal of the Royal Society Interface*, **2012**, 9, 648-56	4.1	34
100	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19 **2020**,		34
99	Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines. *Cell*, **2021**, 184, 5432-5447.e16	56.2	34
98	Deep mutational scanning of SARS-CoV-2 receptor binding domain reveals constraints on folding and ACE2 binding **2020**,		33
97	Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition **2020**,		32
96	Positive Selection in CD8+ T-Cell Epitopes of Influenza Virus Nucleoprotein Revealed by a Comparative Analysis of Human and Swine Viral Lineages. *Journal of Virology*, **2015**, 89, 11275-83	6.6	30
95	Determinants of Zika virus host tropism uncovered by deep mutational scanning. *Nature Microbiology*, **2019**, 4, 876-887	26.6	29
94	Linking influenza virus evolution within and between human hosts. *Virus Evolution*, **2020**, 6, veaa010	3.7	29
93	Genetic and structural basis for recognition of SARS-CoV-2 spike protein by a two-antibody cocktail **2021**,		28
92	Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016 **2021**,		28
91	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV. *PLoS Pathogens*, **2018**, 14, e1007159	7.6	27
90	Probing the role of PrP repeats in conformational conversion and amyloid assembly of chimeric yeast prions. *Journal of Biological Chemistry*, **2007**, 282, 34204-12	5.4	27
89	Mutational escape from the polyclonal antibody response to SARS-CoV-2 infection is largely shaped by a single class of antibodies **2021**,		27

88	Neutralizing antibodies correlate with protection from SARS-CoV-2 in humans during a fishery vessel outbreak with high attack rate **2020**,		26
87	An experimentally informed evolutionary model improves phylogenetic fit to divergent lactamase homologs. *Molecular Biology and Evolution*, **2014**, 31, 2753-69	8.3	24
86	: Interactive visualization tool for deep mutational scanning data. *Journal of Open Source Software*, **2020**, 5,	5.2	24
85	Comprehensive mapping of adaptation of the avian influenza polymerase protein PB2 to humans. *ELife*, **2019**, 8,	8.9	24
84	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry.. *Science*, **2022**, 375, eabm8143	33.3	23
83	Reconciling disparate estimates of viral genetic diversity during human influenza infections. *Nature Genetics*, **2019**, 51, 1298-1301	36.3	22
82	Different genetic barriers for resistance to HA stem antibodies in influenza H3 and H1 viruses. *Science*, **2020**, 368, 1335-1340	33.3	22
81	Cooperating H3N2 Influenza Virus Variants Are Not Detectable in Primary Clinical Samples. *MSphere*, **2018**, 3,	5	21
80	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses.. *Nature*, **2022**,	50.4	19
79	Estimating the frequency of multiplets in single-cell RNA sequencing from cell-mixing experiments. *PeerJ*, **2018**, 6, e5578	3.1	17
78	A human coronavirus evolves antigenically to escape antibody immunity		17
77	Comprehensive profiling of translation initiation in influenza virus infected cells. *PLoS Pathogens*, **2019**, 15, e1007518	7.6	16
76	Sera from Individuals with Narrowly Focused Influenza Virus Antibodies Rapidly Select Viral Escape Mutations. *Journal of Virology*, **2018**, 92,	6.6	15
75	phydms: software for phylogenetic analyses informed by deep mutational scanning. *PeerJ*, **2017**, 5, e3657	7.1	14
74	Structural basis for broad sarbecovirus neutralization by a human monoclonal antibody **2021**,		14
73	Destabilized adaptive influenza variants critical for innate immune system escape are potentiated by host chaperones. *PLoS Biology*, **2018**, 16, e3000008	9.7	14
72	Influenza viruses with receptor-binding N1 neuraminidases occur sporadically in several lineages and show no attenuation in cell culture or mice. *Journal of Virology*, **2015**, 89, 3737-45	6.6	13
71	Deep Mutational Scanning Comprehensively Maps How Zika Envelope Protein Mutations Affect Viral Growth and Antibody Escape. *Journal of Virology*, **2019**, 93,	6.6	12

70	Elicitation of broadly protective sarbecovirus immunity by receptor-binding domain nanoparticle vaccines **2021**,		12
69	Antibodies to the SARS-CoV-2 receptor-binding domain that maximize breadth and resistance to viral escape **2021**,		12
68	Deep Mutational Scan of the Highly Conserved Influenza A Virus M1 Matrix Protein Reveals Substantial Intrinsic Mutational Tolerance. *Journal of Virology*, **2019**, 93,	6.6	11
67	Enhanced ER proteostasis and temperature differentially impact the mutational tolerance of influenza hemagglutinin. *ELife*, **2018**, 7,	8.9	11
66	The SARS-CoV-2 mRNA-1273 vaccine elicits more RBD-focused neutralization, but with broader antibody binding within the RBD **2021**,		11
65	An antibody-escape calculator for mutations to the SARS-CoV-2 receptor-binding domain. **2021**,		10
64	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses		10
63	Identification of Antibodies Targeting the H3N2 Hemagglutinin Receptor Binding Site following Vaccination of Humans. *Cell Reports*, **2019**, 29, 4460-4470.e8	10.6	10
62	Modeling site-specific amino-acid preferences deepens phylogenetic estimates of viral sequence divergence. *Virus Evolution*, **2018**, 4, vey033	3.7	10
61	Selection analysis identifies clusters of unusual mutational changes in Omicron lineage BA.1 that likely impact Spike function.. *Molecular Biology and Evolution*, **2022**,	8.3	10
60	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak **2020**,		9
59	Attenuated Influenza Virions Expressing the SARS-CoV-2 Receptor-Binding Domain Induce Neutralizing Antibodies in Mice. *Viruses*, **2020**, 12,	6.2	9
58	Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. **2022**,		8
57	Massively Parallel Profiling of HIV-1 Resistance to the Fusion Inhibitor Enfuvirtide. *Viruses*, **2019**, 11,	6.2	7
56	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy.. *PLoS Pathogens*, **2022**, 18, e1010248	7.6	7
55	Broadly neutralizing antibodies target a hemagglutinin anchor epitope.. *Nature*, **2021**,	50.4	7
54	Author response: Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin **2019**,		7
53	Antibody-mediated broad sarbecovirus neutralization through ACE2 molecular mimicry **2021**,		7

52	Accurate measurement of the effects of all amino-acid mutations to influenza hemagglutinin		7
51	Stabilization of the SARS-CoV-2 Spike Receptor-Binding Domain Using Deep Mutational Scanning and Structure-Based Design. *Frontiers in Immunology*, **2021**, 12, 710263	8.4	7
50	Defining the risk of SARS-CoV-2 variants on immune protection.. *Nature*, **2022**,	50.4	7
49	alignparse: A Python package for parsing complex features from high-throughput long-read sequencing. *Journal of Open Source Software*, **2019**, 4,	5.2	6
48	Single-cell virus sequencing of influenza infections that trigger innate immunity		6
47	Phage-DMS: A Comprehensive Method for Fine Mapping of Antibody Epitopes. *IScience*, **2020**, 23, 101622	6.1	6
46	Recovery of Deleted Deep Sequencing Data Sheds More Light on the Early Wuhan SARS-CoV-2 Epidemic. *Molecular Biology and Evolution*, **2021**, 38, 5211-5224	8.3	6
45	Shifting mutational constraints in the SARS-CoV-2 receptor-binding domain during viral evolution		6
44	Author response: Extreme heterogeneity of influenza virus infection in single cells **2018**,		5
43	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy **2021** ,		5
42	Mapping person-to-person variation in viral mutations that escape polyclonal serum targeting influenza hemagglutinin		5
41	Identification of positive selection in genes is greatly improved by using experimentally informed site-specific models		5
40	Neutralizing Monoclonal Antibodies That Target the Spike Receptor Binding Domain Confer Fc Receptor-Independent Protection against SARS-CoV-2 Infection in Syrian Hamsters. *MBio*, **2021**, 12, e0239521	7.8	5
39	When two are better than one: Modeling the mechanisms of antibody mixtures. *PLoS Computational Biology*, **2020**, 16, e1007830	5	4
38	Antibody Neutralization of an Influenza Virus that Uses Neuraminidase for Receptor Binding. *Viruses*, **2020**, 12,	6.2	4
37	Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants		4
36	Cell-Culture Adaptation of H3N2 Influenza Virus Impacts Acid Stability and Reduces Airborne Transmission in Ferret Model. *Viruses*, **2021**, 13,	6.2	4
35	Multivalent designed proteins protect against SARS-CoV-2 variants of concern **2021**,		4

34	APOBEC3C Tandem Domain Proteins Create Super Restriction Factors against HIV-1. *MBio*, **2020**, 11,	7.8	3
33	Reconciling disparate estimates of viral genetic diversity during human influenza infections		3
32	Humoral immunogenicity of the seasonal influenza vaccine before and after CAR-T-cell therapy **2021**,		3
31	High-resolution mapping of the neutralizing and binding specificities of polyclonal sera post-HIV Env trimer vaccination. *ELife*, **2021**, 10,	8.9	3
30	An antibody-escape estimator for mutations to the SARS-CoV-2 receptor-binding domain.. *Virus Evolution*, **2022**, 8, veac021	3.7	3
29	Multivalent designed proteins neutralize SARS-CoV-2 variants of concern and confer protection against infection in mice.. *Science Translational Medicine*, **2022**, 14, eabn1252	17.5	3
28	Structural changes in the SARS-CoV-2 spike E406W mutant escaping a clinical monoclonal antibody cocktail. **2022**,		2
27	Author response: The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin **2014**,		2
26	Structure, receptor recognition and antigenicity of the human coronavirus CCoV-HuPn-2018 spike glycoprotein		2
25	Expanding the Atlas of Functional Missense Variation for Human Genes		2
24	dms-view: Interactive visualization tool for deep mutational scanning data		2
23	Attenuated influenza virions expressing the SARS-CoV-2 receptor-binding domain induce neutralizing antibodies in mice **2020**,		2
22	Quantifying the effects of single mutations on viral escape from broad and narrow antibodies to an H1 influenza hemagglutinin		2
21	Author response: Improving pandemic influenza risk assessment **2014**,		2
20	Author response: Stability-mediated epistasis constrains the evolution of an influenza protein **2013**,		2
19	Comprehensive Profiling of Mutations to Influenza Virus PB2 That Confer Resistance to the Cap-Binding Inhibitor Pimodivir. *Viruses*, **2021**, 13,	6.2	2
18	Recovery of deleted deep sequencing data sheds more light on the early Wuhan SARS-CoV-2 epidemic		2
17	Functional development of a V3/glycan-specific broadly neutralizing antibody isolated from a case of HIV superinfection. *ELife*, **2021**, 10,	8.9	2

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16	Dynamics of infection-elicited SARS-CoV-2 antibodies in children over time. **2022,**	1
15	Influenza H3 and H1 hemagglutinins have different genetic barriers for resistance to broadly neutralizing stem antibodies	1
14	Humoral immunogenicity of the seasonal influenza vaccine before and after CAR-T-cell therapy: a prospective observational study **2021**, 9,	1
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 mutationsin ovo	1
11	Deep mutational scanning comprehensively maps how Zika envelope protein mutations affect viral growth and antibody escape	1
10	Linking influenza virus evolution within and between human hosts	1
9	alignparse: A Python package for parsing complex features from high-throughput long-read sequencing	1
8	The inherent mutational tolerance and antigenic evolvability of influenza hemagglutinin	1
7	A public broadly neutralizing antibody class targets a membrane-proximal anchor epitope of influenza virus hemagglutinin	1
6	613. Transmission of Influenza Virus in Mother and Infant Transmission Events in Nepal. *Open Forum Infectious Diseases*, **2018**, 5, S223-S224	1 1
5	Deep Mutational Scanning to Map How Zika Envelope Protein Mutations Affect Viral Growth and Antibody Escape. *Proceedings (mdpi)*, **2020**, 50, 93	0.3
4	When two are better than one: Modeling the mechanisms of antibody mixtures **2020**, 16, e1007830	
3	When two are better than one: Modeling the mechanisms of antibody mixtures **2020**, 16, e1007830	
2	When two are better than one: Modeling the mechanisms of antibody mixtures **2020**, 16, e1007830	
1	When two are better than one: Modeling the mechanisms of antibody mixtures **2020**, 16, e1007830	