David Fushman

List of Publications by Year
in descending order

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137 papers	8,633 citations	44042 48 h-index	48277 88 g-index
147 all docs	147 docs citations	147 times ranked	7202 citing authors

#	Article	IF	Citations
1	Backbone NMR resonance assignment of the intrinsically disordered UBact protein from Nitrospira nitrosa. Biomolecular NMR Assignments, 2022, , 1.	0.4	0
2	Tsg101/ESCRT-I recruitment regulated by the dual binding modes of K63-linked diubiquitin. Structure, 2022, 30, 289-299.e6.	1.6	5
3	Site-Specific Detection and Characterization of Ubiquitin Carbamylation. Biochemistry, 2022, 61, 712-721.	1.2	3
4	Ubiquitin is a carbon dioxideâ€“binding protein. Science Advances, 2021, 7, eabi5507.	4.7	13
5	A novel recognition site for polyubiquitin and ubiquitin-like signals in an unexpected region of proteasomal subunit Rpn1. Journal of Biological Chemistry, 2021, 297, 101052.	1.6	8
6	In vivo modulation of ubiquitin chains by N-methylated non-proteinogenic cyclic peptides. RSC Chemical Biology, 2021, 2, 513-522.	2.0	16
7	Polyubiquitin and ubiquitin-like signals share common recognition sites on proteasomal subunit Rpn1. Journal of Biological Chemistry, 2021, 296, 100450.	1.6	7
8	15N NMR studies provide insights into physico-chemical properties of room-temperature ionic liquids. Physical Chemistry Chemical Physics, 2021, 23, 12395-12407.	1.3	1
9	Branched ubiquitin chain binding and deubiquitination by UCH37 facilitate proteasome clearance of stress-induced inclusions. ELife, 2021, 10, .	2.8	20
10	Branching via K11 and K48 Bestows Ubiquitin Chains with a Unique Interdomain Interface and Enhanced Affinity for Proteasomal Subunit Rpn1. Structure, 2020, 28, 29-43.e6.	1.6	49
11	SOS1 interacts with Grb2 through regions that induce closed nSH3 conformations. Journal of Chemical Physics, 2020, 153, 045106.	1.2	14
12	Mechanism of Catalysis by <scp>l</scp>-Asparaginase. Biochemistry, 2020, 59, 1927-1945.	1.2	36
13	High-Affinity Interactions of the nSH3/cSH3 Domains of Grb2 with the C-Terminal Proline-Rich Domain of SOS1. Journal of the American Chemical Society, 2020, 142, 3401-3411.	6.6	25
14	Structural basis for DNA damage-induced phosphoregulation of MDM2 RING domain. Nature Communications, 2020, 11, 2094.	5.8	20
15	Crosstalk between Lys63- and Lys11-polyubiquitin signaling at DNA damage sites is driven by Cezanne. Genes and Development, 2019, 33, 1702-1717.	2.7	25
16	Ubiquitin Chains Bearing Genetically Encoded Photo-Cross-Linkers Enable Efficient Covalent Capture of (Poly)ubiquitin-Binding Domains. Biochemistry, 2019, 58, 883-886.	1.2	11
17	De novo macrocyclic peptides that specifically modulate Lys48-linked ubiquitin chains. Nature Chemistry, 2019, 11, 644-652.	6.6	63
18	A binding cooperativity switch driven by synergistic structural swelling of an osmo-regulatory protein pair. Nature Communications, 2019, 10, 1995.	5.8	15

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19	Structure Based Search for Multiple Binding Sites of SOS1 PR Domain Recognizes an Uncovered Motif Favoring GRB2-SOS1 Association. Biophysical Journal, 2019, 116, 169a.	0.2	0
20	Topâ€‹down analysis of novel synthetic branched proteins. Journal of Mass Spectrometry, 2019, 54, 19-25.	0.7	6
21	Top-Down Analysis of Branched Proteins Using Mass Spectrometry. Analytical Chemistry, 2018, 90, 4032-4038.	3.2	12
22	Impact of different ionization states of phosphorylated Serine-65 on ubiquitin structure and interactions. Scientific Reports, 2018, 8, 2651.	1.6	5
23	Neutron scattering in the biological sciences: progress and prospects. Acta Crystallographica Section D: Structural Biology, 2018, 74, 1129-1168.	1.1	47
24	Autoinhibition in Ras effectors Raf, PI3KÎ±, and RASSF5: a comprehensive review underscoring the challenges in pharmacological intervention. Biophysical Reviews, 2018, 10, 1263-1282.	1.5	40
25	Allosteric KRas4B Can Modulate SOS1 Fast and Slow Ras Activation Cycles. Biophysical Journal, 2018, 115, 629-641.	0.2	24
26	The dynamic mechanism of RASSF5 and MST kinase activation by Ras. Physical Chemistry Chemical Physics, 2017, 19, 6470-6480.	1.3	22
27	Intrinsic protein disorder in oncogenic KRAS signaling. Cellular and Molecular Life Sciences, 2017, 74, 3245-3261.	2.4	45
28	Probing the Binding Modes of a Multidomain Protein to Lipid-based Nanoparticles by Relaxation-based NMR. Journal of Physical Chemistry Letters, 2017, 8, 2535-2540.	2.1	11
29	Identification of primary and secondary <scp>UBA</scp> footprints on the surface of ubiquitin in cellâ€‹mimicking crowded solution. FEBS Letters, 2017, 591, 979-990.	1.3	9
30	Polyubiquitin-Photoactivatable Crosslinking Reagents for Mapping Ubiquitin Interactome Identify Rpn1 as a Proteasome Ubiquitin-Associating Subunit. Cell Chemical Biology, 2017, 24, 443-457.e6.	2.5	37
31	Exploring Polyubiquitin as a Flexible Multiple-Ligand Binding Platform. Structure, 2017, 25, 1-3.	1.6	30
32	Graded Structural Polymorphism in a Bacterial Thermosensor Protein. Journal of the American Chemical Society, 2017, 139, 792-802.	6.6	28
33	Structural Basis for the Inhibitory Effects of Ubistatins in the Ubiquitin-Proteasome Pathway. Structure, 2017, 25, 1839-1855.e11.	1.6	15
34	Hydrophobic Patch of Ubiquitin is Important for its Optimal Activation by Ubiquitin Activating Enzyme E1. Analytical Chemistry, 2017, 89, 7852-7860.	3.2	16
35	Preparing to read the ubiquitin code: top-down analysis of unanchored ubiquitin tetramers. Journal of Mass Spectrometry, 2016, 51, 629-637.	0.7	8
36	RASSF5: An MST activator and tumor suppressor in vivo but opposite in vitro. Current Opinion in Structural Biology, 2016, 41, 217-224.	2.6	29

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37	Characterizing polyubiquitinated forms of the neurodegenerative ubiquitin mutant <scp>UBB</scp>⁺¹. FEBS Letters, 2016, 590, 4573-4585.	1.3	4
38	Preparing to read the ubiquitin code: characterization of ubiquitin trimers by topâ€down mass spectrometry. Journal of Mass Spectrometry, 2016, 51, 315-321.	0.7	8
39	Linkage via K27 Bestows Ubiquitin Chains with Unique Properties among Polyubiquitins. Structure, 2016, 24, 423-436.	1.6	56
40	Linkage-specific conformational ensembles of non-canonical polyubiquitin chains. Physical Chemistry Chemical Physics, 2016, 18, 5771-5788.	1.3	58
41	Base-CP proteasome can serve as a platform for stepwise lid formation. Bioscience Reports, 2015, 35, .	1.1	18
42	Changing the topology of protein backbone: the effect of backbone cyclization on the structure and dynamics of a SH3 domain. Frontiers in Chemistry, 2015, 3, 26.	1.8	6
43	Polyhydroxylated [60]fullerene binds specifically to functional recognition sites on a monomeric and a dimeric ubiquitin. Nanoscale, 2015, 7, 7197-7205.	2.8	35
44	Disassembly of Lys11 and Mixed Linkage Polyubiquitin Conjugates Provides Insights into Function of Proteasomal Deubiquitinases Rpn11 and Ubp6. Journal of Biological Chemistry, 2015, 290, 4688-4704.	1.6	42
45	DNA-Damage-Inducible 1 Protein (Ddi1) Contains an Uncharacteristic Ubiquitin-like Domain that Binds Ubiquitin. Structure, 2015, 23, 542-557.	1.6	71
46	Information content of long-range NMR data for the characterization of conformational heterogeneity. Journal of Biomolecular NMR, 2015, 62, 353-371.	1.6	19
47	Unexpected Trypsin Cleavage at Ubiquitinated Lysines. Analytical Chemistry, 2015, 87, 8144-8148.	3.2	16
48	Preparing to read the ubiquitin code: a middleâ€out strategy for characterization of all lysineâ€linked diubiquitins. Journal of Mass Spectrometry, 2014, 49, 1272-1278.	0.7	7
49	Nonenzymatic Rubylation and Ubiquitination of Proteins for Structural and Functional Studies. Angewandte Chemie - International Edition, 2014, 53, 6120-6125.	7.2	20
50	Extended ubiquitin species are protein-based DUB inhibitors. Nature Chemical Biology, 2014, 10, 664-670.	3.9	31
51	Alanine Scan of Core Positions in Ubiquitin Reveals Links between Dynamics, Stability, and Function. Journal of Molecular Biology, 2014, 426, 1377-1389.	2.0	21
52	HierarchicalO(N) computation of small-angle scattering profiles and their associated derivatives. Journal of Applied Crystallography, 2014, 47, 755-761.	1.9	5
53	Deriving quantitative dynamics information for proteins and RNAs using ROTDIF with a graphical user interface. Journal of Biomolecular NMR, 2013, 57, 333-352.	1.6	41
54	Analyses of the Effects of All Ubiquitin Point Mutants on Yeast Growth Rate. Journal of Molecular Biology, 2013, 425, 1363-1377.	2.0	212

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55	Mixed-Linkage Ubiquitin Chains Send Mixed Messages. Structure, 2013, 21, 727-740.	1.6	88
56	Nonenzymatic assembly of branched polyubiquitin chains for structural and biochemical studies. Bioorganic and Medicinal Chemistry, 2013, 21, 3421-3429.	1.4	35
57	Unique Structural, Dynamical, and Functional Properties of K11-Linked Polyubiquitin Chains. Structure, 2013, 21, 1168-1181.	1.6	56
58	Recovering a Representative Conformational Ensemble from Underdetermined Macromolecular Structural Data. Journal of the American Chemical Society, 2013, 135, 16595-16609.	6.6	106
59	Recognition and Cleavage of Related to Ubiquitin 1 (Rub1) and Rub1-Ubiquitin Chains by Components of the Ubiquitin-Proteasome System. Molecular and Cellular Proteomics, 2012, 11, 1595-1611.	2.5	43
60	Evidence for Cooperative and Domain-specific Binding of the Signal Transducing Adaptor Molecule 2 (STAM2) to Lys63-linked Diubiquitin. Journal of Biological Chemistry, 2012, 287, 18687-18699.	1.6	21
61	Rpn1 and Rpn2 Coordinate Ubiquitin Processing Factors at Proteasome. Journal of Biological Chemistry, 2012, 287, 14659-14671.	1.6	99
62	Proteomic Identification and Analysis of K63-Linked Ubiquitin Conjugates. Analytical Chemistry, 2012, 84, 10121-10128.	3.2	16
63	Structural and biochemical studies of the open state of Lys48-linked diubiquitin. Biochimica Et Biophysica Acta - Molecular Cell Research, 2012, 1823, 2046-2056.	1.9	40
64	A hierarchical algorithm for fast debye summation with applications to small angle scattering. Journal of Computational Chemistry, 2012, 33, 1981-1996.	1.5	21
65	High Relaxivity Supramolecular Adducts Between Humanâ€Liver Fattyâ€Acidâ€Binding Protein and Amphiphilic Gd^{III} Complexes: Structural Basis for the Design of Intracellular Targeting MRI Probes. Chemistry - A European Journal, 2012, 18, 9919-9928.	1.7	25
66	Determining Protein Dynamics from 15N Relaxation Data by Using DYNAMICS. Methods in Molecular Biology, 2012, 831, 485-511.	0.4	12
67	Controlled enzymatic synthesis of natural-linkage, defined-length polyubiquitin chains using lysines with removable protecting groups. Chemical Communications, 2011, 47, 2026.	2.2	36
68	Nonenzymatic Assembly of Natural Polyubiquitin Chains of Any Linkage Composition and Isotopic Labeling Scheme. Journal of the American Chemical Society, 2011, 133, 17855-17868.	6.6	85
69	Structure and recognition of polyubiquitin chains of different lengths and linkage. F1000 Biology Reports, 2011, 3, 26.	4.0	54
70	Density functional calculations of backbone 15N shielding tensors in beta-sheet and turn residues of protein G. Journal of Biomolecular NMR, 2011, 50, 19-33.	1.6	14
71	Fast approximations of the rotational diffusion tensor and their application to structural assembly of molecular complexes. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2268-2281.	1.5	5
72	Longâ€Lived States to Monitor Protein Unfolding by Proton NMR. ChemPhysChem, 2011, 12, 2729-2734.	1.0	41

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73	Segmental Isotopic Labeling of Ubiquitin Chains To Unravel Monomerâ€Specific Molecular Behavior. Angewandte Chemie - International Edition, 2011, 50, 11210-11214.	7.2	30
74	Condensed E. coli cultures for highly efficient production of proteins containing unnatural amino acids. Bioorganic and Medicinal Chemistry Letters, 2010, 20, 5613-5616.	1.0	11
75	Structural Assembly of Molecular Complexes Based on Residual Dipolar Couplings. Journal of the American Chemical Society, 2010, 132, 8961-8972.	6.6	22
76	Exploring the Linkage Dependence of Polyubiquitin Conformations Using Molecular Modeling. Journal of Molecular Biology, 2010, 395, 803-814.	2.0	59
77	Perturbing the Ubiquitin Pathway Reveals How Mitosis Is Hijacked to Denucleate and Regulate Cell Proliferation and Differentiation In Vivo. PLoS ONE, 2010, 5, e13331.	1.1	31
78	Density functional calculations of chemical shielding of backbone 15N in helical residues of protein G. Journal of Biomolecular NMR, 2009, 45, 245-253.	1.6	16
79	Avid interactions underlie the Lys63-linked polyubiquitin binding specificities observed for UBA domains. Nature Structural and Molecular Biology, 2009, 16, 883-889.	3.6	78
80	Improvement and analysis of computational methods for prediction of residual dipolar couplings. Journal of Magnetic Resonance, 2009, 201, 25-33.	1.2	38
81	Evidence for Bidentate Substrate Binding as the Basis for the K48 Linkage Specificity of Otubain 1. Journal of Molecular Biology, 2009, 386, 1011-1023.	2.0	126
82	Structure of the S5a:K48-Linked Diubiquitin Complex and Its Interactions with Rpn13. Molecular Cell, 2009, 35, 280-290.	4.5	133
83	Together, Rpn10 and Dsk2 Can Serve as a Polyubiquitin Chain-Length Sensor. Molecular Cell, 2009, 36, 1018-1033.	4.5	107
84	Density functional calculations of 15N chemical shifts in solvated dipeptides. Journal of Biomolecular NMR, 2008, 41, 77-88.	1.6	22
85	1H, 13C, and 15N resonance assignment of the ubiquitin-like domain from Dsk2p. Biomolecular NMR Assignments, 2008, 2, 147-149.	0.4	3
86	Mutations in the Hydrophobic Core of Ubiquitin Differentially Affect Its Recognition by Receptor Proteins. Journal of Molecular Biology, 2008, 375, 979-996.	2.0	43
87	Affinity Makes the Difference: Nonselective Interaction of the UBA Domain of Ubiquilin-1 with Monomeric Ubiquitin and Polyubiquitin Chains. Journal of Molecular Biology, 2008, 377, 162-180.	2.0	146
88	Crystal Structure and Solution NMR Studies of Lys48-linked Tetraubiquitin at Neutral pH. Journal of Molecular Biology, 2007, 367, 204-211.	2.0	153
89	Mapping the Interactions between Lys48 and Lys63-Linked Di-ubiquitins and a Ubiquitin-Interacting Motif of S5a. Journal of Molecular Biology, 2007, 368, 753-766.	2.0	31
90	A Model of Interdomain Mobility in a Multidomain Protein. Journal of the American Chemical Society, 2007, 129, 3315-3327.	6.6	88

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91	Structural Assembly of Multidomain Proteins and Protein Complexes Guided by the Overall Rotational Diffusion Tensor. Journal of the American Chemical Society, 2007, 129, 7894-7902.	6.6	38
92	Analysis of 'downhill' protein folding; Analysis of protein-folding cooperativity (Reply). Nature, 2007, 445, E17-E18.	13.7	30
93	Effects of cyclization on conformational dynamics and binding properties of Lys48-linked di-ubiquitin. Protein Science, 2007, 16, 369-378.	3.1	18
94	Variability of the15N Chemical Shielding Tensors in the B3 Domain of Protein G from15N Relaxation Measurements at Several Fields. Implications for Backbone Order Parameters. Journal of the American Chemical Society, 2006, 128, 7855-7870.	6.6	83
95	An Efficient Computational Method for Predicting Rotational Diffusion Tensors of Globular Proteins Using an Ellipsoid Representation. Journal of the American Chemical Society, 2006, 128, 15432-15444.	6.6	50
96	Interdomain mobility in di-ubiquitin revealed by NMR. Proteins: Structure, Function and Bioinformatics, 2006, 63, 787-796.	1.5	82
97	Atom-by-atom analysis of global downhill protein folding. Nature, 2006, 442, 317-321.	13.7	231
98	Measurement of 15N relaxation in deuterated amide groups in proteins using direct nitrogen detection. Journal of Biomolecular NMR, 2006, 36, 27-36.	1.6	31
99	Analysis of interdomain dynamics in a two-domain protein using residual dipolar couplings together with15N relaxation data. Magnetic Resonance in Chemistry, 2006, 44, S143-S151.	1.1	19
100	Spin-state selection for increased confidence in cross-correlation rates measurements. Journal of Biomolecular NMR, 2005, 31, 149-154.	1.6	11
101	Diverse polyubiquitin interaction properties of ubiquitin-associated domains. Nature Structural and Molecular Biology, 2005, 12, 708-714.	3.6	312
102	Various strategies of using residual dipolar couplings in NMR-driven protein docking: Application to Lys48-linked di-ubiquitin and validation against 15N-relaxation data. Proteins: Structure, Function and Bioinformatics, 2005, 60, 367-381.	1.5	78
103	Using NMR Spectroscopy to Monitor Ubiquitin Chain Conformation and Interactions with Ubiquitinâ€Binding Domains. Methods in Enzymology, 2005, 399, 177-192.	0.4	32
104	Structural Determinants for Selective Recognition of a Lys48-Linked Polyubiquitin Chain by a UBA Domain. Molecular Cell, 2005, 18, 687-698.	4.5	203
105	Solution Conformation of Lys63-linked Di-ubiquitin Chain Provides Clues to Functional Diversity of Polyubiquitin Signaling. Journal of Biological Chemistry, 2004, 279, 7055-7063.	1.6	296
106	Ubistatins Inhibit Proteasome-Dependent Degradation by Binding the Ubiquitin Chain. Science, 2004, 306, 117-120.	6.0	183
107	Efficient and accurate determination of the overall rotational diffusion tensor of a molecule from 15N relaxation data using computer program ROTDIF. Journal of Magnetic Resonance, 2004, 168, 336-345.	1.2	73
108	Determining domain orientation in macromolecules by using spin-relaxation and residual dipolar coupling measurements. Progress in Nuclear Magnetic Resonance Spectroscopy, 2004, 44, 189-214.	3.9	90

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109	Polyubiquitin chains: polymeric protein signals. Current Opinion in Chemical Biology, 2004, 8, 610-616.	2.8	921
110	Characterization of the Overall Rotational Diffusion of a Protein From ¹⁵N Relaxation Measurements and Hydrodynamic Calculations. , 2004, 278, 139-160.		9
111	Direct measurement of the 15N CSA/dipolar relaxation interference from coupled HSQC spectra. Journal of Biomolecular NMR, 2003, 26, 181-186.	1.6	19
112	Characterization of the overall and local dynamics of a protein with intermediate rotational anisotropy: Differentiating between conformational exchange and anisotropic diffusion in the B3 domain of protein G. Journal of Biomolecular NMR, 2003, 27, 261-275.	1.6	114
113	Direct measurement of the transverse and longitudinal15N chemical shift anisotropy-dipolar cross-correlation rate constants using1H-coupled HSQC spectra. Magnetic Resonance in Chemistry, 2003, 41, 837-842.	1.1	15
114	Structural Properties of Polyubiquitin Chains in Solution. Journal of Molecular Biology, 2002, 324, 637-647.	2.0	259
115	Characterization of Inter-Domain Orientations in Solution Using the NMR Relaxation Approach. , 2002, , 53-77.		5
116	Rescuing a destabilized protein fold through backbone cyclization. Journal of Molecular Biology, 2001, 308, 1045-1062.	2.0	98
117	Simulated and NMR-Derived Backbone Dynamics of a Protein with Significant Flexibility:Â A Comparison of Spectral Densities for the Î²ARK1 PH Domain. Journal of the American Chemical Society, 2001, 123, 3021-3036.	6.6	54
118	Nuclear Magnetic Resonance Relaxation in Determination of Residue-Specific 15N Chemical Shift Tensors in Proteins in Solution: Protein Dynamics, Structure, and Applications of Transverse Relaxation Optimized Spectroscopy. Methods in Enzymology, 2001, 339, 109-126.	0.4	37
119	Determination of the Rotational Diffusion Tensor of Macromolecules in Solution from NMR Relaxation Data with a Combination of Exact and Approximate Methodsâ€"Application to the Determination of Interdomain Orientation in Multidomain Proteins. Journal of Magnetic Resonance, 2001, 149, 204-217.	1.2	66
120	Peptide chemical ligation inside living cells: in vivo generation of a circular protein domain. Bioorganic and Medicinal Chemistry, 2001, 9, 2479-2484.	1.4	58
121	The Virtual NMR Spectrometer: A Computer Program for Efficient Simulation of NMR Experiments Involving Pulsed Field Gradients. Journal of Magnetic Resonance, 2000, 145, 262-275.	1.2	36
122	The Effect of Finite Sampling on the Determination of Orientational Properties:Â A Theoretical Treatment with Application to Interatomic Vectors in Proteins. Journal of the American Chemical Society, 2000, 122, 10640-10649.	6.6	35
123	The effect of noncollinearity of 15N-1H dipolar and 15N CSA tensors and rotational anisotropy on 15N relaxation, CSA/dipolar cross correlation, and TROSY. Journal of Biomolecular NMR, 1999, 13, 139-147.	1.6	55
124	An Approach to Direct Determination of Protein Dynamics from15N NMR Relaxation at Multiple Fields, Independent of Variable15N Chemical Shift Anisotropy and Chemical Exchange Contributions. Journal of the American Chemical Society, 1999, 121, 8577-8582.	6.6	84
125	Solution Structure of the Proapoptotic Molecule BID. Cell, 1999, 96, 625-634.	13.5	370
126	Direct Determination of Changes of Interdomain Orientation on Ligation:Â Use of the Orientational Dependence of15N NMR Relaxation in Abl SH(32)â€. Biochemistry, 1999, 38, 10225-10230.	1.2	116

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127	Model-Independent Analysis of15N Chemical Shift Anisotropy from NMR Relaxation Data. Ubiquitin as a Test Example. Journal of the American Chemical Society, 1998, 120, 7109-7110.	6.6	88
128	Solution structure and dynamics of the bioactive retroviral M domain from rous sarcoma virus. Journal of Molecular Biology, 1998, 279, 921-928.	2.0	45
129	Direct Measurement of15N Chemical Shift Anisotropy in Solution. Journal of the American Chemical Society, 1998, 120, 10947-10952.	6.6	154
130	The Solution Structure and Dynamics of the Pleckstrin Homology Domain of G Protein-coupled Receptor Kinase 2 (Î²-Adrenergic Receptor Kinase 1). Journal of Biological Chemistry, 1998, 273, 2835-2843.	1.6	75
131	Solution Structures of FcÎµRI Î±-Chain Mimics:Â A Î²-Hairpin Peptide and Its Retroenantiomer. Journal of the American Chemical Society, 1997, 119, 5321-5328.	6.6	44
132	The main-chain dynamics of the dynamin pleckstrin homology (PH) domain in solution: analysis of 15N relaxation with monomer/dimer equilibration. Journal of Molecular Biology, 1997, 266, 173-194.	2.0	224
133	Identification of the Binding Site for Acidic Phospholipids on the PH Domain of Dynamin: Implications for Stimulation of GTPase Activity. Journal of Molecular Biology, 1996, 255, 14-21.	2.0	251
134	Backbone dynamics of proteins studied by two-dimensional heteronuclear NMR spectroscopy and molecular dynamics simulations. International Journal of Quantum Chemistry, 1996, 59, 291-300.	1.0	2
135	Determination of the Backbone Mobility of Ribonuclease T1 and its 2â€²GMP Complex Using Molecular Dynamics Simulations and NMR Relaxation Data. Journal of Biomolecular Structure and Dynamics, 1994, 11, 1377-1402.	2.0	48
136	Backbone dynamics of ribonuclease T1 and its complex with 2?GMP studied by two-dimensional heteronuclear NMR spectroscopy. Journal of Biomolecular NMR, 1994, 4, 61-78.	1.6	117
137	Surface Fractality of Proteins From Theory and NMR Data. Journal of Biomolecular Structure and Dynamics, 1990, 7, 1333-1344.	2.0	20