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List of Publications by Year
in descending order

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108 papers	6,899 citations	61857 43 h-index	64668 79 g-index
118 all docs	118 docs citations	118 times ranked	7041 citing authors

#	Article	IF	Citations
1	A FRET-Based Biosensor for the Src N-Terminal Regulatory Element. Biosensors, 2022, 12, 96.	2.3	1
2	Molecular and cellular insight into Escherichia coli SslE and its role during biofilm maturation. Npj Biofilms and Microbiomes, 2022, 8, 9.	2.9	8
3	Structural Insights into the Intrinsically Disordered GPCR C-Terminal Region, Major Actor in Arrestin-GPCR Interaction. Biomolecules, 2022, 12, 617.	1.8	7
4	Tailoring the NIRâ€II Photoluminescence of Single Thiolated Au₂₅ Nanoclusters by Selective Binding to Proteins**. Chemistry - A European Journal, 2022, 28, .	1.7	13
5	Cover Feature: Tailoring the NIRâ€II Photoluminescence of Single Thiolated Au₂₅ Nanoclusters by Selective Binding to Proteins (Chem. Eur. J. 39/2022). Chemistry - A European Journal, 2022, 28, .	1.7	0
6	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. Journal of Chemical Theory and Computation, 2021, 17, 2014-2021.	2.3	13
7	Interdomain linkers tailor the stability of immunoglobulin repeats in polyproteins. Biochemical and Biophysical Research Communications, 2021, 550, 43-48.	1.0	2
8	Structural Insights into the Interaction of the Intrinsically Disordered Co-activator TIF2 with Retinoic Acid Receptor Heterodimer (RXR/RAR). Journal of Molecular Biology, 2021, 433, 166899.	2.0	14
9	An Integrative Structural Biology Analysis of Von Willebrand Factor Binding and Processing by ADAMTS-13 in Solution. Journal of Molecular Biology, 2021, 433, 166954.	2.0	3
10	Structure and thermodynamics of transient protein-protein complexes by chemometric decomposition of SAXS datasets. Structure, 2021, 29, 1074-1090.e4.	1.6	7
11	The diversity of molecular interactions involving intrinsically disordered proteins: A molecular modeling perspective. Computational and Structural Biotechnology Journal, 2021, 19, 3817-3828.	1.9	6
12	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. Nucleic Acids Research, 2021, 49, D404-D411.	6.5	95
13	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	3.2	70
14	Siteâ€Specific Isotopic Labeling (SSIL): Access to Highâ€Resolution Structural and Dynamic Information in Lowâ€Complexity Proteins. ChemBioChem, 2020, 21, 769-775.	1.3	12
15	Predicting Secondary Structure Propensities in IDPs Using Simple Statistics from Three-Residue Fragments. Journal of Molecular Biology, 2020, 432, 5447-5459.	2.0	10
16	Flanking Regions Determine the Structure of the Poly-Glutamine in Huntingtin through Mechanisms Common among Glutamine-Rich Human Proteins. Structure, 2020, 28, 733-746.e5.	1.6	45
17	Robust Cell-Free Expression of Sub-Pathological and Pathological Huntingtin Exon-1 for NMR Studies. General Approaches for the Isotopic Labeling of Low-Complexity Proteins. Biomolecules, 2020, 10, 1458.	1.8	11
18	The importance of definitions in the study of polyQ regions: A tale of thresholds, impurities and sequence context. Computational and Structural Biotechnology Journal, 2020, 18, 306-313.	1.9	18

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19	IDPs and their complexes in GPCR and nuclear receptor signaling. Progress in Molecular Biology and Translational Science, 2020, 174, 105-155.	0.9	6
20	Molecular basis for fibroblast growth factor 23 O-glycosylation by GalNAc-T3. Nature Chemical Biology, 2020, 16, 351-360.	3.9	52
21	Integrative Biophysics: Protein Interaction and Disorder. Journal of Molecular Biology, 2020, 432, 2843-2845.	2.0	3
22	Evidence of the Reduced Abundance of Proline cis Conformation in Protein Poly Proline Tracts. Journal of the American Chemical Society, 2020, 142, 7976-7986.	6.6	18
23	Structural Characterization of Proteinâ€“Protein Interactions with pyDockSAXS. Methods in Molecular Biology, 2020, 2112, 131-144.	0.4	7
24	Structural Analyses of Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. Methods in Molecular Biology, 2020, 2141, 249-269.	0.4	8
25	Interplay of Protein Disorder in Retinoic Acid Receptor Heterodimer and Its Corepressor Regulates Gene Expression. Structure, 2019, 27, 1270-1285.e6.	1.6	50
26	Double Monoubiquitination Modifies the Molecular Recognition Properties of p15PAF Promoting Binding to the Reader Module of Dnmt1. ACS Chemical Biology, 2019, 14, 2315-2326.	1.6	12
27	Oncogenic mutations at the EGFR ectodomain structurally converge to remove a steric hindrance on a kinase-coupled cryptic epitope. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10009-10018.	3.3	46
28	Investigating the Formation of Structural Elements in Proteins Using Local Sequence-Dependent Information and a Heuristic Search Algorithm. Molecules, 2019, 24, 1150.	1.7	2
29	Realistic Ensemble Models of Intrinsically Disordered Proteins Using a Structure-Encoding Coil Database. Structure, 2019, 27, 381-391.e2.	1.6	49
30	A General Strategy to Access Structural Information at Atomic Resolution in Polyglutamine Homorepeats. Angewandte Chemie - International Edition, 2018, 57, 3598-3601.	7.2	30
31	A General Strategy to Access Structural Information at Atomic Resolution in Polyglutamine Homorepeats. Angewandte Chemie, 2018, 130, 3660-3663.	1.6	8
32	Solution scattering approaches to dynamical ordering in biomolecular systems. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 253-274.	1.1	39
33	Protein Flexibility and Synergy of HMG Domains Underlie U-Turn Bending of DNA by TFAM in Solution. Biophysical Journal, 2018, 114, 2386-2396.	0.2	16
34	Hybrid parallelization of a multi-tree path search algorithm: Application to highly-flexible biomolecules. Parallel Computing, 2018, 77, 84-100.	1.3	9
35	Noninvasive Structural Analysis of Intermediate Species During Fibrillation: An Application of Small-Angle X-Ray Scattering. Methods in Molecular Biology, 2018, 1779, 209-239.	0.4	5
36	Conformational Characterization of Intrinsically Disordered Proteins and Its Biological Significance. , 2018, , 381-399.		5

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37	The Unique Domain Forms a Fuzzy Intramolecular Complex in Src Family Kinases. Structure, 2017, 25, 630-640.e4.	1.6	72
38	Disulfide driven folding for a conditionally disordered protein. Scientific Reports, 2017, 7, 16994.	1.6	14
39	Small-angle scattering studies of intrinsically disordered proteins and their complexes. Current Opinion in Structural Biology, 2017, 42, 15-23.	2.6	76
40	Structural Analysis of Multi-component Amyloid Systems by Chemometric SAXS Data Decomposition. Structure, 2017, 25, 5-15.	1.6	49
41	Structural Characterization of Highly Flexible Proteins by Small-Angle Scattering. Advances in Experimental Medicine and Biology, 2017, 1009, 107-129.	0.8	29
42	The metastasis suppressor KISS1 is an intrinsically disordered protein slightly more extended than a random coil. PLoS ONE, 2017, 12, e0172507.	1.1	6
43	Disentangling polydispersity in the PCNAâ”p15PAF complex, a disordered, transient and multivalent macromolecular assembly. Nucleic Acids Research, 2017, 45, 1501-1515.	6.5	33
44	Conformational Characterization of Intrinsically Disordered Proteins and Its Biological Significance. , 2017, , 1-20.		2
45	Ensemble Structure of the Highly Flexible Complex Formed between Vesicular Stomatitis Virus Unassembled Nucleoprotein and its Phosphoprotein Chaperone. Journal of Molecular Biology, 2016, 428, 2671-2694.	2.0	16
46	Activeâ€Siteâ€Directed Inhibitors of Prolyl Oligopeptidase Abolish Its Conformational Dynamics. ChemBioChem, 2016, 17, 913-917.	1.3	14
47	pyDockSAXS: proteinâ€“protein complex structure by SAXS and computational docking. Nucleic Acids Research, 2015, 43, W356-W361.	6.5	61
48	The hexameric structure of the human mitochondrial replicative helicase Twinkle. Nucleic Acids Research, 2015, 43, 4284-4295.	6.5	40
49	Dynamic interplay between catalytic and lectin domains of GalNAc-transferases modulates protein O-glycosylation. Nature Communications, 2015, 6, 6937.	5.8	77
50	Structure of p15PAFâ€“PCNA complex and implications for clamp sliding during DNA replication and repair. Nature Communications, 2015, 6, 6439.	5.8	65
51	A Three-protein Charge Zipper Stabilizes a Complex Modulating Bacterial Gene Silencing. Journal of Biological Chemistry, 2015, 290, 21200-21212.	1.6	18
52	p15PAF Is an Intrinsically Disordered Protein with Nonrandom Structural Preferences at Sites of Interaction with Other Proteins. Biophysical Journal, 2014, 106, 865-874.	0.2	54
53	Lipid binding by the Unique and SH3 domains of c-Src suggests a new regulatory mechanism. Scientific Reports, 2013, 3, 1295.	1.6	84
54	Conformational transitions in human translin enable nucleic acid binding. Nucleic Acids Research, 2013, 41, 9956-9966.	6.5	11

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55	Measurement and Analysis of NMR Residual Dipolar Couplings for the Study of Intrinsically Disordered Proteins. Methods in Molecular Biology, 2012, 895, 115-125.	0.4	11
56	Structural characterization of intrinsically disordered proteins by the combined use of NMR and SAXS. Biochemical Society Transactions, 2012, 40, 955-962.	1.6	77
57	Analysis of Intrinsically Disordered Proteins by Small-Angle X-ray Scattering. , 2012, 896, 107-122.		38
58	Structural analysis of intrinsically disordered proteins by small-angle X-ray scattering. Molecular BioSystems, 2012, 8, 151-167.	2.9	291
59	Defining the Nature of Thermal Intermediate in 3 State Folding Proteins: Apoflavodoxin, a Study Case. PLoS Computational Biology, 2012, 8, e1002647.	1.5	14
60	Flexible-meccano: a tool for the generation of explicit ensemble descriptions of intrinsically disordered proteins and their associated experimental observables. Bioinformatics, 2012, 28, 1463-1470.	1.8	324
61	Structural Analysis of an Equilibrium Folding Intermediate in the Apoflavodoxin Native Ensemble by Small-Angle X-ray Scattering. Journal of Molecular Biology, 2011, 406, 604-619.	2.0	27
62	Human mitochondrial transcription factor A induces a U-turn structure in the light strand promoter. Nature Structural and Molecular Biology, 2011, 18, 1281-1289.	3.6	168
63	Lowâ€resolution structural approaches to study biomolecular assemblies. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2011, 1, 283-297.	6.2	4
64	Protein loop compaction and the origin of the effect of arginine and glutamic acid mixtures on solubility, stability and transient oligomerization of proteins. European Biophysics Journal, 2011, 40, 1327-1338.	1.2	15
65	Indirect DNA Readout by an H-NS Related Protein: Structure of the DNA Complex of the C-Terminal Domain of Ler. PLoS Pathogens, 2011, 7, e1002380.	2.1	53
66	Effect of interdomain dynamics on the structure determination of modular proteins by small-angle scattering. European Biophysics Journal, 2010, 39, 769-780.	1.2	102
67	Human mitochondrial mTERF wraps around DNA through a left-handed superhelical tandem repeat. Nature Structural and Molecular Biology, 2010, 17, 891-893.	3.6	46
68	Proteins in dynamic equilibrium. Nature, 2010, 468, 1046-1048.	13.7	74
69	Structural Disorder within Sendai Virus Nucleoprotein and Phosphoprotein: Insight into the Structural Basis of Molecular Recognition. Protein and Peptide Letters, 2010, 17, 952-960.	0.4	25
70	Structure and Dynamics of Ribosomal Protein L12: An Ensemble Model Based on SAXS and NMR Relaxation. Biophysical Journal, 2010, 98, 2374-2382.	0.2	67
71	The Dimeric Structure and the Bivalent Recognition of H3K4me3 by the Tumor Suppressor ING4 Suggests a Mechanism for Enhanced Targeting of the HBO1 Complex to Chromatin. Journal of Molecular Biology, 2010, 396, 1117-1127.	2.0	36
72	Design and Structure of an Equilibrium Protein Folding Intermediate: A Hint into Dynamical Regions of Proteins. Journal of Molecular Biology, 2010, 400, 922-934.	2.0	25

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73	Structural Characterization of Proteinâ€“Protein Complexes by Integrating Computational Docking with Small-angle Scattering Data. Journal of Molecular Biology, 2010, 403, 217-230.	2.0	64
74	Quantitative Determination of the Conformational Properties of Partially Folded and Intrinsically Disordered Proteins Using NMR Dipolar Couplings. Structure, 2009, 17, 1169-1185.	1.6	160
75	ProtSA: a web application for calculating sequence specific protein solvent accessibilities in the unfolded ensemble. BMC Bioinformatics, 2009, 10, 104.	1.2	77
76	Structural characterization of Î±â€synuclein in an aggregation prone state. Protein Science, 2009, 18, 1840-1846.	3.1	97
77	Structural characterization of unphosphorylated STAT5a oligomerization equilibrium in solution by smallâ€angle Xâ€ray scattering. Protein Science, 2009, 18, 716-726.	3.1	26
78	Weak oligomerization of lowâ€molecularâ€weight protein tyrosine phosphatase is conserved from mammals to bacteria. FEBS Journal, 2009, 276, 4346-4357.	2.2	8
79	Dynamic interactions of proteins in complex networks: a more structured view. FEBS Journal, 2009, 276, 5390-5405.	2.2	104
80	Low-Resolution Structures of Transient Proteinâˆ'Protein Complexes Using Small-Angle X-ray Scattering. Journal of the American Chemical Society, 2009, 131, 4378-4386.	6.6	59
81	Structural Characterization of the Natively Unfolded N-Terminal Domain of Human c-Src Kinase: Insights into the Role of Phosphorylation of the Unique Domain. Journal of Molecular Biology, 2009, 391, 136-148.	2.0	74
82	A Self-Consistent Description of the Conformational Behavior of Chemically Denatured Proteins from NMR and Small Angle Scattering. Biophysical Journal, 2009, 97, 2839-2845.	0.2	120
83	On the Use of low-resolution Data to Improve Structure Prediction of Proteins and Protein Complexes. Journal of Chemical Theory and Computation, 2009, 5, 3129-3137.	2.3	7
84	Structural Relationships Among the Ribosomal Stalk Proteins from the Three Domains of Life. Journal of Molecular Evolution, 2008, 67, 154-167.	0.8	46
85	Domain Conformation of Tau Protein Studied by Solution Small-Angle X-ray Scattering. Biochemistry, 2008, 47, 10345-10353.	1.2	187
86	Structural Characterization of the Active and Inactive States of Src Kinase in Solution by Small-Angle X-ray Scattering. Journal of Molecular Biology, 2008, 376, 492-505.	2.0	49
87	Interaction of Human Complement with Sbi, a Staphylococcal Immunoglobulin-binding Protein. Journal of Biological Chemistry, 2008, 283, 17579-17593.	1.6	139
88	Structural Characterization of the Ribosomal P1Aâˆ'P2B Protein Dimer by Small-Angle X-ray Scattering and NMR Spectroscopy. Biochemistry, 2007, 46, 1988-1998.	1.2	25
89	Structural Characterization of Flexible Proteins Using Small-Angle X-ray Scattering. Journal of the American Chemical Society, 2007, 129, 5656-5664.	6.6	1,080
90	Amino Acid Bulkiness Defines the Local Conformations and Dynamics of Natively Unfolded Î±-Synuclein and Tau. Journal of the American Chemical Society, 2007, 129, 3032-3033.	6.6	61

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91	Protein Tyrosine Phosphatase Oligomerization Studied by a Combination of15N NMR Relaxation and129Xe NMR. Effect of Buffer Containing Arginine and Glutamic Acid. Journal of the American Chemical Society, 2007, 129, 5946-5953.	6.6	16
92	Highly Populated Turn Conformations in Natively Unfolded Tau Protein Identified from Residual Dipolar Couplings and Molecular Simulation. Journal of the American Chemical Society, 2007, 129, 5235-5243.	6.6	208
93	Residual Dipolar Couplings in Short Peptides Reveal Systematic Conformational Preferences of Individual Amino Acids. Journal of the American Chemical Society, 2006, 128, 13508-13514.	6.6	55
94	Sequence-Specific Solvent Accessibilities of Protein Residues in Unfolded Protein Ensembles. Biophysical Journal, 2006, 91, 4536-4543.	0.2	48
95	Protein backbone dynamics from Nâ€“HN dipolar couplings in partially aligned systems: a comparison of motional models in the presence of structural noise. Journal of Magnetic Resonance, 2005, 173, 328-338.	1.2	25
96	Identification of slow correlated motions in proteins using residual dipolar and hydrogen-bond scalar couplings. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13885-13890.	3.3	220
97	A structural model for unfolded proteins from residual dipolar couplings and small-angle x-ray scattering. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17002-17007.	3.3	413
98	Defining Long-Range Order and Local Disorder in Native Î±-Synuclein Using Residual Dipolar Couplings. Journal of the American Chemical Society, 2005, 127, 17968-17969.	6.6	223
99	Interpretation of NMR relaxation properties of Pin1, a two-domain protein, based on Brownian dynamic simulations. Journal of Biomolecular NMR, 2004, 29, 21-35.	1.6	27
100	Macromolecular crowding in biological systems: hydrodynamics and NMR methods. Journal of Molecular Recognition, 2004, 17, 397-407.	1.1	47
101	Anisotropic Small Amplitude Peptide Plane Dynamics in Proteins from Residual Dipolar Couplings. Journal of the American Chemical Society, 2004, 126, 4907-4920.	6.6	64
102	Local Dynamic Amplitudes on the Protein Backbone from Dipolar Couplings: Toward the Elucidation of Slower Motions in Biomolecules. Journal of the American Chemical Society, 2004, 126, 7760-7761.	6.6	46
103	Combined Use of NMR Relaxation Measurements and Hydrodynamic Calculations To Study Protein Association. Evidence for Tetramers of Low Molecular Weight Protein Tyrosine Phosphatase in Solution. Journal of the American Chemical Society, 2003, 125, 916-923.	6.6	38
104	Peptide Binding Induces Large Scale Changes in Inter-domain Mobility in Human Pin1. Journal of Biological Chemistry, 2003, 278, 26174-26182.	1.6	87
105	Lanthanide Modulation of the Orientation of Macromolecules Induced by Purple Membrane. Journal of the American Chemical Society, 2002, 124, 374-375.	6.6	12
106	NMR measurement of the off rate from the first calcium-binding site of the synaptotagmin I C2A domain. FEBS Letters, 2002, 516, 93-96.	1.3	26
107	Interpretation of 15N NMR relaxation data of globular proteins using hydrodynamic calculations with HYDRONMR. Journal of Biomolecular NMR, 2002, 23, 139-150.	1.6	76
108	An Analytical Solution to the Problem of the Orientation of Rigid Particles by Planar Obstacles. Application to Membrane Systems and to the Calculation of Dipolar Couplings in Protein NMR Spectroscopy. Journal of the American Chemical Society, 2001, 123, 12037-12047.	6.6	54