

Julie D Forman-Kay

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

171 papers	17,923 citations	73 h-index	132 g-index
204 ext. papers	20,551 ext. citations	9 avg, IF	6.89 L-index

#	Paper	IF	Citations
171	A recurrent SHANK3 frameshift variant in Autism Spectrum Disorder. <i>Npj Genomic Medicine</i> , 2021 , 6, 91	6.2	1
170	Configurational Entropy of Folded Proteins and Its Importance for Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
169	Phosphorylation-dependent regulation of messenger RNA transcription, processing and translation within biomolecular condensates. <i>Current Opinion in Cell Biology</i> , 2021 , 69, 30-40	9	11
168	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,	11.5	11
167	-Linked--Acetylglucosaminylation 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	16.4	2
166	Recessive variants impair actin remodeling and cause glomerulopathy in humans and mice. <i>Science Advances</i> , 2021 , 7,	14.3	6
165	Identifying molecular features that are associated with biological function of intrinsically disordered protein regions. <i>ELife</i> , 2021 , 10,	8.9	3
164	FUS-ALS mutants alter FMRP phase separation equilibrium and impair protein translation. <i>Science Advances</i> , 2021 , 7,	14.3	6
163	Global Proximity Interactome of the Human Macroautophagy Pathway. <i>Autophagy</i> , 2021 , 1-13	10.2	4
162	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021 , 49, D404-D411	20.1	31
161	Phase Separation as a Missing Mechanism for Interpretation of Disease Mutations. <i>Cell</i> , 2020 , 183, 1742-1756	47.56	34
160	Comparative roles of charge, , 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	11.5	56
159	Extended Experimental Inferential Structure Determination Method in Determining the Structural Ensembles of Disordered Protein States. <i>Communications Chemistry</i> , 2020 , 3,	6.3	21
158	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	17.4	6
157	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , 2020 , 77, 1176-1192.e16	17.6	32
156	Whence Blobs? Phylogenetics of functional protein condensates. <i>Biochemical Society Transactions</i> , 2020 , 48, 2151-2158	5.1	3
155	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	16.4	23

154	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	16.4	41
153	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	15.1	35
152	Phospho-dependent phase separation of FMRP and CAPRIN1 recapitulates regulation of translation and deadenylation. <i>Science</i> , 2019 , 365, 825-829	33.3	128
151	First-generation predictors of biological protein phase separation. <i>Current Opinion in Structural Biology</i> , 2019 , 58, 88-96	8.1	62
150	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	5.7	11
149	Entropy and Information within Intrinsically Disordered Protein Regions. <i>Entropy</i> , 2019 , 21,	2.8	22
148	Oxidative Inhibition of Pbp1 Phase Separation. <i>Biochemistry</i> , 2019 , 58, 3057-3059	3.2	0
147	Translating Material Science into Biological Function. <i>Molecular Cell</i> , 2019 , 75, 1-2	17.6	21
146	Properties of Stress Granule and P-Body Proteomes. <i>Molecular Cell</i> , 2019 , 76, 286-294	17.6	105
145	Proteome-wide signatures of function in highly diverged intrinsically disordered regions. <i>ELife</i> , 2019 , 8,	8.9	53
144	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	11.5	125
143	Theories for Sequence-Dependent Phase Behaviors of Biomolecular Condensates. <i>Biochemistry</i> , 2018 , 57, 2499-2508	3.2	115
142	RGG/RG Motif Regions in RNA Binding and Phase Separation. <i>Journal of Molecular Biology</i> , 2018 , 430, 4650-4665	6.5	166
141	CFTR structure. <i>Journal of Cystic Fibrosis</i> , 2018 , 17, S5-S8	4.1	11
140	Multivalent Interactions with Fbw7 and Pin1 Facilitate Recognition of c-Jun by the SCF Ubiquitin Ligase. <i>Structure</i> , 2018 , 26, 28-39.e2	5.2	17
139	Complex regulatory mechanisms mediated by the interplay of multiple post-translational modifications. <i>Current Opinion in Structural Biology</i> , 2018 , 48, 58-67	8.1	68
138	Pi-Pi contacts are an overlooked protein feature relevant to phase separation. <i>ELife</i> , 2018 , 7,	8.9	302
137	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	11.5	31

136	Interplay of buried histidine protonation and protein stability in prion misfolding. <i>Scientific Reports</i> , 2017 , 7, 882	4.9	14
135	An evolutionary switch in ND2 enables Src kinase regulation of NMDA receptors. <i>Nature Communications</i> , 2017 , 8, 15220	17.4	8
134	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	4.3	51
133	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCF ubiquitin ligase. <i>Nature Communications</i> , 2017 , 8, 13943	17.4	28
132	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	11.5	227
131	Phenotypic profiling of CFTR modulators in patient-derived respiratory epithelia. <i>Npj Genomic Medicine</i> , 2017 , 2, 12	6.2	46
130	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	5.4	13
129	Molecular structural analysis of a novel and de-novo mutation in the SERPINC1 gene associated with type 1 antithrombin deficiency. <i>British Journal of Haematology</i> , 2017 , 177, 654-656	4.5	3
128	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	6	73
127	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	2.9	61
126	Liquid-liquid phase separation in cellular signaling systems. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 180-186	8.1	116
125	Sequence-Specific Polyampholyte Phase Separation in Membraneless Organelles. <i>Physical Review Letters</i> , 2016 , 117, 178101	7.4	149
124	Role of CBS and Bateman Domains in Phosphorylation-Dependent Regulation of a CLC Anion Channel. <i>Biophysical Journal</i> , 2016 , 111, 1876-1886	2.9	3
123	Modulation of Intrinsically Disordered Protein Function by Post-translational Modifications. <i>Journal of Biological Chemistry</i> , 2016 , 291, 6696-705	5.4	262
122	Dynamic Protein Interaction Networks and New Structural Paradigms in Signaling. <i>Chemical Reviews</i> , 2016 , 116, 6424-62	68.1	118
121	Finding Our Way in the Dark Proteome. <i>Journal of the American Chemical Society</i> , 2016 , 138, 9730-42	16.4	93
120	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, 360-73	6.3	21
119	Development and characterization of synthetic antibodies binding to the cystic fibrosis conductance regulator. <i>MAbs</i> , 2016 , 8, 1167-76	6.6	3

118	Conformations of a Metastable SH3 Domain Characterized by smFRET and an Excluded-Volume Polymer Model. <i>Biophysical Journal</i> , 2016 , 110, 1510-1522	2.9	15
117	A New Phase in ALS Research. <i>Structure</i> , 2016 , 24, 1435-6	5.2	5
116	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, 22862-78	5.4	15
115	Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. <i>Nature</i> , 2015 , 519, 106-9	50.4	344
114	c.1058C>T variant in the SERPINC1 gene is pathogenic for antithrombin deficiency. <i>British Journal of Haematology</i> , 2015 , 170, 123-5	4.5	2
113	Phase transition of a disordered nuage protein generates environmentally responsive membraneless organelles. <i>Molecular Cell</i> , 2015 , 57, 936-947	17.6	952
112	The effect of intrachain electrostatic repulsion on conformational disorder and dynamics of the Sic1 protein. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 4088-97	3.4	43
111	Clinical presentation and molecular basis of congenital antithrombin deficiency in children: a cohort study. <i>British Journal of Haematology</i> , 2014 , 166, 130-9	4.5	14
110	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014 , 42, D326-35	20.1	159
109	From sequence and forces to structure, function, and evolution of intrinsically disordered proteins. <i>Structure</i> , 2013 , 21, 1492-9	5.2	144
108	Characterization of disordered proteins with ENSEMBLE. <i>Bioinformatics</i> , 2013 , 29, 398-9	7.2	115
107	Interaction of the eukaryotic initiation factor 4E with 4E-BP2 at a dynamic bipartite interface. <i>Structure</i> , 2013 , 21, 2186-96	5.2	64
106	Structural changes of CFTR R region upon phosphorylation: a plastic platform for intramolecular and intermolecular interactions. <i>FEBS Journal</i> , 2013 , 280, 4407-16	5.7	44
105	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	11.5	110
104	What's in a name? Why these proteins are intrinsically disordered: Why these proteins are intrinsically disordered. <i>Intrinsically Disordered Proteins</i> , 2013 , 1, e24157		171
103	Dynamics intrinsic to cystic fibrosis transmembrane conductance regulator function and stability. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2013 , 3, a009522	5.4	24
102	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	3.7	19
101	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	3.7	24

100	Dynamic complexes of intrinsically disordered proteins and their regulation by post-translational modifications. <i>FASEB Journal</i> , 2013 , 27, 459.1	0.9	
99	Probing the diverse landscape of protein flexibility and binding. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 643-50	8.1	87
98	Ensemble modeling of protein disordered states: experimental restraint contributions and validation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 556-72	4.2	95
97	Composite low affinity interactions dictate recognition of the cyclin-dependent kinase inhibitor Sic1 by the SCFCdc4 ubiquitin ligase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 3287-92	11.5	51
96	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, 28480-94	5.4	42
95	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <i>Nucleic Acids Research</i> , 2012 , 40, 6353-66	20.1	75
94	Phosphorylation-dependent 14-3-3 protein interactions regulate CFTR biogenesis. <i>Molecular Biology of the Cell</i> , 2012 , 23, 996-1009	3.5	45
93	Differential dynamic engagement within 24 SH3 domain: peptide complexes revealed by co-linear chemical shift perturbation analysis. <i>PLoS ONE</i> , 2012 , 7, e51282	3.7	27
92	Structural signature of the MYPT1-PP1 interaction. <i>Journal of the American Chemical Society</i> , 2011 , 133, 73-80	16.4	37
91	NMR spectroscopy to study the dynamics and interactions of CFTR. <i>Methods in Molecular Biology</i> , 2011 , 741, 377-403	1.4	9
90	NMR evidence for differential phosphorylation-dependent interactions in WT and DeltaF508 CFTR. <i>EMBO Journal</i> , 2010 , 29, 263-77	13	87
89	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, 18404-9	11.5	57
88	The ubiquitin binding region of the Smurf HECT domain facilitates polyubiquitylation and binding of ubiquitylated substrates. <i>Journal of Biological Chemistry</i> , 2010 , 285, 6308-15	5.4	55
87	Sequence determinants of compaction in intrinsically disordered proteins. <i>Biophysical Journal</i> , 2010 , 98, 2383-90	2.9	252
86	NMR characterization of copper-binding domains 4-6 of ATP7B. <i>Biochemistry</i> , 2010 , 49, 8468-77	3.2	33
85	Protein dynamics and conformational disorder in molecular recognition. <i>Journal of Molecular Recognition</i> , 2010 , 23, 105-16	2.6	277
84	¹⁵ N H/D-SOLEXSY experiment for accurate measurement of amide solvent exchange rates: application to denatured drkN SH3. <i>Journal of Biomolecular NMR</i> , 2010 , 46, 227-44	3	48
83	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	5.2	208

82	Structural diversity in free and bound states of intrinsically disordered protein phosphatase 1 regulators. <i>Structure</i> , 2010 , 18, 1094-103	5.2	94
81	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, 1241-50	7	13
80	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, 26918-27	5.4	25
79	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, 359-74	6.5	126
78	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, 409-24	6.5	9
77	Calculation of residual dipolar couplings from disordered state ensembles using local alignment. <i>Journal of the American Chemical Society</i> , 2008 , 130, 7804-5	16.4	61
76	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, 8711-22	5.4	54
75	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, 17772-7	11.5	257
74	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	0.6	11
73	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, 1826-35	16.4	27
72	CFTR regulatory region interacts with NBD1 predominantly via multiple transient helices. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 738-45	17.6	233
71	Atomic-level characterization of disordered protein ensembles. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 3-14	8.1	360
70	Synuclein-gamma targeting peptide inhibitor that enhances sensitivity of breast cancer cells to antimicrotubule drugs. <i>Cancer Research</i> , 2007 , 67, 626-33	10.1	48
69	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, 9650-5	11.5	186
68	Autoinhibition of the HECT-type ubiquitin ligase Smurf2 through its C2 domain. <i>Cell</i> , 2007 , 130, 651-62	56.2	206
67	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, 1494-510	6.5	99
66	Structural determinants for high-affinity binding in a Nedd4 WW3* domain-Comm PY motif complex. <i>Structure</i> , 2006 , 14, 543-53	5.2	67
65	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	5.4	45

64	Characterization of the hydrodynamic properties of the folding transition state of an SH3 domain by magnetization transfer NMR spectroscopy. <i>Biochemistry</i> , 2006 , 45, 6434-45	3.2	6
63	A change in conformational dynamics underlies the activation of Eph receptor tyrosine kinases. <i>EMBO Journal</i> , 2006 , 25, 4686-96	13	82
62	Tryptophan solvent exposure in folded and unfolded states of an SH3 domain by 19F and 1H NMR. <i>Biochemistry</i> , 2006 , 45, 14120-8	3.2	30
61	Hydration and packing along the folding pathway of SH3 domains by pressure-dependent NMR. <i>Biochemistry</i> , 2006 , 45, 4711-9	3.2	27
60	Sensitivity of secondary structure propensities to sequence differences between alpha- and gamma-synuclein: implications for fibrillation. <i>Protein Science</i> , 2006 , 15, 2795-804	6.3	547
59	NMR dynamics-derived insights into the binding properties of a peptide interacting with an SH2 domain. <i>Biochemistry</i> , 2005 , 44, 694-703	3.2	27
58	Measuring pK(a) values in protein folding transition state ensembles by NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2005 , 127, 8904-5	16.4	15
57	Structural comparison of the unstable drkN SH3 domain and a stable mutant. <i>Biochemistry</i> , 2005 , 44, 15550-60	3.2	31
56	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, 40707-14	5.4	19
55	Affinity and specificity of interactions between Nedd4 isoforms and the epithelial Na ⁺ channel. <i>Journal of Biological Chemistry</i> , 2003 , 278, 20019-28	5.4	74
54	Aromatic and methyl NOEs highlight hydrophobic clustering in the unfolded state of an SH3 domain. <i>Biochemistry</i> , 2003 , 42, 8687-95	3.2	77
53	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	6.5	15
52	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, 4545-50	11.5	79
51	A "three-pronged" binding mechanism for the SAP/SH2D1A SH2 domain: structural basis and relevance to the XLP syndrome. <i>EMBO Journal</i> , 2002 , 21, 314-23	13	73
50	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, 13560-5	11.5	282
49	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, 14053-8	11.5	63
48	Measurement of side-chain carboxyl pK(a) values of glutamate and aspartate residues in an unfolded protein by multinuclear NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2002 , 124, 5714-7	16.4	62
47	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, 101-12	6.5	158

46	Cooperative interactions and a non-native buried Trp in the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , 2002 , 322, 163-78	6.5	63
45	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, 605-20	6.5	46
44	Multidimensional NMR methods for protein structure determination. <i>IUBMB Life</i> , 2001 , 52, 291-302	4.7	95
43	Solution structure of a Nedd4 WW domain-ENaC peptide complex. <i>Nature Structural Biology</i> , 2001 , 8, 407-12		181
42	Slow dynamics in folded and unfolded states of an SH3 domain. <i>Journal of the American Chemical Society</i> , 2001 , 123, 11341-52	16.4	408
41	Dramatic stabilization of an SH3 domain by a single substitution: roles of the folded and unfolded states. <i>Journal of Molecular Biology</i> , 2001 , 307, 913-28	6.5	73
40	Calculation of ensembles of structures representing the unfolded state of an SH3 domain. <i>Journal of Molecular Biology</i> , 2001 , 308, 1011-32	6.5	184
39	Structural characterization of proteins with an attached ATCUN motif by paramagnetic relaxation enhancement NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2001 , 123, 9843-7	16.4	145
38	Sequential assignment of proline-rich regions in proteins: application to modular binding domain complexes. <i>Journal of Biomolecular NMR</i> , 2000 , 16, 253-9	3	64
37	Similarities between the spectrin SH3 domain denatured state and its folding transition state. <i>Journal of Molecular Biology</i> , 2000 , 297, 1217-29	6.5	90
36	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	6.5	147
35	Analysis of deuterium relaxation-derived methyl axis order parameters and correlation with local structure. <i>Journal of Biomolecular NMR</i> , 1999 , 13, 181-5	3	74
34	A simple in vivo assay for increased protein solubility. <i>Protein Science</i> , 1999 , 8, 1908-11	6.3	140
33	Diversity in protein recognition by PTB domains. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 690-5	8.1	103
32	Novel mode of ligand binding by the SH2 domain of the human XLP disease gene product SAP/SH2D1A. <i>Current Biology</i> , 1999 , 9, 1355-62	6.3	97
31	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	16.4	40
30	NOE data demonstrating a compact unfolded state for an SH3 domain under non-denaturing conditions. <i>Journal of Molecular Biology</i> , 1999 , 289, 619-38	6.5	149
29	Correlation between binding and dynamics at SH2 domain interfaces. <i>Nature Structural Biology</i> , 1998 , 5, 156-63		97

28	Structure of a Numb PTB domain-peptide complex suggests a basis for diverse binding specificity. <i>Nature Structural Biology</i> , 1998 , 5, 1075-83		98
27	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	3.6	34
26	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, 1153-64	6.5	49
25	NMR structure of neuromedin C, a neurotransmitter with an amino terminal Cull-, Nill-binding (ATCUN) motif. <i>Chemical Biology and Drug Design</i> , 1997 , 49, 500-9		26
24	NMR studies of unfolded states of an SH3 domain in aqueous solution and denaturing conditions. <i>Biochemistry</i> , 1997 , 36, 3959-70	3.2	128
23	Characterization of the backbone dynamics of folded and denatured states of an SH3 domain. <i>Biochemistry</i> , 1997 , 36, 2390-402	3.2	148
22	Comprehensive NOE characterization of a partially folded large fragment of staphylococcal nuclease Delta131Delta, using NMR methods with improved resolution. <i>Journal of Molecular Biology</i> , 1997 , 272, 9-20	6.5	56
21	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	6.5	134
20	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	3	69
19	pH titration studies of an SH2 domain-phosphopeptide complex: unusual histidine and phosphate pKa values. <i>Protein Science</i> , 1997 , 6, 1910-9	6.3	37
18	Correlation between dynamics and high affinity binding in an SH2 domain interaction. <i>Biochemistry</i> , 1996 , 35, 361-8	3.2	225
17	Characterization of the phosphotyrosine-binding domain of the Drosophila Shc protein. <i>Journal of Biological Chemistry</i> , 1996 , 271, 31855-62	5.4	15
16	Structural, Dynamic, and Folding Studies of SH2 and SH3 Domains 1996 , 35-47		
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, 868-78	3.2	289
14	Structural characterization of folded and unfolded states of an SH3 domain in equilibrium in aqueous buffer. <i>Biochemistry</i> , 1995 , 34, 6784-94	3.2	170
13	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	16.4	73
12	Structural and dynamic characterization of the phosphotyrosine binding region of a Src homology 2 domain--phosphopeptide complex by NMR relaxation, proton exchange, and chemical shift approaches. <i>Biochemistry</i> , 1995 , 34, 11353-62	3.2	60
11	Backbone 1H and 15N 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, 845-58	3	617

10	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, 727-34	3.2	387
9	Backbone dynamics of a free and phosphopeptide-complexed Src homology 2 domain studied by ^{15}N NMR relaxation. <i>Biochemistry</i> , 1994 , 33, 5984-6003	3.2	1979
8	Two-dimensional NMR experiments for correlating carbon-13.β. 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	16.4	399
7	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, 3442-52	3.2	116
6	High-resolution three-dimensional structure of reduced recombinant human thioredoxin in solution. <i>Biochemistry</i> , 1991 , 30, 2685-98	3.2	137
5	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, 209-16	6.5	43
4	Studies on the solution conformation of human thioredoxin using heteronuclear ^{15}N - ^1H nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1990 , 29, 1566-72	3.2	86
3	A proton nuclear magnetic resonance assignment and secondary structure determination of recombinant human thioredoxin. <i>Biochemistry</i> , 1989 , 28, 7088-97	3.2	26
2	Integrating multiple experimental data to determine conformational ensembles of an intrinsically disordered protein		3
1	O-GlcNAcylation reduces phase separation and aggregation of the EWS N-terminal low complexity region		1