Chun Tang

List of Publications by Year
in descending order

76	5,021	159585 30	95266 68
papers	citations	h-index	g-index

91	91	91	6014
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural basis of N6-adenosine methylation by the METTL3â€“METTL14 complex. Nature, 2016, 534, 575-578.	27.8	807
2	Visualization of transient encounter complexes in proteinâ€“protein association. Nature, 2006, 444, 383-386.	27.8	397
3	Open-to-closed transition in apo maltose-binding protein observed by paramagnetic NMR. Nature, 2007, 449, 1078-1082.	27.8	390
4	Entropic switch regulates myristate exposure in the HIV-1 matrix protein. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 517-522.	7.1	293
5	Practical aspects of 1H transverse paramagnetic relaxation enhancement measurements on macromolecules. Journal of Magnetic Resonance, 2007, 184, 185-195.	2.1	239
6	Antiviral Inhibition of the HIV-1 Capsid Protein. Journal of Molecular Biology, 2003, 327, 1013-1020.	4.2	204
7	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. Current Opinion in Structural Biology, 2007, 17, 603-616.	5.7	201
8	FRET-based dynamic structural biology: Challenges, perspectives and an appeal for open-science practices. ELife, 2021, 10, .	6.0	152
9	Structure of the N-terminal 283-residue fragment of the immature HIV-1 Gag polyprotein. Nature Structural Biology, 2002, 9, 537-43.	9.7	151
10	Structure of the Antiviral Assembly Inhibitor CAP-1 Complex with the HIV-1 CA Protein. Journal of Molecular Biology, 2007, 373, 355-366.	4.2	144
11	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. Nature, 2008, 455, 693-696.	27.8	123
12	Replica exchange simulations of transient encounter complexes in proteinâ€“protein association. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12855-12860.	7.1	107
13	Hemi-methylated DNA opens a closed conformation of UHRF1 to facilitate its histone recognition. Nature Communications, 2016, 7, 11197.	12.8	100
14	Solution structure of the RNA recognition domain of METTL3-METTL14 N6-methyladenosine methyltransferase. Protein and Cell, 2019, 10, 272-284.	11.0	99
15	Requirement for p62 acetylation in the aggregation of ubiquitylated proteins under nutrient stress. Nature Communications, 2019, 10, 5792.	12.8	83
16	Visualization of Transient Ultra-Weak Protein Self-Association in Solution Using Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2008, 130, 4048-4056.	13.7	80
17	Noncovalent Dimerization of Ubiquitin. Angewandte Chemie - International Edition, 2012, 51, 469-472.	13.8	80
18	Role of Electrostatic Interactions in Transient Encounter Complexes in Proteinâ^'Protein Association Investigated by Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2007, 129, 12954-12955.	13.7	73

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19	Two Distinct Buckling Modes in Carbon Nanotube Bending. Nano Letters, 2007, 7, 143-148.	9.1	62
20	Structural basis of nonribosomal peptide macrocyclization in fungi. Nature Chemical Biology, 2016, 12, 1001-1003.	8.0	54
21	Exploration of Multi-State Conformational Dynamics and Underlying Global Functional Landscape of Maltose Binding Protein. PLoS Computational Biology, 2012, 8, e1002471.	3.2	50
22	Lys63-linked ubiquitin chain adopts multiple conformational states for specific target recognition. ELife, 2015, 4, .	6.0	50
23	Transient proteinâ€“protein interactions visualized by solution NMR. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 115-122.	2.3	49
24	Modeling Protein Excited-state Structures from â€œOver-lengthâ€•Chemical Cross-links. Journal of Biological Chemistry, 2017, 292, 1187-1196.	3.4	48
25	Molecular mechanism for Rabex-5 GEF activation by Rabaptin-5. ELife, 2014, 3, .	6.0	47
26	Carboxylate-Selective Chemical Cross-Linkers for Mass Spectrometric Analysis of Protein Structures. Analytical Chemistry, 2018, 90, 1195-1201.	6.5	42
27	Ubiquitin S65 phosphorylation engenders a pH-sensitive conformational switch. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6770-6775.	7.1	40
28	Lipid-dependent conformational dynamics underlie the functional versatility of T-cell receptor. Cell Research, 2017, 27, 505-525.	12.0	38
29	NMR Model of Prglâ€“SipD Interaction and Its Implications in the Needle-Tip Assembly of the Salmonella Type III Secretion System. Journal of Molecular Biology, 2014, 426, 2958-2969.	4.2	36
30	Protein Structural Ensembles Visualized by Solvent Paramagnetic Relaxation Enhancement. Angewandte Chemie - International Edition, 2017, 56, 1002-1006.	13.8	34
31	A simple and reliable approach to docking proteinâ€“protein complexes from very sparse NOE-derived intermolecular distance restraints. Journal of Biomolecular NMR, 2006, 36, 37-44.	2.8	32
32	Characterizing Dynamic Proteinâˆ’Protein Interactions Using Differentially Scaled Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2009, 131, 17291-17297.	13.7	30
33	Characterization of the Interaction between the Salmonella Type III Secretion System Tip Protein SipD and the Needle Protein PrgI by Paramagnetic Relaxation Enhancement. Journal of Biological Chemistry, 2011, 286, 4922-4930.	3.4	30
34	PolyUbiquitin Chain Linkage Topology Selects the Functions from the Underlying Binding Landscape. PLoS Computational Biology, 2014, 10, e1003691.	3.2	30
35	Theory and practice of using solvent paramagnetic relaxation enhancement to characterize protein conformational dynamics. Methods, 2018, 148, 48-56.	3.8	28
36	Nicotinamide phosphoribosyltransferase secreted from microglia via exosome during ischemic injury. Journal of Neurochemistry, 2019, 150, 723-737.	3.9	28

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37	Structural basis for the recognition of K48-linked Ub chain by proteasomal receptor Rpn13. Cell Discovery, 2019, 5, 19.	6.7	27
38	Visualizing the Ensemble Structures of Protein Complexes Using Chemical Cross-Linking Coupled with Mass Spectrometry. Biophysics Reports, 2015, 1, 127-138.	0.8	26
39	Cerebral Ischemia Is Exacerbated by Extracellular Nicotinamide Phosphoribosyltransferase via a Non-Enzymatic Mechanism. PLoS ONE, 2013, 8, e85403.	2.5	24
40	Visualizing an Ultraâ€Weak Proteinâ€“Protein Interaction in Phosphorylation Signaling. Angewandte Chemie - International Edition, 2014, 53, 11501-11505.	13.8	24
41	Conjoined Use of EM and NMR in RNA Structure Refinement. PLoS ONE, 2015, 10, e0120445.	2.5	24
42	Characterizing Protein Dynamics with Integrative Use of Bulk and Single-Molecule Techniques. Biochemistry, 2018, 57, 305-313.	2.5	21
43	Characterization of protein unfolding by fast cross-linking mass spectrometry using di-ortho-phthalaldehyde cross-linkers. Nature Communications, 2022, 13, 1468.	12.8	20
44	Subtle Dynamics of holo Glutamine Binding Protein Revealed with a Rigid Paramagnetic Probe. Biochemistry, 2014, 53, 1403-1409.	2.5	19
45	NAMPT inhibitor and metabolite protect mouse brain from cryoinjury through distinct mechanisms. Neuroscience, 2015, 291, 230-240.	2.3	18
46	A decadentate Gd(III)-coordinating paramagnetic cosolvent for protein relaxation enhancement measurement. Journal of Biomolecular NMR, 2014, 58, 149-154.	2.8	17
47	Understanding the graphene quantum dots-ubiquitin interaction by identifying the interaction sites. Carbon, 2017, 121, 285-291.	10.3	17
48	Lanthanoid tagging via an unnatural amino acid for protein structure characterization. Journal of Biomolecular NMR, 2017, 67, 273-282.	2.8	17
49	NASR: An Effective Approach for Simultaneous Noise and Artifact Suppression in NMR Spectroscopy. Analytical Chemistry, 2013, 85, 2523-2528.	6.5	15
50	Specific cell surface labeling of GPCRs using split GFP. Scientific Reports, 2016, 6, 20568.	3.3	15
51	Tightening the Crosslinking Distance Restraints for Better Resolution of Protein Structure and Dynamics. Structure, 2020, 28, 1160-1167.e3.	3.3	15
52	Characterization of the Raptor/4E-BP1 Interaction by Chemical Cross-linking Coupled with Mass Spectrometry Analysis. Journal of Biological Chemistry, 2014, 289, 4723-4734.	3.4	14
53	Nucleobase Clustering Contributes to the Formation and Hollowing of Repeat-Expansion RNA Condensate. Journal of the American Chemical Society, 2022, 144, 4716-4720.	13.7	14
54	Integrating Non-NMR Distance Restraints to Augment NMR Depiction of Protein Structure and Dynamics. Journal of Molecular Biology, 2020, 432, 2913-2929.	4.2	13

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55	Accurate Determination of Leucine and Valine Side-chain Conformations using U-[15N/13C/2H]/[1H-(methine/methyl)-Leu/Val] Isotope Labeling, NOE Pattern Recognition, and Methine Cî³â€“Hî³/Cî²â€“Hî² Residual Dipolar Couplings: Application to the 34-kDa Enzyme IIAChitobiose. Journal of Biomolecular NMR, 2005, 33, 105-121.	2.8	12
56	Structural insights into DNA recognition by AimR of the arbitrium communication system in the SPbeta phage. Cell Discovery, 2019, 5, 29.	6.7	12
57	Protocol for analyzing protein ensemble structures from chemical cross-links using DynaXL. Biophysics Reports, 2017, 3, 100-108.	0.8	10
58	Solution Structure of Enzyme IIAChitobiose from the N,Nâ€²-Diacetylchitobiose Branch of the Escherichia coli Phosphotransferase System. Journal of Biological Chemistry, 2005, 280, 11770-11780.	3.4	9
59	How Phosphorylation by PINK1 Remodels the Ubiquitin System: A Perspective from Structure and Dynamics. Biochemistry, 2020, 59, 26-33.	2.5	9
60	FLIMâ€“FRET-Based Structural Characterization of a Class-A GPCR Dimer in the Cell Membrane. Journal of Molecular Biology, 2020, 432, 4596-4611.	4.2	9
61	Preferential Interactions of a Crowder Protein with the Specific Binding Site of a Native Protein Complex. Journal of Physical Chemistry Letters, 2022, 13, 792-800.	4.6	8
62	Recent Developments in Data-Assisted Modeling of Flexible Proteins. Frontiers in Molecular Biosciences, 2021, 8, 765562.	3.5	8
63	The Conformational Preference of Chemical Cross-linkers Determines the Cross-linking Probability of Reactive Protein Residues. Journal of Physical Chemistry B, 2020, 124, 4446-4453.	2.6	7
64	Discovery of a Novel Androgen Receptor Antagonist Manifesting Evidence to Disrupt the Dimerization of the Ligand-Binding Domain via Attenuating the Hydrogen-Bonding Network Between the Two Monomers. Journal of Medicinal Chemistry, 2021, 64, 17221-17238.	6.4	7
65	Protein dynamics elucidated by NMR technique. Protein and Cell, 2013, 4, 726-730.	11.0	6
66	Ensemble structure description of Lys63-linked diubiquitin. Data in Brief, 2016, 7, 81-88.	1.0	6
67	Ubiquitin is double-phosphorylated by PINK1 for enhanced pH-sensitivity of conformational switch. Protein and Cell, 2019, 10, 908-913.	11.0	6
68	On the necessity of an integrative approach to understand protein structural dynamics. Journal of Zhejiang University: Science B, 2019, 20, 496-502.	2.8	5
69	Protein Structural Ensembles Visualized by Solvent Paramagnetic Relaxation Enhancement. Angewandte Chemie, 2017, 129, 1022-1026.	2.0	4
70	Refining RNA solution structures with the integrative use of label-free paramagnetic relaxation enhancement NMR. Biophysics Reports, 2019, 5, 244-253.	0.8	4
71	Pseudopotentials for coarseâ€grained crossâ€linkâ€assisted modeling of protein structures. Journal of Computational Chemistry, 2021, 42, 2054-2067.	3.3	4
72	Kinetic Constraints in the Specific Interaction between Phosphorylated Ubiquitin and Proteasomal Shuttle Factors. Biomolecules, 2021, 11, 1008.	4.0	2

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73	Hierarchical Conformational Dynamics Confers Thermal Adaptability to preQ1 RNA Riboswitches. Journal of Molecular Biology, 2020, 432, 4523-4543.	4.2	1
74	Preferential Regulation of Transient Proteinâ€“Protein Interaction by the Macromolecular Crowders. Journal of Physical Chemistry B, 2022, 126, 4840-4848.	2.6	1
75	Two Methods to Synthesize C60Nitroxide Derivatives. Fullerenes, Nanotubes, and Carbon Nanostructures, 1999, 7, 297-303.	0.6	0
76	Estimation of protein dynamic states with single molecule fluorescence data analysis at microsecond scale. , 2016, , .		0