

Julie D Forman-Kay

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1564681/publications.pdf>

Version: 2024-02-01

176
papers

22,654
citations

7551

77
h-index

9553

142
g-index

204
all docs

204
docs citations

204
times ranked

16373
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Proximity Interactome of the Human Macroautophagy Pathway. <i>Autophagy</i> , 2022, 18, 1174-1186.	4.3	9
2	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
3	Protein Dynamics to Define and Refine Disordered Protein Ensembles. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1885-1894.	1.2	9
4	Discovering molecular features of intrinsically disordered regions by using evolution for contrastive learning. <i>PLoS Computational Biology</i> , 2022, 18, e1010238.	1.5	16
5	Recessive <i>NOS1AP</i> variants impair actin remodeling and cause glomerulopathy in humans and mice. <i>Science Advances</i> , 2021, 7, .	4.7	21
6	Identifying molecular features that are associated with biological function of intrinsically disordered protein regions. <i>ELife</i> , 2021, 10, .	2.8	47
7	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
8	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
9	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
10	<i>O</i> -Linked- <i>N</i> -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
11	FUS-ALS mutants alter FMRP phase separation equilibrium and impair protein translation. <i>Science Advances</i> , 2021, 7, .	4.7	36
12	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
13	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. <i>Npj Genomic Medicine</i> , 2021, 6, 91.	1.7	9
14	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
15	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
16	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
17	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
18	Phase Separation as a Missing Mechanism for Interpretation of Disease Mutations. <i>Cell</i> , 2020, 183, 1742-1756.	13.5	147

#	ARTICLE	IF	CITATIONS
19	Comparative roles of charge, π - π , 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
20	Extended experimental inferential structure determination method in determining the structural ensembles of disordered protein states. <i>Communications Chemistry</i> , 2020, 3, .	2.0	39
21	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
22	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , 2020, 77, 1176-1192.e16.	4.5	69
23	Whence Blobs? Phylogenetics of functional protein condensates. <i>Biochemical Society Transactions</i> , 2020, 48, 2151-2158.	1.6	7
24	Entropy and Information within Intrinsically Disordered Protein Regions. <i>Entropy</i> , 2019, 21, 662.	1.1	41
25	Oxidative Inhibition of Pbp1 Phase Separation. <i>Biochemistry</i> , 2019, 58, 3057-3059.	1.2	1
26	Translating Material Science into Biological Function. <i>Molecular Cell</i> , 2019, 75, 1-2.	4.5	23
27	Properties of Stress Granule and P-Body Proteomes. <i>Molecular Cell</i> , 2019, 76, 286-294.	4.5	258
28	Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. <i>Science</i> , 2019, 365, 825-829.	6.0	240
29	First-generation predictors of biological protein phase separation. <i>Current Opinion in Structural Biology</i> , 2019, 58, 88-96.	2.6	119
30	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
31	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
32	Proteome-wide signatures of function in highly diverged intrinsically disordered regions. <i>ELife</i> , 2019, 8, .	2.8	131
33	Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. <i>Biochemistry</i> , 2018, 57, 2499-2508.	1.2	184
34	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
35	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
36	Phase Separation in Biology and Disease. <i>Journal of Molecular Biology</i> , 2018, 430, 4603-4606.	2.0	68

#	ARTICLE	IF	CITATIONS
37	Pi-Pi contacts are an overlooked protein feature relevant to phase separation. <i>ELife</i> , 2018, 7, .	2.8	571
38	RGG/RC Motif Regions in RNA Binding and Phase Separation. <i>Journal of Molecular Biology</i> , 2018, 430, 4650-4665.	2.0	297
39	CFTR structure. <i>Journal of Cystic Fibrosis</i> , 2018, 17, S5-S8.	0.3	20
40	A hidden competitive advantage of disorder. <i>Nature</i> , 2017, 543, 325-326.	13.7	4
41	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
42	Interplay of buried histidine protonation and protein stability in prion misfolding. <i>Scientific Reports</i> , 2017, 7, 882.	1.6	17
43	An evolutionary switch in ND2 enables Src kinase regulation of NMDA receptors. <i>Nature Communications</i> , 2017, 8, 15220.	5.8	11
44	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
45	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Communications</i> , 2017, 8, 13943.	5.8	33
46	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
47	Phenotypic profiling of CFTR modulators in patient-derived respiratory epithelia. <i>Npj Genomic Medicine</i> , 2017, 2, 12.	1.7	66
48	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
49	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
50	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
51	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
52	Finding Our Way in the Dark Proteome. <i>Journal of the American Chemical Society</i> , 2016, 138, 9730-9742.	6.6	111
53	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
54	Development and characterization of synthetic antibodies binding to the cystic fibrosis conductance regulator. <i>MAbs</i> , 2016, 8, 1167-1176.	2.6	3

#	ARTICLE	IF	CITATIONS
55	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
56	A New Phase in ALS Research. <i>Structure</i> , 2016, 24, 1435-1436.	1.6	6
57	Liquid-liquid phase separation in cellular signaling systems. <i>Current Opinion in Structural Biology</i> , 2016, 41, 180-186.	2.6	172
58	Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. <i>Physical Review Letters</i> , 2016, 117, 178101.	2.9	224
59	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
60	Modulation of Intrinsically Disordered Protein Function by Post-translational Modifications. <i>Journal of Biological Chemistry</i> , 2016, 291, 6696-6705.	1.6	402
61	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. <i>Chemical Reviews</i> , 2016, 116, 6424-6462.	23.0	161
62	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
63	Phase Transition of a Disordered Nuage Protein Generates Environmentally Responsive Membraneless Organelles. <i>Molecular Cell</i> , 2015, 57, 936-947.	4.5	1,408
64	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
65	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. <i>Nature</i> , 2015, 519, 106-109.	13.7	471
66	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
67	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
68	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
69	From Sequence and Forces to Structure, Function, and Evolution of Intrinsically Disordered Proteins. <i>Structure</i> , 2013, 21, 1492-1499.	1.6	196
70	Characterization of disordered proteins with ENSEMBLE. <i>Bioinformatics</i> , 2013, 29, 398-399.	1.8	141
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	Whatâ€™s in a name? Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013, 1, e24157.	1.9	226
75	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
76	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
77	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
78	Dynamic complexes of intrinsically disordered proteins and their regulation by postâ€translational modifications. <i>FASEB Journal</i> , 2013, 27, 459.1.	0.2	0
79	Composite low affinity interactions dictate recognition of the cyclin-dependent kinase inhibitor Sic1 by the SCF ^{Cdc4} ubiquitin ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3287-3292.	3.3	55
80	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
81	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
82	Phosphorylation-dependent 14-3-3 protein interactions regulate CFTR biogenesis. <i>Molecular Biology of the Cell</i> , 2012, 23, 996-1009.	0.9	53
83	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012, 22, 643-650.	2.6	94
84	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
85	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
86	Structural Signature of the MYPT1â€PP1 Interaction. <i>Journal of the American Chemical Society</i> , 2011, 133, 73-80.	6.6	44
87	NMR Spectroscopy to Study the Dynamics and Interactions of CFTR. <i>Methods in Molecular Biology</i> , 2011, 741, 377-403.	0.4	10
88	Protein dynamics and conformational disorder in molecular recognition. <i>Journal of Molecular Recognition</i> , 2010, 23, 105-116.	1.1	337
89	15NH/D-SOLEXSY 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
90	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

#	ARTICLE	IF	CITATIONS
91	Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. <i>Structure</i> , 2010, 18, 1094-1103.	1.6	110
92	NMR evidence for differential phosphorylation-dependent interactions in WT and \hat{I}^{\prime} F508 CFTR. <i>EMBO Journal</i> , 2010, 29, 263-277.	3.5	103
93	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
94	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
95	Sequence Determinants of Compaction in Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2010, 98, 2383-2390.	0.2	342
96	NMR Characterization of Copper-Binding Domains 4 \hat{a} ~6 of ATP7B,. <i>Biochemistry</i> , 2010, 49, 8468-8477.	1.2	34
97	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
98	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
99	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
100	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
101	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
102	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
103	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
104	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
105	Synuclein- \hat{I}^3 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	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
107	Autoinhibition of the HECT-Type Ubiquitin Ligase Smurf2 through Its C2 Domain. <i>Cell</i> , 2007, 130, 651-662.	13.5	237
108	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

#	ARTICLE	IF	CITATIONS
109	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
110	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
111	Atomic-level characterization of disordered protein ensembles. <i>Current Opinion in Structural Biology</i> , 2007, 17, 3-14.	2.6	409
112	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
113	A change in conformational dynamics underlies the activation of Eph receptor tyrosine kinases. <i>EMBO Journal</i> , 2006, 25, 4686-4696.	3.5	89
114	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
115	Hydration and Packing along the Folding Pathway of SH3 Domains by Pressure-Dependent NMR. <i>Biochemistry</i> , 2006, 45, 4711-4719.	1.2	31
116	Sensitivity of secondary structure propensities to sequence differences between I [±] - and I ³ -synuclein: Implications for fibrillation. <i>Protein Science</i> , 2006, 15, 2795-2804.	3.1	648
117	Structural Determinants for High-Affinity Binding in a Nedd4 WW3 ⁺ — Domain-Comm PY Motif Complex. <i>Structure</i> , 2006, 14, 543-553.	1.6	77
118	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
119	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
120	Measuring pKaValues in Protein Folding Transition State Ensembles by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2005, 127, 8904-8905.	6.6	16
121	Structural Comparison of the Unstable drkN SH3 Domain and a Stable Mutant ⁺ . <i>Biochemistry</i> , 2005, 44, 15550-15560.	1.2	39
122	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
123	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
124	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
125	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
126	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

#	ARTICLE	IF	CITATIONS
127	Solution structure and dynamics of the outer membrane enzyme PagP by NMR. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13560-13565.	3.3	302
128	Structure of a regulatory complex involving the Abl SH3 domain, the Crk SH2 domain, and a Crk-derived phosphopeptide. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14053-14058.	3.3	68
129	Measurement of Side-Chain Carboxyl pKaValues of Glutamate and Aspartate Residues in an Unfolded Protein by Multinuclear NMR Spectroscopy. Journal of the American Chemical Society, 2002, 124, 5714-5717.	6.6	68
130	Distribution of molecular size within an unfolded state ensemble using small-angle X-ray scattering and pulse field gradient NMR techniques. Journal of Molecular Biology, 2002, 316, 101-112.	2.0	181
131	Cooperative Interactions and a Non-native Buried Trp in the Unfolded State of an SH3 Domain. Journal of Molecular Biology, 2002, 322, 163-178.	2.0	64
132	Side-chain Dynamics of the SAP SH2 Domain Correlate with a Binding Hot Spot and a Region with Conformational Plasticity. Journal of Molecular Biology, 2002, 322, 605-620.	2.0	48
133	A "three-pronged" binding mechanism for the SAP/SH2D1A SH2 domain: structural basis and relevance to the XLP syndrome. EMBO Journal, 2002, 21, 314-323.	3.5	82
134	Dramatic stabilization of an SH3 domain by a single substitution: roles of the folded and unfolded states ¹¹ Edited by C. R. Matthews. Journal of Molecular Biology, 2001, 307, 913-928.	2.0	75
135	Calculation of ensembles of structures representing the unfolded state of an SH3 domain. Journal of Molecular Biology, 2001, 308, 1011-1032.	2.0	209
136	Structural Characterization of Proteins with an Attached ATCUN Motif by Paramagnetic Relaxation Enhancement NMR Spectroscopy. Journal of the American Chemical Society, 2001, 123, 9843-9847.	6.6	162
137	Multidimensional NMR Methods for Protein Structure Determination. IUBMB Life, 2001, 52, 291-302.	1.5	110
138	Solution structure of a Nedd4 WW domain-ENaC peptide complex. Nature Structural Biology, 2001, 8, 407-412.	9.7	202
139	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2001, 123, 11341-11352.	6.6	454
140	Sequential assignment of proline-rich regions in proteins: application to modular binding domain complexes. Journal of Biomolecular NMR, 2000, 16, 253-259.	1.6	74
141	Similarities between the spectrin SH3 domain denatured state and its folding transition state ¹¹ Edited by A. R. Fersht. Journal of Molecular Biology, 2000, 297, 1217-1229.	2.0	91
142	Global folds of proteins with low densities of NOEs using residual dipolar couplings: application to the 370-residue maltodextrin-binding protein. Journal of Molecular Biology, 2000, 300, 197-212.	2.0	165
143	The 'dynamics' in the thermodynamics of binding., 1999, 6, 1086-1087.		83
144	Analysis of deuterium relaxation-derived methyl axis order parameters and correlation with local structure. Journal of Biomolecular NMR, 1999, 13, 181-185.	1.6	84

#	ARTICLE	IF	CITATIONS
145	A simple in vivo assay for increased protein solubility. <i>Protein Science</i> , 1999, 8, 1908-1911.	3.1	153
146	Diversity in protein recognition by PTB domains. <i>Current Opinion in Structural Biology</i> , 1999, 9, 690-695.	2.6	118
147	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
148	^1H - ^{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
149	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
150	Correlation between binding and dynamics at SH2 domain interfaces. <i>Nature Structural Biology</i> , 1998, 5, 156-163.	9.7	104
151	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
152	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
153	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
154	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
155	Characterization of the Backbone Dynamics of Folded and Denatured States of an SH3 Domain. <i>Biochemistry</i> , 1997, 36, 2390-2402.	1.2	160
156	Comprehensive NOE characterization of a partially folded large fragment of staphylococcal nuclease (131), using NMR methods with improved resolution. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 272, 9-20.	2.0	57
157	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
158	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
159	pH Titration studies of an SH2 domain-phosphopeptide complex: Unusual histidine and phosphate p <i>K</i> values. <i>Protein Science</i> , 1997, 6, 1910-1919.	3.1	41
160	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
161	Correlation between Dynamics and High Affinity Binding in an SH2 Domain Interaction. <i>Biochemistry</i> , 1996, 35, 361-368.	1.2	235
162	Characterization of the Phosphotyrosine-binding Domain of the Drosophila Shc Protein. <i>Journal of Biological Chemistry</i> , 1996, 271, 31855-31862.	1.6	16

#	ARTICLE	IF	CITATIONS
163	Structural, Dynamic, and Folding Studies of SH2 and SH3 Domains. , 1996, , 35-47.		0
164	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
165	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
166	NMR Pulse Schemes for the Sequence-Specific Assignment of Arginine Guanidino ^{15}N and ^1H Chemical Shifts in Proteins. <i>Journal of the American Chemical Society</i> , 1995, 117, 3556-3564.	6.6	80
167	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
168	Backbone ^1H 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
169	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
170	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
171	Two-dimensional NMR experiments for correlating carbon- ^{13}C and proton δ/ϵ 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
172	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
173	High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. <i>Biochemistry</i> , 1991, 30, 2685-2698.	1.2	151
174	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
175	Studies on the solution conformation of human thioredoxin using heteronuclear nitrogen- ^{15}N -proton nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1990, 29, 1566-1572.	1.2	87
176	A proton nuclear magnetic resonance assignment and secondary structure determination of recombinant human thioredoxin. <i>Biochemistry</i> , 1989, 28, 7088-7097.	1.2	26