

# Hao Song

## List of Publications by Year in descending order

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45  
papers

13,474  
citations

212478

28  
h-index

252626

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docs citations

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times ranked

28345  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of differential receptor usage for naturally occurring CD55-binding and -nonbinding coxsackievirus B3 strains. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	2
2	Target-Based Virtual Screening and LC/MS-Guided Isolation Procedure for Identifying Phloroglucinol-Terpenoid Inhibitors of SARS-CoV-2. Journal of Natural Products, 2022, 85, 327-336.	1.5	13
3	The antigenicity of SARS-CoV-2 Delta variants aggregated 10 high-frequency mutations in RBD has not changed sufficiently to replace the current vaccine strain. Signal Transduction and Targeted Therapy, 2022, 7, 18.	7.1	9
4	A broadly protective antibody that targets the flavivirus NS1 protein. Science, 2021, 371, 190-194.	6.0	66
5	Structural basis for the inhibition of the SARS-CoV-2 main protease by the anti-HCV drug nardaprevir. Signal Transduction and Targeted Therapy, 2021, 6, 51.	7.1	20
6	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. Cell, 2021, 184, 4380-4391.e14.	13.5	261
7	Structural basis of malarial parasite RIFIN-mediated immune escape against LAIR1. Cell Reports, 2021, 36, 109600.	2.9	7
8	Structures of the four-Ålg-like domain LILRB2 and the four-domain LILRB1 and HLA-G1 complex. Cellular and Molecular Immunology, 2020, 17, 966-975.	4.8	38
9	Broad host range of SARS-CoV-2 and the molecular basis for SARS-CoV-2 binding to cat ACE2. Cell Discovery, 2020, 6, 68.	3.1	132
10	Molecular basis of Coxsackievirus A10 entry using the two-in-one attachment and uncoating receptor KRM1. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18711-18718.	3.3	18
11	Molecular basis of EphA2 recognition by gHgL from gammaherpesviruses. Nature Communications, 2020, 11, 5964.	5.8	22
12	Structure-Based Modification of an Anti-neuraminidase Human Antibody Restores Protection Efficacy against the Drifted Influenza Virus. MBio, 2020, 11, .	1.8	12
13	Both Boceprevir and GC376 efficaciously inhibit SARS-CoV-2 by targeting its main protease. Nature Communications, 2020, 11, 4417.	5.8	394
14	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. Current Biology, 2020, 30, 2196-2203.e3.	1.8	480
15	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet, The, 2020, 395, 565-574.	6.3	9,430
16	Structures of the <scp>SARS</scp> â€CoVâ€2 nucleocapsid and their perspectives for drug design. EMBO Journal, 2020, 39, e105938.	3.5	198
17	Structural insight into RNA synthesis by influenza D polymerase. Nature Microbiology, 2019, 4, 1750-1759.	5.9	58
18	Disrupting LILRB4/APOE Interaction by an Efficacious Humanized Antibody Reverses T-cell Suppression and Blocks AML Development. Cancer Immunology Research, 2019, 7, 1244-1257.	1.6	51

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19	Molecular Basis of Arthritogenic Alphavirus Receptor MXRA8 Binding to Chikungunya Virus Envelope Protein. <i>Cell</i> , 2019, 177, 1714-1724.e12.	13.5	75
20	Human Neonatal Fc Receptor Is the Cellular Uncoating Receptor for Enterovirus B. <i>Cell</i> , 2019, 177, 1553-1565.e16.	13.5	69
21	Avian-to-Human Receptor-Binding Adaptation of Avian H7N9 Influenza Virus Hemagglutinin. <i>Cell Reports</i> , 2019, 29, 2217-2228.e5.	2.9	27
22	Crystal Structure of African Swine Fever Virus dUTPase Reveals a Potential Drug Target. <i>MBio</i> , 2019, 10, .	1.8	24
23	Cryo-EM Structure of the African Swine Fever Virus. <i>Cell Host and Microbe</i> , 2019, 26, 836-843.e3.	5.1	113
24	Crystal Structure of the Capsid Protein from Zika Virus. <i>Journal of Molecular Biology</i> , 2018, 430, 948-962.	2.0	98
25	Structures of Zika Virus E & NS1: Relations with Virus Infection and Host Immune Responses. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1062, 77-87.	0.8	13
26	Genomic characterizations of H4 subtype avian influenza viruses from live poultry markets in Sichuan province of China, 2014–2015. <i>Science China Life Sciences</i> , 2018, 61, 1123-1126.	2.3	12
27	Zika Virus Envelope Protein and Antibody Complexes. <i>Sub-Cellular Biochemistry</i> , 2018, 88, 147-168.	1.0	10
28	An unexpected N-terminal loop in PD-1 dominates binding by nivolumab. <i>Nature Communications</i> , 2017, 8, 14369.	5.8	192
29	The crystal structure of Zika virus NS5 reveals conserved drug targets. <i>EMBO Journal</i> , 2017, 36, 919-933.	3.5	107
30	Structure of the S1 subunit C-terminal domain from bat-derived coronavirus HKU5 spike protein. <i>Virology</i> , 2017, 507, 101-109.	1.1	13
31	Avian-to-Human Receptor-Binding Adaptation by Influenza A Virus Hemagglutinin H4. <i>Cell Reports</i> , 2017, 20, 1201-1214.	2.9	57
32	Crystal Structure of the Marburg Virus Nucleoprotein Core Domain Chaperoned by a VP35 Peptide Reveals a Conserved Drug Target for Filovirus. <i>Journal of Virology</i> , 2017, 91, .	1.5	31
33	Structural basis of anti-PD-L1 monoclonal antibody avelumab for tumor therapy. <i>Cell Research</i> , 2017, 27, 151-153.	5.7	116
34	Crystal structure of the C-terminal fragment of NS1 protein from yellow fever virus. <i>Science China Life Sciences</i> , 2017, 60, 1403-1406.	2.3	11
35	Two classes of protective antibodies against Pseudorabies virus variant glycoprotein B: Implications for vaccine design. <i>PLoS Pathogens</i> , 2017, 13, e1006777.	2.1	34
36	Contribution of intertwined loop to membrane association revealed by Zika virus NS1 structure. <i>EMBO Journal</i> , 2016, 35, 2170-2178.	3.5	126

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37	Zika virus NS1 structure reveals diversity of electrostatic surfaces among flaviviruses. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 456-458.	3.6	165
38	Structures of the Zika Virus Envelope Protein and Its Complex with a Flavivirus Broadly Protective Antibody. <i>Cell Host and Microbe</i> , 2016, 19, 696-704.	5.1	426
39	Crystal clear: visualizing the intervention mechanism of the PD-1/PD-L1 interaction by two cancer therapeutic monoclonal antibodies. <i>Protein and Cell</i> , 2016, 7, 866-877.	4.8	44
40	An Open Receptor-Binding Cavity of Hemagglutinin-Esterase-Fusion Glycoprotein from Newly-Identified Influenza D Virus: Basis for Its Broad Cell Tropism. <i>PLoS Pathogens</i> , 2016, 12, e1005411.	2.1	92
41	Microarray analysis of MicroRNA expression in peripheral blood mononuclear cells of critically ill patients with influenza A (H1N1). <i>BMC Infectious Diseases</i> , 2013, 13, 257.	1.3	66
42	Structures and Receptor Binding of Hemagglutinins from Human-Infecting H7N9 Influenza Viruses. <i>Science</i> , 2013, 342, 243-247.	6.0	237
43	Crystal structures of the two membrane-proximal Ig-like domains (D3D4) of LILRB1/B2: alternative models for their involvement in peptide-HLA binding. <i>Protein and Cell</i> , 2013, 4, 761-770.	4.8	14
44	ACVR1, a Therapeutic Target of Fibrodysplasia Ossificans Progressiva, Is Negatively Regulated by miR-148a. <i>International Journal of Molecular Sciences</i> , 2012, 13, 2063-2077.	1.8	36
45	Reply to "Nuclear Export Signal and Immunodominant CD8+T Cell Epitope in Influenza A Virus Matrix Protein 1". <i>Journal of Virology</i> , 2012, 86, 10259-10260.	1.5	1