

Julie D Forman-Kay

List of Publications by Year in descending order

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176
papers

22,654
citations

7551

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9553

142
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204
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204
docs citations

204
times ranked

16373
citing authors

#	ARTICLE	IF	CITATIONS
1	Backbone Dynamics of a Free and a Phosphopeptide-Complexed Src Homology 2 Domain Studied by ¹⁵ N NMR Relaxation. <i>Biochemistry</i> , 1994, 33, 5984-6003.	1.2	2,136
2	Phase Transition of a Disordered Nuage Protein Generates Environmentally Responsive Membraneless Organelles. <i>Molecular Cell</i> , 2015, 57, 936-947.	4.5	1,408
3	Sensitivity of secondary structure propensities to sequence differences between $\hat{1}\pm$ - and $\hat{1}^3$ -synuclein: Implications for fibrillation. <i>Protein Science</i> , 2006, 15, 2795-2804.	3.1	648
4	Backbone ¹ H and ¹⁵ N resonance assignments of the N-terminal SH3 domain of drk in folded and unfolded states using enhanced-sensitivity pulsed field gradient NMR techniques. <i>Journal of Biomolecular NMR</i> , 1994, 4, 845-858.	1.6	644
5	Pi-Pi contacts are an overlooked protein feature relevant to phase separation. <i>ELife</i> , 2018, 7, .	2.8	571
6	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. <i>Nature</i> , 2015, 519, 106-109.	13.7	471
7	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. <i>Journal of the American Chemical Society</i> , 2001, 123, 11341-11352.	6.6	454
8	Two-dimensional NMR experiments for correlating carbon-13.beta. and proton.delta./epsilon. chemical shifts of aromatic residues in ¹³ C-labeled proteins via scalar couplings. <i>Journal of the American Chemical Society</i> , 1993, 115, 11054-11055.	6.6	424
9	A heteronuclear correlation experiment for simultaneous determination of ¹⁵ N longitudinal decay and chemical exchange rates of systems in slow equilibrium. <i>Journal of Biomolecular NMR</i> , 1994, 4, 727-734.	1.6	417
10	Atomic-level characterization of disordered protein ensembles. <i>Current Opinion in Structural Biology</i> , 2007, 17, 3-14.	2.6	409
11	Modulation of Intrinsically Disordered Protein Function by Post-translational Modifications. <i>Journal of Biological Chemistry</i> , 2016, 291, 6696-6705.	1.6	402
12	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8194-E8203.	3.3	381
13	Sequence Determinants of Compaction in Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2010, 98, 2383-2390.	0.2	342
14	Protein dynamics and conformational disorder in molecular recognition. <i>Journal of Molecular Recognition</i> , 2010, 23, 105-116.	1.1	337
15	Comparison of the Backbone Dynamics of a Folded and an Unfolded SH3 Domain Existing in Equilibrium in Aqueous Buffer. <i>Biochemistry</i> , 1995, 34, 868-878.	1.2	313
16	Dynamic equilibrium engagement of a polyvalent ligand with a single-site receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17772-17777.	3.3	304
17	Solution structure and dynamics of the outer membrane enzyme PagP by NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13560-13565.	3.3	302
18	RGG/RG Motif Regions in RNA Binding and Phase Separation. <i>Journal of Molecular Biology</i> , 2018, 430, 4650-4665.	2.0	297

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19	CFTR regulatory region interacts with NBD1 predominantly via multiple transient helices. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 738-745.	3.6	267
20	Properties of Stress Granule and P-Body Proteomes. <i>Molecular Cell</i> , 2019, 76, 286-294.	4.5	258
21	Phosphoregulated FMRP phase separation models activity-dependent translation through bidirectional control of mRNA granule formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4218-4227.	3.3	249
22	Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. <i>Science</i> , 2019, 365, 825-829.	6.0	240
23	Structure/Function Implications in a Dynamic Complex of the Intrinsically Disordered Sic1 with the Cdc4 Subunit of an SCF Ubiquitin Ligase. <i>Structure</i> , 2010, 18, 494-506.	1.6	239
24	Autoinhibition of the HECT-Type Ubiquitin Ligase Smurf2 through Its C2 Domain. <i>Cell</i> , 2007, 130, 651-662.	13.5	237
25	Correlation between Dynamics and High Affinity Binding in an SH2 Domain Interaction. <i>Biochemistry</i> , 1996, 35, 361-368.	1.2	235
26	What's in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
27	Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. <i>Physical Review Letters</i> , 2016, 117, 178101.	2.9	224
28	Calculation of ensembles of structures representing the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , 2001, 308, 1011-1032.	2.0	209
29	Polyelectrostatic interactions of disordered ligands suggest a physical basis for ultrasensitivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9650-9655.	3.3	207
30	Solution structure of a Nedd4 WW domain-ENaC peptide complex. <i>Nature Structural Biology</i> , 2001, 8, 407-412.	9.7	202
31	From Sequence and Forces to Structure, Function, and Evolution of Intrinsically Disordered Proteins. <i>Structure</i> , 2013, 21, 1492-1499.	1.6	196
32	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014, 42, D326-D335.	6.5	195
33	Structural Characterization of Folded and Unfolded States of an SH3 Domain in Equilibrium in Aqueous Buffer. <i>Biochemistry</i> , 1995, 34, 6784-6794.	1.2	186
34	Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. <i>Biochemistry</i> , 2018, 57, 2499-2508.	1.2	184
35	Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. <i>Journal of Molecular Biology</i> , 2002, 316, 101-112.	2.0	181
36	Liquid-liquid phase separation in cellular signaling systems. <i>Current Opinion in Structural Biology</i> , 2016, 41, 180-186.	2.6	172

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37	Global folds of proteins with low densities of NOEs using residual dipolar couplings: application to the 370-residue maltodextrin-binding protein. <i>Journal of Molecular Biology</i> , 2000, 300, 197-212.	2.0	165
38	NOE data demonstrating a compact unfolded state for an SH3 domain under non-denaturing conditions. <i>Journal of Molecular Biology</i> , 1999, 289, 619-638.	2.0	163
39	Structural Characterization of Proteins with an Attached ATCLIN Motif by Paramagnetic Relaxation Enhancement NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2001, 123, 9843-9847.	6.6	162
40	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. <i>Chemical Reviews</i> , 2016, 116, 6424-6462.	23.0	161
41	Characterization of the Backbone Dynamics of Folded and Denatured States of an SH3 Domain. <i>Biochemistry</i> , 1997, 36, 2390-2402.	1.2	160
42	Comparative roles of charge, $\langle i \rangle$, and hydrophobic interactions in sequence-dependent phase separation of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28795-28805.	3.3	159
43	A simple in vivo assay for increased protein solubility. <i>Protein Science</i> , 1999, 8, 1908-1911.	3.1	153
44	High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. <i>Biochemistry</i> , 1991, 30, 2685-2698.	1.2	151
45	Phase Separation as a Missing Mechanism for Interpretation of Disease Mutations. <i>Cell</i> , 2020, 183, 1742-1756.	13.5	147
46	Contributions to protein entropy and heat capacity from bond vector motions measured by NMR spin relaxation. <i>Journal of Molecular Biology</i> , 1997, 272, 790-804.	2.0	146
47	Structure and Disorder in an Unfolded State under Nondenaturing Conditions from Ensemble Models Consistent with a Large Number of Experimental Restraints. <i>Journal of Molecular Biology</i> , 2009, 391, 359-374.	2.0	144
48	Regulatory R region of the CFTR chloride channel is a dynamic integrator of phospho-dependent intra- and intermolecular interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4427-36.	3.3	142
49	Characterization of disordered proteins with ENSEMBLE. <i>Bioinformatics</i> , 2013, 29, 398-399.	1.8	141
50	NMR Studies of Unfolded States of an SH3 Domain in Aqueous Solution and Denaturing Conditions. <i>Biochemistry</i> , 1997, 36, 3959-3970.	1.2	134
51	Proteome-wide signatures of function in highly diverged intrinsically disordered regions. <i>ELife</i> , 2019, 8, .	2.8	131
52	Relationship between electrostatics and redox function in human thioredoxin: characterization of pH titration shifts using two-dimensional homo- and heteronuclear NMR. <i>Biochemistry</i> , 1992, 31, 3442-3452.	1.2	124
53	Conformational Ensembles of an Intrinsically Disordered Protein Consistent with NMR, SAXS, and Single-Molecule FRET. <i>Journal of the American Chemical Society</i> , 2020, 142, 15697-15710.	6.6	120
54	First-generation predictors of biological protein phase separation. <i>Current Opinion in Structural Biology</i> , 2019, 58, 88-96.	2.6	119

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55	Diversity in protein recognition by PTB domains. <i>Current Opinion in Structural Biology</i> , 1999, 9, 690-695.	2.6	118
56	Structure of a Numb PTB domain-peptide complex suggests a basis for diverse binding specificity. <i>Nature Structural Biology</i> , 1998, 5, 1075-1083.	9.7	112
57	Finding Our Way in the Dark Proteome. <i>Journal of the American Chemical Society</i> , 2016, 138, 9730-9742.	6.6	111
58	Multidimensional NMR Methods for Protein Structure Determination. <i>IUBMB Life</i> , 2001, 52, 291-302.	1.5	110
59	Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. <i>Structure</i> , 2010, 18, 1094-1103.	1.6	110
60	Improved Structural Characterizations of the drkN SH3 Domain Unfolded State Suggest a Compact Ensemble with Native-like and Non-native Structure. <i>Journal of Molecular Biology</i> , 2007, 367, 1494-1510.	2.0	109
61	Novel mode of ligand binding by the SH2 domain of the human XLP disease gene product SAP/SH2D1A. <i>Current Biology</i> , 1999, 9, 1355-1362.	1.8	108
62	Ensemble modeling of protein disordered states: Experimental restraint contributions and validation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 556-572.	1.5	107
63	Correlation between binding and dynamics at SH2 domain interfaces. <i>Nature Structural Biology</i> , 1998, 5, 156-163.	9.7	104
64	NMR evidence for differential phosphorylation-dependent interactions in WT and F508 CFTR. <i>EMBO Journal</i> , 2010, 29, 263-277.	3.5	103
65	Random-phase-approximation theory for sequence-dependent, biologically functional liquid-liquid phase separation of intrinsically disordered proteins. <i>Journal of Molecular Liquids</i> , 2017, 228, 176-193.	2.3	103
66	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <i>Nucleic Acids Research</i> , 2012, 40, 6353-6366.	6.5	97
67	Charge pattern matching as a "fuzzy" mode of molecular recognition for the functional phase separations of intrinsically disordered proteins. <i>New Journal of Physics</i> , 2017, 19, 115003.	1.2	96
68	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
69	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012, 22, 643-650.	2.6	94
70	Similarities between the spectrin SH3 domain denatured state and its folding transition state ¹¹ Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 2000, 297, 1217-1229.	2.0	91
71	Complex regulatory mechanisms mediated by the interplay of multiple post-translational modifications. <i>Current Opinion in Structural Biology</i> , 2018, 48, 58-67.	2.6	90
72	A change in conformational dynamics underlies the activation of Eph receptor tyrosine kinases. <i>EMBO Journal</i> , 2006, 25, 4686-4696.	3.5	89

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73	Studies on the solution conformation of human thioredoxin using heteronuclear nitrogen-15-proton nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1990, 29, 1566-1572.	1.2	87
74	Site-specific contributions to the pH dependence of protein stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4545-4550.	3.3	86
75	Direct Binding of the Corrector VX-809 to Human CFTR NBD1: Evidence of an Allosteric Coupling between the Binding Site and the NBD1:CL4 Interface. <i>Molecular Pharmacology</i> , 2017, 92, 124-135.	1.0	85
76	Analysis of deuterium relaxation-derived methyl axis order parameters and correlation with local structure. <i>Journal of Biomolecular NMR</i> , 1999, 13, 181-185.	1.6	84
77	The 'dynamics' in the thermodynamics of binding. , 1999, 6, 1086-1087.		83
78	A π -three-pronged π ™ binding mechanism for the SAP/SH2D1A SH2 domain: structural basis and relevance to the XLP syndrome. <i>EMBO Journal</i> , 2002, 21, 314-323.	3.5	82
79	NMR Pulse Schemes for the Sequence-Specific Assignment of Arginine Guanidino 15N and 1H Chemical Shifts in Proteins. <i>Journal of the American Chemical Society</i> , 1995, 117, 3556-3564.	6.6	80
80	Aromatic and Methyl NOEs Highlight Hydrophobic Clustering in the Unfolded State of an SH3 Domain. <i>Biochemistry</i> , 2003, 42, 8687-8695.	1.2	80
81	Affinity and Specificity of Interactions between Nedd4 Isoforms and the Epithelial Na ⁺ Channel. <i>Journal of Biological Chemistry</i> , 2003, 278, 20019-20028.	1.6	80
82	Structural Determinants for High-Affinity Binding in a Nedd4 WW3 π - Domain-Comm PY Motif Complex. <i>Structure</i> , 2006, 14, 543-553.	1.6	77
83	Triple-resonance NOESY-based experiments with improved spectral resolution: applications to structural characterization of unfolded, partially folded and folded proteins. <i>Journal of Biomolecular NMR</i> , 1997, 9, 181-200.	1.6	75
84	Dramatic stabilization of an SH3 domain by a single substitution: roles of the folded and unfolded states. Edited by C. R. Matthews. <i>Journal of Molecular Biology</i> , 2001, 307, 913-928.	2.0	75
85	Sequential assignment of proline-rich regions in proteins: application to modular binding domain complexes. <i>Journal of Biomolecular NMR</i> , 2000, 16, 253-259.	1.6	74
86	Interaction of the Eukaryotic Initiation Factor 4E with 4E-BP2 at a Dynamic Bipartite Interface. <i>Structure</i> , 2013, 21, 2186-2196.	1.6	74
87	Structural and Dynamic Characterization of the Phosphotyrosine Binding Region of an Src Homology 2 Domain-Phosphopeptide Complex by NMR Relaxation, Proton Exchange, and Chemical Shift Approaches. <i>Biochemistry</i> , 1995, 34, 11353-11362.	1.2	71
88	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , 2020, 77, 1176-1192.e16.	4.5	69
89	Structure of a regulatory complex involving the Abl SH3 domain, the Crk SH2 domain, and a Crk-derived phosphopeptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14053-14058.	3.3	68
90	Measurement of Side-Chain Carboxyl pKa Values of Glutamate and Aspartate Residues in an Unfolded Protein by Multinuclear NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 5714-5717.	6.6	68

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91	Phase Separation in Biology and Disease. <i>Journal of Molecular Biology</i> , 2018, 430, 4603-4606.	2.0	68
92	Calculation of Residual Dipolar Couplings from Disordered State Ensembles Using Local Alignment. <i>Journal of the American Chemical Society</i> , 2008, 130, 7804-7805.	6.6	67
93	Phenotypic profiling of CFTR modulators in patient-derived respiratory epithelia. <i>Npj Genomic Medicine</i> , 2017, 2, 12.	1.7	66
94	Cooperative Interactions and a Non-native Buried Trp in the Unfolded State of an SH3 Domain. <i>Journal of Molecular Biology</i> , 2002, 322, 163-178.	2.0	64
95	The Ubiquitin Binding Region of the Smurf HECT Domain Facilitates Polyubiquitylation and Binding of Ubiquitylated Substrates. <i>Journal of Biological Chemistry</i> , 2010, 285, 6308-6315.	1.6	63
96	Congenital Chloride-losing Diarrhea Causing Mutations in the STAS Domain Result in Misfolding and Mistrafficking of SLC26A3. <i>Journal of Biological Chemistry</i> , 2008, 283, 8711-8722.	1.6	60
97	Coupling of tandem Smad ubiquitination regulatory factor (Smurf) WW domains modulates target specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18404-18409.	3.3	60
98	Comprehensive NOE characterization of a partially folded large fragment of staphylococcal nuclease $^{\text{13C}}$, using NMR methods with improved resolution 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 272, 9-20.	2.0	57
99	$^{15}\text{N}/\text{D}$ -SOLESY experiment for accurate measurement of amide solvent exchange rates: application to denatured drkN SH3. <i>Journal of Biomolecular NMR</i> , 2010, 46, 227-244.	1.6	57
100	Composite low affinity interactions dictate recognition of the cyclin-dependent kinase inhibitor Sic1 by the SCF $\langle \text{sup} \rangle \text{Cdc4} \langle \text{sup} \rangle$ ubiquitin ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3287-3292.	3.3	55
101	The Effect of Intrachain Electrostatic Repulsion on Conformational Disorder and Dynamics of the Sic1 Protein. <i>Journal of Physical Chemistry B</i> , 2014, 118, 4088-4097.	1.2	55
102	High populations of non-native structures in the denatured state are compatible with the formation of the native folded state. <i>Journal of Molecular Biology</i> , 1998, 284, 1153-1164.	2.0	54
103	Structural changes of CFTR R region upon phosphorylation: a plastic platform for intramolecular and intermolecular interactions. <i>FEBS Journal</i> , 2013, 280, 4407-4416.	2.2	54
104	Phosphorylation-dependent 14-3-3 protein interactions regulate CFTR biogenesis. <i>Molecular Biology of the Cell</i> , 2012, 23, 996-1009.	0.9	53
105	Synuclein- β Targeting Peptide Inhibitor that Enhances Sensitivity of Breast Cancer Cells to Antimicrotubule Drugs. <i>Cancer Research</i> , 2007, 67, 626-633.	0.4	52
106	Identification of a molecular locus for normalizing dysregulated GABA release from interneurons in the Fragile X brain. <i>Molecular Psychiatry</i> , 2020, 25, 2017-2035.	4.1	52
107	An Expanded WW Domain Recognition Motif Revealed by the Interaction between Smad7 and the E3 Ubiquitin Ligase Smurf2*. <i>Journal of Biological Chemistry</i> , 2006, 281, 17069-17075.	1.6	50
108	Determination of the positions of bound water molecules in the solution structure of reduced human thioredoxin by heteronuclear three-dimensional nuclear magnetic resonance spectroscopy. <i>Journal of Molecular Biology</i> , 1991, 220, 209-216.	2.0	49

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109	NMR Experiments for Studies of Dilute and Condensed Protein Phases: Application to the Phase-Separating Protein CAPRIN1. <i>Journal of the American Chemical Society</i> , 2020, 142, 2471-2489.	6.6	49
110	Side-chain Dynamics of the SAP SH2 Domain Correlate with a Binding Hot Spot and a Region with Conformational Plasticity. <i>Journal of Molecular Biology</i> , 2002, 322, 605-620.	2.0	48
111	Conformational Changes Relevant to Channel Activity and Folding within the first Nucleotide Binding Domain of the Cystic Fibrosis Transmembrane Conductance Regulator. <i>Journal of Biological Chemistry</i> , 2012, 287, 28480-28494.	1.6	48
112	Synergy of cAMP and calcium signaling pathways in CFTR regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2086-E2095.	3.3	48
113	Identifying molecular features that are associated with biological function of intrinsically disordered protein regions. <i>ELife</i> , 2021, 10, .	2.8	47
114	Structural Signature of the MYPT1~PP1 Interaction. <i>Journal of the American Chemical Society</i> , 2011, 133, 73-80.	6.6	44
115	¹ H~ ¹³ C Dipole~Dipole Cross-Correlated Spin Relaxation As a Probe of Dynamics in Unfolded Proteins:~% Application to the DrkN SH3 Domain. <i>Journal of the American Chemical Society</i> , 1999, 121, 3555-3556.	6.6	42
116	pH Titration studies of an SH2 domain~phosphopeptide complex: Unusual histidine and phosphate p <i>K</i> _a values. <i>Protein Science</i> , 1997, 6, 1910-1919.	3.1	41
117	Entropy and Information within Intrinsically Disordered Protein Regions. <i>Entropy</i> , 2019, 21, 662.	1.1	41
118	Interaction hot spots for phase separation revealed by NMR studies of a CAPRIN1 condensed phase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
119	Structural Comparison of the Unstable drkN SH3 Domain and a Stable Mutant~%. <i>Biochemistry</i> , 2005, 44, 15550-15560.	1.2	39
120	Extended experimental inferential structure determination method in determining the structural ensembles of disordered protein states. <i>Communications Chemistry</i> , 2020, 3, .	2.0	39
121	Structural, Functional, and Bioinformatic Studies Demonstrate the Crucial Role of an Extended Peptide Binding Site for the SH3 Domain of Yeast Abp1p. <i>Journal of Biological Chemistry</i> , 2009, 284, 26918-26927.	1.6	36
122	FUS-ALS mutants alter FMRP phase separation equilibrium and impair protein translation. <i>Science Advances</i> , 2021, 7, .	4.7	36
123	Tryptophan Solvent Exposure in Folded and Unfolded States of an SH3 Domain by 19F and 1H NMR. <i>Biochemistry</i> , 2006, 45, 14120-14128.	1.2	35
124	NMR studies of tandem WW domains of Nedd4 in complex with a PY motif-containing region of the epithelial sodium channel. <i>Biochemistry and Cell Biology</i> , 1998, 76, 341-350.	0.9	34
125	NMR Characterization of Copper-Binding Domains 4~6 of ATP7B. <i>Biochemistry</i> , 2010, 49, 8468-8477.	1.2	34
126	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Communications</i> , 2017, 8, 13943.	5.8	33

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127	Hydration and Packing along the Folding Pathway of SH3 Domains by Pressure-Dependent NMR. <i>Biochemistry</i> , 2006, 45, 4711-4719.	1.2	31
128	Differential Dynamic Engagement within 24 SH3 Domain: Peptide Complexes Revealed by Co-Linear Chemical Shift Perturbation Analysis. <i>PLoS ONE</i> , 2012, 7, e51282.	1.1	31
129	NMR structure of neuromedin C, a neurotransmitter with an amino terminal Cu ^{II} ; Ni ^{II} -binding (ATCUN) motif. <i>Chemical Biology and Drug Design</i> , 1997, 49, 500-509.	1.2	30
130	Allosteric Coupling between the Intracellular Coupling Helix 4 and Regulatory Sites of the First Nucleotide-binding Domain of CFTR. <i>PLoS ONE</i> , 2013, 8, e74347.	1.1	30
131	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCFFbw7 Ubiquitin Ligase. <i>Structure</i> , 2018, 26, 28-39.e2.	1.6	29
132	Phosphorylation-dependent regulation of messenger RNA transcription, processing and translation within biomolecular condensates. <i>Current Opinion in Cell Biology</i> , 2021, 69, 30-40.	2.6	29
133	Oxygen as a Paramagnetic Probe of Clustering and Solvent Exposure in Folded and Unfolded States of an SH3 Domain. <i>Journal of the American Chemical Society</i> , 2007, 129, 1826-1835.	6.6	28
134	NMR Dynamics-Derived Insights into the Binding Properties of a Peptide Interacting with an SH2 Domain. <i>Biochemistry</i> , 2005, 44, 694-703.	1.2	27
135	A proton nuclear magnetic resonance assignment and secondary structure determination of recombinant human thioredoxin. <i>Biochemistry</i> , 1989, 28, 7088-7097.	1.2	26
136	Disorder in a Target for the Smad2 Mad Homology 2 Domain and Its Implications for Binding and Specificity. <i>Journal of Biological Chemistry</i> , 2004, 279, 40707-40714.	1.6	26
137	O-Linked-N-Acetylglucosamylation of the RNA-Binding Protein EWS N-Terminal Low Complexity Region Reduces Phase Separation and Enhances Condensate Dynamics. <i>Journal of the American Chemical Society</i> , 2021, 143, 11520-11534.	6.6	26
138	Dynamics Intrinsic to Cystic Fibrosis Transmembrane Conductance Regulator Function and Stability. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2013, 3, a009522-a009522.	2.9	24
139	Binding screen for cystic fibrosis transmembrane conductance regulator correctors finds new chemical matter and yields insights into cystic fibrosis therapeutic strategy. <i>Protein Science</i> , 2016, 25, 360-373.	3.1	24
140	The ZIP5 Ectodomain Co-Localizes with PrP and May Acquire a PrP-Like Fold That Assembles into a Dimer. <i>PLoS ONE</i> , 2013, 8, e72446.	1.1	23
141	Conformations of a Metastable SH3 Domain Characterized by smFRET and an Excluded-Volume Polymer Model. <i>Biophysical Journal</i> , 2016, 110, 1510-1522.	0.2	23
142	Translating Material Science into Biological Function. <i>Molecular Cell</i> , 2019, 75, 1-2.	4.5	23
143	What are the distinguishing features and size requirements of biomolecular condensates and their implications for RNA-containing condensates?. <i>Rna</i> , 2022, 28, 36-47.	1.6	23
144	Recessive <i>NOS1AP</i> variants impair actin remodeling and cause glomerulopathy in humans and mice. <i>Science Advances</i> , 2021, 7, .	4.7	21

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145	Deletion of Phenylalanine 508 in the First Nucleotide-binding Domain of the Cystic Fibrosis Transmembrane Conductance Regulator Increases Conformational Exchange and Inhibits Dimerization. <i>Journal of Biological Chemistry</i> , 2015, 290, 22862-22878.	1.6	20
146	CFTR structure. <i>Journal of Cystic Fibrosis</i> , 2018, 17, S5-S8.	0.3	20
147	Interplay of buried histidine protonation and protein stability in prion misfolding. <i>Scientific Reports</i> , 2017, 7, 882.	1.6	17
148	Non-cooperative 4E-BP2 folding with exchange between eIF4E-binding and binding-incompatible states tunes cap-dependent translation inhibition. <i>Nature Communications</i> , 2020, 11, 3146.	5.8	17
149	Characterization of the Phosphotyrosine-binding Domain of the Drosophila Shc Protein. <i>Journal of Biological Chemistry</i> , 1996, 271, 31855-31862.	1.6	16
150	Corrigendum to the Paper by Mok et al. (1999) NOE Data Demonstrating a Compact Unfolded State for an SH3 Domain under Non-denaturing Conditions. <i>Journal of Molecular Biology</i> , 2003, 329, 185-187.	2.0	16
151	Measuring pKa Values in Protein Folding Transition State Ensembles by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2005, 127, 8904-8905.	6.6	16
152	Clinical presentation and molecular basis of congenital antithrombin deficiency in children: a cohort study. <i>British Journal of Haematology</i> , 2014, 166, 130-139.	1.2	16
153	Discovering molecular features of intrinsically disordered regions by using evolution for contrastive learning. <i>PLoS Computational Biology</i> , 2022, 18, e1010238.	1.5	16
154	Megakaryocyte and platelet abnormalities in a patient with a W33C mutation in the conserved SH3-like domain of myosin heavy chain IIA. <i>Thrombosis and Haemostasis</i> , 2009, 102, 1241-1250.	1.8	15
155	Stabilization of a nucleotide-binding domain of the cystic fibrosis transmembrane conductance regulator yields insight into disease-causing mutations. <i>Journal of Biological Chemistry</i> , 2017, 292, 14147-14164.	1.6	15
156	Molecular oxygen as a paramagnetic NMR probe of protein solvent exposure and topology. <i>Concepts in Magnetic Resonance Part A: Bridging Education and Research</i> , 2008, 32A, 239-253.	0.2	14
157	Augmentation of Cystic Fibrosis Transmembrane Conductance Regulator Function in Human Bronchial Epithelial Cells via SLC6A14-Dependent Amino Acid Uptake. Implications for Treatment of Cystic Fibrosis. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 755-764.	1.4	12
158	An evolutionary switch in ND2 enables Src kinase regulation of NMDA receptors. <i>Nature Communications</i> , 2017, 8, 15220.	5.8	11
159	Structural Studies of FF Domains of the Transcription Factor CA150 Provide Insights into the Organization of FF Domain Tandem Arrays. <i>Journal of Molecular Biology</i> , 2009, 393, 409-424.	2.0	10
160	Configurational Entropy of Folded Proteins and Its Importance for Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3420.	1.8	10
161	NMR Spectroscopy to Study the Dynamics and Interactions of CFTR. <i>Methods in Molecular Biology</i> , 2011, 741, 377-403.	0.4	10
162	Global Proximity Interactome of the Human Macroautophagy Pathway. <i>Autophagy</i> , 2022, 18, 1174-1186.	4.3	9

#	ARTICLE	IF	CITATIONS
163	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. <i>Npj Genomic Medicine</i> , 2021, 6, 91.	1.7	9
164	Protein Dynamics to Define and Refine Disordered Protein Ensembles. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1885-1894.	1.2	9
165	Characterization of the Hydrodynamic Properties of the Folding Transition State of an SH3 Domain by Magnetization Transfer NMR Spectroscopy. <i>Biochemistry</i> , 2006, 45, 6434-6445.	1.2	8
166	Role of CBS and Bateman Domains in Phosphorylation-Dependent Regulation of a CLC Anion Channel. <i>Biophysical Journal</i> , 2016, 111, 1876-1886.	0.2	7
167	Whence Blobs? Phylogenetics of functional protein condensates. <i>Biochemical Society Transactions</i> , 2020, 48, 2151-2158.	1.6	7
168	A New Phase in ALS Research. <i>Structure</i> , 2016, 24, 1435-1436.	1.6	6
169	A hidden competitive advantage of disorder. <i>Nature</i> , 2017, 543, 325-326.	13.7	4
170	c.1058C>T variant in the <i>SERPINC1</i> gene is pathogenic for antithrombin deficiency. <i>British Journal of Haematology</i> , 2015, 170, 123-125.	1.2	3
171	Development and characterization of synthetic antibodies binding to the cystic fibrosis conductance regulator. <i>MAbs</i> , 2016, 8, 1167-1176.	2.6	3
172	Molecular structural analysis of a novel and de novo mutation in the <i>SERPINC1</i> gene associated with type 1 antithrombin deficiency. <i>British Journal of Haematology</i> , 2017, 177, 654-656.	1.2	3
173	Oxidative Inhibition of Pbp1 Phase Separation. <i>Biochemistry</i> , 2019, 58, 3057-3059.	1.2	1
174	Structure and Function Implications of Conformational Ensembles Consistent with NMR, SAXS, and smFRET Data. The Disordered Protein SIC1 Before and After Multisite Phosphorylation. <i>Biophysical Journal</i> , 2020, 118, 60a.	0.2	1
175	Dynamic complexes of intrinsically disordered proteins and their regulation by post-translational modifications. <i>FASEB Journal</i> , 2013, 27, 459.1.	0.2	0
176	Structural, Dynamic, and Folding Studies of SH2 and SH3 Domains. , 1996, , 35-47.		0