

Zihe Rao

List of Publications by Year in descending order

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Version: 2024-02-01

146
papers

17,667
citations

34105

52
h-index

16183

124
g-index

165
all docs

165
docs citations

165
times ranked

20946
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of SARS-CoV-2 main protease in complex with protease inhibitor PF-07321332. <i>Protein and Cell</i> , 2022, 13, 689-693.	11.0	136
2	Structural basis for replicase polyprotein cleavage and substrate specificity of main protease from SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2117142119.	7.1	64
3	Structures of Omicron spike complexes and implications for neutralizing antibody development. <i>Cell Reports</i> , 2022, 39, 110770.	6.4	47
4	Antibody engineering improves neutralization activity against K417 spike mutant SARS-CoV-2 variants. <i>Cell and Bioscience</i> , 2022, 12, 63.	4.8	4
5	The Life of SARS-CoV-2 Inside Cells: Replication and Transcription Complex Assembly and Function. <i>Annual Review of Biochemistry</i> , 2022, 91, 381-401.	11.1	9
6	Cryo-EM Structure of an Extended SARS-CoV-2 Replication and Transcription Complex Reveals an Intermediate State in Cap Synthesis. <i>Cell</i> , 2021, 184, 184-193.e10.	28.9	201
7	High-throughput screening identifies established drugs as SARS-CoV-2 PLpro inhibitors. <i>Protein and Cell</i> , 2021, 12, 877-888.	11.0	95
8	Structures of Foot-and-mouth Disease Virus with neutralizing antibodies derived from recovered natural host reveal a mechanism for cross-serotype neutralization. <i>PLoS Pathogens</i> , 2021, 17, e1009507.	4.7	9
9	Cryo-EM structure of <i>Mycobacterium smegmatis</i> DyP-loaded encapsulin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	32
10	Architecture of the mycobacterial succinate dehydrogenase with a membrane-embedded Rieske FeS cluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
11	A SARS-CoV-2 neutralizing antibody with extensive Spike binding coverage and modified for optimal therapeutic outcomes. <i>Nature Communications</i> , 2021, 12, 2623.	12.8	64
12	Inhibition mechanism of SARS-CoV-2 main protease by ebiselen and its derivatives. <i>Nature Communications</i> , 2021, 12, 3061.	12.8	149
13	Structural basis for SARS-CoV-2 neutralizing antibodies with novel binding epitopes. <i>PLoS Biology</i> , 2021, 19, e3001209.	5.6	31
14	Coupling of N7-methyltransferase and 5' exoribonuclease with SARS-CoV-2 polymerase reveals mechanisms for capping and proofreading. <i>Cell</i> , 2021, 184, 3474-3485.e11.	28.9	111
15	Structural basis for recognition and regulation of arenavirus polymerase L by Z protein. <i>Nature Communications</i> , 2021, 12, 4134.	12.8	17
16	Cryo-EM structure of mycobacterial cytochrome bd reveals two oxygen access channels. <i>Nature Communications</i> , 2021, 12, 4621.	12.8	24
17	Structural biology of SARS-CoV-2 and implications for therapeutic development. <i>Nature Reviews Microbiology</i> , 2021, 19, 685-700.	28.6	259
18	Mass spectrometry reveals potential of β -lactams as SARS-CoV-2 M ^{pro} inhibitors. <i>Chemical Communications</i> , 2021, 57, 1430-1433.	4.1	35

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19	Double lock of a potent human therapeutic monoclonal antibody against SARS-CoV-2. <i>National Science Review</i> , 2021, 8, nwa297.	9.5	24
20	Remdesivir overcomes the S861 roadblock in SARS-CoV-2 polymerase elongation complex. <i>Cell Reports</i> , 2021, 37, 109882.	6.4	12
21	Dual activities of ACC synthase: Novel clues regarding the molecular evolution of <i>ACS</i> genes. <i>Science Advances</i> , 2021, 7, eabg8752.	10.3	14
22	Structure of <i>Mycobacterium tuberculosis</i> cytochrome bcc in complex with Q203 and TB47, two anti-TB drug candidates. <i>ELife</i> , 2021, 10, .	6.0	22
23	Nanometer-resolution in situ structure of the SARS-CoV-2 postfusion spike protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
24	Conformational Changes in a Macrolide Antibiotic Binding Protein From <i>Mycobacterium smegmatis</i> Upon ADP Binding. <i>Frontiers in Microbiology</i> , 2021, 12, 780954.	3.5	0
25	Structural Insight into African Swine Fever Virus dUTPase Reveals a Novel Folding Pattern in the dUTPase Family. <i>Journal of Virology</i> , 2020, 94, .	3.4	10
26	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. <i>Nature Communications</i> , 2020, 11, 38.	12.8	28
27	Architecture of a SARS-CoV-2 mini replication and transcription complex. <i>Nature Communications</i> , 2020, 11, 5874.	12.8	147
28	Structural basis for neutralization of SARS-CoV-2 and SARS-CoV by a potent therapeutic antibody. <i>Science</i> , 2020, 369, 1505-1509.	12.6	358
29	Structural basis of trehalose recycling by the ABC transporter LpqY-SugABC. <i>Science Advances</i> , 2020, 6, .	10.3	19
30	Serotype specific epitopes identified by neutralizing antibodies underpin immunogenic differences in Enterovirus B. <i>Nature Communications</i> , 2020, 11, 4419.	12.8	13
31	Structures of Echovirus 30 in complex with its receptors inform a rational prediction for enterovirus receptor usage. <i>Nature Communications</i> , 2020, 11, 4421.	12.8	18
32	Cryo-EM structure of trimeric <i>Mycobacterium smegmatis</i> succinate dehydrogenase with a membrane-anchor SdhF. <i>Nature Communications</i> , 2020, 11, 4245.	12.8	20
33	Structures of fungal and plant acetoxyacid synthases. <i>Nature</i> , 2020, 586, 317-321.	27.8	37
34	Cryo-EM snapshots of mycobacterial arabinosyltransferase complex EmbB2-AcpM2. <i>Protein and Cell</i> , 2020, 11, 505-517.	11.0	13
35	Structural basis for the inhibition of SARS-CoV-2 main protease by antineoplastic drug carmofur. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 529-532.	8.2	339
36	Structural analysis of a trimeric assembly of the mitochondrial dynamin-like GTPase Mgm1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4061-4070.	7.1	42

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37	Structure of Mpro from SARS-CoV-2 and discovery of its inhibitors. <i>Nature</i> , 2020, 582, 289-293.	27.8	3,133
38	Crystal structure of the African swine fever virus structural protein p35 reveals its role for core shell assembly. <i>Protein and Cell</i> , 2020, 11, 600-605.	11.0	9
39	Structural Basis for the Inhibition of Mycobacterial MmpL3 by NITD-349 and SPIRO. <i>Journal of Molecular Biology</i> , 2020, 432, 4426-4434.	4.2	27
40	Structures of <i>Mycobacterium tuberculosis</i> Penicillin-Binding Protein 3 in Complex with Five β -Lactam Antibiotics Reveal Mechanism of Inactivation. <i>Molecular Pharmacology</i> , 2020, 97, 287-294.	2.3	20
41	Structural basis for the broad substrate specificity of two acyl-CoA dehydrogenases FadE5 from mycobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16324-16332.	7.1	7
42	Identification of Interferon Receptor IFNAR2 As a Novel HCV Entry Factor by Using Chemical Probes. <i>ACS Chemical Biology</i> , 2020, 15, 1232-1241.	3.4	5
43	Design, Synthesis, and Evaluation of Novel Enterovirus 71 Inhibitors as Therapeutic Drug Leads for the Treatment of Human Hand, Foot, and Mouth Disease. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 1233-1244.	6.4	12
44	Architecture of the herpesvirus genome-packaging complex and implications for DNA translocation. <i>Protein and Cell</i> , 2020, 11, 339-351.	11.0	53
45	Structure of the RNA-dependent RNA polymerase from COVID-19 virus. <i>Science</i> , 2020, 368, 779-782.	12.6	1,228
46	Crystal Structure of African Swine Fever Virus pS273R Protease and Implications for Inhibitor Design. <i>Journal of Virology</i> , 2020, 94, .	3.4	28
47	Structure of severe fever with thrombocytopenia syndrome virus L protein elucidates the mechanisms of viral transcription initiation. <i>Nature Microbiology</i> , 2020, 5, 864-871.	13.3	38
48	Structures of cell wall arabinosyltransferases with the anti-tuberculosis drug ethambutol. <i>Science</i> , 2020, 368, 1211-1219.	12.6	82
49	Structure-based design of antiviral drug candidates targeting the SARS-CoV-2 main protease. <i>Science</i> , 2020, 368, 1331-1335.	12.6	1,135
50	Structures of the portal vertex reveal essential protein-protein interactions for Herpesvirus assembly and maturation. <i>Protein and Cell</i> , 2020, 11, 366-373.	11.0	33
51	Structure of African swine fever virus p15 reveals its dual role for membrane-association and DNA binding. <i>Protein and Cell</i> , 2020, 11, 606-612.	11.0	8
52	Structural Basis for RNA Replication by the SARS-CoV-2 Polymerase. <i>Cell</i> , 2020, 182, 417-428.e13.	28.9	672
53	Structural insights into G domain dimerization and pathogenic mutation of OPA1. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	25
54	Hepatitis A Virus Capsid Structure. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a031807.	6.2	18

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55	Divergent engagements between adeno-associated viruses with their cellular receptor AAVR. <i>Nature Communications</i> , 2019, 10, 3760.	12.8	52
56	Architecture of African swine fever virus and implications for viral assembly. <i>Science</i> , 2019, 366, 640-644.	12.6	252
57	Crystal structure and biochemical study on argininosuccinate lyase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 510, 116-121.	2.1	1
58	Crystal Structures of Membrane Transporter MmpL3, an Anti-TB Drug Target. <i>Cell</i> , 2019, 176, 636-648.e13.	28.9	172
59	The crystal structure of the phosphotriesterase from <i>M.Âtuberculosis</i> , another member of phosphotriesterase-like lactonase family. <i>Biochemical and Biophysical Research Communications</i> , 2019, 510, 224-229.	2.1	4
60	Delicate structural coordination of the Severe Acute Respiratory Syndrome coronavirus Nsp13 upon ATP hydrolysis. <i>Nucleic Acids Research</i> , 2019, 47, 6538-6550.	14.5	256
61	Structural basis for neutralization of hepatitis A virus informs a rational design of highly potent inhibitors. <i>PLoS Biology</i> , 2019, 17, e3000229.	5.6	12
62	Purification and characterization of the extracellular region of human receptor tyrosine kinase like orphan receptor 2 (ROR2). <i>Protein Expression and Purification</i> , 2019, 158, 74-80.	1.3	4
63	Structural analysis of molybdopterin synthases from two mycobacterial pathogens. <i>Biochemical and Biophysical Research Communications</i> , 2019, 511, 21-27.	2.1	0
64	Adeno-associated virus 2 bound to its cellular receptor AAVR. <i>Nature Microbiology</i> , 2019, 4, 675-682.	13.3	76
65	Structural basis for enzymatic photocatalysis in chlorophyll biosynthesis. <i>Nature</i> , 2019, 574, 722-725.	27.8	88
66	Double Lock of a Human Neutralizing and Protective Monoclonal Antibody Targeting the Yellow Fever Virus Envelope. <i>Cell Reports</i> , 2019, 26, 438-446.e5.	6.4	49
67	Structural Adaptations of Norovirus GII.17/13/21 Lineage through Two Distinct Evolutionary Paths. <i>Journal of Virology</i> , 2019, 93, .	3.4	16
68	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. <i>Nature Microbiology</i> , 2019, 4, 414-419.	13.3	73
69	Identification of serotonin 2A receptor as a novel HCV entry factor by a chemical biology strategy. <i>Protein and Cell</i> , 2019, 10, 178-195.	11.0	11
70	Structural characterization of the HCoV-229E fusion core. <i>Biochemical and Biophysical Research Communications</i> , 2018, 497, 705-712.	2.1	8
71	Structural basis for GTP hydrolysis and conformational change of MFN1 in mediating membrane fusion. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 233-243.	8.2	78
72	Crystal structure of the apurinic/aprimidinic endonuclease IV from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 498, 111-118.	2.1	7

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73	Pushing the resolution limit by correcting the Ewald sphere effect in single-particle Cryo-EM reconstructions. <i>Nature Communications</i> , 2018, 9, 1552.	12.8	83
74	Cryo-EM structure of a herpesvirus capsid at 3.1 Å... <i>Science</i> , 2018, 360, .	12.6	93
75	Structural basis for neutralization of Japanese encephalitis virus by two potent therapeutic antibodies. <i>Nature Microbiology</i> , 2018, 3, 287-294.	13.3	42
76	Discovery of the first macrolide antibiotic binding protein in <i>Mycobacterium tuberculosis</i> : a new antibiotic resistance drug target. <i>Protein and Cell</i> , 2018, 9, 971-975.	11.0	6
77	Structures of Coxsackievirus A10 unveil the molecular mechanisms of receptor binding and viral uncoating. <i>Nature Communications</i> , 2018, 9, 4985.	12.8	52
78	Seneca Valley virus attachment and uncoating mediated by its receptor anthrax toxin receptor 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13087-13092.	7.1	30
79	Structural properties of the peroxiredoxin AhpC2 from the hyperthermophilic eubacterium <i>Aquifex aeolicus</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2797-2805.	2.4	4
80	Crystal structure of a membrane-bound O-acyltransferase. <i>Nature</i> , 2018, 562, 286-290.	27.8	87
81	An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018, 362, .	12.6	117
82	Structure of the herpes simplex virus type 2 C-capsid with capsid-vertex-specific component. <i>Nature Communications</i> , 2018, 9, 3668.	12.8	31
83	Structural basis for signal recognition and transduction by platelet-activating-factor receptor. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 488-495.	8.2	58
84	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. <i>MBio</i> , 2018, 9, .	4.1	26
85	Structural and Biochemical Characterization of Endoribonuclease Nsp15 Encoded by Middle East Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2018, 92, .	3.4	97
86	Structural Biology and Synchrotron Radiation. , 2018, , 81-104.		0
87	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 770-775.	7.1	42
88	Oncoprotein <sc>CIP</sc> 2A is stabilized via interaction with tumor suppressor <sc>PP</sc> 2A/B56. <i>EMBO Reports</i> , 2017, 18, 437-450.	4.5	84
89	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017, 8, 14.	12.8	117
90	The binding of a monoclonal antibody to the apical region of SCARB2 blocks EV71 infection. <i>Protein and Cell</i> , 2017, 8, 590-600.	11.0	18

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91	Structural Insight into Nucleoprotein Conformation Change Chaperoned by VP35 Peptide in Marburg Virus. <i>Journal of Virology</i> , 2017, 91, .	3.4	27
92	Crystal structure of l -glutamate N -acetyltransferase ArgA from <i>Mycobacterium tuberculosis</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1800-1807.	2.3	6
93	Structural Insight into the Activation of PknI Kinase from <i>M.Âtuberculosis</i> via Dimerization of the Extracellular Sensor Domain. <i>Structure</i> , 2017, 25, 1286-1294.e4.	3.3	5
94	Crystal structure of a tankyrase 1â€“telomere repeat factor 1 complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 320-327.	0.8	19
95	Structural insight into dephosphorylation by trehalose 6â€“phosphate phosphatase (OtsB2) from <i>Mycobacterium tuberculosis</i> . <i>FASEB Journal</i> , 2016, 30, 3989-3996.	0.5	19
96	Structures of human mitofusin 1 provide insight into mitochondrial tethering. <i>Journal of Cell Biology</i> , 2016, 215, 621-629.	5.2	141
97	Structural basis of Zika virus helicase in recognizing its substrates. <i>Protein and Cell</i> , 2016, 7, 562-570.	11.0	72
98	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016, 1, 16150.	13.3	36
99	Crystal structure of a PP2A B56-BubR1 complex and its implications for PP2A substrate recruitment and localization. <i>Protein and Cell</i> , 2016, 7, 516-526.	11.0	70
100	Structural views of quinone oxidoreductase from <i>MycobacteriumÂtuberculosis</i> reveal large conformational changes induced by the coâ€“factor. <i>FEBS Journal</i> , 2015, 282, 2697-2707.	4.7	8
101	A Unique Human Norovirus Lineage with a Distinct HBGA Binding Interface. <i>PLoS Pathogens</i> , 2015, 11, e1005025.	4.7	42
102	Studies on Inhibition of Proliferation of Enterovirus-71 by Compound YZ-LY-0. <i>International Journal of Biological Sciences</i> , 2015, 11, 1337-1347.	6.4	3
103	Structural View and Substrate Specificity of Papain-like Protease from Avian Infectious Bronchitis Virus. <i>Journal of Biological Chemistry</i> , 2015, 290, 7160-7168.	3.4	28
104	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. <i>Nature Communications</i> , 2015, 6, 8316.	12.8	43
105	Structural basis and functional analysis of the SARS coronavirus nsp14â€“nsp10 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9436-9441.	7.1	431
106	Peptidyl Aldehyde NK-1.8k Suppresses Enterovirus 71 and Enterovirus 68 Infection by Targeting Protease 3C. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2636-2646.	3.2	36
107	Prediction of host - pathogen protein interactions between <i>Mycobacterium tuberculosis</i> and <i>Homo sapiens</i> using sequence motifs. <i>BMC Bioinformatics</i> , 2015, 16, 100.	2.6	51
108	Structures of Coxsackievirus A16 Capsids with Native Antigenicity: Implications for Particle Expansion, Receptor Binding, and Immunogenicity. <i>Journal of Virology</i> , 2015, 89, 10500-10511.	3.4	58

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109	Structures of the yeast dynamin-like GTPase Sey1p provide insight into homotypic ER fusion. <i>Journal of Cell Biology</i> , 2015, 210, 961-972.	5.2	46
110	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015, 517, 85-88.	27.8	158
111	Structure Elucidation of Coxsackievirus A16 in Complex with GPP3 Informs a Systematic Review of Highly Potent Capsid Binders to Enteroviruses. <i>PLoS Pathogens</i> , 2015, 11, e1005165.	4.7	20
112	Molecular architecture of the ErbB2 extracellular domain homodimer. <i>Oncotarget</i> , 2015, 6, 1695-1706.	1.8	44
113	Mechanism of Dephosphorylation of Glucosyl-3-phosphoglycerate by a Histidine Phosphatase. <i>Journal of Biological Chemistry</i> , 2014, 289, 21242-21251.	3.4	9
114	Cyclophilin A Associates with Enterovirus-71 Virus Capsid and Plays an Essential Role in Viral Infection as an Uncoating Regulator. <i>PLoS Pathogens</i> , 2014, 10, e1004422.	4.7	74
115	Current progress in antiviral strategies. <i>Trends in Pharmacological Sciences</i> , 2014, 35, 86-102.	8.7	199
116	Suramin inhibits EV71 infection. <i>Antiviral Research</i> , 2014, 103, 1-6.	4.1	36
117	Molecular mechanism of SCARB2-mediated attachment and uncoating of EV71. <i>Protein and Cell</i> , 2014, 5, 692-703.	11.0	95
118	Structure of the nisin leader peptidase NisP revealing a C-terminal autocleavage activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1499-1505.	2.5	26
119	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 282-288.	8.2	88
120	Homotypic dimerization of a maltose kinase for molecular scaffolding. <i>Scientific Reports</i> , 2014, 4, 6418.	3.3	7
121	The newly emerged SARS-Like coronavirus HCoV-EMC also has an "Achilles heel" current effective inhibitor targeting a 3C-like protease. <i>Protein and Cell</i> , 2013, 4, 248-250.	11.0	146
122	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013, 4, 1929.	12.8	148
123	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 424-429.	8.2	347
124	New nsp8 isoform suggests mechanism for tuning viral RNA synthesis. <i>Protein and Cell</i> , 2010, 1, 198-204.	11.0	16
125	Crystal structures of NAC domains of human nascent polypeptide-associated complex (NAC) and its \hat{I} -NAC subunit. <i>Protein and Cell</i> , 2010, 1, 406-416.	11.0	26
126	Opening Up the Group II Chaperonins. <i>Structure</i> , 2010, 18, 1221-1222.	3.3	1

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127	Molecular Characterization of a Class I P450 Electron Transfer System from <i>Novosphingobium aromaticivorans</i> DSM12444. <i>Journal of Biological Chemistry</i> , 2010, 285, 27372-27384.	3.4	74
128	Crystal structure and mutagenesis analysis of chitinase CrChi1 from the nematophagous fungus <i>Clonostachys rosea</i> in complex with the inhibitor caffeine. <i>Microbiology (United Kingdom)</i> , 2010, 156, 3566-3574.	1.8	50
129	Crystal structure of an avian influenza polymerase PAN reveals an endonuclease active site. <i>Nature</i> , 2009, 458, 909-913.	27.8	437
130	Structures of Two Coronavirus Main Proteases: Implications for Substrate Binding and Antiviral Drug Design. <i>Journal of Virology</i> , 2008, 82, 2515-2527.	3.4	388
131	Structure of the Main Protease from a Global Infectious Human Coronavirus, HCoV-HKU1. <i>Journal of Virology</i> , 2008, 82, 8647-8655.	3.4	83
132	History of protein crystallography in China. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1035-1042.	4.0	4
133	Production of Authentic SARS-CoV Mpro with Enhanced Activity: Application as a Novel Tag-cleavage Endopeptidase for Protein Overproduction. <i>Journal of Molecular Biology</i> , 2007, 366, 965-975.	4.2	221
134	Drug Design Targeting the Main Protease, the Achilles Heel of Coronaviruses. <i>Current Pharmaceutical Design</i> , 2006, 12, 4573-4590.	1.9	145
135	Insights into SARS-CoV transcription and replication from the structure of the nsp7â€“nsp8 hexadecamer. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 980-986.	8.2	255
136	YjiX: From Structure â€œTuâ€•Function. <i>Structure</i> , 2005, 13, 1401-1402.	3.3	0
137	Design of Wide-Spectrum Inhibitors Targeting Coronavirus Main Proteases. <i>PLoS Biology</i> , 2005, 3, e324.	5.6	547
138	Crystal Structure of Mitochondrial Respiratory Membrane Protein Complex II. <i>Cell</i> , 2005, 121, 1043-1057.	28.9	689
139	Protective humoral responses to severe acute respiratory syndrome-associated coronavirus: implications for the design of an effective protein-based vaccine. <i>Journal of General Virology</i> , 2004, 85, 3109-3113.	2.9	69
140	A preliminary study on functional domains of small heat shock protein Hsp16.3 *. <i>Progress in Natural Science: Materials International</i> , 2004, 14, 21-25.	4.4	1
141	The crystal structures of severe acute respiratory syndrome virus main protease and its complex with an inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13190-13195.	7.1	879
142	Crystallization and preliminary X-ray diffraction analysis of FKBP12 complexed with a new neurotrophic ligand*. <i>Progress in Natural Science: Materials International</i> , 2003, 13, 765-767.	4.4	2
143	Phylogeny reconstruction based on protein phylogenetic profiles of organisms*. <i>Progress in Natural Science: Materials International</i> , 2003, 13, 109-113.	4.4	1
144	Six-helix bundle assembly and characterization of heptad repeat regions from the F protein of Newcastle disease virus. <i>Journal of General Virology</i> , 2002, 83, 623-629.	2.9	43

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145	Crystallization and preliminary X-ray crystallographic analysis of yeast prion protein Ure2p with shortened N-terminal. Science Bulletin, 2001, 46, 1012-1014.	1.7	1
146	High-level expression and secondary structure analysis of the bovine mature prion protein. Science Bulletin, 2000, 45, 1312-1315.	1.7	1