

Maikun Teng

List of Publications by Year in descending order

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96
papers

2,136
citations

236925

25
h-index

265206

42
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98
all docs

98
docs citations

98
times ranked

3306
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Structural basis of the ligand binding and signaling mechanism of melatonin receptors. <i>Nature Communications</i> , 2022, 13, 454. | 12.8 | 19 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | <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 |
| 7 | Antibiotic binding releases autoinhibition of the TipA multidrug-resistance transcriptional regulator. <i>Journal of Biological Chemistry</i> , 2020, 295, 17865-17876. | 3.4 | 2 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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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|----|--|------|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Crystal Structure of Human SSRP1 Middle Domain Reveals a Role in DNA Binding. <i>Scientific Reports</i> , 2016, 5, 18688. | 3.3 | 29 |
| 29 | Acetylation of Aurora B by TIP60 ensures accurate chromosomal segregation. <i>Nature Chemical Biology</i> , 2016, 12, 226-232. | 8.0 | 77 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | mFASD: a structure-based algorithm for discriminating different types of metal-binding sites. <i>Bioinformatics</i> , 2015, 31, 1938-1944. | 4.1 | 28 |
| 35 | 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 |
| 36 | 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 |

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|----|---|------|-----------|
| 37 | 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 |
| 38 | Crystal Structure of Arginine Methyltransferase 6 from <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2014, 9, e87267. | 2.5 | 21 |
| 39 | Mitotic Regulator Mis18 ¹² 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 |
| 40 | Crystal structure of phospholipase PA2 ^{1b} , a protease ¹ -activated receptor agonist from the <i>Trimeresurus stejnegeri</i> snake venom. <i>FEBS Letters</i> , 2014, 588, 4604-4612. | 2.8 | 6 |
| 41 | Crystal structure of DnaT ⁸⁴ -153 ² -dT10 ssDNA complex reveals a novel single-stranded DNA binding mode. <i>Nucleic Acids Research</i> , 2014, 42, 9470-9483. | 14.5 | 15 |
| 42 | 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 |
| 43 | 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 |
| 44 | The multiple nucleotide ¹ -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 |
| 45 | 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 |
| 46 | AhV _{aPA} -induced vasoconstriction involves the IP3Rs-mediated Ca ²⁺ releasing. <i>Toxicon</i> , 2013, 70, 107-113. | 1.6 | 2 |
| 47 | 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 |
| 48 | Structural peculiarities of the (MHF1 ¹ -MHF2) ₄ octamer provide a long DNA binding patch to anchor the MHF ¹ -FANCM complex to chromatin: A solution SAXS study. <i>FEBS Letters</i> , 2013, 587, 2912-2917. | 2.8 | 3 |
| 49 | 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 |
| 50 | Structural insights into the role of the Chl4 ¹ -lml3 complex in kinetochore assembly. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2412-2419. | 2.5 | 7 |
| 51 | A small disturbance, but a serious disease: The possible mechanism of D52H ¹ -mutant of human PRS1 that causes gout. <i>IUBMB Life</i> , 2013, 65, 518-525. | 3.4 | 16 |
| 52 | 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 |
| 53 | The structure of the FANCM ¹ -MHF complex reveals physical features for functional assembly. <i>Nature Communications</i> , 2012, 3, 782. | 12.8 | 53 |
| 54 | Crystal structure of agkisacuetin, a Gpib ¹ -binding snake Ca ²⁺ -type lectin that inhibits platelet adhesion and aggregation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1707-1711. | 2.6 | 21 |

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|----|---|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | Crystal structure of human osteoclast stimulating factor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 245-251. | 2.6 | 6 |
| 61 | Monomeric tRNA (m ⁷ G46) methyltransferase from <i>Escherichia coli</i> presents a novel structure at the function-essential insertion. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 512-515. | 2.6 | 11 |
| 62 | 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 |
| 63 | 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 |
| 64 | 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 |
| 65 | 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 |
| 66 | 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 |
| 67 | Crystallization and preliminary crystallographic analysis of tRNA (m ⁷ G46) methyltransferase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 743-745. | 0.7 | 4 |
| 68 | 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 |
| 69 | 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 |
| 70 | 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 |
| 71 | 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 |
| 72 | 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 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | Comparison of protein interaction networks reveals species conservation and divergence. <i>BMC Bioinformatics</i> , 2006, 7, 457. | 2.6 | 44 |
| 75 | NetAlign: a web-based tool for comparison of protein interaction networks. <i>Bioinformatics</i> , 2006, 22, 2175-2177. | 4.1 | 67 |
| 76 | 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 |
| 77 | 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 |
| 78 | 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 |
| 79 | 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 |
| 80 | How does agkicetin-C bind on platelet glycoprotein Ib α and achieve its platelet effects?. <i>Toxicon</i> , 2005, 45, 561-570. | 1.6 | 16 |
| 81 | 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 |
| 82 | 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 |
| 83 | 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 pallasvenom</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 974-977. | 2.5 | 52 |
| 84 | 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 |
| 85 | Hydrogen peroxide produced by two amino acid oxidases mediates antibacterial actions. <i>Journal of Microbiology</i> , 2004, 42, 336-9. | 2.8 | 33 |
| 86 | Purification, N-terminal sequencing, partial characterization, crystallization and preliminary crystallographic analysis of two glycosylated serine proteinases from <i>Agkistrodon acutusvenom</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 547-550. | 2.5 | 11 |
| 87 | Purification, crystallization and preliminary crystallographic analysis of AHP IX-bp, a zinc ion and pH-dependent coagulation factor IX binding protein from <i>Agkistrodon halys Pallas</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 730-733. | 2.5 | 14 |
| 88 | 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 |
| 89 | 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 acutusvenom</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2310-2312. | 2.5 | 12 |
| 90 | 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 |

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|----|--|-----|-----------|
| 91 | Purification, N-terminal sequencing, crystallization and preliminary X-ray diffraction analysis of atratoxin, a new short-chain $\hat{\pm}$ -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 |
| 92 | 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 |
| 93 | 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 |
| 94 | 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 |
| 95 | 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 |
| 96 | 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 |