

Maikun Teng

List of Publications by Year in descending order

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96
papers

2,136
citations

236925

25
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265206

42
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98
all docs

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docs citations

98
times ranked

3306
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of the Cysteine-rich Secretory Protein Stecrisp Reveals That the Cysteine-rich Domain Has a K ⁺ Channel Inhibitor-like Fold. <i>Journal of Biological Chemistry</i> , 2005, 280, 12405-12412.	3.4	132
2	Human Zwint-1 Specifies Localization of Zeste White 10 to Kinetochores and Is Essential for Mitotic Checkpoint Signaling. <i>Journal of Biological Chemistry</i> , 2004, 279, 54590-54598.	3.4	106
3	Crystal structures of acutolysin A, a three-disulfide hemorrhagic zinc metalloproteinase from the snake venom of <i>Agkistrodon acutus</i> . <i>Journal of Molecular Biology</i> , 1998, 283, 657-668.	4.2	105
4	Blocking Effect and Crystal Structure of Natrin Toxin, a Cysteine-Rich Secretory Protein from <i>Naja atra</i> Venom that Targets the BKCa Channel. <i>Biochemistry</i> , 2005, 44, 10145-10152.	2.5	99
5	The structure of the ARE-binding domains of Hu antigen R (HuR) undergoes conformational changes during RNA binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 373-380.	2.5	90
6	Loss-of-Function Mutations in the PRPS1 Gene Cause a Type of Nonsyndromic X-linked Sensorineural Deafness, DFN2. <i>American Journal of Human Genetics</i> , 2010, 86, 65-71.	6.2	88
7	Mitotic Regulator Mis18 ² Interacts with and Specifies the Centromeric Assembly of Molecular Chaperone Holliday Junction Recognition Protein (HJURP). <i>Journal of Biological Chemistry</i> , 2014, 289, 8326-8336.	3.4	78
8	Acetylation of Aurora B by TIP60 ensures accurate chromosomal segregation. <i>Nature Chemical Biology</i> , 2016, 12, 226-232.	8.0	77
9	NetAlign: a web-based tool for comparison of protein interaction networks. <i>Bioinformatics</i> , 2006, 22, 2175-2177.	4.1	67
10	Core Structure of the Yeast Spt4-Spt5 Complex: A Conserved Module for Regulation of Transcription Elongation. <i>Structure</i> , 2008, 16, 1649-1658.	3.3	61
11	Crystal Structure of Human Vacuolar Protein Sorting Protein 29 Reveals a Phosphodiesterase/Nuclease-like Fold and Two Protein-Protein Interaction Sites. <i>Journal of Biological Chemistry</i> , 2005, 280, 22962-22967.	3.4	56
12	Crystal Structures and Amidolytic Activities of Two Glycosylated Snake Venom Serine Proteinases. <i>Journal of Biological Chemistry</i> , 2005, 280, 10524-10529.	3.4	53
13	The structure of the FANCMâ€‘MHF complex reveals physical features for functional assembly. <i>Nature Communications</i> , 2012, 3, 782.	12.8	53
14	Purification, partial characterization, crystallization and structural determination of AHP-LAAO, a novel L-amino-acid oxidase with cell apoptosis-inducing activity from <i>Agkistrodon halys pallas</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 974-977.	2.5	52
15	BubR1 phosphorylates CENP-E as a switch enabling the transition from lateral association to end-on capture of spindle microtubules. <i>Cell Research</i> , 2019, 29, 562-578.	12.0	46
16	Comparison of protein interaction networks reveals species conservation and divergence. <i>BMC Bioinformatics</i> , 2006, 7, 457.	2.6	44
17	Structural Determinants for the Strict Monomethylation Activity by <i>Trypanosoma brucei</i> Protein Arginine Methyltransferase 7. <i>Structure</i> , 2014, 22, 756-768.	3.3	43
18	Hydrogen peroxide produced by two amino acid oxidases mediates antibacterial actions. <i>Journal of Microbiology</i> , 2004, 42, 336-9.	2.8	33

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19	Structural Analysis of Rtt106p Reveals a DNA Binding Role Required for Heterochromatin Silencing. <i>Journal of Biological Chemistry</i> , 2010, 285, 4251-4262.	3.4	32
20	Epitope mapping and structural analysis of an anti-ErbB2 antibody A21: Molecular basis for tumor inhibitory mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 938-949.	2.6	31
21	Crystal structure of a membrane-bound L -amino acid deaminase from <i>Proteus vulgaris</i> . <i>Journal of Structural Biology</i> , 2016, 195, 306-315.	2.8	30
22	Crystal Structure of Human SSRP1 Middle Domain Reveals a Role in DNA Binding. <i>Scientific Reports</i> , 2016, 5, 18688.	3.3	29
23	Structural Insights into the Down-regulation of Overexpressed p185 Protein of Transformed Cells by the Antibody chA21*. <i>Journal of Biological Chemistry</i> , 2011, 286, 31676-31683.	3.4	28
24	Structural Analysis of Shu Proteins Reveals a DNA Binding Role Essential for Resisting Damage. <i>Journal of Biological Chemistry</i> , 2012, 287, 20231-20239.	3.4	28
25	mFASD: a structure-based algorithm for discriminating different types of metal-binding sites. <i>Bioinformatics</i> , 2015, 31, 1938-1944.	4.1	28
26	Purification, characterization and conformational analysis of a haemorrhagin from the venom of <i>Agkistrodon acutus</i> . <i>Toxicon</i> , 1997, 35, 283-292.	1.6	27
27	Structural insights into the interaction of the ribosomal P stalk protein P2 with a type II ribosome-inactivating protein ricin. <i>Scientific Reports</i> , 2016, 6, 37803.	3.3	22
28	Crystal structure of agkisacucetin, a GPIb-binding snake C-type lectin that inhibits platelet adhesion and aggregation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1707-1711.	2.6	21
29	Crystal Structure of Arginine Methyltransferase 6 from <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2014, 9, e87267.	2.5	21
30	Crystal structure of the C-terminal conserved domain of human GRP, a galectin-related protein, reveals a function mode different from those of galectins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1582-1588.	2.6	20
31	Crystal structure and activating effect on RyRs of AhV_TL-I, a glycosylated thrombin-like enzyme from <i>Agkistrodon halys</i> snake venom. <i>Archives of Toxicology</i> , 2013, 87, 535-545.	4.2	20
32	Structural basis of the ligand binding and signaling mechanism of melatonin receptors. <i>Nature Communications</i> , 2022, 13, 454.	12.8	19
33	Structural basis of the autolysis of AaHIV suggests a novel target recognizing model for ADAM/reprolysin family proteins. <i>Biochemical and Biophysical Research Communications</i> , 2009, 386, 159-164.	2.1	18
34	Differentially expressed mitochondrial genes in breast cancer cells: Potential new targets for anti-cancer therapies. <i>Gene</i> , 2017, 596, 45-52.	2.2	18
35	In vitro assessment and phase I randomized clinical trial of anfibatide a snake venom derived anti-thrombotic agent targeting human platelet GPIIb/IIIa. <i>Scientific Reports</i> , 2021, 11, 11663.	3.3	18
36	Crystal structure of the two-subunit tRNA m1A58 methyltransferase TRM6-TRM61 from <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2016, 6, 32562.	3.3	17

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37	How does agkicetin-C bind on platelet glycoprotein Ib \pm and achieve its platelet effects?. <i>Toxicon</i> , 2005, 45, 561-570.	1.6	16
38	A small disturbance, but a serious disease: The possible mechanism of D52H μ mutant of human PRS1 that causes gout. <i>IUBMB Life</i> , 2013, 65, 518-525.	3.4	16
39	A cellular endolysosome-modulating pore-forming protein from a toad is negatively regulated by its paralog under oxidizing conditions. <i>Journal of Biological Chemistry</i> , 2020, 295, 10293-10306.	3.4	16
40	Crystal structure of DnaT ^{84μ153} -dT10 ssDNA complex reveals a novel single-stranded DNA binding mode. <i>Nucleic Acids Research</i> , 2014, 42, 9470-9483.	14.5	15
41	Purification, crystallization and preliminary crystallographic analysis of AHP IX-bp, a zinc ion and pH-dependent coagulation factor IX binding protein from <i>Agkistrodon halysPallas</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 730-733.	2.5	14
42	Structural Insights into the Association of Hif1 with Histones H2A-H2B Dimer and H3-H4 Tetramer. <i>Structure</i> , 2016, 24, 1810-1820.	3.3	14
43	Interface switch mediates signal transmission in a two-component system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30433-30440.	7.1	14
44	Crystal and EM Structures of Human Phosphoribosyl Pyrophosphate Synthase I (PRS1) Provide Novel Insights into the Disease-Associated Mutations. <i>PLoS ONE</i> , 2015, 10, e0120304.	2.5	14
45	Structural and biochemical studies reveal UbiG/Coq3 as a class of novel membrane-binding proteins. <i>Biochemical Journal</i> , 2015, 470, 105-114.	3.7	13
46	Purification, partial characterization and crystallization of acucetin, a protein containing both disintegrin-like and cysteine-rich domains released by auto-proteolysis of a P-III-type metalloproteinase AaH-IV from <i>Agkistrodon acutus</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2310-2312.	2.5	12
47	Stejnihagin, a novel snake metalloproteinase from <i>Trimeresurus stejnegeri</i> venom, inhibited L-type Ca ²⁺ channels. <i>Toxicon</i> , 2009, 53, 309-315.	1.6	12
48	Structure of saxthrombin, a thrombin-like enzyme from <i>Gloydius saxatilis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 862-865.	0.7	12
49	Structural Insights into the Neutralization Mechanism of Monoclonal Antibody 6C2 against Ricin. <i>Journal of Biological Chemistry</i> , 2013, 288, 25165-25172.	3.4	12
50	Purification, N-terminal sequencing, partial characterization, crystallization and preliminary crystallographic analysis of two glycosylated serine proteinases from <i>Agkistrodon acutus</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 547-550.	2.5	11
51	The Atomic Resolution Crystal Structure of Atratoxin Determined by Single Wavelength Anomalous Diffraction Phasing. <i>Journal of Biological Chemistry</i> , 2004, 279, 39094-39104.	3.4	11
52	Monomeric tRNA (m ⁷ G46) methyltransferase from <i>Escherichia coli</i> presents a novel structure at the function μ essential insertion. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 512-515.	2.6	11
53	Structural and biochemical insights into the DNA-binding mode of Mj Spt4p:Spt5 complex at the exit tunnel of RNAPII. <i>Journal of Structural Biology</i> , 2015, 192, 418-425.	2.8	11
54	Structure of the DNA-binding domain of the response regulator SaeR from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1768-1776.	2.5	11

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55	Expression, purification, crystallization and preliminary X-ray diffraction analysis of human phosphoribosyl pyrophosphate synthetase 1 (PRS1). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 432-434.	0.7	10
56	Crystal structure of NusG N-terminal (NGN) domain from <i>Methanocaldococcus jannaschii</i> and its interaction with rpoE ³ . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 787-793.	2.6	10
57	N114S mutation causes loss of ATP-induced aggregation of human phosphoribosylpyrophosphate synthetase 1. <i>Biochemical and Biophysical Research Communications</i> , 2009, 379, 1120-1125.	2.1	10
58	Structure of Rot, a global regulator of virulence genes in <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2467-2476.	2.5	10
59	Structural analysis of Dis3l2, an exosome-independent exonuclease from <i>Schizosaccharomyces pombe</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1284-1294.	2.5	10
60	Crystal structure of <i>Staphylococcus aureus</i> peptidyl-tRNA hydrolase at a 2.25 Å... resolution. <i>Acta Biochimica Et Biophysica Sinica</i> , 2015, 47, gmv114.	2.0	9
61	The DNA-binding mechanism of the TCS response regulator ArlR from <i>Staphylococcus aureus</i> . <i>Journal of Structural Biology</i> , 2019, 208, 107388.	2.8	8
62	Purification, partial characterization, crystallization and preliminary X-ray diffraction of two cysteine-rich secretory proteins from <i>Naja atra</i> and <i>Trimeresurus stejnegeri</i> venoms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1108-1111.	2.5	7
63	Structural insights into the role of the Chl4-Iml3 complex in kinetochore assembly. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2412-2419.	2.5	7
64	Structural and histone binding ability characterization of the ARB2 domain of a histone deacetylase Hda1 from <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2016, 6, 33905.	3.3	7
65	Crystal structure of HLA-B*5801, a protective HLA allele for HIV-1 infection. <i>Protein and Cell</i> , 2016, 7, 761-765.	11.0	7
66	Crystal structure of human osteoclast stimulating factor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 245-251.	2.6	6
67	Crystal structure of phospholipase PA2 ^b , a protease-activated receptor agonist from the <i>Trimeresurus stejnegeri</i> snake venom. <i>FEBS Letters</i> , 2014, 588, 4604-4612.	2.8	6
68	Structural insights into the methyl donor recognition model of a novel membrane-binding protein UbiG. <i>Scientific Reports</i> , 2016, 6, 23147.	3.3	6
69	Identification of novel enriched recurrent chimeric COL7A1-UCN2 in human laryngeal cancer samples using deep sequencing. <i>BMC Cancer</i> , 2018, 18, 248.	2.6	6
70	Purification, N-terminal sequencing, crystallization and preliminary structural determination of atratoxin-b, a short-chain β -neurotoxin from <i>Naja atra</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1038-1042.	2.5	5
71	Preliminary crystallographic analysis of the RNA-binding domain of HuR and its poly(U)-binding properties. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 546-550.	0.7	5
72	Structural analysis of Ca ²⁺ -binding pocket of synaptotagmin 5 C2A domain. <i>International Journal of Biological Macromolecules</i> , 2017, 95, 946-953.	7.5	5

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73	Purification, N-terminal sequencing, crystallization and preliminary X-ray diffraction analysis of atratoxin, a new short-chain β -neurotoxin from the venom of <i>Naja naja atra</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 839-842.	2.5	4
74	Expression, purification, crystallization and preliminary X-ray characterization of the GRP carbohydrate-recognition domain from <i>Homo sapiens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 474-476.	0.7	4
75	Crystallization and preliminary crystallographic analysis of tRNA (m7G46) methyltransferase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 743-745.	0.7	4
76	Crystallographic Analysis of the Catalytic Mechanism of Phosphopantothoenoylcysteine Synthetase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2019, 431, 764-776.	4.2	4
77	A newly identified photolyase from <i>Arthrospira platensis</i> possesses a unique methenyltetrahydrofolate chromophore-binding pattern. <i>FEBS Letters</i> , 2020, 594, 740-750.	2.8	4
78	<i>Caulobacter crescentus</i> sliding clamp employs a noncanonical regulatory model of DNA replication. <i>FEBS Journal</i> , 2020, 287, 2292-2311.	4.7	4
79	Crystal structure of cytoplasmic acetoacetyl-CoA thiolase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 6-13.	0.8	4
80	Heterologous Expression of the Single-Mutation Glucose Isomerase (GIG138P) Gene in <i>Streptomyces lividans</i> and Its Genetic Instability. <i>Current Microbiology</i> , 2001, 42, 241-247.	2.2	3
81	Crystallization and preliminary crystallographic studies of the single-chain variable fragment of antibody chA21 in complex with an N-terminal fragment of ErbB2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 692-694.	0.7	3
82	Structural peculiarities of the (MHF1-MHF2) ₄ octamer provide a long DNA binding patch to anchor the MHF-FANCM complex to chromatin: A solution SAXS study. <i>FEBS Letters</i> , 2013, 587, 2912-2917.	2.8	3
83	The multiple nucleotide-divalent cation binding modes of <i>Saccharomyces cerevisiae</i> CK2 ₁ indicate a possible co-substrate hydrolysis product (ADP/GDP) release pathway. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 501-513.	2.5	3
84	Crystal structure determination of alkaline haemorrhagin AaH III from snake venom of <i>Agkistrodon acutus</i> . <i>Science in China Series C: Life Sciences</i> , 1997, 40, 351-355.	1.3	2
85	Construction of Double-Copy Glucose Isomerase Gene Engineering Strain of <i>Streptomyces diastaticus</i> by Homologous Recombination. <i>Current Microbiology</i> , 2002, 44, 273-279.	2.2	2
86	AhV ₁ -induced vasoconstriction involves the IP3Rs-mediated Ca ²⁺ releasing. <i>Toxicon</i> , 2013, 70, 107-113.	1.6	2
87	Crystallographic analysis of RsmA, a ribosomal RNA small subunit methyltransferase A from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1063-1066.	0.8	2
88	The crystal structure of the Hsp90 co-chaperone Cpr7 from <i>Saccharomyces cerevisiae</i> . <i>Journal of Structural Biology</i> , 2017, 197, 379-387.	2.8	2
89	Antibiotic binding releases autoinhibition of the TipA multidrug-resistance transcriptional regulator. <i>Journal of Biological Chemistry</i> , 2020, 295, 17865-17876.	3.4	2
90	0.27-nm resolution crystal structure of Haemorrhagin I from snake venom of <i>Agkistrodon acutus</i> . <i>Science Bulletin</i> , 1997, 42, 333-337.	1.7	1

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91	X-ray absorption near edge structure study on Acutolysin-C, a zinc-metalloproteinase from <i>Agkistrodon acutus</i> venom: Insight into the acid-inactive mechanism. <i>Spectrochimica Acta, Part B: Atomic Spectroscopy</i> , 2007, 62, 1246-1251.	2.9	1
92	Structural and functional insight into the N-terminal domain of the clathrin adaptor Ent5 from <i>Saccharomyces cerevisiae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 786-793.	2.1	1
93	Functional and structural characterization of a novel catechol-O-methyltransferase from <i>Schizosaccharomyces pombe</i> . <i>IUBMB Life</i> , 2019, 71, 330-339.	3.4	1
94	The structural mechanism for the nucleoside triphosphate and diphosphate hydrolysis activity of Ntdp from <i>Staphylococcus aureus</i> . <i>FEBS Journal</i> , 2021, 288, 6019-6034.	4.7	1
95	The C-terminus of ubiquitin plays a critical role in deamidase Lpg2148 recognition. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 2943-2948.	2.1	0
96	Defining A Global Map of Functional Group-based 3D Ligand-binding Motifs. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 765-779.	6.9	0