Volker Dotsch

List of Publications by Year
in descending order

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		15495	18115
235	16,754	65	120
papers	citations	h-index	g-index
271	271	271	18867
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	p63, a p53 Homolog at 3q27â€“29, Encodes Multiple Products with Transactivating, Death-Inducing, and Dominant-Negative Activities. Molecular Cell, 1998, 2, 305-316.	4.5	1,943
2	Phosphorylation of the Autophagy Receptor Optineurin Restricts <i>Salmonella</i> Growth. Science, 2011, 333, 228-233.	6.0	1,125
3	Nix is a selective autophagy receptor for mitochondrial clearance. EMBO Reports, 2010, 11, 45-51.	2.0	1,045
4	Interactions between Autophagy Receptors and Ubiquitin-like Proteins Form the Molecular Basis for Selective Autophagy. Molecular Cell, 2014, 53, 167-178.	4.5	849
5	Intramolecular Masking of Nuclear Import Signal on NF-AT4 by Casein Kinase I and MEKK1. Cell, 1998, 93, 851-861.	13.5	291
6	Processing of multi-dimensional NMR data with the new software PROSA. Journal of Biomolecular NMR, 1992, 2, 619-629.	1.6	281
7	Loss of p63 and its microRNA-205 target results in enhanced cell migration and metastasis in prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15312-15317.	3.3	251
8	Preparative scale expression of membrane proteins in Escherichia coli-based continuous exchange cell-free systems. Nature Protocols, 2007, 2, 2945-2957.	5.5	240
9	High level cell-free expression and specific labeling of integral membrane proteins. FEBS Journal, 2004, 271, 568-580.	0.2	230
10	Phosphorylation of the mitochondrial autophagy receptor Nix enhances its interaction with LC3 proteins. Scientific Reports, 2017, 7, 1131.	1.6	203
11	HUWE1 E3 ligase promotes PINK1/PARKIN-independent mitophagy by regulating AMBRA1 activation via IKKÎ±. Nature Communications, 2018, 9, 3755.	5.8	198
12	High-Resolution Macromolecular NMR Spectroscopy Inside Living Cells. Journal of the American Chemical Society, 2001, 123, 2446-2447.	6.6	187
13	Evaluation of detergents for the soluble expression of Î±-helical and Î²-barrel-type integral membrane proteins by a preparative scale individual cell-free expression system. FEBS Journal, 2005, 272, 6024-6038.	2.2	186
14	A C-Terminal Inhibitory Domain Controls the Activity of p63 by an Intramolecular Mechanism. Molecular and Cellular Biology, 2002, 22, 8601-8611.	1.1	183
15	Longâ€Range Distance Measurements on Nucleic Acids in Cells by Pulsed EPR Spectroscopy. Angewandte Chemie - International Edition, 2011, 50, 5070-5074.	7.2	163
16	Solution NMR Structure of Proteorhodopsin. Angewandte Chemie - International Edition, 2011, 50, 11942-11946.	7.2	162
17	Low-Conductivity Buffers for High-Sensitivity NMR Measurements. Journal of the American Chemical Society, 2002, 124, 12013-12019.	6.6	161
18	In-Cell NMR Spectroscopyâ€. Biochemistry, 2001, 40, 14317-14323.	1.2	159

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19	Conformational Switches Modulate Protein Interactions in Peptide Antibiotic Synthetases. Science, 2006, 312, 273-276.	6.0	149
20	The parallel G-quadruplex structure of vertebrate telomeric repeat sequences is not the preferred folding topology under physiological conditions. Nucleic Acids Research, 2011, 39, 5768-5775.	6.5	143
21	E3-Independent Monoubiquitination of Ubiquitin-Binding Proteins. Molecular Cell, 2007, 26, 891-898.	4.5	132
22	Structural and functional analysis of the GABARAP interaction motif (GIM). EMBO Reports, 2017, 18, 1382-1396.	2.0	129
23	Evaluation of Parameters Critical to Observing Proteins Inside LivingEscherichiacoliby In-Cell NMR Spectroscopy. Journal of the American Chemical Society, 2001, 123, 8895-8901.	6.6	127
24	Investigating macromolecules inside cultured and injected cells by in-cell NMR spectroscopy. Nature Protocols, 2006, 1, 2701-2709.	5.5	120
25	Cell-free expression as an emerging technique for the large scale production of integral membrane protein. FEBS Journal, 2006, 273, 4141-4153.	2.2	119
26	DNA Damage in Oocytes Induces a Switch of the Quality Control Factor TAp63Î± from Dimer to Tetramer. Cell, 2011, 144, 566-576.	13.5	117
27	Structural basis for the selectivity of the external thioesterase of the surfactin synthetase. Nature, 2008, 454, 907-911.	13.7	112
28	Oocyte DNA damage quality control requires consecutive interplay of CHK2 and CK1 to activate p63. Nature Structural and Molecular Biology, 2018, 25, 261-269.	3.6	112
29	Cell-free production of G protein-coupled receptors for functional and structural studies. Journal of Structural Biology, 2007, 158, 482-493.	1.3	111
30	TECPR2 Cooperates with LC3C to Regulate COPII-Dependent ER Export. Molecular Cell, 2015, 60, 89-104.	4.5	111
31	Structural Basis for Tail-Anchored Membrane Protein Biogenesis by the Get3-Receptor Complex. Science, 2011, 333, 758-762.	6.0	110
32	Involvement of the ubiquitin-like domain of TBK1/IKK-i kinases in regulation of IFN-inducible genes. EMBO Journal, 2007, 26, 3451-3462.	3.5	108
33	Gain-of-function mutation in ADULT syndrome reveals the presence of a second transactivation domain in p63. Human Molecular Genetics, 2002, 11, 799-804.	1.4	104
34	Unusual Rel-like architecture in the DNA-binding domain of the transcription factor NFATc. Nature, 1997, 385, 172-176.	13.7	103
35	High-Resolution Insight into G-Overhang Architecture. Journal of the American Chemical Society, 2013, 135, 2816-2824.	6.6	103
36	Solution Structure of the Core NFATC1/DNA Complex. Cell, 1998, 92, 687-696.	13.5	101

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37	Evaluation of Parameters Critical for Observing Nucleic Acids Inside Living <i>Xenopus laevis</i> Oocytes by In-Cell NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 15761-15768.	6.6	96
38	Definition of the Switch Surface in the Solution Structure of Cdc42Hsâ€,â€¡. Biochemistry, 1997, 36, 8755-8766.	1.2	95
39	Production of membrane proteins using cellâ€free expression systems. Proteomics, 2008, 8, 3933-3946.	1.3	95
40	New Carbon-Detected Protein NMR Experiments Using CryoProbes. Journal of the American Chemical Society, 2000, 122, 3554-3555.	6.6	92
41	Advances in cell-free protein synthesis for the functional and structural analysis of membrane proteins. New Biotechnology, 2011, 28, 262-271.	2.4	92
42	Structural basis for phosphorylation-triggered autophagic clearance of <i>Salmonella</i>. Biochemical Journal, 2013, 454, 459-466.	1.7	92
43	Inâ€Cell NMR and EPR Spectroscopy of Biomacromolecules. Angewandte Chemie - International Edition, 2014, 53, 10300-10314.	7.2	91
44	Regulation of Phosphoribosyl-Linked Serine Ubiquitination by Deubiquitinases DupA and DupB. Molecular Cell, 2020, 77, 164-179.e6.	4.5	91
45	In-Cell NMR Spectroscopy. Methods in Enzymology, 2005, 394, 17-41.	0.4	89
46	The GYF domain is a novel structural fold that is involved in lymphoid signaling through proline-rich sequences. Nature Structural Biology, 1999, 6, 656-660.	9.7	86
47	Characterization of the Interaction of GABARAPL-1 with the LIR Motif of NBR1. Journal of Molecular Biology, 2011, 410, 477-487.	2.0	86
48	Structural evolution of C-terminal domains in the p53 family. EMBO Journal, 2007, 26, 3463-3473.	3.5	85
49	Methyl Groups as Probes for Proteins and Complexes in In-Cell NMR Experiments. Journal of the American Chemical Society, 2004, 126, 7119-7125.	6.6	84
50	Cell-free expression and stable isotope labelling strategies for membrane proteins. Journal of Biomolecular NMR, 2010, 46, 33-43.	1.6	81
51	Cell-Free Expression and Assembly of ATP Synthase. Journal of Molecular Biology, 2011, 413, 593-603.	2.0	81
52	Caspase-2 is an initiator caspase responsible for pore-forming toxin-mediated apoptosis. EMBO Journal, 2012, 31, 2615-2628.	3.5	81
53	Donated chemical probes for open science. ELife, 2018, 7, .	2.8	80
54	A method for integrative structure determination of protein-protein complexes. Bioinformatics, 2012, 28, 3282-3289.	1.8	78

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55	Molecular Crowding Drives Active Pin1 into Nonspecific Complexes with Endogenous Proteins Prior to Substrate Recognition. Journal of the American Chemical Society, 2013, 135, 13796-13803.	6.6	76
56	Membrane protein production in <i>Escherichia coli</i> cellâ€free lysates. FEBS Letters, 2015, 589, 1713-1722.	1.3	76
57	Analyzing native membrane protein assembly in nanodiscs by combined non-covalent mass spectrometry and synthetic biology. ELife, 2017, 6, .	2.8	75
58	An Activation Switch in the Ligand Binding Pocket of the C5a Receptor. Journal of Biological Chemistry, 2001, 276, 3394-3400.	1.6	74
59	CUL3-KBTBD6/KBTBD7Âubiquitin Ligase Cooperates with GABARAP Proteins to Spatially Restrict TIAM1-RAC1 Signaling. Molecular Cell, 2015, 57, 995-1010.	4.5	74
60	A Methylation-Dependent Electrostatic Switch Controls DNA Repair and Transcriptional Activation by E. coli Ada. Molecular Cell, 2005, 20, 117-129.	4.5	73
61	Membrane Protein Expression in Cell-Free Systems. Methods in Molecular Biology, 2010, 601, 165-186.	0.4	73
62	Structural investigation of the C-terminal catalytic fragment of presenilin 1. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9644-9649.	3.3	72
63	Efficient Strategy for the Rapid Backbone Assignment of Membrane Proteins. Journal of the American Chemical Society, 2005, 127, 13504-13505.	6.6	71
64	Actin Binding to the Central Domain of WASP/Scar Proteins Plays a Critical Role in the Activation of the Arp2/3 Complex. Journal of Biological Chemistry, 2006, 281, 10589-10597.	1.6	71
65	The role of protein-solvent interactions in protein unfolding. Current Opinion in Biotechnology, 1996, 7, 428-432.	3.3	69
66	Cell Free Expression and Functional Reconstitution of Eukaryotic Drug Transporters. Biochemistry, 2008, 47, 4552-4564.	1.2	68
67	Diseaseâ€linked TDPâ€43 hyperphosphorylation suppresses TDPâ€43 condensation and aggregation. EMBO Journal, 2022, 41, e108443.	3.5	68
68	Characterization of co-translationally formed nanodisc complexes with small multidrug transporters, proteorhodopsin and with the E. coli MraY translocase. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 3098-3106.	1.4	67
69	Modified lipid and protein dynamics in nanodiscs. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 1222-1229.	1.4	67
70	The Large Extracellular Loop of Organic Cation Transporter 1 Influences Substrate Affinity and Is Pivotal for Oligomerization. Journal of Biological Chemistry, 2011, 286, 37874-37886.	1.6	64
71	Endoplasmic Reticulum Targeting and Insertion of Tail-Anchored Membrane Proteins by the GET Pathway. Cold Spring Harbor Perspectives in Biology, 2013, 5, a013334-a013334.	2.3	64
72	Segmental Isotopic Labeling of a Central Domain in a Multidomain Protein by Protein <i>Trans</i>â€splicing Using Only One Robust DnaE Intein. Angewandte Chemie - International Edition, 2009, 48, 6128-6131.	7.2	63

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73	Non-oncogenic roles of TAp73: from multiciliogenesis to metabolism. Cell Death and Differentiation, 2018, 25, 144-153.	5.0	63
74	A systematic approach to increase the efficiency of membrane protein production in cell-free expression systems. Protein Expression and Purification, 2012, 82, 308-316.	0.6	62
75	Quantitative Identification of the Protonation State of Histidines in Vitro and in Vivoâ€. Biochemistry, 2003, 42, 9227-9234.	1.2	61
76	Preparative scale cell-free expression systems: New tools for the large scale preparation of integral membrane proteins for functional and structural studies. Methods, 2007, 41, 355-369.	1.9	61
77	Selective autophagy maintains centrosome integrity and accurate mitosis by turnover of centriolar satellites. Nature Communications, 2019, 10, 4176.	5.8	61
78	Elimination of13CÎ± Splitting in Protein NMR Spectra by Deconvolution with Maximum Entropy Reconstruction. Journal of the American Chemical Society, 2003, 125, 2382-2383.	6.6	60
79	Functional properties of cell-free expressed human endothelin A and endothelin B receptors in artificial membrane environments. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2182-2192.	1.4	58
80	Lipid Requirements for the Enzymatic Activity of MraY Translocases and in Vitro Reconstitution of the Lipid II Synthesis Pathway. Journal of Biological Chemistry, 2016, 291, 2535-2546.	1.6	57
81	Carbon-Detected NMR Experiments To Investigate Structure and Dynamics of Biological Macromolecules. ChemBioChem, 2001, 2, 247-251.	1.3	56
82	Differential altered stability and transcriptional activity of Î”Np63 mutants in distinct ectodermal dysplasias. Journal of Cell Science, 2011, 124, 2200-2207.	1.2	56
83	Preparative Scale Cell-free Production and Quality Optimization of MraY Homologues in Different Expression Modes. Journal of Biological Chemistry, 2011, 286, 38844-38853.	1.6	54
84	Co-translational association of cell-free expressed membrane proteins with supplied lipid bilayers. Molecular Membrane Biology, 2013, 30, 75-89.	2.0	54
85	The E. coli S30 lysate proteome: A prototype for cell-free protein production. New Biotechnology, 2018, 40, 245-260.	2.4	54
86	Inâ€Cell Solidâ€State NMR as a Tool to Study Proteins in Large Complexes. ChemBioChem, 2012, 13, 534-537.	1.3	53
87	Co-translational formation and pharmacological characterization of beta1-adrenergic receptor/nanodisc complexes with different lipid environments. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1306-1316.	1.4	53
88	Quality control in oocytes by p63 is based on a spring-loaded activation mechanism on the molecular and cellular level. ELife, 2016, 5, .	2.8	52
89	The Molecular Pharmacology and In Vivo Activity of 2-(4-Chloro-6-(2,3-dimethylphenylamino)pyrimidin-2-ylthio)octanoic acid (YS121), a Dual Inhibitor of Microsomal Prostaglandin E₂ Synthase-1 and 5-Lipoxygenase. Journal of Pharmacology and Experimental Therapeutics, 2010, 332, 840-848.	1.3	49
90	Fluorescenceâ€based <scp>ATG</scp>8 sensors monitor localization and function of <scp>LC</scp>3/<scp>GABARAP</scp> proteins. EMBO Journal, 2017, 36, 549-564.	3.5	49

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91	In-Cell NMR Spectroscopy. ChemBioChem, 2005, 6, 1601-1606.	1.3	48
92	Single-Molecule Force Spectroscopy from Nanodiscs: An Assay to Quantify Folding, Stability, and Interactions of Native Membrane Proteins. ACS Nano, 2012, 6, 961-971.	7.3	47
93	Modulation of G-protein coupled receptor sample quality by modified cell-free expression protocols: A case study of the human endothelin A receptor. Journal of Structural Biology, 2010, 172, 94-106.	1.3	46
94	The guanylate kinase domain of the MAGUK PSD-95 binds dynamically to a conserved motif in MAP1a. Nature Structural and Molecular Biology, 2007, 14, 155-163.	3.6	43
95	Intrinsic aggregation propensity of the p63 and p73 TI domains correlates with p53R175H interaction and suggests further significance of aggregation events in the p53 family. Cell Death and Differentiation, 2016, 23, 1952-1960.	5.0	43
96	Strategies for the Cell-Free Expression of Membrane Proteins. Methods in Molecular Biology, 2010, 607, 187-212.	0.4	42
97	In-cell NMR spectroscopy. Progress in Nuclear Magnetic Resonance Spectroscopy, 2007, 51, 91-101.	3.9	41
98	Preparative Scale Production of Functional Mouse Aquaporin 4 Using Different Cell-Free Expression Modes. PLoS ONE, 2010, 5, e12972.	1.1	41
99	Optimization of amino acid type-specific 13C and 15N labeling for the backbone assignment of membrane proteins by solution- and solid-state NMR with the UPLABEL algorithm. Journal of Biomolecular NMR, 2011, 49, 75-84.	1.6	41
100	Structural Evolution and Dynamics of the p53 Proteins. Cold Spring Harbor Perspectives in Medicine, 2017, 7, a028308.	2.9	41
101	An atypical LIR motif within UBA5 (ubiquitin like modifier activating enzyme 5) interacts with GABARAP proteins and mediates membrane localization of UBA5. Autophagy, 2020, 16, 256-270.	4.3	41
102	Amino-Acid-Type-Selective Triple-Resonance Experiments. Journal of Magnetic Resonance Series B, 1996, 110, 107-111.	1.6	39
103	Transmembrane segment enhanced labeling as a tool for the backbone assignment of Î±-helical membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8262-8267.	3.3	38
104	A Universal Expression Tag for Structural and Functional Studies of Proteins. ChemBioChem, 2012, 13, 959-963.	1.3	38
105	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degraders. Journal of Medicinal Chemistry, 2021, 64, 10682-10710.	2.9	38
106	Systems for the Cell-Free Synthesis of Proteins. Methods in Molecular Biology, 2012, 800, 201-225.	0.4	37
107	Crystal Structure of a PCP/Sfp Complex Reveals the Structural Basis for Carrier Protein Posttranslational Modification. Chemistry and Biology, 2014, 21, 552-562.	6.2	37
108	Combination of cell-free expression and NMR spectroscopy as a new approach for structural investigation of membrane proteins. Magnetic Resonance in Chemistry, 2006, 44, S17-S23.	1.1	36

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109	A Disulfide Bridge Network within the Soluble Periplasmic Domain Determines Structure and Function of the Outer Membrane Protein RCSF. Journal of Biological Chemistry, 2011, 286, 18775-18783.	1.6	36
110	Combining <i>in Vitro</i> Folding with Cell Free Protein Synthesis for Membrane Protein Expression. Biochemistry, 2016, 55, 4212-4219.	1.2	36
111	Cell cycle arrest in mitosis promotes interferon-induced necroptosis. Cell Death and Differentiation, 2019, 26, 2046-2060.	5.0	36
112	Ubiquitination in the ERAD Process. International Journal of Molecular Sciences, 2020, 21, 5369.	1.8	36
113	New approaches to structure determination by NMR spectroscopy. Current Opinion in Structural Biology, 1998, 8, 619-623.	2.6	35
114	Optimization of13C direct detection NMR methods. Journal of Biomolecular NMR, 2004, 30, 175-179.	1.6	35
115	Characterization of Molecular Interactions between ACP and Halogenase Domains in the Curacin A Polyketide Synthase. ACS Chemical Biology, 2012, 7, 378-386.	1.6	35
116	Requirements on Paramagnetic Relaxation Enhancement Data for Membrane Protein Structure Determination by NMR. Structure, 2012, 20, 1019-1027.	1.6	35
117	Hydrophobic supplements in cellâ€free systems: Designing artificial environments for membrane proteins. Engineering in Life Sciences, 2014, 14, 365-379.	2.0	35
118	The CUE Domain of Cue1 Aligns Growing Ubiquitin Chains with Ubc7 for Rapid Elongation. Molecular Cell, 2016, 62, 918-928.	4.5	34
119	Apoptosis inhibitor 5 is an endogenous inhibitor of caspaseâ€2. EMBO Reports, 2017, 18, 733-744.	2.0	34
120	Structural and functional dissection of the DH and PH domains of oncogenic Bcr-Abl tyrosine kinase. Nature Communications, 2017, 8, 2101.	5.8	33
121	LILBID and nESI: Different Native Mass Spectrometry Techniques as Tools in Structural Biology. Journal of the American Society for Mass Spectrometry, 2019, 30, 181-191.	1.2	33
122	Cellâ€free expression profiling of <i>E. coli</i> inner membrane proteins. Proteomics, 2010, 10, 1762-1779.	1.3	32
123	Cell-free expression and in meso crystallisation of an integral membrane kinase for structure determination. Cellular and Molecular Life Sciences, 2014, 71, 4895-4910.	2.4	32
124	A New Structural Domain in the Escherichia coli RcsC Hybrid Sensor Kinase Connects Histidine Kinase and Phosphoreceiver Domains. Journal of Molecular Biology, 2006, 364, 68-79.	2.0	30
125	Screening for Lipid Requirements of Membrane Proteins by Combining Cell-Free Expression with Nanodiscs. Methods in Enzymology, 2015, 556, 351-369.	0.4	30
126	DNA Damaged Induced Cell Death in Oocytes. Molecules, 2020, 25, 5714.	1.7	30

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127	Improved pulse sequences for sequence specific assignment of aromatic proton resonances in proteins. Journal of Biomolecular NMR, 2007, 37, 205-224.	1.6	29
128	Mechanism of TAp73 inhibition by Î”Np63 and structural basis of p63/p73 hetero-tetramerization. Cell Death and Differentiation, 2016, 23, 1930-1940.	5.0	29
129	From Nanodiscs to Isotropic Bicelles: A Procedure for Solution Nuclear Magnetic Resonance Studies of Detergent-Sensitive Integral Membrane Proteins. Structure, 2016, 24, 1830-1841.	1.6	29
130	Artificial Environments for the Co-Translational Stabilization of Cell-Free Expressed Proteins. PLoS ONE, 2013, 8, e56637.	1.1	29
131	Structural Basis for the Functional Switch of theE. coliAda Proteinâ€‚â€¡. Biochemistry, 2001, 40, 4261-4271.	1.2	28
132	Site-specific inhibition of the small ubiquitin-like modifier (SUMO)-conjugating enzyme Ubc9 selectively impairs SUMO chain formation. Journal of Biological Chemistry, 2017, 292, 15340-15351.	1.6	28
133	Rat Organic Cation Transporter 1 Contains Three Binding Sites for Substrate 1-Methyl-4-phenylpyridinium per Monomer. Molecular Pharmacology, 2019, 95, 169-182.	1.0	28
134	p63 uses a switch-like mechanism to set the threshold for induction of apoptosis. Nature Chemical Biology, 2020, 16, 1078-1086.	3.9	28
135	Editing for Amino-Acid Type in CBCACONH Experiments Based on the13CÎ²â€“13CÎ³ Coupling. Journal of Magnetic Resonance Series B, 1996, 111, 310-313.	1.6	27
136	Cell-Free Production of Integral Membrane Proteins on a Preparative Scale. , 2007, 375, 57-78.		27
137	Functional Expression of the PorAH Channel from Corynebacterium glutamicum in Cell-free Expression Systems. Journal of Biological Chemistry, 2011, 286, 32525-32532.	1.6	27
138	Combinatorial triple-selective labeling as a tool to assist membrane protein backbone resonance assignment. Journal of Biomolecular NMR, 2012, 52, 197-210.	1.6	27
139	Fast Mapping of Proteinâˆ’Protein Interfaces by NMR Spectroscopy. Journal of the American Chemical Society, 2003, 125, 14250-14251.	6.6	26
140	Solution Structure of the Escherichia coli YojN Histidine-phosphotransferase Domain and its Interaction with Cognate Phosphoryl Receiver Domains. Journal of Molecular Biology, 2004, 343, 1035-1048.	2.0	26
141	Control mechanisms in germ cells mediated by p53 family proteins. Journal of Cell Science, 2017, , .	1.2	26
142	Protein aggregation of the p63 transcription factor underlies severe skin fragility in AEC syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E906-E915.	3.3	26
143	Protein labeling strategies for liquid-state NMR spectroscopy using cell-free synthesis. Progress in Nuclear Magnetic Resonance Spectroscopy, 2018, 105, 1-22.	3.9	26
144	Efficient identification of amino acid types for fast protein backbone assignments. Journal of Biomolecular NMR, 2001, 21, 269-273.	1.6	25

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145	Ubiquitin linkages make a difference. Nature Structural and Molecular Biology, 2009, 16, 1209-1210.	3.6	25
146	FAM96A is a novel pro-apoptotic tumor suppressor in gastrointestinal stromal tumors. International Journal of Cancer, 2015, 137, 1318-1329.	2.3	25
147	Systematic optimization of cell-free synthesized human endothelin B receptor folding. Methods, 2018, 147, 73-83.	1.9	25
148	The UBA domain of conjugating enzyme Ubc1/Ube2K facilitates assembly of K48/K63â€•branched ubiquitin chains. EMBO Journal, 2021, 40, e106094.	3.5	25
149	Induced structure of a helical switch as a mechanism to regulate enzymatic activity. Nature Structural and Molecular Biology, 2005, 12, 1019-1020.	3.6	24
150	A General Model for Preferential Hetero-oligomerization of LIN-2/7 Domains. Journal of Biological Chemistry, 2005, 280, 38528-38536.	1.6	24
151	NmerA of Tn<i>501</i> Mercuric Ion Reductase: Structural Modulation of the p<i>K</i>_a Values of the Metal Binding Cysteine Thiols,. Biochemistry, 2010, 49, 8988-8998.	1.2	24
152	Investigation of Quadruplex Structure Under Physiological Conditions Using In-Cell NMR. Topics in Current Chemistry, 2012, 330, 47-65.	4.0	24
153	From Gene to Function: Cell-Free Electrophysiological and Optical Analysis of Ion Pumps in Nanodiscs. Biophysical Journal, 2017, 113, 1331-1341.	0.2	24
154	Biosynthesis of membrane dependent proteins in insect cell lysates: identification of limiting parameters for folding and processing. Biological Chemistry, 2015, 396, 1097-1107.	1.2	23
155	The p63 C-terminus is essential for murine oocyte integrity. Nature Communications, 2021, 12, 383.	5.8	23
156	Selective Identification of Threonine, Valine, and Isoleucine Sequential Connectivities with a TVI-CBCACONH Experiment. Journal of Magnetic Resonance Series B, 1996, 110, 304-308.	1.6	22
157	Demonstrating Ligandability of the LC3A and LC3B Adapter Interface. Journal of Medicinal Chemistry, 2021, 64, 3720-3746.	2.9	22
158	Structural diversity of p63 and p73 isoforms. Cell Death and Differentiation, 2022, 29, 921-937.	5.0	22
159	NMR Studies Reveal the Role of Biomembranes in Modulating Ligand Binding and Release by Intracellular Bile Acid Binding Proteins. Journal of Molecular Biology, 2009, 394, 852-863.	2.0	21
160	Structure and Biophysical Characterization of the S-Adenosylmethionine-dependent O-Methyltransferase PaMTH1, a Putative Enzyme Accumulating during Senescence of Podospora anserina. Journal of Biological Chemistry, 2015, 290, 16415-16430.	1.6	20
161	Insights into Cotranslational Membrane Protein Insertion by Combined LILBID-Mass Spectrometry and NMR Spectroscopy. Analytical Chemistry, 2017, 89, 12314-12318.	3.2	20
162	The synaptic vesicle protein <scp>SV</scp>31 assembles into a dimer and transports Zn²⁺. Journal of Neurochemistry, 2017, 140, 280-293.	2.1	19

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163	Inâ€Cell NMR Spectroscopy of Functional Riboswitch Aptamers in Eukaryotic Cells. Angewandte Chemie - International Edition, 2021, 60, 865-872.	7.2	19
164	Probing metallo-Î²-lactamases with molecular fragments identified by consensus docking. Bioorganic and Medicinal Chemistry Letters, 2015, 25, 5243-5246.	1.0	18
165	Regulation of the Activity in the p53 Family Depends on the Organization of the Transactivation Domain. Structure, 2018, 26, 1091-1100.e4.	1.6	18
166	Peak picking NMR spectral data using non-negative matrix factorization. BMC Bioinformatics, 2014, 15, 46.	1.2	17
167	High-Level Cell-Free Production of Membrane Proteins with Nanodiscs. Methods in Molecular Biology, 2014, 1118, 109-130.	0.4	16
168	Chain Assembly and Disassembly Processes Differently Affect the Conformational Space of Ubiquitin Chains. Structure, 2018, 26, 249-258.e4.	1.6	16
169	Deletions and loss-of-function variants in TP63 associated with orofacial clefting. European Journal of Human Genetics, 2019, 27, 1101-1112.	1.4	16
170	Cell-Free Expression of G-Protein-Coupled Receptors. Methods in Molecular Biology, 2015, 1261, 171-195.	0.4	16
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