

Nicholas C Wu

List of Publications by Year in descending order

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96
papers

9,651
citations

81900
39
h-index

49909
87
g-index

133
all docs

133
docs citations

133
times ranked

15342
citing authors

#	ARTICLE	IF	CITATIONS
1	A highly conserved cryptic epitope in the receptor binding domains of SARS-CoV-2 and SARS-CoV. Science, 2020, 368, 630-633.	12.6	1,379
2	Isolation of potent SARS-CoV-2 neutralizing antibodies and protection from disease in a small animal model. Science, 2020, 369, 956-963.	12.6	1,287
3	Structural basis of a shared antibody response to SARS-CoV-2. Science, 2020, 369, 1119-1123.	12.6	536
4	Cross-reactive Antibody Response between SARS-CoV-2 and SARS-CoV Infections. Cell Reports, 2020, 31, 107725.	6.4	353
5	Limiting Cholesterol Biosynthetic Flux Spontaneously Engages Type I IFN Signaling. Cell, 2015, 163, 1716-1729.	28.9	322
6	Serological assays for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), March 2020. Eurosurveillance, 2020, 25, .	7.0	309
7	Structural and functional ramifications of antigenic drift in recent SARS-CoV-2 variants. Science, 2021, 373, 818-823.	12.6	309
8	A Therapeutic Non-self-reactive SARS-CoV-2 Antibody Protects from Lung Pathology in a COVID-19 Hamster Model. Cell, 2020, 183, 1058-1069.e19.	28.9	305
9	Structure-guided multivalent nanobodies block SARS-CoV-2 infection and suppress mutational escape. Science, 2021, 371, .	12.6	304
10	A Comprehensive Biophysical Description of Pairwise Epistasis throughout an Entire Protein Domain. Current Biology, 2014, 24, 2643-2651.	3.9	281
11	A Broadly Neutralizing Antibody Targets the Dynamic HIV Envelope Trimer Apex via a Long, Rigidified, and Anionic I ² -Hairpin Structure. Immunity, 2017, 46, 690-702.	14.3	216
12	A structural explanation for the low effectiveness of the seasonal influenza H3N2 vaccine. PLoS Pathogens, 2017, 13, e1006682.	4.7	188
13	Cross-Neutralization of a SARS-CoV-2 Antibody to a Functionally Conserved Site Is Mediated by Avidity. Immunity, 2020, 53, 1272-1280.e5.	14.3	185
14	Adaptation in protein fitness landscapes is facilitated by indirect paths. ELife, 2016, 5, .	6.0	184
15	Recognition of the SARS-CoV-2 receptor binding domain by neutralizing antibodies. Biochemical and Biophysical Research Communications, 2021, 538, 192-203.	2.1	165
16	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.	7.1	156
17	An Alternative Binding Mode of IGHV3-53 Antibodies to the SARS-CoV-2 Receptor Binding Domain. Cell Reports, 2020, 33, 108274.	6.4	152
18	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. Scientific Reports, 2014, 4, 4942.	3.3	147

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19	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.	4.2	133
20	Antibody 27F3 Broadly Targets Influenza A Group 1 and 2 Hemagglutinins through a Further Variation in VH1-69 Antibody Orientation on the HA Stem. <i>Cell Reports</i> , 2017, 20, 2935-2943.	6.4	103
21	Chromosomal DNA deletion confers phage resistance to <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2014, 4, 4738.	3.3	84
22	Structural insights into the design of novel anti-influenza therapies. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 115-121.	8.2	81
23	Influenza Hemagglutinin Structures and Antibody Recognition. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020, 10, a038778.	6.2	79
24	Bispecific antibodies targeting distinct regions of the spike protein potentially neutralize SARS-CoV-2 variants of concern. <i>Science Translational Medicine</i> , 2021, 13, eabj5413.	12.4	79
25	Human airway cells prevent SARS-CoV-2 multibasic cleavage site cell culture adaptation. <i>ELife</i> , 2021, 10, .	6.0	77
26	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.	4.0	67
27	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.	4.7	66
28	Genome-wide identification of interferon-sensitive mutations enables influenza vaccine design. <i>Science</i> , 2018, 359, 290-296.	12.6	64
29	The in vivo ISGylome links ISG15 to metabolic pathways and autophagy upon <i>Listeria monocytogenes</i> infection. <i>Nature Communications</i> , 2019, 10, 5383.	12.8	63
30	Systematic Identification of H274Y Compensatory Mutations in Influenza A Virus Neuraminidase by High-Throughput Screening. <i>Journal of Virology</i> , 2013, 87, 1193-1199.	3.4	61
31	Diversity of Functionally Permissive Sequences in the Receptor-Binding Site of Influenza Hemagglutinin. <i>Cell Host and Microbe</i> , 2017, 21, 742-753.e8.	11.0	59
32	A complex epistatic network limits the mutational reversibility in the influenza hemagglutinin receptor-binding site. <i>Nature Communications</i> , 2018, 9, 1264.	12.8	58
33	In vitro evolution of an influenza broadly neutralizing antibody is modulated by hemagglutinin receptor specificity. <i>Nature Communications</i> , 2017, 8, 15371.	12.8	55
34	A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody. <i>PLoS Pathogens</i> , 2020, 16, e1009089.	4.7	55
35	Different genetic barriers for resistance to HA stem antibodies in influenza H3 and H1 viruses. <i>Science</i> , 2020, 368, 1335-1340.	12.6	51
36	Functional Constraint Profiling of a Viral Protein Reveals Discordance of Evolutionary Conservation and Functionality. <i>PLoS Genetics</i> , 2015, 11, e1005310.	3.5	50

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37	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.	11.0	49
38	Accurate viral population assembly from ultra-deep sequencing data. <i>Bioinformatics</i> , 2014, 30, i329-i337.	4.1	48
39	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.	2.2	48
40	RIOK3 Is an Adaptor Protein Required for IRF3-Mediated Antiviral Type I Interferon Production. <i>Journal of Virology</i> , 2014, 88, 7987-7997.	3.4	46
41	Bacterial glycosyltransferase-mediated cell-surface chemoenzymatic glycan modification. <i>Nature Communications</i> , 2019, 10, 1799.	12.8	46
42	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.	6.4	46
43	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.	11.0	45
44	Sequence signatures of two public antibody clonotypes that bind SARS-CoV-2 receptor binding domain. <i>Nature Communications</i> , 2021, 12, 3815.	12.8	44
45	A large-scale systematic survey reveals recurring molecular features of public antibody responses to SARS-CoV-2. <i>Immunity</i> , 2022, 55, 1105-1117.e4.	14.3	44
46	Structure-Activity Relationships in Metal-Binding Pharmacophores for Influenza Endonuclease. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 10206-10217.	6.4	42
47	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.	11.0	42
48	Kaposi's Sarcoma-Associated Herpesvirus ORF18 and ORF30 Are Essential for Late Gene Expression during Lytic Replication. <i>Journal of Virology</i> , 2014, 88, 11369-11382.	3.4	40
49	Major antigenic site B of human influenza H3N2 viruses has an evolving local fitness landscape. <i>Nature Communications</i> , 2020, 11, 1233.	12.8	40
50	High-throughput profiling of point mutations across the HIV-1 genome. <i>Retrovirology</i> , 2014, 11, 124.	2.0	35
51	Structural Biology of Influenza Hemagglutinin: An Amaranthine Adventure. <i>Viruses</i> , 2020, 12, 1053.	3.3	35
52	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
53	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, 10157-10164.	3.4	33
54	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.	7.1	33

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55	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.	11.0	32
56	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.	7.1	29
57	COVID-19 vaccines: Knowing the unknown. <i>European Journal of Immunology</i> , 2020, 50, 939-943.	2.9	28
58	A benchmark study on error-correction by read-pairing and tag-clustering in amplicon-based deep sequencing. <i>BMC Genomics</i> , 2016, 17, 108.	2.8	27
59	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020, 21, 71.	8.8	26
60	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.	7.1	25
61	HIV-1 Quasispecies Delineation by Tag Linkage Deep Sequencing. <i>PLoS ONE</i> , 2014, 9, e97505.	2.5	25
62	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.	2.8	24
63	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.	7.1	23
64	A cross-neutralizing antibody between HIV-1 and influenza virus. <i>PLoS Pathogens</i> , 2021, 17, e1009407.	4.7	23
65	MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. <i>BMC Genomics</i> , 2019, 20, 423.	2.8	22
66	Identification of Antibodies Targeting the H3N2 Hemagglutinin Receptor Binding Site following Vaccination of Humans. <i>Cell Reports</i> , 2019, 29, 4460-4470.e8.	6.4	22
67	A high-affinity antibody against the CSP N-terminal domain lacks <i>Plasmodium falciparum</i> inhibitory activity. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	21
68	Diverse immunoglobulin gene usage and convergent epitope targeting in neutralizing antibody responses to SARS-CoV-2. <i>Cell Reports</i> , 2021, 35, 109109.	6.4	21
69	Antigenic evolution of human influenza H3N2 neuraminidase is constrained by charge balancing. <i>ELife</i> , 2021, 10, .	6.0	21
70	Clinical Correlations of Transcriptional Profile in Patients Infected With Avian Influenza H7N9 Virus. <i>Journal of Infectious Diseases</i> , 2018, 218, 1238-1248.	4.0	18
71	A Comprehensive Functional Map of the Hepatitis C Virus Genome Provides a Resource for Probing Viral Proteins. <i>MBio</i> , 2014, 5, e01469-14.	4.1	16
72	Convergent Evolution in Breadth of Two VH6-1-Encoded Influenza Antibody Clonotypes from a Single Donor. <i>Cell Host and Microbe</i> , 2020, 28, 434-444.e4.	11.0	16

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73	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.	1.6	14
74	Neutralizing Antibodies to SARS-CoV-2 Selected from a Human Antibody Library Constructed Decades Ago. <i>Advanced Science</i> , 2022, 9, e2102181.	11.2	14
75	High-resolution genetic profile of viral genomes: why it matters. <i>Current Opinion in Virology</i> , 2015, 14, 62-70.	5.4	13
76	High-throughput identification of protein mutant stability computed from a double mutant fitness landscape. <i>Protein Science</i> , 2016, 25, 530-539.	7.6	13
77	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, 724-727.	3.0	11
78	Annotating Protein Functional Residues by Coupling High-Throughput Fitness Profile and Homologous-Structure Analysis. <i>MBio</i> , 2016, 7, .	4.1	11
79	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.	7.1	11
80	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.	2.9	7
81	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.	7.1	6
82	Quantifying perinatal transmission of Hepatitis B viral quasispecies by tag linkage deep sequencing. <i>Scientific Reports</i> , 2017, 7, 10168.	3.3	6
83	Development of a versatile, target-oriented tiling microarray assay for measuring allele-specific gene expression. <i>Genomics</i> , 2010, 96, 308-315.	2.9	4
84	VGA: A method for viral quasispecies assembly from ultra-deep sequencing data. , 2014, , .		3
85	Interactions between Influenza A Virus Nucleoprotein and Gene Segment Untranslated Regions Facilitate Selective Modulation of Viral Gene Expression. <i>Journal of Virology</i> , 2022, 96, e0020522.	3.4	3
86	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, 806-811.	1.1	2
87	Quantifying the Evolutionary Constraints and Potential of Hepatitis C Virus NS5A Protein. <i>MSystems</i> , 2021, 6, .	3.8	2
88	Application of Deep Mutational Scanning in Hepatitis C Virus. <i>Methods in Molecular Biology</i> , 2019, 1911, 183-190.	0.9	2
89	Dynamics of B-Cell Repertoires and Emergence of Cross-Reactive Responses in COVID-19 Patients with Different Disease Severity. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
90	Neutralizing Antibody Response to Sarbecovirus Is Delayed in Sequential Heterologous Immunization. <i>Viruses</i> , 2022, 14, 1382.	3.3	2

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91	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. Lecture Notes in Computer Science, 2016, , 164-175.	1.3	1
92	Reconstruction of influenza a virus variants from PacBio reads. , 2014, , .		0
93	2SNV: Quasispecies reconstruction from PacBio reads. , 2015, , .		0
94	Deception through Mimicry: A Cellular Antiviral Strategy. Cell, 2018, 175, 1728-1729.	28.9	0
95	Novel Rigid Glycomimetics to Inhibit Influenza Infection. FASEB Journal, 2019, 33, .	0.5	0
96	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0