Yi Shi

List of Publications by Year in descending order

107 papers	7,497 citations	76326 40 h-index	62596 80 g-index
116 all docs	116 docs citations	116 times ranked	13030 citing authors

#	Article	IF	Citations
1	Cryo-EM structures of MERS-CoV and SARS-CoV spike glycoproteins reveal the dynamic receptor binding domains. Nature Communications, 2017, 8, 15092.	12.8	649
2	Structures of the Zika Virus Envelope Protein and Its Complex with a Flavivirus Broadly Protective Antibody. Cell Host and Microbe, 2016, 19, 696-704.	11.0	426
3	Both Boceprevir and GC376 efficaciously inhibit SARS-CoV-2 by targeting its main protease. Nature Communications, 2020, 11, 4417.	12.8	394
4	SARS-CoV-2 501Y.V2 variants lack higher infectivity but do have immune escape. Cell, 2021, 184, 2362-2371.e9.	28.9	332
5	Single-Cell Sequencing of Peripheral Mononuclear Cells Reveals Distinct Immune Response Landscapes of COVID-19 and Influenza Patients. Immunity, 2020, 53, 685-696.e3.	14.3	299
6	Bat-derived influenza-like viruses H17N10 and H18N11. Trends in Microbiology, 2014, 22, 183-191.	7.7	270
7	ORF3a of the COVID-19 virus SARS-CoV-2 blocks HOPS complex-mediated assembly of the SNARE complex required for autolysosome formation. Developmental Cell, 2021, 56, 427-442.e5.	7.0	250
8	Structures and Receptor Binding of Hemagglutinins from Human-Infecting H7N9 Influenza Viruses. Science, 2013, 342, 243-247.	12.6	237
9	Ebola Viral Glycoprotein Bound to Its Endosomal Receptor Niemann-Pick C1. Cell, 2016, 164, 258-268.	28.9	226
10	Structural and Biochemical Characterization of the nsp12-nsp7-nsp8 Core Polymerase Complex from SARS-CoV-2. Cell Reports, 2020, 31, 107774.	6.4	216
11	Enabling the 'host jump': structural determinants of receptor-binding specificity in influenza A viruses. Nature Reviews Microbiology, 2014, 12, 822-831.	28.6	213
12	Molecular determinants of human neutralizing antibodies isolated from a patient infected with Zika virus. Science Translational Medicine, 2016, 8, 369ra179.	12.4	194
13	An unexpected N-terminal loop in PD-1 dominates binding by nivolumab. Nature Communications, 2017, 8, 14369.	12.8	192
14	Zika virus NS1 structure reveals diversity of electrostatic surfaces among flaviviruses. Nature Structural and Molecular Biology, 2016, 23, 456-458.	8.2	165
15	Contribution of intertwined loop to membrane association revealed by Zika virus fullâ€length <scp>NS</scp>1 structure. EMBO Journal, 2016, 35, 2170-2178.	7.8	126
16	A potent broad-spectrum protective human monoclonal antibody crosslinking two haemagglutinin monomers of influenza A virus. Nature Communications, 2015, 6, 7708.	12.8	124
17	Structural basis of anti-PD-L1 monoclonal antibody avelumab for tumor therapy. Cell Research, 2017, 27, 151-153.	12.0	116
18	The crystal structure of Zika virus <scp>NS</scp> 5 reveals conserved drug targets. EMBO Journal, 2017, 36, 919-933.	7.8	107

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19	Structural Biology of the Zika Virus. Trends in Biochemical Sciences, 2017, 42, 443-456.	7.5	98
20	Structures of phlebovirus glycoprotein Gn and identification of a neutralizing antibody epitope. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7564-E7573.	7.1	98
21	Crystal Structure of the Capsid Protein from Zika Virus. Journal of Molecular Biology, 2018, 430, 948-962.	4.2	98
22	Comparative study on virus shedding patterns in nasopharyngeal and fecal specimens of COVID-19 patients. Science China Life Sciences, 2021, 64, 486-488.	4.9	95
23	Crystal structure of the swine-origin A (H1N1)-2009 influenza A virus hemagglutinin (HA) reveals similar antigenicity to that of the 1918 pandemic virus. Protein and Cell, 2010, 1, 459-467.	11.0	94
24	Dominant subtype switch in avian influenza viruses during 2016â€“2019 in China. Nature Communications, 2020, 11, 5909.	12.8	93
25	An Open Receptor-Binding Cavity of Hemagglutinin-Esterase-Fusion Glycoprotein from Newly-Identified Influenza D Virus: Basis for Its Broad Cell Tropism. PLoS Pathogens, 2016, 12, e1005411.	4.7	92
26	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. PLoS Pathogens, 2016, 12, e1005883.	4.7	92
27	Azithromycin Protects against Zika Virus Infection by Upregulating Virus-Induced Type I and III Interferon Responses. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	83
28	Integrated gut virome and bacteriome dynamics in COVID-19 patients. Gut Microbes, 2021, 13, 1-21.	9.8	81
29	Inference of person-to-person transmission of COVID-19 reveals hidden super-spreading events during the early outbreak phase. Nature Communications, 2020, 11, 5006.	12.8	80
30	Longitudinal analysis of antibody dynamics in COVID-19 convalescents reveals neutralizing responses up to 16 months after infection. Nature Microbiology, 2022, 7, 423-433.	13.3	78
31	Human Neonatal Fc Receptor Is the Cellular Uncoating Receptor for Enterovirus B. Cell, 2019, 177, 1553-1565.e16.	28.9	69
32	A broadly protective antibody that targets the flavivirus NS1 protein. Science, 2021, 371, 190-194.	12.6	66
33	Remarkably similar CTLA-4 binding properties of therapeutic ipilimumab and tremelimumab antibodies. Oncotarget, 2017, 8, 67129-67139.	1.8	65
34	Alternate binding modes of anti-CRISPR viral suppressors AcrF1/2 to Csy surveillance complex revealed by cryo-EM structures. Cell Research, 2017, 27, 853-864.	12.0	64
35	Structural insight into RNA synthesis by influenza D polymerase. Nature Microbiology, 2019, 4, 1750-1759.	13.3	58
36	Structural basis of nectin-1 recognition by pseudorabies virus glycoprotein D. PLoS Pathogens, 2017, 13, e1006314.	4.7	55

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37	Disrupting LILRB4/APOE Interaction by an Efficacious Humanized Antibody Reverses T-cell Suppression and Blocks AML Development. Cancer Immunology Research, 2019, 7, 1244-1257.	3.4	51
38	Structural insight into arenavirus replication machinery. Nature, 2020, 579, 615-619.	27.8	51
39	Structural Basis of SARS-CoV-2 Polymerase Inhibition by Favipiravir. Innovation(China), 2021, 2, 100080.	9.1	51
40	Double Lock of a Human Neutralizing and Protective Monoclonal Antibody Targeting the Yellow Fever Virus Envelope. Cell Reports, 2019, 26, 438-446.e5.	6.4	49
41	Potent neutralizing monoclonal antibodies against Ebola virus infection. Scientific Reports, 2016, 6, 25856.	3.3	46
42	Adaptation of avian influenza A (H6N1) virus from avian to human receptorâ€binding preference. EMBO Journal, 2015, 34, 1661-1673.	7.8	44
43	Crystal clear: visualizing the intervention mechanism of the PD-1/PD-L1 interaction by two cancer therapeutic monoclonal antibodies. Protein and Cell, 2016, 7, 866-877.	11.0	44
44	A novel virtual screening procedure identifies Pralatrexate as inhibitor of SARS-CoV-2 RdRp and it reduces viral replication in vitro. PLoS Computational Biology, 2020, 16, e1008489.	3.2	42
45	Selective inhibition of Ebola entry with selective estrogen receptor modulators by disrupting the endolysosomal calcium. Scientific Reports, 2017, 7, 41226.	3.3	41
46	Structureâ€"function analysis of neutralizing antibodies to H7N9 influenza from naturally infected humans. Nature Microbiology, 2019, 4, 306-315.	13.3	41
47	Antibiotic resistance gene reservoir in live poultry markets. Journal of Infection, 2019, 78, 445-453.	3.3	40
48	The effect of whey protein on viral infection and replication of SARS-CoV-2 and pangolin coronavirus in vitro. Signal Transduction and Targeted Therapy, 2020, 5, 275.	17.1	40
49	Expert consensus on acute exacerbation of chronic obstructive pulmonary disease in the People's Republic of China. International Journal of COPD, 2014, 9, 381.	2.3	39
50	Neutralization mechanism of human monoclonal antibodies against Rift Valley fever virus. Nature Microbiology, 2019, 4, 1231-1241.	13.3	39
51	Structures of the fourÂIg-like domain LILRB2 and the four-domain LILRB1 and HLA-G1 complex. Cellular and Molecular Immunology, 2020, 17, 966-975.	10.5	38
52	Peptide-dependent Conformational Fluctuation Determines the Stability of the Human Leukocyte Antigen Class I Complex. Journal of Biological Chemistry, 2014, 289, 24680-24690.	3.4	37
53	Pediatric Drug Nitazoxanide: A Potential Choice for Control of Zika. Open Forum Infectious Diseases, 2017, 4, ofx009.	0.9	35
54	Structure and receptor-binding properties of an airborne transmissible avian influenza A virus hemagglutinin H5 (VN1203mut). Protein and Cell, 2013, 4, 502-511.	11.0	34

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55	Two classes of protective antibodies against Pseudorabies virus variant glycoprotein B: Implications for vaccine design. PLoS Pathogens, 2017, 13, e1006777.	4.7	34
56	Mycobacterium tuberculosis Mce2E suppresses the macrophage innate immune response and promotes epithelial cell proliferation. Cellular and Molecular Immunology, 2019, 16, 380-391.	10.5	32
57	Downregulated miR-451a as a feature of the plasma cfRNA landscape reveals regulatory networks of IL-6/IL-6R-associated cytokine storms in COVID-19 patients. Cellular and Molecular Immunology, 2021, 18, 1064-1066.	10.5	31
58	Emerging HxNy Influenza A Viruses. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a038406.	6.2	30
59	Avian influenza A (H7N9) virus: from low pathogenic to highly pathogenic. Frontiers of Medicine, 2021, 15, 507-527.	3.4	30
60	Structures of human-infecting Thogotovirus fusogens support a common ancestor with insect baculovirus. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8905-E8912.	7.1	29
61	Structural basis for preferential avian receptor binding by the human-infecting H10N8 avian influenza virus. Nature Communications, 2015, 6, 5600.	12.8	28
62	An autoimmune disease variant of IgG1 modulates B cell activation and differentiation. Science, 2018, 362, 700-705.	12.6	28
63	Structural and functional analysis of an anchorless fibronectin-binding protein FBPS from Gram-positive bacterium Streptococcus suis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13869-13874.	7.1	27
64	Avian-to-Human Receptor-Binding Adaptation of Avian H7N9 Influenza Virus Hemagglutinin. Cell Reports, 2019, 29, 2217-2228.e5.	6.4	27
65	Plasticity of human CD8Î±Î± binding to peptideâ€“HLA-A*2402. Molecular Immunology, 2011, 48, 2198-2202.	2.2	26
66	Tracing the origins of SARS-CoV-2: lessons learned from the past. Cell Research, 2021, 31, 1139-1141.	12.0	25
67	Mycobacterium tuberculosis protein kinase G acts as an unusual ubiquitinating enzyme to impair host immunity. EMBO Reports, 2021, 22, e52175.	4.5	23
68	Structural insight into multistage inhibition of CRISPR-Cas12a by AcrVA4. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18928-18936.	7.1	21
69	Structural basis for the inhibition of the SARS-CoV-2 main protease by the anti-HCV drug narlaprevir. Signal Transduction and Targeted Therapy, 2021, 6, 51.	17.1	20
70	Cryo-EM structures of Lassa and Machupo virus polymerases complexed with cognate regulatory Z proteins identify targets for antivirals. Nature Microbiology, 2021, 6, 921-931.	13.3	20
71	Effects of a Single Escape Mutation on T Cell and HIV-1 Co-adaptation. Cell Reports, 2016, 15, 2279-2291.	6.4	19
72	Novel cyclo-peptides inhibit Ebola pseudotyped virus entry by targeting primed GP protein. Antiviral Research, 2018, 155, 1-11.	4.1	18

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73	Landscapes and dynamic diversifications of B-cell receptor repertoires in COVID-19 patients. Human Immunology, 2022, 83, 119-129.	2.4	17
74	An adenovirus serotype 2-vectored ebolavirus vaccine generates robust antibody and cell-mediated immune responses in mice and rhesus macaques. Emerging Microbes and Infections, 2018, 7, 1-12.	6.5	16
75	Superimposed Epitopes Restricted by the Same HLA Molecule Drive Distinct HIV-Specific CD8+ T Cell Repertoires. Journal of Immunology, 2014, 193, 77-84.	0.8	15
76	Conserved VÎ´1 Binding Geometry in a Setting of Locus-Disparate pHLA Recognition by Î´/Î±Î² T Cell Receptors (TCRs): Insight into Recognition of HIV Peptides by TCRs. Journal of Virology, 2017, 91, .	3.4	15
77	Light chain modulates heavy chain conformation to change protection profile of monoclonal antibodies against influenza A viruses. Cell Discovery, 2019, 5, 21.	6.7	15
78	Special features of the 2009 pandemic swine-origin influenza A H1N1 hemagglutinin and neuraminidase. Science Bulletin, 2011, 56, 1747-1752.	1.7	14
79	Crystal structures of the two membrane-proximal Ig-like domains (D3D4) of LILRB1/B2: alternative models for their involvement in peptide-HLA binding. Protein and Cell, 2013, 4, 761-770.	11.0	14
80	NÎ±-Terminal Acetylation for T Cell Recognition: Molecular Basis of MHC Class Iâ€“Restricted NÎ±-Acetylpeptide Presentation. Journal of Immunology, 2014, 192, 5509-5519.	0.8	14
81	Structures of Zika Virus E & NS1: Relations with Virus Infection and Host Immune Responses. Advances in Experimental Medicine and Biology, 2018, 1062, 77-87.	1.6	13
82	CASCIRE surveillance network and work on avian influenza viruses. Science China Life Sciences, 2017, 60, 1386-1391.	4.9	12
83	Structure-Based Modification of an Anti-neuraminidase Human Antibody Restores Protection Efficacy against the Drifted Influenza Virus. MBio, 2020, 11, .	4.1	12
84	Ribavirin is effective against drug-resistant H7N9 influenza virus infections. Protein and Cell, 2016, 7, 611-614.	11.0	11
85	Crystal structure of the C-terminal fragment of NS1 protein from yellow fever virus. Science China Life Sciences, 2017, 60, 1403-1406.	4.9	11
86	Cryo-EM structure of the varicella-zoster virus A-capsid. Nature Communications, 2020, 11, 4795.	12.8	10
87	The Genome Resequencing of TCR Loci inGallus gallusRevealed Their Distinct Evolutionary Features in Avians. ImmunoHorizons, 2020, 4, 33-46.	1.8	10
88	In vitro assembly of Ebola virus nucleocapsid-like complex expressed in E. coli. Protein and Cell, 2016, 7, 888-898.	11.0	9
89	New Virus, New Challenge. Innovation(China), 2020, 1, 100005.	9.1	9
90	The virulence of Legionella pneumophila is positively correlated with its ability to stimulate NF-ÎºB activation. Future Microbiology, 2018, 13, 1247-1259.	2.0	5

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91	Salt bridge-forming residues positioned over viral peptides presented by MHC class I impacts T-cell recognition in a binding-dependent manner. Molecular Immunology, 2019, 112, 274-282.	2.2	5
92	Intact Glycopeptide Analysis of Influenza A/H1N1/09 Neuraminidase Revealing the Effects of Host and Glycosite Location on Siteâ€Specific Glycan Structures. Proteomics, 2019, 19, 1800202.	2.2	5
93	Identification of antibiotic resistance genes and associated mobile genetic elements in permafrost. Science China Life Sciences, 2021, 64, 2210-2213.	4.9	5
94	Analysis of SARS-CoV-2 variants B.1.617: host tropism, proteolytic activation, cellâ€“cell fusion, and neutralization sensitivity. Emerging Microbes and Infections, 2022, 11, 1024-1036.	6.5	5
95	Current knowledge of COVID-19: Advances, challenges and future perspectives. Biosafety and Health, 2021, 3, 202-209.	2.7	4
96	Meclizine Inhibits Pseudorabies Virus Replication by Interfering With Virus Entry and Release. Frontiers in Microbiology, 2021, 12, 795593.	3.5	4
97	The S190R mutation in the hemagglutinin protein of pandemic H1N1 2009 influenza virus increased its pathogenicity in mice. Science China Life Sciences, 2018, 61, 836-843.	4.9	3
98	Third Tofo Advanced Study Week on Emerging and Re-emerging Viruses, 2018. Antiviral Research, 2019, 162, 142-150.	4.1	3
99	Legionella pneumophila Risk from Cooling Tower Systems in China. Applied and Environmental Microbiology, 2022, 88, AEM0192121.	3.1	3
100	Discs large homolog 1 regulates B-cell proliferation and antibody production. International Immunology, 2019, 31, 759-770.	4.0	2
101	Diversity and abundance of resistome in rhizosphere soil. Science China Life Sciences, 2020, 63, 1946-1949.	4.9	1
102	Significance of electron microscopic examination in the diagnosis of pulmonary neoplasms. Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research, 1995, 7, 61-65.	2.2	0
103	Linking innate and adaptive immunity. Science Bulletin, 2012, 57, 4100-4102.	1.7	0
104	Title is missing!. , 2020, 16, e1008489.		0
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107	Title is missing!. , 2020, 16, e1008489.		0