

Zhong-zhou Chen

List of Publications by Year in descending order

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95
papers

3,950
citations

172457

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128289

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98
docs citations

98
times ranked

6033
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis of Human Parainfluenza Virus 3 Unassembled Nucleoprotein in Complex with Its Viral Chaperone. <i>Journal of Virology</i> , 2022, 96, JVI0164821.	3.4	6
2	Structure of Rift Valley Fever Virus RNA-Dependent RNA Polymerase. <i>Journal of Virology</i> , 2022, 96, JVI0171321.	3.4	13
3	Structural Insights into the Ligand-Binding and -Releasing Mechanism of <i>Helicoverpa armigera</i> Pheromone-Binding Protein PBP1. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1190.	4.1	4
4	Structural insights into the interactions and epigenetic functions of human nucleic acid repair protein ALKBH6. <i>Journal of Biological Chemistry</i> , 2022, 298, 101671.	3.4	10
5	The Novel Protease Activities of JMJD5, JMJD6, JMJD7 and Arginine Methylation Activities of Arginine Methyltransferases Are Likely Coupled. <i>Biomolecules</i> , 2022, 12, 347.	4.0	3
6	The basis of a more contagious 501Y.V1 variant of SARS-CoV-2. <i>Cell Research</i> , 2021, 31, 720-722.	12.0	129
7	The Function of the PRRSV-Host Interactions and Their Effects on Viral Replication and Propagation in Antiviral Strategies. <i>Vaccines</i> , 2021, 9, 364.	4.4	21
8	Novel insights into the function of an N-terminal region of DENV2 NS4B for the optimal helicase activity of NS3. <i>Virus Research</i> , 2021, 295, 198318.	2.2	7
9	The stability of R-spine defines RAF inhibitor resistance: A comprehensive analysis of oncogenic BRAF mutants with in-frame insertion of $\pm C\text{-}\hat{I}^{24}$ loop. <i>Science Advances</i> , 2021, 7, .	10.3	13
10	Structure and Function of N-Terminal Zinc Finger Domain of SARS-CoV-2 NSP2. <i>Virologica Sinica</i> , 2021, 36, 1104-1112.	3.0	25
11	501Y.V2 and 501Y.V3 variants of SARS-CoV-2 lose binding to bamlanivimab <i>in vitro</i> . <i>MAbs</i> , 2021, 13, 1919285.	5.2	65
12	Global distribution of soapberries (<i>Sapindus</i> L.) habitats under current and future climate scenarios. <i>Scientific Reports</i> , 2021, 11, 19740.	3.3	6
13	Structures and Functional Diversities of ASFV Proteins. <i>Viruses</i> , 2021, 13, 2124.	3.3	37
14	Amyotrophy Induced by a High-Fat Diet Is Closely Related to Inflammation and Protein Degradation Determined by Quantitative Phosphoproteomic Analysis in Skeletal Muscle of C57BL/6 J Mice. <i>Journal of Nutrition</i> , 2020, 150, 294-302.	2.9	11
15	JMJD5 couples with CDK9 to release the paused RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19888-19895.	7.1	8
16	Structural basis of nucleic acid recognition and 6mA demethylation by human ALKBH1. <i>Cell Research</i> , 2020, 30, 272-275.	12.0	36
17	Crystal structures of REF6 and its complex with DNA reveal diverse recognition mechanisms. <i>Cell Discovery</i> , 2020, 6, 17.	6.7	18
18	The potential underlying mechanism of the leukemia caused by <i>MLL</i> fusion and potential treatments. <i>Molecular Carcinogenesis</i> , 2020, 59, 839-851.	2.7	6

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19	MicroRNA-374a-5p inhibits neuroinflammation in neonatal hypoxic-ischemic encephalopathy via regulating NLRP3 inflammasome targeted Smad6. <i>Life Sciences</i> , 2020, 252, 117664.	4.3	24
20	Aspartic acid at residue 185 modulates the capacity of HP-PRRSV nsp4 to antagonize IFN-I expression. <i>Virology</i> , 2020, 546, 79-87.	2.4	9
21	Helicase of Type 2 Porcine Reproductive and Respiratory Syndrome Virus Strain HV Reveals a Unique Structure. <i>Viruses</i> , 2020, 12, 215.	3.3	18
22	JMJD6 cleaves MePCE to release positive transcription elongation factor b (P-TEFb) in higher eukaryotes. <i>ELife</i> , 2020, 9, .	6.0	20
23	A structure model explaining the binding between a ubiquitous unconventional G-protein (OsYchF1) and a plant-specific C2-domain protein (OsGAP1) from rice. <i>Biochemical Journal</i> , 2020, 477, 3935-3949.	3.7	5
24	Structure and function of cytoplasmic serine hydroxymethyltransferase from <i>Pichia pastoris</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 496, 753-757.	2.1	4
25	Specific Recognition of Arginine Methylated Histone Tails by JMJD5 and JMJD7. <i>Scientific Reports</i> , 2018, 8, 3275.	3.3	23
26	Activating mutations in MEK1 enhance homodimerization and promote tumorigenesis. <i>Science Signaling</i> , 2018, 11, .	3.6	37
27	A novel glycosylated anti-CD20 monoclonal antibody from transgenic cattle. <i>Scientific Reports</i> , 2018, 8, 13208.	3.3	8
28	Architecture of the native major royal jelly protein 1 oligomer. <i>Nature Communications</i> , 2018, 9, 3373.	12.8	47
29	Structures of glycolate oxidase from <i>Nicotiana benthamiana</i> reveal a conserved pH sensor affecting the binding of FMN. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 3050-3056.	2.1	6
30	Design and Functional Characterization of a Novel Abscisic Acid Analog. <i>Scientific Reports</i> , 2017, 7, 43863.	3.3	18
31	Class I histone deacetylases are major histone decrotonylases: evidence for critical and broad function of histone crotonylation in transcription. <i>Cell Research</i> , 2017, 27, 898-915.	12.0	216
32	Human apo-SRP72 and SRP68/72 complex structures reveal the molecular basis of protein translocation. <i>Journal of Molecular Cell Biology</i> , 2017, 9, 220-230.	3.3	15
33	Catching Sirtuin-2 Intermediates One Structure at the Time. <i>Cell Chemical Biology</i> , 2017, 24, 248-249.	5.2	6
34	Structural Biology of the Arterivirus nsp11 Endoribonucleases. <i>Journal of Virology</i> , 2017, 91, .	3.4	30
35	Clipping of arginine-methylated histone tails by JMJD5 and JMJD7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7717-E7726.	7.1	48
36	Analysis of crystal structure of Arabidopsis MPK6 and generation of its mutants with higher activity. <i>Scientific Reports</i> , 2016, 6, 25646.	3.3	13

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37	ATP binding by the P-loop NTPase OsYchF1 (an unconventional G protein) contributes to biotic but not abiotic stress responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2648-2653.	7.1	31
38	Structural Basis of Reversible Phosphorylation by Maize Pyruvate Orthophosphate Dikinase Regulatory Protein. <i>Plant Physiology</i> , 2016, 170, 732-741.	4.8	10
39	The amino-terminal structure of human fragile X mental retardation protein obtained using precipitant-immobilized imprinted polymers. <i>Nature Communications</i> , 2015, 6, 6634.	12.8	40
40	Crystal structure of the <i>Locusta migratoria</i> odorant binding protein. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 737-742.	2.1	41
41	A Chaperone Function of NO CATALASE ACTIVITY1 Is Required to Maintain Catalase Activity and for Multiple Stress Responses in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2015, 27, 908-925.	6.6	139
42	Structure of human MDM2 complexed with RPL11 reveals the molecular basis of p53 activation. <i>Genes and Development</i> , 2015, 29, 1524-1534.	5.9	66
43	Mechanistic insights into metal ion activation and operator recognition by the ferric uptake regulator. <i>Nature Communications</i> , 2015, 6, 7642.	12.8	107
44	Structural basis and functions of abscisic acid receptors PYLs. <i>Frontiers in Plant Science</i> , 2015, 6, 88.	3.6	47
45	Zwitterion-Immobilized Imprinted Polymers for Promoting the Crystallization of Proteins. <i>Crystal Growth and Design</i> , 2015, 15, 4932-4937.	3.0	10
46	Structural insights into the substrate specificity and transglycosylation activity of a fungal glycoside hydrolase family 5 β -mannosidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2970-2982.	2.5	27
47	PUF-Based RFID Ownership Transfer Protocol in an Open Environment. , 2014, , .		6
48	The Atomic Resolution Structure of Human AlkB Homolog 7 (ALKBH7), a Key Protein for Programmed Necrosis and Fat Metabolism. <i>Journal of Biological Chemistry</i> , 2014, 289, 27924-27936.	3.4	36
49	Structural basis for the regulatory function of a complex zinc-binding domain in a replicative arterivirus helicase resembling a nonsense-mediated mRNA decay helicase. <i>Nucleic Acids Research</i> , 2014, 42, 3464-3477.	14.5	47
50	The structural basis of urea-induced protein unfolding in β -catenin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2840-2847.	2.5	15
51	Crystal Structures of the Human RNA Demethylase Alkbh5 Reveal Basis for Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2014, 289, 11571-11583.	3.4	143
52	<i>REPRESSOR OF SILENCING5</i> Encodes a Member of the Small Heat Shock Protein Family and Is Required for DNA Demethylation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 2660-2675.	6.6	42
53	Influence of sewage sludge-based activated carbon and temperature on the liquefaction of sewage sludge: Yield and composition of bio-oil, immobilization and risk assessment of heavy metals. <i>Bioresource Technology</i> , 2014, 159, 72-79.	9.6	153
54	Structural Basis of ABA Perception by PYR/PYL/RCAR Receptors. , 2014, , 117-135.		3

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55	Structure-function analysis reveals a novel mechanism for regulation of histone demethylase LSD2/AOF1/KDM1b. <i>Cell Research</i> , 2013, 23, 225-241.	12.0	61
56	Combined Cathepsin S and hs-CRP predicting inflammation of Abdominal Aortic Aneurysm. <i>Clinical Biochemistry</i> , 2013, 46, 1026-1029.	1.9	31
57	Simultaneous determination of metronidazole, chloramphenicol and 10 sulfonamide residues in honey by LC-MS/MS. <i>Analytical Methods</i> , 2013, 5, 1283.	2.7	35
58	The structure of a glycoside hydrolase family 81 endo- β -1,3-glucanase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2027-2038.	2.5	15
59	Structural Insights into the Abscisic Acid Stereospecificity by the ABA Receptors PYR/PYL/RCAR. <i>PLoS ONE</i> , 2013, 8, e67477.	2.5	38
60	Contribution of the C-terminal Regions of Promyelocytic Leukemia Protein (PML) Isoforms II and V to PML Nuclear Body Formation. <i>Journal of Biological Chemistry</i> , 2012, 287, 30729-30742.	3.4	41
61	Crystallization and preliminary X-ray studies of ferric uptake regulator from <i>Magnetospirillum gryphiswaldense</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 902-905.	0.7	1
62	P2PAV: Anti-virus through P2P. , 2012, , .		1
63	Complex Structures of the Abscisic Acid Receptor PYL3/RCAR13 Reveal a Unique Regulatory Mechanism. <i>Structure</i> , 2012, 20, 780-790.	3.3	71
64	Crystallization and preliminary X-ray diffraction studies of the abscisic acid receptor PYL3 and its complex with pyrabactin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 479-482.	0.7	1
65	Sitab: Combating Spam in Tagging Systems via Users' Implicit Tagging Behavior. , 2011, , .		0
66	Enforcing Relaxed Declassifications with Reference Points. , 2011, , .		0
67	Mobile Browser as a Second Factor for Web Authentication. , 2011, , .		2
68	PrivOSN: Practical Privacy in Online Social Network. , 2011, , .		0
69	TEAMA: Trust Evaluation Based Authorization Model for Ad Hoc Networks. , 2011, , .		0
70	Ag Nanoparticles Coated SWCNT with Surface Enhanced Raman Scattering (SERS) Signals. <i>Journal of Nanoscience and Nanotechnology</i> , 2010, 10, 8538-8543.	0.9	5
71	Structural insights into a novel histone demethylase PHF8. <i>Cell Research</i> , 2010, 20, 166-173.	12.0	67
72	A Novel Threshold Distributed Authentication Scheme Using Bilinear Pairings. , 2010, , .		0

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73	SKIP: A Secure Key Issuing Scheme for Peer-to-Peer Networks. , 2009, , .		3
74	Task Based Automatic Examination System for Sequenced Test. , 2009, , .		4
75	Evaluating Network Security With Two-Layer Attack Graphs. , 2009, , .		22
76	Efficient Identity-Based Key Issue with TPM. , 2008, , .		3
77	Function and Regulation of SPLUNC1 Protein in Mycoplasma Infection and Allergic Inflammation. Journal of Immunology, 2007, 179, 3995-4002.	0.8	120
78	Structural basis of the recognition of a methylated histone tail by JMJD2A. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10818-10823.	7.1	131
79	Reversal of Histone Lysine Trimethylation by the JMJD2 Family of Histone Demethylases. Cell, 2006, 125, 467-481.	28.9	908
80	Structural Insights into Histone Demethylation by JMJD2 Family Members. Cell, 2006, 125, 691-702.	28.9	341
81	A common intermediate for prebiotic synthesis of proteins and nucleosides: a density functional theory (DFT) study on the formation of penta-coordinate phosphorus carboxylicâ€“phosphoric mixed anhydride from N-phosphoryl amino acids. Computational and Theoretical Chemistry, 2004, 672, 51-60.	1.5	13
82	Theoretical Study on the Rearrangement of \hat{I}^2 -OH and \hat{I}^3 -OH in ESI Mass Spectrometry by N-Phosphorylation. Journal of Physical Chemistry A, 2004, 108, 7686-7690.	2.5	5
83	Synthesis and matrix assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometry study of phosphopeptide. International Journal of Peptide Research and Therapeutics, 2003, 10, 57-62.	0.1	9
84	Phosphoryl group differentiating \hat{I}^2 -amino acids from \hat{I}^3 - and \hat{I}^1 -amino acids in prebiotic peptide formation. International Journal of Quantum Chemistry, 2003, 94, 232-241.	2.0	10
85	Activity Difference between \hat{I}^1 -COOH and \hat{I}^2 -COOH in N-Phosphorylaspartic Acids. Journal of Organic Chemistry, 2003, 68, 4052-4058.	3.2	25
86	Hydrolysis of Dipeptide N-Heptyl Esters with Newlase F. Journal of Chemical Research, 2003, 2003, 1-1.	1.3	1
87	Synthesis and matrix assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometry study of phosphopeptide. International Journal of Peptide Research and Therapeutics, 2003, 10, 57-62.	0.1	1
88	Activities of \hat{I}^1 -COOH vs \hat{I}^3 -COOH in N-Phosphoryl Amino Acids: A Theoretical Study. Journal of Physical Chemistry A, 2002, 106, 11565-11569.	2.5	9
89	The use of crude lipase in deprotection of C-terminal protecting groups. Journal of Molecular Catalysis B: Enzymatic, 2002, 18, 243-249.	1.8	12
90	Negative-ion electrospray ionization tandem mass spectrometry of N-phosphoryl amino acids and dipeptides. Rapid Communications in Mass Spectrometry, 2002, 16, 790-796.	1.5	14

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91	Orientation of the peptide formation of N-phosphoryl amino acids in solution. Science Bulletin, 2002, 47, 1866.	1.7	5
92	Differentiation of α -COOH from β -COOH in aspartic acids by N-phosphorylation. International Journal of Quantum Chemistry, 2001, 83, 41-51.	2.0	11
93	Differentiation of α -COOH from β -COOH in glutamic acid by N-phosphorylation. Computational and Theoretical Chemistry, 2001, 574, 163-175.	1.5	6
94	Differentiation of α -COOH from β -COOH in aspartic acids by N-phosphorylation. International Journal of Quantum Chemistry, 2001, 83, 41-51.	2.0	0
95	Crystal Structures of REF6 and Its Complex with DNA Reveal Diverse Recognition Mechanisms. SSRN Electronic Journal, 0, , .	0.4	0