Adam S Dingens

List of Publications by Citations

Source: https://exaly.com/author-pdf/2204893/adam-s-dingens-publications-by-citations.pdf
Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

39 papers	3,908 citations	26 h-index	52 g-index
52 ext. papers	6,023 ext. citations	17.6 avg, IF	6.44 L-index

#	Paper	IF	Citations
39	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
38	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
37	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19. *Science*, **2021**, 371, 850-854	33.3	395
36	Protocol and Reagents for Pseudotyping Lentiviral Particles with SARS-CoV-2 Spike Protein for Neutralization Assays. *Viruses*, **2020**, 12,	6.2	360
35	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
34	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
33	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
32	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. *Nature*, **2021**, 597, 97-102	50.4	118
31	Genetic and structural basis for SARS-CoV-2 variant neutralization by a two-antibody cocktail. *Nature Microbiology*, **2021**, 6, 1233-1244	26.6	72
30	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. *Cell*, **2019**, 178, 567-584.e19	56.2	64
29	Experimental Estimation of the Effects of All Amino-Acid Mutations to HIVas Envelope Protein on Viral Replication in Cell Culture. *PLoS Pathogens*, **2016**, 12, e1006114	7.6	57
28	Comprehensive Mapping of HIV-1 Escape from a Broadly Neutralizing Antibody. *Cell Host and Microbe*, **2017**, 21, 777-787.e4	23.4	51
27	Cooperation between distinct viral variants promotes growth of H3N2 influenza in cell culture. *ELife*, **2016**, 5, e13974	8.9	51
26	Mapping mutational effects along the evolutionary landscape of HIV envelope. *ELife*, **2018**, 7,	8.9	50
25	Restriction of HIV-1 Escape by a Highly Broad and Potent Neutralizing Antibody. *Cell*, **2020**, 180, 471-489.e22	56.2	47
24	Protocol and reagents for pseudotyping lentiviral particles with SARS-CoV-2 Spike protein for neutralization assays		45
23	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

22	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
21	Dynamics of neutralizing antibody titers in the months after SARS-CoV-2 infection		38
20	HIV-specific CD4-induced Antibodies Mediate Broad and Potent Antibody-dependent Cellular Cytotoxicity Activity and Are Commonly Detected in Plasma From HIV-infected humans. *EBioMedicine*, **2015**, 2, 1464-77	8.8	36
19	Prospective mapping of viral mutations that escape antibodies used to treat COVID-19 **2020**,		34
18	Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition **2020**,		32
17	Bacterial vaginosis and adverse outcomes among full-term infants: a cohort study. *BMC Pregnancy and Childbirth*, **2016**, 16, 278	3.2	29
16	Genetic and structural basis for recognition of SARS-CoV-2 spike protein by a two-antibody cocktail **2021**,		28
15	Complete map of SARS-CoV-2 RBD mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-CoV016 **2021**,		28
14	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV. *PLoS Pathogens*, **2018**, 14, e1007159	7.6	27
13	Neutralizing antibodies correlate with protection from SARS-CoV-2 in humans during a fishery vessel outbreak with high attack rate **2020**,		26
12	The Broad Neutralizing Antibody Responses after HIV-1 Superinfection Are Not Dominated by Antibodies Directed to Epitopes Common in Single Infection. *PLoS Pathogens*, **2015**, 11, e1004973	7.6	24
11	: Interactive visualization tool for deep mutational scanning data. *Journal of Open Source Software*, **2020**, 5,	5.2	24
10	Superinfection Drives HIV Neutralizing Antibody Responses from Several B Cell Lineages that Contribute to a Polyclonal Repertoire. *Cell Reports*, **2018**, 23, 682-691	10.6	16
9	Comprehensive Characterization of Humoral Correlates of Human Immunodeficiency Virus 1 Superinfection Acquisition in High-risk Kenyan Women. *EBioMedicine*, **2017**, 18, 216-224	8.8	14
8	Prediction of VRC01 neutralization sensitivity by HIV-1 gp160 sequence features. *PLoS Computational Biology*, **2019**, 15, e1006952	5	13
7	Antibodies to the SARS-CoV-2 receptor-binding domain that maximize breadth and resistance to viral escape **2021**,		12
6	Serological identification of SARS-CoV-2 infections among children visiting a hospital during the initial Seattle outbreak **2020**,		9
5	Massively Parallel Profiling of HIV-1 Resistance to the Fusion Inhibitor Enfuvirtide. *Viruses*, **2019**, 11,	6.2	7

4	High-resolution mapping of the neutralizing and binding specificities of polyclonal sera post-HIV Env trimer vaccination. *ELife*, **2021**, 10,	8.9	3
3	dms-view: Interactive visualization tool for deep mutational scanning data		2
2	Functional development of a V3/glycan-specific broadly neutralizing antibody isolated from a case of HIV superinfection. *ELife*, **2021**, 10,	8.9	2
1	Complete functional mapping of infection- and vaccine-elicited antibodies against the fusion peptide of HIV		1