

# David Fushman

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5570817/publications.pdf>

Version: 2024-02-01

137  
papers

8,633  
citations

43973

48  
h-index

48187

88  
g-index

147  
all docs

147  
docs citations

147  
times ranked

7202  
citing authors

#	ARTICLE	IF	CITATIONS
1	Polyubiquitin chains: polymeric protein signals. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 610-616.	2.8	921
2	Solution Structure of the Proapoptotic Molecule BID. <i>Cell</i> , 1999, 96, 625-634.	13.5	370
3	Diverse polyubiquitin interaction properties of ubiquitin-associated domains. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 708-714.	3.6	312
4	Solution Conformation of Lys63-linked Di-ubiquitin Chain Provides Clues to Functional Diversity of Polyubiquitin Signaling. <i>Journal of Biological Chemistry</i> , 2004, 279, 7055-7063.	1.6	296
5	Structural Properties of Polyubiquitin Chains in Solution. <i>Journal of Molecular Biology</i> , 2002, 324, 637-647.	2.0	259
6	Identification of the Binding Site for Acidic Phospholipids on the PH Domain of Dynamin: Implications for Stimulation of GTPase Activity. <i>Journal of Molecular Biology</i> , 1996, 255, 14-21.	2.0	251
7	Atom-by-atom analysis of global downhill protein folding. <i>Nature</i> , 2006, 442, 317-321.	13.7	231
8	The main-chain dynamics of the dynamin pleckstrin homology (PH) domain in solution: analysis of <sup>15</sup> N relaxation with monomer/dimer equilibration. <i>Journal of Molecular Biology</i> , 1997, 266, 173-194.	2.0	224
9	Analyses of the Effects of All Ubiquitin Point Mutants on Yeast Growth Rate. <i>Journal of Molecular Biology</i> , 2013, 425, 1363-1377.	2.0	212
10	Structural Determinants for Selective Recognition of a Lys48-Linked Polyubiquitin Chain by a UBA Domain. <i>Molecular Cell</i> , 2005, 18, 687-698.	4.5	203
11	Ubistatins Inhibit Proteasome-Dependent Degradation by Binding the Ubiquitin Chain. <i>Science</i> , 2004, 306, 117-120.	6.0	183
12	Direct Measurement of <sup>15</sup> N Chemical Shift Anisotropy in Solution. <i>Journal of the American Chemical Society</i> , 1998, 120, 10947-10952.	6.6	154
13	Crystal Structure and Solution NMR Studies of Lys48-linked Tetraubiquitin at Neutral pH. <i>Journal of Molecular Biology</i> , 2007, 367, 204-211.	2.0	153
14	Affinity Makes the Difference: Nonselective Interaction of the UBA Domain of Ubiquilin-1 with Monomeric Ubiquitin and Polyubiquitin Chains. <i>Journal of Molecular Biology</i> , 2008, 377, 162-180.	2.0	146
15	Structure of the S5a:K48-Linked Diubiquitin Complex and Its Interactions with Rpn13. <i>Molecular Cell</i> , 2009, 35, 280-290.	4.5	133
16	Evidence for Bidentate Substrate Binding as the Basis for the K48 Linkage Specificity of Otubain 1. <i>Journal of Molecular Biology</i> , 2009, 386, 1011-1023.	2.0	126
17	Backbone dynamics of ribonuclease T1 and its complex with 2'GMP studied by two-dimensional heteronuclear NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 1994, 4, 61-78.	1.6	117
18	Direct Determination of Changes of Interdomain Orientation on Ligation: Use of the Orientational Dependence of <sup>15</sup> N NMR Relaxation in Abl SH(32). <i>Biochemistry</i> , 1999, 38, 10225-10230.	1.2	116

#	ARTICLE	IF	CITATIONS
19	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. <i>Journal of Biomolecular NMR</i> , 2003, 27, 261-275.	1.6	114
20	Together, Rpn10 and Dsk2 Can Serve as a Polyubiquitin Chain-Length Sensor. <i>Molecular Cell</i> , 2009, 36, 1018-1033.	4.5	107
21	Recovering a Representative Conformational Ensemble from Underdetermined Macromolecular Structural Data. <i>Journal of the American Chemical Society</i> , 2013, 135, 16595-16609.	6.6	106
22	Rpn1 and Rpn2 Coordinate Ubiquitin Processing Factors at Proteasome. <i>Journal of Biological Chemistry</i> , 2012, 287, 14659-14671.	1.6	99
23	Rescuing a destabilized protein fold through backbone cyclization. <i>Journal of Molecular Biology</i> , 2001, 308, 1045-1062.	2.0	98
24	Determining domain orientation in macromolecules by using spin-relaxation and residual dipolar coupling measurements. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2004, 44, 189-214.	3.9	90
25	Model-Independent Analysis of <sup>15</sup> N Chemical Shift Anisotropy from NMR Relaxation Data. Ubiquitin as a Test Example. <i>Journal of the American Chemical Society</i> , 1998, 120, 7109-7110.	6.6	88
26	A Model of Interdomain Mobility in a Multidomain Protein. <i>Journal of the American Chemical Society</i> , 2007, 129, 3315-3327.	6.6	88
27	Mixed-Linkage Ubiquitin Chains Send Mixed Messages. <i>Structure</i> , 2013, 21, 727-740.	1.6	88
28	Nonenzymatic Assembly of Natural Polyubiquitin Chains of Any Linkage Composition and Isotopic Labeling Scheme. <i>Journal of the American Chemical Society</i> , 2011, 133, 17855-17868.	6.6	85
29	An Approach to Direct Determination of Protein Dynamics from <sup>15</sup> N NMR Relaxation at Multiple Fields, Independent of Variable <sup>15</sup> N Chemical Shift Anisotropy and Chemical Exchange Contributions. <i>Journal of the American Chemical Society</i> , 1999, 121, 8577-8582.	6.6	84
30	Variability of the <sup>15</sup> N Chemical Shielding Tensors in the B3 Domain of Protein G from <sup>15</sup> N Relaxation Measurements at Several Fields. Implications for Backbone Order Parameters. <i>Journal of the American Chemical Society</i> , 2006, 128, 7855-7870.	6.6	83
31	Interdomain mobility in di-ubiquitin revealed by NMR. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 787-796.	1.5	82
32	Various strategies of using residual dipolar couplings in NMR-driven protein docking: Application to Lys48-linked di-ubiquitin and validation against <sup>15</sup> N-relaxation data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 367-381.	1.5	78
33	Avid interactions underlie the Lys63-linked polyubiquitin binding specificities observed for UBA domains. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 883-889.	3.6	78
34	The Solution Structure and Dynamics of the Pleckstrin Homology Domain of G Protein-coupled Receptor Kinase 2 ( <sup>β</sup> 2-Adrenergic Receptor Kinase 1). <i>Journal of Biological Chemistry</i> , 1998, 273, 2835-2843.	1.6	75
35	Efficient and accurate determination of the overall rotational diffusion tensor of a molecule from <sup>15</sup> N relaxation data using computer program ROTDIF. <i>Journal of Magnetic Resonance</i> , 2004, 168, 336-345.	1.2	73
36	DNA-Damage-Inducible 1 Protein (Ddi1) Contains an Uncharacteristic Ubiquitin-like Domain that Binds Ubiquitin. <i>Structure</i> , 2015, 23, 542-557.	1.6	71

#	ARTICLE	IF	CITATIONS
37	Determination of the Rotational Diffusion Tensor of Macromolecules in Solution from NMR Relaxation Data with a Combination of Exact and Approximate Methods Application to the Determination of Interdomain Orientation in Multidomain Proteins. <i>Journal of Magnetic Resonance</i> , 2001, 149, 204-217.	1.2	66
38	De novo macrocyclic peptides that specifically modulate Lys48-linked ubiquitin chains. <i>Nature Chemistry</i> , 2019, 11, 644-652.	6.6	63
39	Exploring the Linkage Dependence of Polyubiquitin Conformations Using Molecular Modeling. <i>Journal of Molecular Biology</i> , 2010, 395, 803-814.	2.0	59
40	Peptide chemical ligation inside living cells: in vivo generation of a circular protein domain. <i>Bioorganic and Medicinal Chemistry</i> , 2001, 9, 2479-2484.	1.4	58
41	Linkage-specific conformational ensembles of non-canonical polyubiquitin chains. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 5771-5788.	1.3	58
42	Unique Structural, Dynamical, and Functional Properties of K11-Linked Polyubiquitin Chains. <i>Structure</i> , 2013, 21, 1168-1181.	1.6	56
43	Linkage via K27 Bestows Ubiquitin Chains with Unique Properties among Polyubiquitins. <i>Structure</i> , 2016, 24, 423-436.	1.6	56
44	The effect of noncollinearity of $^{15}\text{N}$ - $^1\text{H}$ dipolar and $^{15}\text{N}$ CSA tensors and rotational anisotropy on $^{15}\text{N}$ relaxation, CSA/dipolar cross correlation, and TROSY. <i>Journal of Biomolecular NMR</i> , 1999, 13, 139-147.	1.6	55
45	Simulated and NMR-Derived Backbone Dynamics of a Protein with Significant Flexibility: A Comparison of Spectral Densities for the $\hat{1}^2$ ARK1 PH Domain. <i>Journal of the American Chemical Society</i> , 2001, 123, 3021-3036.	6.6	54
46	Structure and recognition of polyubiquitin chains of different lengths and linkage. <i>F1000 Biology Reports</i> , 2011, 3, 26.	4.0	54
47	An Efficient Computational Method for Predicting Rotational Diffusion Tensors of Globular Proteins Using an Ellipsoid Representation. <i>Journal of the American Chemical Society</i> , 2006, 128, 15432-15444.	6.6	50
48	Branching via K11 and K48 Bestows Ubiquitin Chains with a Unique Interdomain Interface and Enhanced Affinity for Proteasomal Subunit Rpn1. <i>Structure</i> , 2020, 28, 29-43.e6.	1.6	49
49	Determination of the Backbone Mobility of Ribonuclease T1 and its $2\hat{2}\hat{2}$ GMP Complex Using Molecular Dynamics Simulations and NMR Relaxation Data. <i>Journal of Biomolecular Structure and Dynamics</i> , 1994, 11, 1377-1402.	2.0	48
50	Neutron scattering in the biological sciences: progress and prospects. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1129-1168.	1.1	47
51	Solution structure and dynamics of the bioactive retroviral M domain from rous sarcoma virus. <i>Journal of Molecular Biology</i> , 1998, 279, 921-928.	2.0	45
52	Intrinsic protein disorder in oncogenic KRAS signaling. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3245-3261.	2.4	45
53	Solution Structures of Fc $\hat{1}$ RI $\hat{1}$ -Chain Mimics: A $\hat{1}^2$ -Hairpin Peptide and Its Retroenantiomer. <i>Journal of the American Chemical Society</i> , 1997, 119, 5321-5328.	6.6	44
54	Mutations in the Hydrophobic Core of Ubiquitin Differentially Affect Its Recognition by Receptor Proteins. <i>Journal of Molecular Biology</i> , 2008, 375, 979-996.	2.0	43

#	ARTICLE	IF	CITATIONS
55	Recognition and Cleavage of Related to Ubiquitin 1 (Rub1) and Rub1-Ubiquitin Chains by Components of the Ubiquitin-Proteasome System. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1595-1611.	2.5	43
56	Disassembly of Lys11 and Mixed Linkage Polyubiquitin Conjugates Provides Insights into Function of Proteasomal Deubiquitinases Rpn11 and Ubp6. <i>Journal of Biological Chemistry</i> , 2015, 290, 4688-4704.	1.6	42
57	Long-lived States to Monitor Protein Unfolding by Proton NMR. <i>ChemPhysChem</i> , 2011, 12, 2729-2734.	1.0	41
58	Deriving quantitative dynamics information for proteins and RNAs using ROTDIF with a graphical user interface. <i>Journal of Biomolecular NMR</i> , 2013, 57, 333-352.	1.6	41
59	Structural and biochemical studies of the open state of Lys48-linked diubiquitin. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2012, 1823, 2046-2056.	1.9	40
60	Autoinhibition in Ras effectors Raf, PI3K, and RASSF5: a comprehensive review underscoring the challenges in pharmacological intervention. <i>Biophysical Reviews</i> , 2018, 10, 1263-1282.	1.5	40
61	Structural Assembly of Multidomain Proteins and Protein Complexes Guided by the Overall Rotational Diffusion Tensor. <i>Journal of the American Chemical Society</i> , 2007, 129, 7894-7902.	6.6	38
62	Improvement and analysis of computational methods for prediction of residual dipolar couplings. <i>Journal of Magnetic Resonance</i> , 2009, 201, 25-33.	1.2	38
63	Nuclear Magnetic Resonance Relaxation in Determination of Residue-Specific <sup>15</sup> N Chemical Shift Tensors in Proteins in Solution: Protein Dynamics, Structure, and Applications of Transverse Relaxation Optimized Spectroscopy. <i>Methods in Enzymology</i> , 2001, 339, 109-126.	0.4	37
64	Polyubiquitin-Photoactivatable Crosslinking Reagents for Mapping Ubiquitin Interactome Identify Rpn1 as a Proteasome Ubiquitin-Associating Subunit. <i>Cell Chemical Biology</i> , 2017, 24, 443-457.e6.	2.5	37
65	The Virtual NMR Spectrometer: A Computer Program for Efficient Simulation of NMR Experiments Involving Pulsed Field Gradients. <i>Journal of Magnetic Resonance</i> , 2000, 145, 262-275.	1.2	36
66	Controlled enzymatic synthesis of natural-linkage, defined-length polyubiquitin chains using lysines with removable protecting groups. <i>Chemical Communications</i> , 2011, 47, 2026.	2.2	36
67	Mechanism of Catalysis by Asparaginase. <i>Biochemistry</i> , 2020, 59, 1927-1945.	1.2	36
68	The Effect of Finite Sampling on the Determination of Orientational Properties: A Theoretical Treatment with Application to Interatomic Vectors in Proteins. <i>Journal of the American Chemical Society</i> , 2000, 122, 10640-10649.	6.6	35
69	Nonenzymatic assembly of branched polyubiquitin chains for structural and biochemical studies. <i>Bioorganic and Medicinal Chemistry</i> , 2013, 21, 3421-3429.	1.4	35
70	Polyhydroxylated [60]fullerene binds specifically to functional recognition sites on a monomeric and a dimeric ubiquitin. <i>Nanoscale</i> , 2015, 7, 7197-7205.	2.8	35
71	Using NMR Spectroscopy to Monitor Ubiquitin Chain Conformation and Interactions with Ubiquitin-binding Domains. <i>Methods in Enzymology</i> , 2005, 399, 177-192.	0.4	32
72	Measurement of <sup>15</sup> N relaxation in deuterated amide groups in proteins using direct nitrogen detection. <i>Journal of Biomolecular NMR</i> , 2006, 36, 27-36.	1.6	31

#	ARTICLE	IF	CITATIONS
73	Mapping the Interactions between Lys48 and Lys63-Linked Di-ubiquitins and a Ubiquitin-Interacting Motif of S5a. <i>Journal of Molecular Biology</i> , 2007, 368, 753-766.	2.0	31
74	Extended ubiquitin species are protein-based DUB inhibitors. <i>Nature Chemical Biology</i> , 2014, 10, 664-670.	3.9	31
75	Perturbing the Ubiquitin Pathway Reveals How Mitosis Is Hijacked to Denucleate and Regulate Cell Proliferation and Differentiation In Vivo. <i>PLoS ONE</i> , 2010, 5, e13331.	1.1	31
76	Analysis of 'downhill' protein folding; Analysis of protein-folding cooperativity (Reply). <i>Nature</i> , 2007, 445, E17-E18.	13.7	30
77	Segmental Isotopic Labeling of Ubiquitin Chains To Unravel Monomer-Specific Molecular Behavior. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 11210-11214.	7.2	30
78	Exploring Polyubiquitin as a Flexible Multiple-Ligand Binding Platform. <i>Structure</i> , 2017, 25, 1-3.	1.6	30
79	RASSF5: An MST activator and tumor suppressor in vivo but opposite in vitro. <i>Current Opinion in Structural Biology</i> , 2016, 41, 217-224.	2.6	29
80	Graded Structural Polymorphism in a Bacterial Thermosensor Protein. <i>Journal of the American Chemical Society</i> , 2017, 139, 792-802.	6.6	28
81	High Relaxivity Supramolecular Adducts Between Human Liver Fatty Acid-Binding Protein and Amphiphilic Gd <sup>III</sup> Complexes: Structural Basis for the Design of Intracellular Targeting MRI Probes. <i>Chemistry - A European Journal</i> , 2012, 18, 9919-9928.	1.7	25
82	Crosstalk between Lys63- and Lys11-polyubiquitin signaling at DNA damage sites is driven by Cezanne. <i>Genes and Development</i> , 2019, 33, 1702-1717.	2.7	25
83	High-Affinity Interactions of the nSH3/cSH3 Domains of Grb2 with the C-Terminal Proline-Rich Domain of SOS1. <i>Journal of the American Chemical Society</i> , 2020, 142, 3401-3411.	6.6	25
84	Allosteric KRas4B Can Modulate SOS1 Fast and Slow Ras Activation Cycles. <i>Biophysical Journal</i> , 2018, 115, 629-641.	0.2	24
85	Density functional calculations of 15N chemical shifts in solvated dipeptides. <i>Journal of Biomolecular NMR</i> , 2008, 41, 77-88.	1.6	22
86	Structural Assembly of Molecular Complexes Based on Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2010, 132, 8961-8972.	6.6	22
87	The dynamic mechanism of RASSF5 and MST kinase activation by Ras. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 6470-6480.	1.3	22
88	Evidence for Cooperative and Domain-specific Binding of the Signal Transducing Adaptor Molecule 2 (STAM2) to Lys63-linked Diubiquitin. <i>Journal of Biological Chemistry</i> , 2012, 287, 18687-18699.	1.6	21
89	A hierarchical algorithm for fast debye summation with applications to small angle scattering. <i>Journal of Computational Chemistry</i> , 2012, 33, 1981-1996.	1.5	21
90	Alanine Scan of Core Positions in Ubiquitin Reveals Links between Dynamics, Stability, and Function. <i>Journal of Molecular Biology</i> , 2014, 426, 1377-1389.	2.0	21

#	ARTICLE	IF	CITATIONS
91	Surface Fractality of Proteins From Theory and NMR Data. Journal of Biomolecular Structure and Dynamics, 1990, 7, 1333-1344.	2.0	20
92	Nonenzymatic Rubylation and Ubiquitination of Proteins for Structural and Functional Studies. Angewandte Chemie - International Edition, 2014, 53, 6120-6125.	7.2	20
93	Structural basis for DNA damage-induced phosphoregulation of MDM2 RING domain. Nature Communications, 2020, 11, 2094.	5.8	20
94	Branched ubiquitin chain binding and deubiquitination by UCH37 facilitate proteasome clearance of stress-induced inclusions. ELife, 2021, 10, .	2.8	20
95	Direct measurement of the 15N CSA/dipolar relaxation interference from coupled HSQC spectra. Journal of Biomolecular NMR, 2003, 26, 181-186.	1.6	19
96	Analysis of interdomain dynamics in a two-domain protein using residual dipolar couplings together with 15N relaxation data. Magnetic Resonance in Chemistry, 2006, 44, S143-S151.	1.1	19
97	Information content of long-range NMR data for the characterization of conformational heterogeneity. Journal of Biomolecular NMR, 2015, 62, 353-371.	1.6	19
98	Effects of cyclization on conformational dynamics and binding properties of Lys48-linked di-ubiquitin. Protein Science, 2007, 16, 369-378.	3.1	18
99	Base-CP proteasome can serve as a platform for stepwise lid formation. Bioscience Reports, 2015, 35, .	1.1	18
100	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
101	Proteomic Identification and Analysis of K63-Linked Ubiquitin Conjugates. Analytical Chemistry, 2012, 84, 10121-10128.	3.2	16
102	Unexpected Trypsin Cleavage at Ubiquitinated Lysines. Analytical Chemistry, 2015, 87, 8144-8148.	3.2	16
103	Hydrophobic Patch of Ubiquitin is Important for its Optimal Activation by Ubiquitin Activating Enzyme E1. Analytical Chemistry, 2017, 89, 7852-7860.	3.2	16
104	<i>In vivo</i> modulation of ubiquitin chains by <i>N</i> -methylated non-proteinogenic cyclic peptides. RSC Chemical Biology, 2021, 2, 513-522.	2.0	16
105	Direct measurement of the transverse and longitudinal 15N chemical shift anisotropy-dipolar cross-correlation rate constants using 1H-coupled HSQC spectra. Magnetic Resonance in Chemistry, 2003, 41, 837-842.	1.1	15
106	Structural Basis for the Inhibitory Effects of Ubistatins in the Ubiquitin-Proteasome Pathway. Structure, 2017, 25, 1839-1855.e11.	1.6	15
107	A binding cooperativity switch driven by synergistic structural swelling of an osmo-regulatory protein pair. Nature Communications, 2019, 10, 1995.	5.8	15
108	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

#	ARTICLE	IF	CITATIONS
109	SOS1 interacts with Grb2 through regions that induce closed nSH3 conformations. <i>Journal of Chemical Physics</i> , 2020, 153, 045106.	1.2	14
110	Ubiquitin is a carbon dioxide-binding protein. <i>Science Advances</i> , 2021, 7, eabi5507.	4.7	13
111	Top-Down Analysis of Branched Proteins Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 4032-4038.	3.2	12
112	Determining Protein Dynamics from 15N Relaxation Data by Using DYNAMICS. <i>Methods in Molecular Biology</i> , 2012, 831, 485-511.	0.4	12
113	Spin-state selection for increased confidence in cross-correlation rates measurements. <i>Journal of Biomolecular NMR</i> , 2005, 31, 149-154.	1.6	11
114	Condensed E. coli cultures for highly efficient production of proteins containing unnatural amino acids. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 5613-5616.	1.0	11
115	Probing the Binding Modes of a Multidomain Protein to Lipid-based Nanoparticles by Relaxation-based NMR. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 2535-2540.	2.1	11
116	Ubiquitin Chains Bearing Genetically Encoded Photo-Cross-Linkers Enable Efficient Covalent Capture of (Poly)ubiquitin-Binding Domains. <i>Biochemistry</i> , 2019, 58, 883-886.	1.2	11
117	Characterization of the Overall Rotational Diffusion of a Protein From <sup>15</sup> N Relaxation Measurements and Hydrodynamic Calculations. , 2004, 278, 139-160.		9
118	Identification of primary and secondary UBA footprints on the surface of ubiquitin in cell-mimicking crowded solution. <i>FEBS Letters</i> , 2017, 591, 979-990.	1.3	9
119	Preparing to read the ubiquitin code: top-down analysis of unanchored ubiquitin tetramers. <i>Journal of Mass Spectrometry</i> , 2016, 51, 629-637.	0.7	8
120	Preparing to read the ubiquitin code: characterization of ubiquitin trimers by top-down mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2016, 51, 315-321.	0.7	8
121	A novel recognition site for polyubiquitin and ubiquitin-like signals in an unexpected region of proteasomal subunit Rpn1. <i>Journal of Biological Chemistry</i> , 2021, 297, 101052.	1.6	8
122	Preparing to read the ubiquitin code: a middle-out strategy for characterization of all lysine-linked diubiquitins. <i>Journal of Mass Spectrometry</i> , 2014, 49, 1272-1278.	0.7	7
123	Polyubiquitin and ubiquitin-like signals share common recognition sites on proteasomal subunit Rpn1. <i>Journal of Biological Chemistry</i> , 2021, 296, 100450.	1.6	7
124	Changing the topology of protein backbone: the effect of backbone cyclization on the structure and dynamics of a SH3 domain. <i>Frontiers in Chemistry</i> , 2015, 3, 26.	1.8	6
125	Top-down analysis of novel synthetic branched proteins. <i>Journal of Mass Spectrometry</i> , 2019, 54, 19-25.	0.7	6
126	Characterization of Inter-Domain Orientations in Solution Using the NMR Relaxation Approach. , 2002, 53-77.		5



#	ARTICLE	IF	CITATIONS
127	Fast approximations of the rotational diffusion tensor and their application to structural assembly of molecular complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2268-2281.	1.5	5
128	Impact of different ionization states of phosphorylated Serine-65 on ubiquitin structure and interactions. <i>Scientific Reports</i> , 2018, 8, 2651.	1.6	5
129	HierarchicalO(N) computation of small-angle scattering profiles and their associated derivatives. <i>Journal of Applied Crystallography</i> , 2014, 47, 755-761.	1.9	5
130	Tsg101/ESCRT-I recruitment regulated by the dual binding modes of K63-linked diubiquitin. <i>Structure</i> , 2022, 30, 289-299.e6.	1.6	5
131	Characterizing polyubiquitinated forms of the neurodegenerative ubiquitin mutant $\langle \text{scp} \rangle \text{UBB} \langle \text{scp} \rangle \langle \text{sup} \rangle + 1 \langle \text{sup} \rangle$ . <i>FEBS Letters</i> , 2016, 590, 4573-4585.	1.3	4
132	$^1\text{H}$ , $^{13}\text{C}$ , and $^{15}\text{N}$ resonance assignment of the ubiquitin-like domain from Dsk2p. <i>Biomolecular NMR Assignments</i> , 2008, 2, 147-149.	0.4	3
133	Site-Specific Detection and Characterization of Ubiquitin Carbamylation. <i>Biochemistry</i> , 2022, 61, 712-721.	1.2	3
134	Backbone dynamics of proteins studied by two-dimensional heteronuclear NMR spectroscopy and molecular dynamics simulations. <i>International Journal of Quantum Chemistry</i> , 1996, 59, 291-300.	1.0	2
135	$^{15}\text{N}$ NMR studies provide insights into physico-chemical properties of room-temperature ionic liquids. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 12395-12407.	1.3	1
136	Structure Based Search for Multiple Binding Sites of SOS1 PR Domain Recognizes an Uncovered Motif Favoring GRB2-SOS1 Association. <i>Biophysical Journal</i> , 2019, 116, 169a.	0.2	0
137	Backbone NMR resonance assignment of the intrinsically disordered UBact protein from <i>Nitrospira nitrosa</i> . <i>Biomolecular NMR Assignments</i> , 2022, , 1.	0.4	0