

Nicholas C Wu

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.

110
papers

6,095
citations

34
h-index

77
g-index

133
ext. papers

8,305
ext. citations

13.4
avg, IF

6.43
L-index

#	Paper	IF	Citations
110	A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2.. <i>Immunity</i> , 2022 ,	32.3	2
109	Interactions between Influenza A Virus Nucleoprotein and Gene Segment Untranslated Regions Facilitate Selective Modulation of Viral Gene Expression.. <i>Journal of Virology</i> , 2022 , e0020522	6.6	
108	A large-scale systematic survey of SARS-CoV-2 antibodies reveals recurring molecular features 2021 ,		3
107	Neutralizing Antibodies to SARS-CoV-2 Selected from a Human Antibody Library Constructed Decades Ago. <i>Advanced Science</i> , 2021 , e2102181	13.6	6
106	Dynamics of B-cell repertoires and emergence of cross-reactive responses in COVID-19 patients with different disease severity 2021 ,		2
105	A cross-neutralizing antibody between HIV-1 and influenza virus. <i>PLoS Pathogens</i> , 2021 , 17, e1009407	7.6	9
104	Ultrapotent bispecific antibodies neutralize emerging SARS-CoV-2 variants 2021 ,		6
103	Quantifying the Evolutionary Constraints and Potential of Hepatitis C Virus NS5A Protein. <i>MSystems</i> , 2021 , 6,	7.6	1
102	Human airway cells prevent SARS-CoV-2 multibasic cleavage site cell culture adaptation. <i>ELife</i> , 2021 , 10,	8.9	42
101	Dynamics of B cell repertoires and emergence of cross-reactive responses in patients with different severities of COVID-19. <i>Cell Reports</i> , 2021 , 35, 109173	10.6	14
100	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. <i>Science</i> , 2021 , 373, 818-823	33.3	148
99	A combination of cross-neutralizing antibodies synergizes to prevent SARS-CoV-2 and SARS-CoV pseudovirus infection. <i>Cell Host and Microbe</i> , 2021 , 29, 806-818.e6	23.4	24
98	Diverse immunoglobulin gene usage and convergent epitope targeting in neutralizing antibody responses to SARS-CoV-2. <i>Cell Reports</i> , 2021 , 35, 109109	10.6	7
97	Sequence signatures of two public antibody clonotypes that bind SARS-CoV-2 receptor binding domain. <i>Nature Communications</i> , 2021 , 12, 3815	17.4	15
96	Homologous and heterologous serological response to the N-terminal domain of SARS-CoV-2 in humans and mice. <i>European Journal of Immunology</i> , 2021 , 51, 2296-2305	6.1	2
95	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
94	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants 2021 ,		26

93	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. <i>Science</i> , 2021 , 371,	33.3	149
92	A combination of cross-neutralizing antibodies synergizes to prevent SARS-CoV-2 and SARS-CoV pseudovirus infection 2021 ,		3
91	Bispecific antibodies targeting distinct regions of the spike protein potently neutralize SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2021 , 13, eabj5413	17.5	18
90	Antigenic evolution of human influenza H3N2 neuraminidase is constrained by charge balancing. <i>ELife</i> , 2021 , 10,	8.9	4
89	Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. <i>Eurosurveillance</i> , 2020 , 25,	19.8	220
88	Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. <i>Cell Reports</i> , 2020 , 31, 107725	10.6	263
87	COVID-19 vaccines: Knowing the unknown. <i>European Journal of Immunology</i> , 2020 , 50, 939-943	6.1	14
86	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
85	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
84	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020 , 21, 71	18.3	11
83	Major antigenic site B of human influenza H3N2 viruses has an evolving local fitness landscape. <i>Nature Communications</i> , 2020 , 11, 1233	17.4	23
82	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
81	Convergent Evolution in Breadth of Two V6-1-Encoded Influenza Antibody Clonotypes from a Single Donor. <i>Cell Host and Microbe</i> , 2020 , 28, 434-444.e4	23.4	8
80	A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody. <i>PLoS Pathogens</i> , 2020 , 16, e1009089	7.6	33
79	Cross-reactive antibody response between SARS-CoV-2 and SARS-CoV infections 2020 ,		40
78	Structural basis of a public antibody response to SARS-CoV-2 2020 ,		14
77	An alternative binding mode of IGHV3-53 antibodies to the SARS-CoV-2 receptor binding domain 2020 ,		8
76	Cross-neutralization of a SARS-CoV-2 antibody to a functionally conserved site is mediated by avidity 2020 ,		13

75	A SARS-CoV-2 neutralizing antibody protects from lung pathology in a COVID-19 hamster model 2020 ,		15
74	A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody 2020 ,		2
73	Immunity against cancer cells may promote their proliferation and metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 426-431	11.5	4
72	Influenza Hemagglutinin Structures and Antibody Recognition. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020 , 10,	5.4	21
71	Structural Biology of Influenza Hemagglutinin: An Amaranthine Adventure. <i>Viruses</i> , 2020 , 12,	6.2	12
70	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
69	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
68	An influenza A hemagglutinin small-molecule fusion inhibitor identified by a new high-throughput fluorescence polarization screen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 18431-18438	11.5	13
67	Structural basis of a shared antibody response to SARS-CoV-2. <i>Science</i> , 2020 , 369, 1119-1123	33.3	338
66	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
65	A high-affinity antibody against the CSP N-terminal domain lacks Plasmodium falciparum inhibitory activity. <i>Journal of Experimental Medicine</i> , 2020 , 217,	16.6	5
64	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. <i>BMC Genomics</i> , 2019 , 20, 423	4.5	7
63	Preventing an Antigenically Disruptive Mutation in Egg-Based H3N2 Seasonal Influenza Vaccines by Mutational Incompatibility. <i>Cell Host and Microbe</i> , 2019 , 25, 836-844.e5	23.4	27
62	Conformational Plasticity in the HIV-1 Fusion Peptide Facilitates Recognition by Broadly Neutralizing Antibodies. <i>Cell Host and Microbe</i> , 2019 , 25, 873-883.e5	23.4	25
61	Bacterial glycosyltransferase-mediated cell-surface chemoenzymatic glycan modification. <i>Nature Communications</i> , 2019 , 10, 1799	17.4	25
60	Application of Deep Mutational Scanning in Hepatitis C Virus. <i>Methods in Molecular Biology</i> , 2019 , 1911, 183-190	1.4	1
59	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
58	The in vivo ISGylome links ISG15 to metabolic pathways and autophagy upon Listeria monocytogenes infection. <i>Nature Communications</i> , 2019 , 10, 5383	17.4	34

57	Immunodominance and Antigenic Variation of Influenza Virus Hemagglutinin: Implications for Design of Universal Vaccine Immunogens. <i>Journal of Infectious Diseases</i> , 2019 , 219, S38-S45	7	41
56	Multistate design of influenza antibodies improves affinity and breadth against seasonal viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1597-1602	11.5	16
55	Structural insights into the design of novel anti-influenza therapies. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 115-121	17.6	64
54	Genome-wide identification of interferon-sensitive mutations enables influenza vaccine design. <i>Science</i> , 2018 , 359, 290-296	33.3	49
53	A complex epistatic network limits the mutational reversibility in the influenza hemagglutinin receptor-binding site. <i>Nature Communications</i> , 2018 , 9, 1264	17.4	38
52	Fully human agonist antibodies to TrkB using autocrine cell-based selection from a combinatorial antibody library. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E7023-E7032	11.5	19
51	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
50	Deception through Mimicry: A Cellular Antiviral Strategy. <i>Cell</i> , 2018 , 175, 1728-1729	56.2	
49	Recurring and Adaptable Binding Motifs in Broadly Neutralizing Antibodies to Influenza Virus Are Encoded on the D3-9 Segment of the Ig Gene. <i>Cell Host and Microbe</i> , 2018 , 24, 569-578.e4	23.4	25
48	Structure-Activity Relationships in Metal-Binding Pharmacophores for Influenza Endonuclease. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 10206-10217	8.3	22
47	Clinical Correlations of Transcriptional Profile in Patients Infected With Avian Influenza H7N9 Virus. <i>Journal of Infectious Diseases</i> , 2018 , 218, 1238-1248	7	10
46	Systematic identification of anti-interferon function on hepatitis C virus genome reveals p7 as an immune evasion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2018-2023	11.5	18
45	Immunochemical engineering of cell surfaces to generate virus resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 4655-4660	11.5	4
44	A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic Hairpin Structure. <i>Immunity</i> , 2017 , 46, 690-702	32.3	146
43	In vitro evolution of an influenza broadly neutralizing antibody is modulated by hemagglutinin receptor specificity. <i>Nature Communications</i> , 2017 , 8, 15371	17.4	38
42	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Journal of Computational Biology</i> , 2017 , 24, 558-570	1.7	10
41	Diversity of Functionally Permissive Sequences in the Receptor-Binding Site of Influenza Hemagglutinin. <i>Cell Host and Microbe</i> , 2017 , 21, 742-753.e8	23.4	40
40	A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. <i>PLoS Pathogens</i> , 2017 , 13, e1006682	7.6	143

39	Antibody 27F3 Broadly Targets Influenza A Group 1 and 2 Hemagglutinins through a Further Variation in V1-69 Antibody Orientation on the HA Stem. <i>Cell Reports</i> , 2017 , 20, 2935-2943	10.6	64
38	Quantifying perinatal transmission of Hepatitis B viral quasispecies by tag linkage deep sequencing. <i>Scientific Reports</i> , 2017 , 7, 10168	4.9	5
37	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
36	Structure-based optimization and synthesis of antiviral drug Arbidol analogues with significantly improved affinity to influenza hemagglutinin. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2017 , 27, 3744-3748	2.9	34
35	Annotating Protein Functional Residues by Coupling High-Throughput Fitness Profile and Homologous-Structure Analysis. <i>MBio</i> , 2016 , 7,	7.8	8
34	Coupling high-throughput genetics with phylogenetic information reveals an epistatic interaction on the influenza A virus M segment. <i>BMC Genomics</i> , 2016 , 17, 46	4.5	20
33	A benchmark study on error-correction by read-pairing and tag-clustering in amplicon-based deep sequencing. <i>BMC Genomics</i> , 2016 , 17, 108	4.5	24
32	Adaptation in protein fitness landscapes is facilitated by indirect paths. <i>ELife</i> , 2016 , 5,	8.9	88
31	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Lecture Notes in Computer Science</i> , 2016 , 164-175	0.9	1
30	High-throughput identification of protein mutant stability computed from a double mutant fitness landscape. <i>Protein Science</i> , 2016 , 25, 530-9	6.3	11
29	Applications of High-Fidelity Sequencing Protocol to RNA Viruses 2016 , 85-104		
28	High-resolution genetic profile of viral genomes: why it matters. <i>Current Opinion in Virology</i> , 2015 , 14, 62-70	7.5	10
27	Functional Constraint Profiling of a Viral Protein Reveals Discordance of Evolutionary Conservation and Functionality. <i>PLoS Genetics</i> , 2015 , 11, e1005310	6	35
26	Limiting Cholesterol Biosynthetic Flux Spontaneously Engages Type I IFN Signaling. <i>Cell</i> , 2015 , 163, 1716-1722	5.2	203
25	Chromosomal DNA deletion confers phage resistance to <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2014 , 4, 4738	4.9	60
24	Modelling clinical data shows active tissue concentration of daclatasvir is 10-fold lower than its plasma concentration. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 724-7	5.1	10
23	A comprehensive biophysical description of pairwise epistasis throughout an entire protein domain. <i>Current Biology</i> , 2014 , 24, 2643-51	6.3	165
22	Short communication: HIV-1 gag genetic variation in a single acutely infected participant defined by high-resolution deep sequencing. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, 806-11	1.6	2

21	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. <i>Scientific Reports</i> , 2014 , 4, 4942	4.9	113
20	RIOK3 is an adaptor protein required for IRF3-mediated antiviral type I interferon production. <i>Journal of Virology</i> , 2014 , 88, 7987-97	6.6	24
19	High-throughput identification of loss-of-function mutations for anti-interferon activity in the influenza A virus NS segment. <i>Journal of Virology</i> , 2014 , 88, 10157-64	6.6	26
18	VGA: A method for viral quasispecies assembly from ultra-deep sequencing data 2014 ,		1
17	Accurate viral population assembly from ultra-deep sequencing data. <i>Bioinformatics</i> , 2014 , 30, i329-37	7.2	42
16	A quantitative high-resolution genetic profile rapidly identifies sequence determinants of hepatitis C viral fitness and drug sensitivity. <i>PLoS Pathogens</i> , 2014 , 10, e1004064	7.6	51
15	A comprehensive functional map of the hepatitis C virus genome provides a resource for probing viral proteins. <i>MBio</i> , 2014 , 5, e01469-14	7.8	13
14	High-throughput profiling of point mutations across the HIV-1 genome. <i>Retrovirology</i> , 2014 , 11, 124	3.6	24
13	Kaposi's sarcoma-associated herpesvirus ORF18 and ORF30 are essential for late gene expression during lytic replication. <i>Journal of Virology</i> , 2014 , 88, 11369-82	6.6	31
12	HIV-1 quasispecies delineation by tag linkage deep sequencing. <i>PLoS ONE</i> , 2014 , 9, e97505	3.7	21
11	Systematic identification of H274Y compensatory mutations in influenza A virus neuraminidase by high-throughput screening. <i>Journal of Virology</i> , 2013 , 87, 1193-9	6.6	54
10	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010 , 96, 308-15	4.3	4
9	Dynamics of B-Cell Repertoires and Emergence of Cross-Reactive Responses in COVID-19 Patients with Different Disease Severity. <i>SSRN Electronic Journal</i> ,	1	1
8	Influenza H3 and H1 hemagglutinins have different genetic barriers for resistance to broadly neutralizing stem antibodies		1
7	Adaptive potential of a drug-targeted viral protein as a function of environmental stress		1
6	A highly conserved cryptic epitope in the receptor-binding domains of SARS-CoV-2 and SARS-CoV		32
5	Potent SARS-CoV-2 neutralizing antibodies selected from a human antibody library constructed decades ago		6
4	Deep mutational scanning of hemagglutinin helps predict evolutionary fates of human H3N2 influenza variants		4

3	Human organoid systems reveal in vitro correlates of fitness for SARS-CoV-2 B.1.1.7	7
2	Human airway cells prevent SARS-CoV-2 multibasic cleavage site cell culture adaptation	4
1	Antigenic evolution of human influenza H3N2 neuraminidase is constrained by charge balancing	1