Jianxing Song

List of Publications by Year in descending order

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106	3,814	136740	168136
papers	citations	32 h-index	53 g-index

132	132	132	3943
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<scp>CTD</scp> of <scp>SARSâ€CoV</scp>â€2 N protein is a cryptic domain for binding <scp>ATP</scp> and nucleic acid that interplay in modulating phase separation. Protein Science, 2022, 31, 345-356.	3.1	18
2	Myricetin Allosterically Inhibits the Dengue NS2B-NS3 Protease by Disrupting the Active and Locking the Inactive Conformations. ACS Omega, 2022, 7, 2798-2808.	1.6	6
3	A review of the effects of ATP and hydroxychloroquine on the phase separation of the SARS-CoV-2 nucleocapsid protein. Biophysical Reviews, 2022, 14, 709-715.	1.5	4
4	Tethering-induced destabilization and ATP-binding for tandem RRM domains of ALS-causing TDP-43 and hnRNPA1. Scientific Reports, 2021, 11, 1034.	1.6	12
5	ATP biphasically modulates LLPS of SARS-CoV-2 nucleocapsid protein and specifically binds its RNA-binding domain. Biochemical and Biophysical Research Communications, 2021, 541, 50-55.	1.0	36
6	Adenosine triphosphate energyâ€independently controls protein homeostasis with unique structure and diverse mechanisms. Protein Science, 2021, 30, 1277-1293.	3.1	38
7	ATP biphasically modulates LLPS of TDP-43 PLD by specifically binding arginine residues. Communications Biology, 2021, 4, 714.	2.0	21
8	Structural basis of anti-SARS-CoV-2 activity of HCQ: specific binding to N protein to disrupt its interaction with nucleic acids and LLPS. QRB Discovery, 2021, 2, .	0.6	1
9	ATP binds nucleic-acid-binding domains beyond RRM fold. Biochemical and Biophysical Research Communications, 2020, 522, 826-831.	1.0	5
10	ATP is a cryptic binder of TDP-43 RRM domains to enhance stability and inhibit ALS/AD-associated fibrillation. Biochemical and Biophysical Research Communications, 2020, 522, 247-253.	1.0	33
11	ATP differentially antagonizes the crowding-induced destabilization of human Î³S-crystallin and its four cataract-causing mutants. Biochemical and Biophysical Research Communications, 2020, 533, 913-918.	1.0	6
12	Cataract-causing G18V eliminates the antagonization by ATP against the crowding-induced destabilization of human Î³S-crystallin. Biochemical and Biophysical Research Communications, 2020, 530, 554-560.	1.0	4
13	ATP antagonizes the crowding-induced destabilization of the human eye-lens protein Î³S-crystallin. Biochemical and Biophysical Research Communications, 2020, 526, 1112-1117.	1.0	18
14	ALS-causing D169G mutation disrupts the ATP-binding capacity of TDP-43 RRM1 domain. Biochemical and Biophysical Research Communications, 2020, 524, 459-464.	1.0	16
15	Curcumin Allosterically Inhibits the Dengue NS2B-NS3 Protease by Disrupting Its Active Conformation. ACS Omega, 2020, 5, 25677-25686.	1.6	28
16	ATP binds and inhibits the neurodegeneration-associated fibrillization of the FUS RRM domain. Communications Biology, 2019, 2, 223.	2.0	65
17	A unified mechanism for LLPS of ALS/FTLD-causing FUS as well as its modulation by ATP and oligonucleic acids. PLoS Biology, 2019, 17, e3000327.	2.6	91
18	A novel mechanism for ATP to enhance the functional oligomerization of TDP-43 by specific binding. Biochemical and Biophysical Research Communications, 2019, 514, 809-814.	1.0	16

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19	Structurally- and dynamically-driven allostery of the chymotrypsin-like proteases of SARS, Dengue and Zika viruses. Progress in Biophysics and Molecular Biology, 2019, 143, 52-66.	1.4	22
20	TDP-43 NTD can be induced while CTD is significantly enhanced by ssDNA to undergo liquid-liquid phase separation. Biochemical and Biophysical Research Communications, 2018, 499, 189-195.	1.0	36
21	TMEM106B, a risk factor for FTLD and aging, has an intrinsically disordered cytoplasmic domain. PLoS ONE, 2018, 13, e0205856.	1.1	6
22	ATP enhances at low concentrations but dissolves at high concentrations liquid-liquid phase separation (LLPS) of ALS/FTD-causing FUS. Biochemical and Biophysical Research Communications, 2018, 504, 545-551.	1.0	60
23	Environment-transformable sequenceâ€“structure relationship: a general mechanism for proteotoxicity. Biophysical Reviews, 2018, 10, 503-516.	1.5	10
24	ALS-causing cleavages of TDP-43 abolish its RRM2 structure and unlock CTD for enhanced aggregation and toxicity. Biochemical and Biophysical Research Communications, 2017, 485, 826-831.	1.0	12
25	RRM domain of ALS/FTD-causing FUS characteristic of irreversible unfolding spontaneously self-assembles into amyloid fibrils. Scientific Reports, 2017, 7, 1043.	1.6	38
26	ALS-causing profilin-1-mutant forms a non-native helical structure in membrane environments. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 2161-2170.	1.4	19
27	Kinetoplastid membrane proteinâ€11 adopts a fourâ€helix bundle fold in <scp>DPC</scp> micelle. FEBS Letters, 2017, 591, 3793-3804.	1.3	5
28	Solution conformations of Zika NS2B-NS3pro and its inhibition by natural products from edible plants. PLoS ONE, 2017, 12, e0180632.	1.1	78
29	Transforming Cytosolic Proteins into â€œInsolubleâ€•and Membrane-toxic Forms Triggering Diseases/Aging by Genetic, Pathological or Environmental Factors. Protein and Peptide Letters, 2017, 24, 294-306.	0.4	10
30	ALS-Causing Mutations Significantly Perturb the Self-Assembly and Interaction with Nucleic Acid of the Intrinsically Disordered Prion-Like Domain of TDP-43. PLoS Biology, 2016, 14, e1002338.	2.6	160
31	C-Terminal Auto-Regulatory Motif of Hepatitis C Virus NS5B Interacts with Human VAPB-MSP to Form a Dynamic Replication Complex. PLoS ONE, 2016, 11, e0147278.	1.1	11
32	Germline replacement by blastula cell transplantation in the fish medaka. Scientific Reports, 2016, 6, 29658.	1.6	15
33	Inter-domain interactions of TDP-43 as decoded by NMR. Biochemical and Biophysical Research Communications, 2016, 473, 614-619.	1.0	29
34	SALS-linked WT-SOD1 adopts a highly similar helical conformation as FALS-causing L126Z-SOD1 in a membrane environment. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2223-2230.	1.4	19
35	Dnd Is a Critical Specifier of Primordial Germ Cells in the Medaka Fish. Stem Cell Reports, 2016, 6, 411-421.	2.3	56
36	NMR and MD Studies Reveal That the Isolated Dengue NS3 Protease Is an Intrinsically Disordered Chymotrypsin Fold Which Absolutely Requests NS2B for Correct Folding and Functional Dynamics. PLoS ONE, 2015, 10, e0134823.	1.1	42

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37	A monoclonal antibody binds to threonine 49 in the non-structural 1 protein of influenza A virus and interferes with its ability to modulate viral replication. Antiviral Research, 2015, 116, 55-61.	1.9	5
38	Dynamic Principle for Designing Antagonistic/Agonistic Molecules for EphA4 Receptor, the Only Known ALS Modifier. ACS Chemical Biology, 2015, 10, 372-378.	1.6	43
39	Mechanism for transforming cytosolic SOD1 into integral membrane proteins of organelles by ALS-causing mutations. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 1-7.	1.4	27
40	Insoluble Protein Characterization by Circular Dichroism (CD) Spectroscopy and Nuclear Magnetic Resonance (NMR). Methods in Molecular Biology, 2015, 1258, 371-385.	0.4	2
41	Dynamically-Driven Enhancement of the Catalytic Machinery of the SARS 3C-Like Protease by the S284-T285-I286/A Mutations on the Extra Domain. PLoS ONE, 2014, 9, e101941.	1.1	71
42	Disruption of FAT10â€“MAD2 binding inhibits tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5282-91.	3.3	48
43	TDP-43 N terminus encodes a novel ubiquitin-like fold and its unfolded form in equilibrium that can be shifted by binding to ssDNA. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18619-18624.	3.3	128
44	Structural study of hNck2 SH3 domain protein in solution by circular dichroism and X-ray solution scattering. Biophysical Chemistry, 2013, 175-176, 39-46.	1.5	4
45	ALS-causing P56S mutation and splicing variation on the hVAPB MSP domain transform its Î²-sandwich fold into lipid-interacting helical conformations. Biochemical and Biophysical Research Communications, 2013, 431, 398-403.	1.0	17
46	NMR binding and crystal structure reveal that intrinsically-unstructured regulatory domain auto-inhibits PAK4 by a mechanism different from that of PAK1. Biochemical and Biophysical Research Communications, 2013, 438, 169-174.	1.0	21
47	Resolving the paradox for protein aggregation diseases: NMR structure and dynamics of the membrane-embedded P56S-MSP causing ALS imply a common mechanism for aggregation-prone proteins to attack membranes. F1000Research, 2013, 2, 221.	0.8	7
48	Why do proteins aggregate? â€œIntrinsically insoluble proteinsâ€•and â€œdark mediatorsâ€•revealed by studies on â€œinsoluble proteinsâ€•solubilized in pure water. F1000Research, 2013, 2, 94.	0.8	40
49	Unique Structure and Dynamics of the EphA5 Ligand Binding Domain Mediate Its Binding Specificity as Revealed by X-ray Crystallography, NMR and MD Simulations. PLoS ONE, 2013, 8, e74040.	1.1	14
50	Distinctive binding of three antagonistic peptides to the ephrin-binding pocket of the EphA4 receptor. Biochemical Journal, 2012, 445, 47-56.	1.7	47
51	1PT157 Structural properties and folding process of hNck2 SH3 domain(The 50th Annual Meeting of the) Tj ETQq1 1 0.784314 rgBT /O	0.0	0
52	The variable N-terminal region of DDX5 contains structural elements and auto-inhibits its interaction with NS5B of hepatitis C virus. Biochemical Journal, 2012, 446, 37-46.	1.7	13
53	Fusion Gene Vectors Allowing for Simultaneous Drug Selection, Cell Labeling, and Reporter Assay in Vitro and in Vivo. Analytical Chemistry, 2012, 84, 987-993.	3.2	24
54	Interordinal Chimera Formation Between Medaka and Zebrafish for Analyzing Stem Cell Differentiation. Stem Cells and Development, 2012, 21, 2333-2341.	1.1	27

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55	A Î²-sheet structure interacting peptide for intracellular protein delivery into human pluripotent stem cells and their derivatives. Biochemical and Biophysical Research Communications, 2012, 421, 616-620.	1.0	0
56	Mitf is a transcriptional activator of medaka germ genes in culture. Biochimie, 2012, 94, 759-767.	1.3	15
57	VAPC, an Human Endogenous Inhibitor for Hepatitis C Virus (HCV) Infection, Is Intrinsically Unstructured but Forms a â€œFuzzy Complexâ€•with HCV NS5B. PLoS ONE, 2012, 7, e40341.	1.1	12
58	A Small Molecule Agonist of EphA2 Receptor Tyrosine Kinase Inhibits Tumor Cell Migration In Vitro and Prostate Cancer Metastasis In Vivo. PLoS ONE, 2012, 7, e42120.	1.1	103
59	"Dark Mediators" of Proteins as Revealed by NMR in Water: Residue-selective Anion Bindings that are Masked by Pre-existing Buffer. Nature Precedings, 2012, , .	0.1	0
60	Solubilization of M2 Transmembrane Peptide of Influenza A in Pure Water: Implications for Emergence of Proteins and Protein-embedded Primeval Membranes in Unsalted Oceans. Nature Precedings, 2012, , .	0.1	0
61	Protein dynamics at Eph receptor-ligand interfaces as revealed by crystallography, NMR and MD simulations. BMC Biophysics, 2012, 5, 2.	4.4	22
62	Microfibers Fabricated by Nonâ€Covalent Assembly of Peptide and DNA for Viral Vector Encapsulation and Cancer Therapy. Advanced Materials, 2012, 24, 3280-3284.	11.1	15
63	Intrinsically Unstructured Domain 3 of Hepatitis C Virus NS5A Forms a â€œFuzzy Complexâ€•with VAPB-MSP Domain Which Carries ALS-Causing Mutations. PLoS ONE, 2012, 7, e39261.	1.1	39
64	Structural, Stability, Dynamic and Binding Properties of the ALS-Causing T46I Mutant of the hVAPB MSP Domain as Revealed by NMR and MD Simulations. PLoS ONE, 2011, 6, e27072.	1.1	28
65	A Disalicylic Acidâ€Furanyl Derivative Inhibits Ephrin Binding to a Subset of Eph Receptors. Chemical Biology and Drug Design, 2011, 78, 667-678.	1.5	39
66	Selective and specific ion binding on proteins at physiologically-relevant concentrations. FEBS Letters, 2011, 585, 3126-3132.	1.3	20
67	Dynamically-Driven Inactivation of the Catalytic Machinery of the SARS 3C-Like Protease by the N214A Mutation on the Extra Domain. PLoS Computational Biology, 2011, 7, e1001084.	1.5	49
68	Structure of the Arabidopsis thaliana DCL4 DUF283 domain reveals a noncanonical double-stranded RNA-binding fold for proteinâ€“protein interaction. Rna, 2010, 16, 474-481.	1.6	84
69	Structural Characterization of the EphA4-Ephrin-B2 Complex Reveals New Features Enabling Eph-Ephrin Binding Promiscuity. Journal of Biological Chemistry, 2010, 285, 644-654.	1.6	84
70	Elimination of the Native Structure and Solubility of the hVAPB MSP Domain by the Pro56Ser Mutation That Causes Amyotrophic Lateral Sclerosis. Biochemistry, 2010, 49, 3887-3897.	1.2	43
71	Structural characterization reveals that viperin is a radical S-adenosyl-l-methionine (SAM) enzyme. Biochemical and Biophysical Research Communications, 2010, 391, 1390-1395.	1.0	79
72	Insight into â€œinsoluble proteinsâ€•with pure water. FEBS Letters, 2009, 583, 953-959.	1.3	51

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73	NMR studies reveal a novel mode for hFADD to bind with the unstructured hRTN3 which initiates the ER-stress activated apoptosis. Biochemical and Biophysical Research Communications, 2009, 383, 433-439.	1.0	5
74	Insights into Protein Aggregation by NMR Characterization of Insoluble SH3 Mutants Solubilized in Salt-Free Water. PLoS ONE, 2009, 4, e7805.	1.1	20
75	NMR structure and dynamics of human ephrinâ€B2 ectodomain: The functionally critical Câ€D and Gâ€H loops are highly dynamic in solution. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1019-1029.	1.5	20
76	Identification, recombinant production and structural characterization of four silk proteins from the Asiatic honeybee Apis cerana. Biomaterials, 2008, 29, 2820-2828.	5.7	44
77	NMR Evidence for Forming Highly Populated Helical Conformations in the Partially Folded hNck2 SH3 Domain. Biophysical Journal, 2008, 95, 4803-4812.	0.2	18
78	A novel nucleolar transcriptional activator ApLLP for long-term memory formation is intrinsically unstructured but functionally active. Biochemical and Biophysical Research Communications, 2008, 366, 585-591.	1.0	17
79	Rational design, solution conformation and identification of functional residues of the soluble and structured Nogo-54, which mimics Nogo-66 in inhibiting the CNS neurite outgrowth. Biochemical and Biophysical Research Communications, 2008, 373, 498-503.	1.0	6
80	Identification and Structural Mechanism for a Novel Interaction between a Ubiquitin Ligase WWP1 and Nogo-A, a Key Inhibitor for Central Nervous System Regeneration. Biochemistry, 2008, 47, 13647-13658.	1.2	19
81	Crystal Structure and NMR Binding Reveal That Two Small Molecule Antagonists Target the High Affinity Ephrin-binding Channel of the EphA4 Receptor. Journal of Biological Chemistry, 2008, 283, 29473-29484.	1.6	66
82	Mechanism for Controlling the Dimer-Monomer Switch and Coupling Dimerization to Catalysis of the Severe Acute Respiratory Syndrome Coronavirus 3C-Like Protease. Journal of Virology, 2008, 82, 4620-4629.	1.5	137
83	Nogo-B receptor possesses an intrinsically unstructured ectodomain and a partially folded cytoplasmic domain. Biochemical and Biophysical Research Communications, 2007, 360, 128-134.	1.0	16
84	The N- and C-termini of the human Nogo molecules are intrinsically unstructured: Bioinformatics, CD, NMR characterization, and functional implications. Proteins: Structure, Function and Bioinformatics, 2007, 68, 100-108.	1.5	38
85	NMR Assignment of the Human EphrinB2 Ectodomain. Journal of Biomolecular NMR, 2007, 38, 171-171.	1.6	1
86	Resurrecting Abandoned Proteins with Pure Water: CD and NMR Studies of Protein Fragments Solubilized in Salt-Free Water. Biophysical Journal, 2006, 91, 4201-4209.	0.2	47
87	Structural Insight into the Binding Diversity between the Human Nck2 SH3 Domains and Proline-Rich Proteinsâ€,â€¡. Biochemistry, 2006, 45, 7171-7184.	1.2	36
88	The catalysis of the SARS 3C-like protease is under extensive regulation by its extra domain. FEBS Journal, 2006, 273, 1035-1045.	2.2	133
89	Nogo goes in the pure water: Solution structure of Nogo-60 and design of the structured and buffer-soluble Nogo-54 for enhancing CNS regeneration. Protein Science, 2006, 15, 1835-1841.	3.1	27
90	Identification of a Novel Nonstructural Protein, VP9, from White Spot Syndrome Virus: Its Structure Reveals a Ferredoxin Fold with Specific Metal Binding Sites. Journal of Virology, 2006, 80, 10419-10427.	1.5	29

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91	Structural Insight into the Binding Diversity between the Tyr-phosphorylated Human EphrinBs and Nck2 SH2 Domain. Journal of Biological Chemistry, 2005, 280, 19205-19212.	1.6	18
92	Molecular Mechanism Underlying the Thermal Stability and pH-induced Unfolding of CHABII. Journal of Molecular Biology, 2005, 348, 205-218.	2.0	35
93	Dissection Study on the Severe Acute Respiratory Syndrome 3C-like Protease Reveals the Critical Role of the Extra Domain in Dimerization of the Enzyme. Journal of Biological Chemistry, 2004, 279, 24765-24773.	1.6	166
94	Structural characterization of the human Nogo-A functional domains. FEBS Journal, 2004, 271, 3512-3522.	0.2	19
95	Tyrosine Phosphorylation of the Well Packed EphrinB Cytoplasmic Î²-Hairpin for Reverse Signaling. Journal of Biological Chemistry, 2003, 278, 24714-24720.	1.6	24
96	Solution Structure and Backbone Dynamics of the Functional Cytoplasmic Subdomain of Human Ephrin B2, a Cell-Surface Ligand with Bidirectional Signaling Propertiesâ€. Biochemistry, 2002, 41, 10942-10949.	1.2	28
97	Stability of protein-bound conformations of bioactive peptides: The folded conformation of an epidermal growth factor-like thrombomodulin fragment is similar to that recognized by thrombin. Biopolymers, 2002, 65, 373-386.	1.2	2
98	A model of dynamic side-chain-side-chain interactions in the alpha-lactalbumin molten globule. Protein Science, 2001, 10, 55-62.	3.1	13
99	Molecular Interactions of the GÎ² Binding Domain of the Ste20p/PAK Family of Protein Kinases. Journal of Biological Chemistry, 2001, 276, 41205-41212.	1.6	14
100	The active-site residue Cys-29 is responsible for the neutral-pH inactivation and the refolding barrier of human cathepsin B. FEBS Letters, 2000, 475, 157-162.	1.3	18
101	A gradual disruption of tight side-chain packing: 2D 1H-NMR characterization of acid-induced unfolding of CHABII. Nature Structural Biology, 1999, 6, 129-134.	9.7	36
102	NMR for the design of functional mimetics of protein-protein interactions: one key is in the building of bridges. Biochemistry and Cell Biology, 1998, 76, 177-188.	0.9	38
103	Contribution of individual residues to formation of the native-like tertiary topology in the Î±-lactalbumin molten globule. Journal of Molecular Biology, 1998, 280, 167-174.	2.0	76
104	On the Convergent Evolution of Animal Toxins. Journal of Biological Chemistry, 1997, 272, 4302-4309.	1.6	314
105	NMR Solution Structure of a Two-Disulfide Derivative of Charybdotoxin:â€‰ Structural Evidence for Conservation of Scorpion Toxin Î±/Î² Motif and Its Hydrophobic Side Chain Packing,. Biochemistry, 1997, 36, 3760-3766.	1.2	31
106	Resolving the paradox for protein aggregation diseases: a common mechanism for aggregated proteins to initially attack membranes without needing aggregates. F1000Research, 0, 2, 221.	0.8	10