

# Allison J Greaney

## 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.

37  
papers

3,660  
citations

19  
h-index

46  
g-index

46  
ext. papers

6,101  
ext. citations

18.8  
avg, IF

6.64  
L-index

#	Paper	IF	Citations
37	Structural changes in the SARS-CoV-2 spike E406W mutant escaping a clinical monoclonal antibody cocktail. <b>2022,</b>		2
36	Selection analysis identifies unusual clustered mutational changes in Omicron lineage BA.1 that likely impact Spike function. <b>2022,</b>		8
35	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses.. <i>Nature</i> , <b>2022,</b>	50.4	19
34	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy.. <i>PLoS Pathogens</i> , <b>2022</b> , 18, e1010248	7.6	7
33	An antibody-escape estimator for mutations to the SARS-CoV-2 receptor-binding domain.. <i>Virus Evolution</i> , <b>2022</b> , 8, veac021	3.7	3
32	Selection analysis identifies clusters of unusual mutational changes in Omicron lineage BA.1 that likely impact Spike function.. <i>Molecular Biology and Evolution</i> , <b>2022,</b>	8.3	10
31	An antibody-escape calculator for mutations to the SARS-CoV-2 receptor-binding domain. <b>2021,</b>		10
30	A SARS-CoV-2 variant elicits an antibody response with a shifted immunodominance hierarchy <b>2021</b> ,		5
29	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> , <b>2021</b> , 29, 463-476.e6	23.4	569
28	Mutational escape from the polyclonal antibody response to SARS-CoV-2 infection is largely shaped by a single class of antibodies <b>2021,</b>		27
27	The SARS-CoV-2 mRNA-1273 vaccine elicits more RBD-focused neutralization, but with broader antibody binding within the RBD <b>2021,</b>		11
26	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> , <b>2021</b> , 2, 100255	18	205
25	Antibodies to the SARS-CoV-2 receptor-binding domain that maximize breadth and resistance to viral escape <b>2021,</b>		12
24	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> , <b>2021</b> , 13,	17.5	74
23	Stabilization of the SARS-CoV-2 Spike Receptor-Binding Domain Using Deep Mutational Scanning and Structure-Based Design. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 710263	8.4	7
22	Mapping mutations to the SARS-CoV-2 RBD that escape binding by different classes of antibodies. <i>Nature Communications</i> , <b>2021</b> , 12, 4196	17.4	106
21	Complete Mapping of Mutations to the SARS-CoV-2 Spike Receptor-Binding Domain that Escape Antibody Recognition. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 44-57.e9	23.4	525

20	Genetic and structural basis for recognition of SARS-CoV-2 spike protein by a two-antibody cocktail <b>2021</b> ,		28
19	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19. <i>Science</i> , <b>2021</b> , 371, 850-854	33.3	395
18	Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016 <b>2021</b> ,		28
17	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , <b>2021</b> , 597, 97-102	50.4	118
16	Genetic and structural basis for SARS-CoV-2 variant neutralization by a two-antibody cocktail. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1233-1244	26.6	72
15	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> , <b>2021</b> , 12, e0239521	7.8	5
14	Frontline Science: Anthrax lethal toxin-induced, NLRP1-mediated IL-1 $\beta$ release is a neutrophil and PAD4-dependent event. <i>Journal of Leukocyte Biology</i> , <b>2020</b> , 108, 773-786	6.5	9
13	Deep mutational scanning of SARS-CoV-2 receptor binding domain reveals constraints on folding and ACE2 binding <b>2020</b> ,		33
12	Attenuated influenza virions expressing the SARS-CoV-2 receptor-binding domain induce neutralizing antibodies in mice <b>2020</b> ,		2
11	Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition <b>2020</b> ,		32
10	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19 <b>2020</b> ,		34
9	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. <i>Cell</i> , <b>2020</b> , 182, 1295-1310.e20	56.2	935
8	Attenuated Influenza Virions Expressing the SARS-CoV-2 Receptor-Binding Domain Induce Neutralizing Antibodies in Mice. <i>Viruses</i> , <b>2020</b> , 12,	6.2	9
7	Sulforaphane inhibits multiple inflammasomes through an Nrf2-independent mechanism. <i>Journal of Leukocyte Biology</i> , <b>2016</b> , 99, 189-99	6.5	93
6	A Diverse Set of Single-domain Antibodies (VHHs) against the Anthrax Toxin Lethal and Edema Factors Provides a Basis for Construction of a Bispecific Agent That Protects against Anthrax Infection. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 21596-21606	5.4	16
5	Bacterial Exotoxins and the Inflammasome. <i>Frontiers in Immunology</i> , <b>2015</b> , 6, 570	8.4	62
4	The Rosetteless gene controls development in the choanoflagellate <i>S. rosetta</i> . <i>ELife</i> , <b>2014</b> , 3,	8.9	54
3	ACE2 binding is an ancestral and evolvable trait of sarbecoviruses		10

2	Comprehensive mapping of mutations to the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human serum antibodies	97
1	Shifting mutational constraints in the SARS-CoV-2 receptor-binding domain during viral evolution	6