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	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
2	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
3	Characterization of protein unfolding by fast cross-linking mass spectrometry using di-ortho-phthalaldehyde cross-linkers. Nature Communications, 2022, 13, 1468.	12.8	20
4	Preferential Regulation of Transient Proteinâ€“Protein Interaction by the Macromolecular Crowders. Journal of Physical Chemistry B, 2022, 126, 4840-4848.	2.6	1
5	FRET-based dynamic structural biology: Challenges, perspectives and an appeal for open-science practices. ELife, 2021, 10, .	6.0	152
6	Kinetic Constraints in the Specific Interaction between Phosphorylated Ubiquitin and Proteasomal Shuttle Factors. Biomolecules, 2021, 11, 1008.	4.0	2
7	Pseudopotentials for coarseâ€grained crossâ€linkâ€assisted modeling of protein structures. Journal of Computational Chemistry, 2021, 42, 2054-2067.	3.3	4
8	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
9	Recent Developments in Data-Assisted Modeling of Flexible Proteins. Frontiers in Molecular Biosciences, 2021, 8, 765562.	3.5	8
10	How Phosphorylation by PINK1 Remodels the Ubiquitin System: A Perspective from Structure and Dynamics. Biochemistry, 2020, 59, 26-33.	2.5	9
11	Tightening the Crosslinking Distance Restraints for Better Resolution of Protein Structure and Dynamics. Structure, 2020, 28, 1160-1167.e3.	3.3	15
12	Hierarchical Conformational Dynamics Confers Thermal Adaptability to preQ1 RNA Riboswitches. Journal of Molecular Biology, 2020, 432, 4523-4543.	4.2	1
13	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
14	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
15	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
16	Ubiquitin is double-phosphorylated by PINK1 for enhanced pH-sensitivity of conformational switch. Protein and Cell, 2019, 10, 908-913.	11.0	6
17	Nicotinamide phosphoribosyltransferase secreted from microglia via exosome during ischemic injury. Journal of Neurochemistry, 2019, 150, 723-737.	3.9	28
18	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

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19	Structural insights into DNA recognition by AimR of the arbitrium communication system in the SPbeta phage. Cell Discovery, 2019, 5, 29.	6.7	12
20	Structural basis for the recognition of K48-linked Ub chain by proteasomal receptor Rpn13. Cell Discovery, 2019, 5, 19.	6.7	27
21	Refining RNA solution structures with the integrative use of label-free paramagnetic relaxation enhancement NMR. Biophysics Reports, 2019, 5, 244-253.	0.8	4
22	Requirement for p62 acetylation in the aggregation of ubiquitylated proteins under nutrient stress. Nature Communications, 2019, 10, 5792.	12.8	83
23	Solution structure of the RNA recognition domain of METTL3-METTL14 N6-methyladenosine methyltransferase. Protein and Cell, 2019, 10, 272-284.	11.0	99
24	Theory and practice of using solvent paramagnetic relaxation enhancement to characterize protein conformational dynamics. Methods, 2018, 148, 48-56.	3.8	28
25	Carboxylate-Selective Chemical Cross-Linkers for Mass Spectrometric Analysis of Protein Structures. Analytical Chemistry, 2018, 90, 1195-1201.	6.5	42
26	Characterizing Protein Dynamics with Integrative Use of Bulk and Single-Molecule Techniques. Biochemistry, 2018, 57, 305-313.	2.5	21
27	Understanding the graphene quantum dots-ubiquitin interaction by identifying the interaction sites. Carbon, 2017, 121, 285-291.	10.3	17
28	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
29	Lanthanoid tagging via an unnatural amino acid for protein structure characterization. Journal of Biomolecular NMR, 2017, 67, 273-282.	2.8	17
30	Lipid-dependent conformational dynamics underlie the functional versatility of T-cell receptor. Cell Research, 2017, 27, 505-525.	12.0	38
31	Modeling Protein Excited-state Structures from â€œOver-lengthâ€•Chemical Cross-links. Journal of Biological Chemistry, 2017, 292, 1187-1196.	3.4	48
32	Protein Structural Ensembles Visualized by Solvent Paramagnetic Relaxation Enhancement. Angewandte Chemie, 2017, 129, 1022-1026.	2.0	4
33	Protein Structural Ensembles Visualized by Solvent Paramagnetic Relaxation Enhancement. Angewandte Chemie - International Edition, 2017, 56, 1002-1006.	13.8	34
34	Protocol for analyzing protein ensemble structures from chemical cross-links using DynaXL. Biophysics Reports, 2017, 3, 100-108.	0.8	10
35	Specific cell surface labeling of GPCRs using split GFP. Scientific Reports, 2016, 6, 20568.	3.3	15
36	Estimation of protein dynamic states with single molecule fluorescence data analysis at microsecond scale. , 2016, , .		0

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37	Structural basis of N6-adenosine methylation by the METTL3â€“METTL14 complex. Nature, 2016, 534, 575-578.	27.8	807
38	Structural basis of nonribosomal peptide macrocyclization in fungi. Nature Chemical Biology, 2016, 12, 1001-1003.	8.0	54
39	Hemi-methylated DNA opens a closed conformation of UHRF1 to facilitate its histone recognition. Nature Communications, 2016, 7, 11197.	12.8	100
40	Ensemble structure description of Lys63-linked diubiquitin. Data in Brief, 2016, 7, 81-88.	1.0	6
41	Transient proteinâ€“protein interactions visualized by solution NMR. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 115-122.	2.3	49
42	Visualizing the Ensemble Structures of Protein Complexes Using Chemical Cross-Linking Coupled with Mass Spectrometry. Biophysics Reports, 2015, 1, 127-138.	0.8	26
43	NAMPT inhibitor and metabolite protect mouse brain from cryoinjury through distinct mechanisms. Neuroscience, 2015, 291, 230-240.	2.3	18
44	Conjoined Use of EM and NMR in RNA Structure Refinement. PLoS ONE, 2015, 10, e0120445.	2.5	24
45	Lys63-linked ubiquitin chain adopts multiple conformational states for specific target recognition. ELife, 2015, 4, .	6.0	50
46	PolyUbiquitin Chain Linkage Topology Selects the Functions from the Underlying Binding Landscape. PLoS Computational Biology, 2014, 10, e1003691.	3.2	30
47	A decadentate Gd(III)-coordinating paramagnetic cosolvent for protein relaxation enhancement measurement. Journal of Biomolecular NMR, 2014, 58, 149-154.	2.8	17
48	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
49	Subtle Dynamics of holo Glutamine Binding Protein Revealed with a Rigid Paramagnetic Probe. Biochemistry, 2014, 53, 1403-1409.	2.5	19
50	Visualizing an Ultraâ€Weak Proteinâ€“Protein Interaction in Phosphorylation Signaling. Angewandte Chemie - International Edition, 2014, 53, 11501-11505.	13.8	24
51	NMR Model of PrgIâ€“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
52	Molecular mechanism for Rabex-5 GEF activation by Rabaptin-5. ELife, 2014, 3, .	6.0	47
53	Protein dynamics elucidated by NMR technique. Protein and Cell, 2013, 4, 726-730.	11.0	6
54	NASR: An Effective Approach for Simultaneous Noise and Artifact Suppression in NMR Spectroscopy. Analytical Chemistry, 2013, 85, 2523-2528.	6.5	15

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55	Cerebral Ischemia Is Exacerbated by Extracellular Nicotinamide Phosphoribosyltransferase via a Non-Enzymatic Mechanism. PLoS ONE, 2013, 8, e85403.	2.5	24
56	Exploration of Multi-State Conformational Dynamics and Underlying Global Functional Landscape of Maltose Binding Protein. PLoS Computational Biology, 2012, 8, e1002471.	3.2	50
57	Noncovalent Dimerization of Ubiquitin. Angewandte Chemie - International Edition, 2012, 51, 469-472.	13.8	80
58	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
59	Characterizing Dynamic Proteinâ^'Protein Interactions Using Differentially Scaled Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2009, 131, 17291-17297.	13.7	30
60	Visualizing transient events in amino-terminal autoprocessing of HIV-1 protease. Nature, 2008, 455, 693-696.	27.8	123
61	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
62	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
63	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
64	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
65	Two Distinct Buckling Modes in Carbon Nanotube Bending. Nano Letters, 2007, 7, 143-148.	9.1	62
66	Practical aspects of 1H transverse paramagnetic relaxation enhancement measurements on macromolecules. Journal of Magnetic Resonance, 2007, 184, 185-195.	2.1	239
67	Open-to-closed transition in apo maltose-binding protein observed by paramagnetic NMR. Nature, 2007, 449, 1078-1082.	27.8	390
68	Elucidating transient macromolecular interactions using paramagnetic relaxation enhancement. Current Opinion in Structural Biology, 2007, 17, 603-616.	5.7	201
69	Visualization of transient encounter complexes in proteinâ€“protein association. Nature, 2006, 444, 383-386.	27.8	397
70	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
71	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
72	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

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73	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
74	Antiviral Inhibition of the HIV-1 Capsid Protein. Journal of Molecular Biology, 2003, 327, 1013-1020.	4.2	204
75	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
76	Two Methods to Synthesize C60Nitroxide Derivatives. Fullerenes, Nanotubes, and Carbon Nanostructures, 1999, 7, 297-303.	0.6	0