

Michael Sattler

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3158603/publications.pdf>

Version: 2024-02-01

308
papers

21,641
citations

12330

69
h-index

12272

133
g-index

361
all docs

361
docs citations

361
times ranked

23710
citing authors

#	ARTICLE	IF	CITATIONS
1	FSP1 is a glutathione-independent ferroptosis suppressor. <i>Nature</i> , 2019, 575, 693-698.	27.8	1,624
2	Heteronuclear multidimensional NMR experiments for the structure determination of proteins in solution employing pulsed field gradients. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1999, 34, 93-158.	7.5	1,490
3	X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed cell death. <i>Nature</i> , 1996, 381, 335-341.	27.8	1,427
4	Structure of Bcl-xL-Bak Peptide Complex: Recognition Between Regulators of Apoptosis. <i>Science</i> , 1997, 275, 983-986.	12.6	1,394
5	A general enhancement scheme in heteronuclear multidimensional NMR employing pulsed field gradients. <i>Journal of Biomolecular NMR</i> , 1994, 4, 301-6.	2.8	728
6	Structure and nucleic-acid binding of the Drosophila Argonaute 2 PAZ domain. <i>Nature</i> , 2003, 426, 465-469.	27.8	405
7	Structure and ligand recognition of the phosphotyrosine binding domain of Shc. <i>Nature</i> , 1995, 378, 584-592.	27.8	370
8	Functional screening identifies CRLF2 in precursor B-cell acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 252-257.	7.1	314
9	Nucleic acid 3' end recognition by the Argonaute2 PAZ domain. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 576-577.	8.2	304
10	SMN tudor domain structure and its interaction with the Sm proteins. <i>Nature Structural Biology</i> , 2001, 8, 27-31.	9.7	285
11	The BCR/ABL Tyrosine Kinase Induces Production of Reactive Oxygen Species in Hematopoietic Cells. <i>Journal of Biological Chemistry</i> , 2000, 275, 24273-24278.	3.4	280
12	Endothelin 1 transcription is controlled by nuclear factor-kappaB in AGE-stimulated cultured endothelial cells. <i>Diabetes</i> , 2000, 49, 1561-1570.	0.6	273
13	Coherence Selection by Gradients without Signal Attenuation: Application to the Three-Dimensional HNCO Experiment. <i>Angewandte Chemie International Edition in English</i> , 1993, 32, 1489-1491.	4.4	226
14	NES consensus redefined by structures of PKI-type and Rev-type nuclear export signals bound to CRM1. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1367-1376.	8.2	226
15	Structural Basis for Recognition of the Intron Branch Site RNA by Splicing Factor 1. <i>Science</i> , 2001, 294, 1098-1102.	12.6	210
16	The SAND domain structure defines a novel DNA-binding fold in transcriptional regulation. <i>Nature Structural Biology</i> , 2001, 8, 626-633.	9.7	204
17	Multi-domain conformational selection underlies pre-mRNA splicing regulation by U2AF. <i>Nature</i> , 2011, 475, 408-411.	27.8	202
18	The small-molecule VEGF receptor inhibitor pazopanib (GW786034B) targets both tumor and endothelial cells in multiple myeloma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19478-19483.	7.1	189

#	ARTICLE	IF	CITATIONS
19	Structural Basis for the Molecular Recognition between Human Splicing Factors U2AF65 and SF1/mBBP. <i>Molecular Cell</i> , 2003, 11, 965-976.	9.7	184
20	Structural basis for dimethylarginine recognition by the Tudor domains of human SMN and SPF30 proteins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1414-1420.	8.2	164
21	NMR approaches for structural analysis of multidomain proteins and complexes in solution. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 80, 26-63.	7.5	164
22	Recognition of a Functional Peroxisome Type 1 Target by the Dynamic Import Receptor Pex5p. <i>Molecular Cell</i> , 2006, 24, 653-663.	9.7	156
23	High-resolution X-ray and NMR Structures of the SMN Tudor Domain: Conformational Variation in the Binding Site for Symmetrically Dimethylated Arginine Residues. <i>Journal of Molecular Biology</i> , 2003, 327, 507-520.	4.2	155
24	A Glycopeptide Dendrimer Inhibitor of the Galactose-specific Lectin LecA and of <i>Pseudomonas aeruginosa</i> Biofilms. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 10631-10635.	13.8	149
25	U2AF-homology motif interactions are required for alternative splicing regulation by SPF45. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 620-629.	8.2	147
26	Active coacervate droplets as a model for membraneless organelles and protocells. <i>Nature Communications</i> , 2020, 11, 5167.	12.8	135
27	Screening of fusion partners for high yield expression and purification of bioactive viscotoxins. <i>Protein Expression and Purification</i> , 2009, 64, 16-23.	1.3	133
28	Structural model of the dimeric Parkinson's protein LRRK2 reveals a compact architecture involving distant interdomain contacts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4357-E4366.	7.1	130
29	Modulation of the Hsp90 Chaperone Cycle by a Stringent Client Protein. <i>Molecular Cell</i> , 2014, 53, 941-953.	9.7	129
30	The three-dimensional structure of the HRDC domain and implications for the Werner and Bloom syndrome proteins. <i>Structure</i> , 1999, 7, 1557-1566.	3.3	126
31	Intron Removal Requires Proofreading of U2AF/3' Splice Site Recognition by DEK. <i>Science</i> , 2006, 312, 1961-1965.	12.6	126
32	Unusual bipartite mode of interaction between the nonsense-mediated decay factors, UPF1 and UPF2. <i>EMBO Journal</i> , 2009, 28, 2293-2306.	7.8	126
33	Determinants of conformational dimerization of Mad2 and its inhibition by p31comet. <i>EMBO Journal</i> , 2006, 25, 1273-1284.	7.8	124
34	The structure of the flock house virus B2 protein, a viral suppressor of RNA interference, shows a novel mode of double-stranded RNA recognition. <i>EMBO Reports</i> , 2005, 6, 1149-1155.	4.5	120
35	Use of deuterium labeling in NMR: overcoming a sizeable problem. <i>Structure</i> , 1996, 4, 1245-1249.	3.3	118
36	Differential inhibition of Arabidopsis superoxide dismutases by peroxynitrite-mediated tyrosine nitration. <i>Journal of Experimental Botany</i> , 2015, 66, 989-999.	4.8	116

#	ARTICLE	IF	CITATIONS
37	BCR/ABL Directly Inhibits Expression of SHIP, an SH2-Containing Polyinositol-5-Phosphatase Involved in the Regulation of Hematopoiesis. <i>Molecular and Cellular Biology</i> , 1999, 19, 7473-7480.	2.3	106
38	Structural Basis for Translational Stalling by Human Cytomegalovirus and Fungal Arginine Attenuator Peptide. <i>Molecular Cell</i> , 2010, 40, 138-146.	9.7	106
39	An Efficient Protocol for NMR Spectroscopy-Based Structure Determination of Protein Complexes in Solution. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 1967-1970.	13.8	104
40	Role of the adapter protein CRKL in signal transduction of normal hematopoietic and BCR/ABL-transformed cells. <i>Leukemia</i> , 1998, 12, 637-644.	7.2	103
41	Structure and VP16 binding of the Mediator Med25 activator interaction domain. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 404-409.	8.2	103
42	Dynamics in multi-domain protein recognition of RNA. <i>Current Opinion in Structural Biology</i> , 2012, 22, 287-296.	5.7	103
43	Structural basis for the assembly of the Sxl-Unr translation regulatory complex. <i>Nature</i> , 2014, 515, 287-290.	27.8	102
44	Activation of hematopoietic growth factor signal transduction pathways by the human oncogene BCR/ABL. <i>Cytokine and Growth Factor Reviews</i> , 1997, 8, 63-79.	7.2	101
45	Structural features of Argonaute-GW182 protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3770-9.	7.1	98
46	A C-terminal HSP90 inhibitor restores glucocorticoid sensitivity and relieves a mouse allograft model of Cushing disease. <i>Nature Medicine</i> , 2015, 21, 276-280.	30.7	92
47	A simultaneous ¹⁵ N, ¹ H- and ¹³ C, ¹ H-HSQC with sensitivity enhancement and a heteronuclear gradient echo. <i>Journal of Biomolecular NMR</i> , 1995, 5, 97-102.	2.8	91
48	Leucine-Rich Repeat Kinase 2 Binds to Neuronal Vesicles through Protein Interactions Mediated by Its C-Terminal WD40 Domain. <i>Molecular and Cellular Biology</i> , 2014, 34, 2147-2161.	2.3	91
49	Hematopoietic growth factors signal through the formation of reactive oxygen species. <i>Blood</i> , 1999, 93, 2928-35.	1.4	91
50	X-Ray Crystallographic and NMR Studies of the Third KH Domain of hnRNP K in Complex with Single-Stranded Nucleic Acids. <i>Structure</i> , 2005, 13, 1055-1067.	3.3	90
51	CH ₂ π-σ-T-Shape Interaction with Histidine Explains Binding of Aromatic Galactosides to <i>Pseudomonas aeruginosa</i> Lectin LecA. <i>ACS Chemical Biology</i> , 2013, 8, 1925-1930.	3.4	90
52	Noncanonical inhibition of caspase-3 by a nuclear microRNA confers endothelial protection by autophagy in atherosclerosis. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	88
53	hnRNP A1 Proofreads 3' Splice Site Recognition by U2AF. <i>Molecular Cell</i> , 2012, 45, 314-329.	9.7	87
54	Structural Basis of Single-Stranded RNA Recognition. <i>Accounts of Chemical Research</i> , 2004, 37, 279-287.	15.6	84

#	ARTICLE	IF	CITATIONS
55	Structural basis for competitive interactions of Pex14 with the import receptors Pex5 and Pex19. <i>EMBO Journal</i> , 2009, 28, 745-754.	7.8	82
56	Prediction of structural domains of TAP reveals details of its interaction with p15 and nucleoporins. <i>EMBO Reports</i> , 2000, 1, 53-58.	4.5	81
57	Topography for Independent Binding of α -Helical and PPII-Helical Ligands to a Peroxisomal SH3 Domain. <i>Molecular Cell</i> , 2002, 10, 1007-1017.	9.7	81
58	Novel modes of protein-RNA recognition in the RNAi pathway. <i>Current Opinion in Structural Biology</i> , 2005, 15, 107-115.	5.7	80
59	Structural basis for terminal loop recognition and stimulation of pri-miRNA-18a processing by hnRNP A1. <i>Nature Communications</i> , 2018, 9, 2479.	12.8	80
60	The Xist RNA A-repeat comprises a novel AUCG tetraloop fold and a platform for multimerization. <i>Rna</i> , 2011, 17, 1973-1982.	3.5	79
61	Transient Electrostatic Interactions Dominate the Conformational Equilibrium Sampled by Multidomain Splicing Factor U2AF65: A Combined NMR and SAXS Study. <i>Journal of the American Chemical Society</i> , 2014, 136, 7068-7076.	13.7	79
62	Efficient segmental isotope labeling of multi-domain proteins using Sortase A. <i>Journal of Biomolecular NMR</i> , 2015, 63, 1-8.	2.8	79
63	Structure of the intracellular domain of the amyloid precursor protein in complex with Fe ⁶⁵ -PTB2. <i>EMBO Reports</i> , 2008, 9, 1134-1140.	4.5	78
64	Telethonin Deficiency Is Associated With Maladaptation to Biomechanical Stress in the Mammalian Heart. <i>Circulation Research</i> , 2011, 109, 758-769.	4.5	78
65	Importance of cycle timing for the function of the molecular chaperone Hsp90. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1020-1028.	8.2	78
66	Structure, dynamics and RNA binding of the multi-domain splicing factor TIA-1. <i>Nucleic Acids Research</i> , 2014, 42, 5949-5966.	14.5	77
67	Structural basis for RNA recognition in roquin-mediated post-transcriptional gene regulation. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 671-678.	8.2	77
68	NMR Structure of the First PHD Finger of Autoimmune Regulator Protein (AIRE1). <i>Journal of Biological Chemistry</i> , 2005, 280, 11505-11512.	3.4	76
69	Structure and Carboxyl-terminal Domain (CTD) Binding of the Set2 SRI Domain That Couples Histone H3 Lys36 Methylation to Transcription*. <i>Journal of Biological Chemistry</i> , 2006, 281, 13-15.	3.4	76
70	The phosphatidylinositol polyphosphate 5-phosphatase SHIP and the protein tyrosine phosphatase SHP-2 form a complex in hematopoietic cells which can be regulated by BCR/ABL and growth factors. <i>Oncogene</i> , 1997, 15, 2379-2384.	5.9	73
71	Solution Structure and Ligand Recognition of the WW Domain Pair of the Yeast Splicing Factor Prp40. <i>Journal of Molecular Biology</i> , 2002, 324, 807-822.	4.2	73
72	High-resolution structures of the IgM Fc domains reveal principles of its hexamer formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10183-10188.	7.1	73

#	ARTICLE	IF	CITATIONS
73	Structural Analysis of Large Protein Complexes Using Solvent Paramagnetic Relaxation Enhancements. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 3993-3997.	13.8	71
74	Novel strategies for sensitivity enhancement in heteronuclear multi-dimensional NMR experiments employing pulsed field gradients. <i>Journal of Biomolecular NMR</i> , 1995, 6, 11-22.	2.8	70
75	Biochemical and NMR analyses of an SF3b155-p14-U2AF-RNA interaction network involved in branch point definition during pre-mRNA splicing. <i>Rna</i> , 2006, 12, 410-425.	3.5	69
76	Genetically Encoded FRET Probe for PKC Activity Based on Pleckstrin. <i>Journal of the American Chemical Society</i> , 2004, 126, 11786-11787.	13.7	67
77	NMR and small-angle scattering-based structural analysis of protein complexes in solution. <i>Journal of Structural Biology</i> , 2011, 173, 472-482.	2.8	67
78	The structural analysis of shark IgNAR antibodies reveals evolutionary principles of immunoglobulins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8155-8160.	7.1	67
79	Molecular basis for CPAP-tubulin interaction in controlling centriolar and ciliary length. <i>Nature Communications</i> , 2016, 7, 11874.	12.8	66
80	Mechanisms of Transformation by the BCR/ABL Oncogene. <i>International Journal of Hematology</i> , 2001, 73, 278-291.	1.6	63
81	Structural Basis for the Cytoskeletal Association of Bcr-Abl/c-Abl. <i>Molecular Cell</i> , 2005, 19, 461-473.	9.7	63
82	In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors. <i>Genome Research</i> , 2018, 28, 699-713.	5.5	62
83	Structure, phosphorylation and U2AF65 binding of the N-terminal domain of splicing factor 1 during 3' splice site recognition. <i>Nucleic Acids Research</i> , 2013, 41, 1343-1354.	14.5	61
84	A Novel Pex14 Protein-interacting Site of Human Pex5 Is Critical for Matrix Protein Import into Peroxisomes. <i>Journal of Biological Chemistry</i> , 2014, 289, 437-448.	3.4	60
85	The AP-1 transcription factor JunB is essential for multiple myeloma cell proliferation and drug resistance in the bone marrow microenvironment. <i>Leukemia</i> , 2017, 31, 1570-1581.	7.2	60
86	Dimerization and Protein Binding Specificity of the U2AF Homology Motif of the Splicing Factor Puf60. <i>Journal of Biological Chemistry</i> , 2009, 284, 630-639.	3.4	59
87	Inhibitors of PEX14 disrupt protein import into glycosomes and kill <i>Trypanosoma</i> parasites. <i>Science</i> , 2017, 355, 1416-1420.	12.6	59
88	A structure refinement protocol combining NMR residual dipolar couplings and small angle scattering restraints. <i>Journal of Biomolecular NMR</i> , 2008, 41, 199-208.	2.8	58
89	Recognition of the 3' splice site RNA by the U2AF heterodimer involves a dynamic population shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7169-E7175.	7.1	57
90	Structural basis of RNA recognition and dimerization by the STAR proteins T-STAR and Sam68. <i>Nature Communications</i> , 2016, 7, 10355.	12.8	57

#	ARTICLE	IF	CITATIONS
91	Structure and Ligand Binding of the Extended Tudor Domain of <i>D. melanogaster</i> Tudor-SN. <i>Journal of Molecular Biology</i> , 2009, 387, 921-934.	4.2	56
92	HuR biological function involves RRM3-mediated dimerization and RNA binding by all three RRMs. <i>Nucleic Acids Research</i> , 2019, 47, 1011-1029.	14.5	56
93	De-Novo Design of Antimicrobial Peptides for Plant Protection. <i>PLoS ONE</i> , 2013, 8, e71687.	2.5	55
94	Structural and biochemical characterization of the yeast exosome component Rrp40. <i>EMBO Reports</i> , 2007, 8, 63-69.	4.5	53
95	Combinatorial recognition of clustered RNA elements by the multidomain RNA-binding protein IMP3. <i>Nature Communications</i> , 2019, 10, 2266.	12.8	53
96	A Dual Parameter FRET Probe for Measuring PKC and PKA Activity in Living Cells. <i>Journal of the American Chemical Society</i> , 2006, 128, 24-25.	13.7	52
97	Segmental, Domain-Selective perdeuteration and Small-Angle Neutron Scattering for Structural Analysis of Multi-Domain Proteins. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 9322-9325.	13.8	52
98	Targeting TRAF6 E3 ligase activity with a small-molecule inhibitor combats autoimmunity. <i>Journal of Biological Chemistry</i> , 2018, 293, 13191-13203.	3.4	52
99	Identification of Wee1 as a novel therapeutic target for mutant RAS-driven acute leukemia and other malignancies. <i>Leukemia</i> , 2015, 29, 27-37.	7.2	51
100	SHIP1, an SH2 Domain Containing Polyinositol-5-phosphatase, Regulates Migration through Two Critical Tyrosine Residues and Forms a Novel Signaling Complex with DOK1 and CRKL. <i>Journal of Biological Chemistry</i> , 2001, 276, 2451-2458.	3.4	50
101	Conformational dynamics modulate the catalytic activity of the molecular chaperone Hsp90. <i>Nature Communications</i> , 2020, 11, 1410.	12.8	50
102	Integrated structural biology to unravel molecular mechanisms of protein-RNA recognition. <i>Methods</i> , 2017, 118-119, 119-136.	3.8	49
103	Constitution and Solution Conformation of the Antibiotic Mersacidin Determined by NMR and Molecular Dynamics. <i>FEBS Journal</i> , 1997, 244, 501-512.	0.2	48
104	Combining NMR and small angle X-ray and neutron scattering in the structural analysis of a ternary protein-RNA complex. <i>Journal of Biomolecular NMR</i> , 2013, 56, 17-30.	2.8	48
105	Pathological glycogenesis through glycogen synthase 1 and suppression of excessive AMP kinase activity in myeloid leukemia cells. <i>Leukemia</i> , 2015, 29, 1555-1563.	7.2	48
106	Dynamic Effects on J-Couplings Across Hydrogen Bonds in Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 644-645.	13.7	47
107	Allosteric modulation of peroxisomal membrane protein recognition by farnesylation of the peroxisomal import receptor PEX19. <i>Nature Communications</i> , 2017, 8, 14635.	12.8	47
108	Structure-function analysis of the DNA-binding domain of a transmembrane transcriptional activator. <i>Scientific Reports</i> , 2017, 7, 1051.	3.3	46

#	ARTICLE	IF	CITATIONS
109	Structure of the histone mRNA hairpin required for cell cycle regulation of histone gene expression. <i>Rna</i> , 2002, 8, 29-46.	3.5	45
110	Crystal Structure and Nuclear Magnetic Resonance Analyses of the SAND Domain from Glucocorticoid Modulatory Element Binding Protein-1 Reveals Deoxyribonucleic Acid and Zinc Binding Regions. <i>Molecular Endocrinology</i> , 2003, 17, 1283-1295.	3.7	45
111	The dynamic duo: Combining NMR and small angle scattering in structural biology. <i>Protein Science</i> , 2014, 23, 669-682.	7.6	45
112	Structural biology of the import pathways of peroxisomal matrix proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 804-813.	4.1	45
113	Celastrol Promotes Weight Loss in Diet-Induced Obesity by Inhibiting the Protein Tyrosine Phosphatases PTP1B and TCPTP in the Hypothalamus. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 11144-11157.	6.4	45
114	Stereospecific assignment of leucine methyl groups with carbon-13 in natural abundance or with random ¹³ C labeling. <i>Journal of the American Chemical Society</i> , 1992, 114, 1126-1127.	13.7	43
115	The DICE-binding Activity of KH Domain 3 of hnRNP K Is Affected by c-Src-mediated Tyrosine Phosphorylation. <i>Journal of Molecular Biology</i> , 2006, 361, 470-481.	4.2	42
116	Structural insights into the interaction of the nuclear exosome helicase Mtr4 with the preribosomal protein Nop53. <i>Rna</i> , 2017, 23, 1780-1787.	3.5	42
117	The multiple Tudor domain-containing protein TDRD1 is a molecular scaffold for mouse Piwi proteins and piRNA biogenesis factors. <i>Rna</i> , 2012, 18, 2056-2072.	3.5	41
118	The MTR4 helicase recruits nuclear adaptors of the human RNA exosome using distinct arch-interacting motifs. <i>Nature Communications</i> , 2019, 10, 3393.	12.8	41
119	Molecular architecture and dynamics of ASH1 mRNA recognition by its mRNA-transport complex. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 152-161.	8.2	40
120	Roquin targets mRNAs in a 3' UTR-specific manner by different modes of regulation. <i>Nature Communications</i> , 2018, 9, 3810.	12.8	40
121	Paramagnetic NMR in drug discovery. <i>Journal of Biomolecular NMR</i> , 2020, 74, 287-309.	2.8	40
122	Novel Pulse Sequences with Sensitivity Enhancement for In-phase Coherence Transfer Employing Pulsed Field Gradients. <i>Journal of Magnetic Resonance Series B</i> , 1995, 108, 235-242.	1.6	39
123	Hsp90 α -Cdc37 Complexes with Protein Kinases Form Cooperatively with Multiple Distinct Interaction Sites. <i>Journal of Biological Chemistry</i> , 2015, 290, 30843-30854.	3.4	39
124	Celastrol-Induced Weight Loss Is Driven by Hypophagia and Independent From UCP1. <i>Diabetes</i> , 2018, 67, 2456-2465.	0.6	39
125	DNA Structure-Specific Cleavage of DNA-Protein Crosslinks by the SPRTN Protease. <i>Molecular Cell</i> , 2020, 80, 102-113.e6.	9.7	39
126	Roquin recognizes a non-canonical hexaloop structure in the 3' UTR of Ox40. <i>Nature Communications</i> , 2016, 7, 11032.	12.8	38

#	ARTICLE	IF	CITATIONS
127	The dynamics of linear polyubiquitin. <i>Science Advances</i> , 2020, 6, .	10.3	38
128	Interferon- α induced degradation of the persistent hepatitis B virus cccDNA form depends on ISG20. <i>EMBO Reports</i> , 2021, 22, e49568.	4.5	38
129	A NMR strategy to unambiguously distinguish nucleic acid hairpin and duplex conformations applied to a Xist RNA A-repeat. <i>Nucleic Acids Research</i> , 2008, 36, 7068-7077.	14.5	37
130	Structural Basis for Homodimerization of the Src-associated during Mitosis, 68-kDa Protein (Sam68) Qua1 Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 28893-28901.	3.4	37
131	A chemical compound inhibiting the Aha1-Hsp90 chaperone complex. <i>Journal of Biological Chemistry</i> , 2017, 292, 17073-17083.	3.4	37
132	The Hsp90 isoforms from <i>S. cerevisiae</i> differ in structure, function and client range. <i>Nature Communications</i> , 2019, 10, 3626.	12.8	36
133	Structural elements in the flexible tail of the co-chaperone p23 coordinate client binding and progression of the Hsp90 chaperone cycle. <i>Nature Communications</i> , 2021, 12, 828.	12.8	36
134	The naturally occurring N6-threonyl adenine in anticodon loop of <i>Schizosaccharomyces pombe</i> tRNA ^I causes formation of a unique U-turn motif. <i>Nucleic Acids Research</i> , 2006, 34, 2878-2886.	14.5	35
135	Chromodomains read the arginine code of post-translational targeting. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 260-263.	8.2	35
136	Structural and Functional Analysis of the Signal-Transducing Linker in the pH-Responsive One-Component System CadC of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 2548-2561.	4.2	35
137	Effects of Fluorophore Attachment on Protein Conformation and Dynamics Studied by spFRET and NMR Spectroscopy. <i>Chemistry - A European Journal</i> , 2017, 23, 14267-14277.	3.3	35
138	A modular toolbox to generate complex polymeric ubiquitin architectures using orthogonal sortase enzymes. <i>Nature Communications</i> , 2021, 12, 6515.	12.8	35
139	Site-Specific Variations of Carbonyl Chemical Shift Anisotropies in Proteins. <i>Journal of the American Chemical Society</i> , 2004, 126, 11424-11425.	13.7	34
140	Structural Characterization of LRRK2 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 3751-3756.	6.4	34
141	Facile Synthesis of a Croconaine-Based Nanoformulation for Optoacoustic Imaging and Photothermal Therapy. <i>Advanced Healthcare Materials</i> , 2021, 10, e2002115.	7.6	34
142	Acriflavine, a clinically approved drug, inhibits SARS-CoV-2 and other betacoronaviruses. <i>Cell Chemical Biology</i> , 2022, 29, 774-784.e8.	5.2	34
143	Thioredoxin as a fusion tag for carrier-driven crystallization. <i>Protein Science</i> , 2008, 17, 2070-2079.	7.6	33
144	A Numb-Mdm2 fuzzy complex reveals an isoform-specific involvement of Numb in breast cancer. <i>Journal of Cell Biology</i> , 2018, 217, 745-762.	5.2	33

#	ARTICLE	IF	CITATIONS
145	A TROSY relayed HCCH-COSY experiment for correlating adenine H2/H8 resonances in uniformly ¹³ C-labeled RNA molecules. <i>Journal of Biomolecular NMR</i> , 2001, 20, 173-176.	2.8	32
146	Challenges and perspectives for structural biology of lncRNAs—the example of the Xist lncRNA A-repeats. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 845-859.	3.3	32
147	Kohärenzselektion durch Gradienten ohne Empfindlichkeitsverlust; Anwendung auf ³ D-HNCO-Experimente. <i>Angewandte Chemie</i> , 1993, 105, 1518-1521.	2.0	31
148	Structural Analysis of Protein Interfaces from ¹³ C Direct-Detected Paramagnetic Relaxation Enhancements. <i>Journal of the American Chemical Society</i> , 2010, 132, 7285-7287.	13.7	31
149	Resolving Resonance Overlap in the NMR Spectra of Proteins from Differential Lanthanide-Induced Shifts. <i>Journal of the American Chemical Society</i> , 1997, 119, 7885-7886.	13.7	30
150	A switch point in the molecular chaperone Hsp90 responding to client interaction. <i>Nature Communications</i> , 2018, 9, 1472.	12.8	30
151	Deconstructing Noncovalent Kelch-like ECH-Associated Protein 1 (Keap1) Inhibitors into Fragments to Reconstruct New Potent Compounds. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4623-4661.	6.4	30
152	A novel NMR experiment for the sequential assignment of proline residues and proline stretches in ¹³ C/ ¹⁵ N-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999, 13, 381-385.	2.8	29
153	Functional and structural characterization of a novel member of the natriuretic family of peptides from the venom of <i>Pseudocerastes persicus</i> . <i>FEBS Letters</i> , 2004, 557, 104-108.	2.8	29
154	A Crystallin Fold in the Interleukin-4-inducing Principle of <i>Schistosoma mansoni</i> Eggs (IPSE/1±-1) Mediates IgE Binding for Antigen-independent Basophil Activation. <i>Journal of Biological Chemistry</i> , 2015, 290, 22111-22126.	3.4	29
155	Immune homeostasis and regulation of the interferon pathway require myeloid-derived Regnase-3. <i>Journal of Experimental Medicine</i> , 2019, 216, 1700-1723.	8.5	29
156	Recent Advances in Half-life Extension Strategies for Therapeutic Peptides and Proteins. <i>Current Pharmaceutical Design</i> , 2019, 24, 4932-4946.	1.9	29
157	De Novo Structure Determination from Residual Dipolar Couplings by NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2002, 41, 437-440.	13.8	28
158	Structural basis for the recognition of spliceosomal SmN/B/B™ proteins by the RBM5 OCRE domain in splicing regulation. <i>ELife</i> , 2016, 5, .	6.0	28
159	Refinement of the protein backbone angle psi in NMR structure calculations. <i>Journal of Biomolecular NMR</i> , 2000, 16, 47-58.	2.8	27
160	The cisproline(i-1)-aromatic(i) interaction: folding of the Ala-cisPro-Tyr peptide characterized by NMR and theoretical approaches. <i>Journal of Biomolecular NMR</i> , 2000, 17, 63-77.	2.8	27
161	Structure and dynamics of the human pleckstrin DEP domain: Distinct molecular features of a novel DEP domain subfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 354-366.	2.6	27
162	Extending the Size of Protein-RNA Complexes Studied by Nuclear Magnetic Resonance Spectroscopy. <i>ChemBioChem</i> , 2005, 6, 1578-1584.	2.6	27

#	ARTICLE	IF	CITATIONS
163	A target function for quaternary structural refinement from small angle scattering and NMR orientational restraints. <i>European Biophysics Journal</i> , 2006, 35, 313-327.	2.2	27
164	Molecular basis for asymmetry sensing of siRNAs by the <i>Drosophila</i> Loqs-PD/Dcr-2 complex in RNA interference. <i>Nucleic Acids Research</i> , 2017, 45, 12536-12550.	14.5	27
165	Structure of the Eps15 ^Δ stonin2 complex provides a molecular explanation for EH-domain ligand specificity. <i>EMBO Journal</i> , 2008, 27, 558-569.	7.8	26
166	Next-Generation Heteronuclear Decoupling for High-Field Biomolecular NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 4475-4479.	13.8	26
167	Deciphering the protein-RNA recognition code: Combining large-scale quantitative methods with structural biology. <i>BioEssays</i> , 2015, 37, 899-908.	2.5	26
168	A novel RNA binding surface of the TAM domain of TIP5/BAZ2A mediates epigenetic regulation of rRNA genes. <i>Nucleic Acids Research</i> , 2015, 43, 5208-5220.	14.5	26
169	Inhibition of Canonical NF- κ B Signaling by a Small Molecule Targeting NEMO-Ubiquitin Interaction. <i>Scientific Reports</i> , 2016, 6, 18934.	3.3	26
170	RNA structure refinement using NMR solvent accessibility data. <i>Scientific Reports</i> , 2017, 7, 5393.	3.3	26
171	Potential of ABCA3 lipid transport function by ivacaftor and genistein. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5225-5234.	3.6	26
172	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. <i>Nature Chemical Biology</i> , 2021, 17, 272-279.	8.0	26
173	PINK1-dependent phosphorylation of Serine111 within the SF3 motif of Rab GTPases impairs effector interactions and LRRK2-mediated phosphorylation at Threonine72. <i>Biochemical Journal</i> , 2020, 477, 1651-1668.	3.7	26
174	Structure of a PH Domain from the <i>C. elegans</i> Muscle Protein UNC-89 Suggests a Novel Function. <i>Structure</i> , 2000, 8, 1079-1087.	3.3	25
175	Efficient Detection of Hydrogen Bonds in Dynamic Regions of RNA by Sensitivity-Optimized NMR Pulse Sequences. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 10487-10490.	13.8	25
176	Developing Inhibitors of the p47phox-p22phox Protein-Protein Interaction by Fragment-Based Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 1156-1177.	6.4	25
177	An autoinhibitory intramolecular interaction proof-reads RNA recognition by the essential splicing factor U2AF2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7140-7149.	7.1	25
178	Client binding shifts the populations of dynamic Hsp90 conformations through an allosteric network. <i>Science Advances</i> , 2021, 7, eabl7295.	10.3	25
179	Production of a de-novo designed antimicrobial peptide in <i>Nicotiana benthamiana</i> . <i>Plant Molecular Biology</i> , 2013, 81, 259-272.	3.9	24
180	Structural basis for cpSRP43 chromodomain selectivity and dynamics in Alb3 insertase interaction. <i>Nature Communications</i> , 2015, 6, 8875.	12.8	24

#	ARTICLE	IF	CITATIONS
181	Identification of small-molecule inhibitors of USP2a. <i>European Journal of Medicinal Chemistry</i> , 2018, 150, 261-267.	5.5	24
182	Inhibition of CPAP tubulin interaction prevents proliferation of centrosome-amplified cancer cells. <i>EMBO Journal</i> , 2019, 38, .	7.8	24
183	Automated evaluation of chemical shift perturbation spectra: New approaches to quantitative analysis of receptor-ligand interaction NMR spectra. <i>Journal of Biomolecular NMR</i> , 2004, 29, 491-504.	2.8	23
184	Probing lipid- and drug-binding domains with fluorescent dyes. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 1162-1173.	3.0	23
185	Investigating the Role of Large-Scale Domain Dynamics in Protein-Protein Interactions. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 54.	3.5	23
186	The Structure of the SPOP-Pdx1 Interface Reveals Insights into the Phosphorylation-Dependent Binding Regulation. <i>Structure</i> , 2019, 27, 327-334.e3.	3.3	23
187	Locus-Conserved Circular RNA cZNF292 Controls Endothelial Cell Flow Responses. <i>Circulation Research</i> , 2022, 130, 67-79.	4.5	23
188	Structure and Phosphatidylinositol-(3,4)- Bisphosphate Binding of the C-Terminal PH Domain of Human Pleckstrin. <i>Structure</i> , 2005, 13, 277-286.	3.3	22
189	Improved Accuracy from Joint X-ray and NMR Refinement of a Protein-RNA Complex Structure. <i>Journal of the American Chemical Society</i> , 2016, 138, 1601-1610.	13.7	22
190	The Co-chaperone Cns1 and the Recruiter Protein Hgh1 Link Hsp90 to Translation Elongation via Chaperoning Elongation Factor 2. <i>Molecular Cell</i> , 2019, 74, 73-87.e8.	9.7	22
191	The Charged Linker Modulates the Conformations and Molecular Interactions of Hsp90. <i>ChemBioChem</i> , 2021, 22, 1084-1092.	2.6	22
192	Orphan GPR116 mediates the insulin sensitizing effects of the hepatokine FNDC4 in adipose tissue. <i>Nature Communications</i> , 2021, 12, 2999.	12.8	22
193	Pitchfork and Gprasp2 Target Smoothed to the Primary Cilium for Hedgehog Pathway Activation. <i>PLoS ONE</i> , 2016, 11, e0149477.	2.5	21
194	Conformational Plasticity of the Lipid Transfer Protein SCP2. <i>Biochemistry</i> , 2007, 46, 7980-7991.	2.5	20
195	Rational Design of Cyclic Peptide Inhibitors of U2AF Homology Motif (UHM) Domains To Modulate Pre-mRNA Splicing. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 10190-10197.	6.4	20
196	Identification of phenothiazine derivatives as UHM-binding inhibitors of early spliceosome assembly. <i>Nature Communications</i> , 2020, 11, 5621.	12.8	20
197	Structural and Functional Analysis of the DEAF-1 and BS69 MYND Domains. <i>PLoS ONE</i> , 2013, 8, e54715.	2.5	20
198	NudC guides client transfer between the Hsp40/70 and Hsp90 chaperone systems. <i>Molecular Cell</i> , 2022, 82, 555-569.e7.	9.7	20

#	ARTICLE	IF	CITATIONS
199	Solution Structure and Molecular Interactions of Lamin B Receptor Tudor Domain. <i>Journal of Biological Chemistry</i> , 2012, 287, 1032-1042.	3.4	19
200	Oral Disinfectants Inhibit Protein-Protein Interactions Mediated by the Anti-Apoptotic Protein Bcl-2 and Induce Apoptosis in Human Oral Tumor Cells. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4487-4491.	13.8	19
201	A Novel Protein-Protein Interaction in the RES (Retention and Splicing) Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 28640-28650.	3.4	19
202	Luciferase Advisor: High-Accuracy Model To Flag False Positive Hits in Luciferase HTS Assays. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 933-942.	5.4	19
203	Croconaine-based nanoparticles enable efficient optoacoustic imaging of murine brain tumors. <i>Photoacoustics</i> , 2021, 22, 100263.	7.8	19
204	Machine learning a model for RNA structure prediction. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa090.	3.2	19
205	Structure of an atypical Tudor domain in the <i>Drosophila</i> Polycomb-like protein. <i>Protein Science</i> , 2010, 19, 1906-1916.	7.6	18
206	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. <i>Rna</i> , 2010, 16, 1205-1216.	3.5	18
207	Artificial Accelerators of the Molecular Chaperone Hsp90 Facilitate Rate-Limiting Conformational Transitions. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 12257-12262.	13.8	18
208	Selective activators of protein phosphatase 5 target the auto-inhibitory mechanism. <i>Bioscience Reports</i> , 2015, 35, .	2.4	18
209	Towards the molecular mechanism of the integration of peroxisomal membrane proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 863-869.	4.1	18
210	The molecular basis of chaperone-mediated interleukin 23 assembly control. <i>Nature Communications</i> , 2019, 10, 4121.	12.8	18
211	Selective Inhibitors of FKBP51 Employ Conformational Selection of Dynamic Invisible States. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9429-9433.	13.8	18
212	Staufen2-mediated RNA recognition and localization requires combinatorial action of multiple domains. <i>Nature Communications</i> , 2019, 10, 1659.	12.8	18
213	Membrane Interactions of the Peroxisomal Proteins PEX5 and PEX14. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 651449.	3.7	18
214	Definition of domain boundaries and crystallization of the SMN Tudor domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 366-368.	2.5	17
215	Tudor hooks up with DNA repair. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 98-99.	8.2	17
216	Strategies for the structural analysis of multi-protein complexes: Lessons from the 3D-Repertoire project. <i>Journal of Structural Biology</i> , 2011, 175, 147-158.	2.8	17

#	ARTICLE	IF	CITATIONS
217	Structural Insight into IAPP-Derived Amyloid Inhibitors and Their Mechanism of Action. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 5771-5781.	13.8	17
218	Current approaches for integrating solution NMR spectroscopy and small-angle scattering to study the structure and dynamics of biomolecular complexes. <i>Journal of Molecular Biology</i> , 2020, 432, 2890-2912.	4.2	17
219	Albumin-binding domain extends half-life of glucagon-like peptide-1. <i>European Journal of Pharmacology</i> , 2021, 890, 173650.	3.5	17
220	Structural effects of m6A modification of the Xist A-repeat AUCG tetraloop and its recognition by YTHDC1. <i>Nucleic Acids Research</i> , 2022, 50, 2350-2362.	14.5	17
221	$\hat{1}\pm\hat{1}^2$ HSQC, an HSQC-Type Experiment with Improved Resolution for I2S Groups. <i>Journal of Magnetic Resonance Series A</i> , 1996, 119, 171-179.	1.6	16
222	Induced folding of the U2AF35 RRM upon binding to U2AF65. <i>FEBS Letters</i> , 2002, 528, 171-176.	2.8	16
223	Structural Analysis of Protein-RNA Complexes in Solution Using NMR Paramagnetic Relaxation Enhancements. <i>Methods in Enzymology</i> , 2015, 558, 333-362.	1.0	16
224	Novel small molecules targeting ciliary transport of Smoothed and oncogenic Hedgehog pathway activation. <i>Scientific Reports</i> , 2016, 6, 22540.	3.3	16
225	Conformational control of small GTPases by AMPylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5772-5781.	7.1	16
226	<i>FARS1</i> -related disorders caused by bi-allelic mutations in cytosolic phenylalanyl-tRNA synthetase genes: Look beyond the lungs!. <i>Clinical Genetics</i> , 2021, 99, 789-801.	2.0	16
227	DNA annealing by Red $\hat{1}^2$ is insufficient for homologous recombination and the additional requirements involve intra- and inter-molecular interactions. <i>Scientific Reports</i> , 2016, 6, 34525.	3.3	15
228	RNA recognition by Roquin in posttranscriptional gene regulation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 455-469.	6.4	15
229	Thymosin $\hat{1}^24$ protects against aortic aneurysm via endocytic regulation of growth factor signaling. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	15
230	Multifaceted N-Degron Recognition and Ubiquitylation by GID/CTLH E3 Ligases. <i>Journal of Molecular Biology</i> , 2022, 434, 167347.	4.2	15
231	Local Structure and Anisotropic Backbone Dynamics from Cross-Correlated NMR Relaxation in Proteins. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 3232-3237.	13.8	14
232	Breaking the protein-RNA recognition code. <i>Cell Cycle</i> , 2014, 13, 3619-3620.	2.6	14
233	Come, sweet death: targeting glycosomal protein import for antitrypanosomal drug development. <i>Current Opinion in Microbiology</i> , 2018, 46, 116-122.	5.1	14
234	Evolutionary divergent PEX3 is essential for glycosome biogenesis and survival of trypanosomatid parasites. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 118520.	4.1	14

#	ARTICLE	IF	CITATIONS
235	Structure-Activity Relationship in Pyrazolo[4,3-c]pyridines, First Inhibitors of PEX14-PEX5 Protein-Protein Interaction with Trypanocidal Activity. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 847-879.	6.4	13
236	Introducing the CSP Analyzer: A novel Machine Learning-based application for automated analysis of two-dimensional NMR spectra in NMR fragment-based screening. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 603-611.	4.1	13
237	SPF45/RBM17-dependent, but not U2AF-dependent, splicing in a distinct subset of human short introns. <i>Nature Communications</i> , 2021, 12, 4910.	12.8	13
238	Ultrashort Broadband Cooperative Pulses for Multidimensional Biomolecular NMR Experiments. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 14498-14502.	13.8	12
239	Structural Insights into BET Client Recognition of Endometrial and Prostate Cancer-Associated SPOP Mutants. <i>Journal of Molecular Biology</i> , 2019, 431, 2213-2221.	4.2	12
240	Proteolysis of Rab32 by Salmonella GtgE induces an inactive GTPase conformation. <i>IScience</i> , 2021, 24, 101940.	4.1	12
241	Speeding Up Biomolecular NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 782-786.	13.8	11
242	Modulation of HIV-1 gene expression by binding of a ULM motif in the Rev protein to UHM-containing splicing factors. <i>Nucleic Acids Research</i> , 2019, 47, 4859-4871.	14.5	11
243	The Photocatalyzed Thiolene reaction: A New Tag to Yield Fast, Selective and reversible Paramagnetic Tagging of Proteins. <i>ChemPhysChem</i> , 2020, 21, 863-869.	2.1	11
244	Translational repression of thymidylate synthase by targeting its mRNA. <i>Nucleic Acids Research</i> , 2013, 41, 4159-4170.	14.5	10
245	Functional role of the flexible N-terminal extension of FKBP38 in catalysis. <i>Scientific Reports</i> , 2013, 3, 2985.	3.3	10
246	Studying Weak and Dynamic Interactions of Posttranslationally Modified Proteins using Expressed Protein Ligation. <i>ACS Chemical Biology</i> , 2014, 9, 347-352.	3.4	10
247	The EBNA-2 N-Terminal Transactivation Domain Folds into a Dimeric Structure Required for Target Gene Activation. <i>PLoS Pathogens</i> , 2015, 11, e1004910.	4.7	10
248	Selective isotope labeling for NMR structure determination of proteins in complex with unlabeled ligands. <i>Journal of Biomolecular NMR</i> , 2019, 73, 183-189.	2.8	10
249	Detection and quantification of the anti-obesity drug celastrol in murine liver and brain. <i>Neurochemistry International</i> , 2020, 136, 104713.	3.8	10
250	Competitive Microtubule Binding of PEX14 Coordinates Peroxisomal Protein Import and Motility. <i>Journal of Molecular Biology</i> , 2021, 433, 166765.	4.2	10
251	Detection of Hydrogen Bonds in Dynamic Regions of RNA by NMR Spectroscopy. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2014, 59, 7.22.1-19.	0.5	9
252	Site-Specific Isotope Labeling of Inosine Phosphoramidites and NMR Analysis of an Inosine-Containing RNA Duplex. <i>Chemistry - A European Journal</i> , 2016, 22, 15350-15359.	3.3	9

#	ARTICLE	IF	CITATIONS
253	Single- and dual-parameter FRET kinase probes based on pleckstrin. <i>Nature Protocols</i> , 2006, 1, 1044-1055.	12.0	8
254	Structure and Molecular Recognition Mechanism of IMP-13 Metallo- β -Lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	8
255	Structural basis of DNA methylation-dependent site selectivity of the Epstein-Barr virus lytic switch protein ZEBRA/Zta/BZLF1. <i>Nucleic Acids Research</i> , 2022, 50, 490-511.	14.5	8
256	^1H , ^{15}N , and ^{13}C resonance assignment of the PH domain from <i>C. elegans</i> UNC-89. <i>Journal of Biomolecular NMR</i> , 1999, 15, 269-270.	2.8	7
257	Adhesion Dance with Raver. <i>Structure</i> , 2009, 17, 781-783.	3.3	7
258	Water envelope has a critical impact on the design of protein-protein interaction inhibitors. <i>Chemical Communications</i> , 2020, 56, 4360-4363.	4.1	7
259	Ferritin-Displayed GLP-1 with Improved Pharmacological Activities and Pharmacokinetics. <i>Molecular Pharmaceutics</i> , 2020, 17, 1663-1673.	4.6	7
260	Inhibitors of glycosomal protein import provide new leads against trypanosomiasis. <i>Microbial Cell</i> , 2017, 4, 229-232.	3.2	7
261	Frequency-selective decoupling with recursively expanded soft pulses in multinuclear NMR. <i>Journal of Magnetic Resonance</i> , 1992, 100, 604-610.	0.5	6
262	In support of the BMRB. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 854-860.	8.2	6
263	^1H , ^{13}C , ^{15}N and ^{31}P chemical shift assignments of a human Xist RNA A-repeat tetraloop hairpin essential for X-chromosome inactivation. <i>Biomolecular NMR Assignments</i> , 2012, 6, 75-77.	0.8	6
264	Autophagy unleashes noncanonical microRNA functions. <i>Autophagy</i> , 2020, 16, 2294-2296.	9.1	6
265	Deep learning model predicts water interaction sites on the surface of proteins using limited-resolution data. <i>Chemical Communications</i> , 2020, 56, 15454-15457.	4.1	6
266	Generation of novel long-acting GLP-1R agonists using DARPins as a scaffold. <i>International Journal of Pharmaceutics</i> , 2021, 607, 121043.	5.2	6
267	Selective Inhibitors of FKBP51 Employ Conformational Selection of Dynamic Invisible States. <i>Angewandte Chemie</i> , 2019, 131, 9529-9533.	2.0	5
268	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , 2021, 22, e53007.	4.5	5
269	Segmental, Domain-Selective perdeuteration and Small-Angle Neutron Scattering for Structural Analysis of Multi-Domain Proteins. <i>Angewandte Chemie</i> , 2017, 129, 9450-9453.	2.0	4
270	Molecular insights on CALX-CBD12 interdomain dynamics from MD simulations, RDCs, and SAXS. <i>Biophysical Journal</i> , 2021, 120, 3664-3675.	0.5	4

#	ARTICLE	IF	CITATIONS
271	Conformational Dynamics from Ambiguous Zinc Coordination in the RanBP2-Type Zinc Finger of RBM5. <i>Journal of Molecular Biology</i> , 2020, 432, 4127-4138.	4.2	4
272	Novel Trypanocidal Inhibitors that Block Glycosome Biogenesis by Targeting PEX3-PEX19 Interaction. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 737159.	3.7	4
273	Letter to the Editor: NMR Assignment of the Drosophila Argonaute2 PAZ Domain. <i>Journal of Biomolecular NMR</i> , 2004, 29, 421-422.	2.8	3
274	NMR Assignment Reveals an α -Helical Fold for the F-Actin Binding Domain of Human Bcr-Abl/c-Abl. <i>Journal of Biomolecular NMR</i> , 2005, 32, 335-335.	2.8	3
275	Backbone assignment of the UHM domain of Puf60 free and bound to five ligands. <i>Biomolecular NMR Assignments</i> , 2008, 2, 211-214.	0.8	3
276	^1H , ^{13}C and ^{15}N chemical shift assignments of IPSE ¹ NLS. <i>Biomolecular NMR Assignments</i> , 2011, 5, 225-227.	0.8	3
277	Expression and purification of a difficult sarcomeric protein: Telethonin. <i>Protein Expression and Purification</i> , 2017, 140, 74-80.	1.3	3
278	Structural Insight into IAPP- α -Derived Amyloid Inhibitors and Their Mechanism of Action. <i>Angewandte Chemie</i> , 2020, 132, 5820-5830.	2.0	3
279	Backbone ^1H , ^{13}C , and ^{15}N resonance assignments of the N-terminal domain of FKBP38 (FKBP38NTD). <i>Journal of Biomolecular NMR</i> , 2006, 36, 37-37.	2.8	2
280	Conformational Selection of Dimethylarginine Recognition by the Survival Motor Neuron Tudor Domain. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 486-490.	13.8	2
281	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. <i>Communications Biology</i> , 2021, 4, 949.	4.4	2
282	What Features of Ligands Are Relevant to the Opening of Cryptic Pockets in Drug Targets?. <i>Informatics</i> , 2022, 9, 8.	3.9	2
283	Extended conformational states dominate the Hsp90 chaperone dynamics. <i>Journal of Biological Chemistry</i> , 2022, 298, 102101.	3.4	2
284	^1H , ^{13}C and ^{15}N backbone resonance assignments of the SAND domains from glucocorticoid modulatory element binding proteins-1 and -2. <i>Journal of Biomolecular NMR</i> , 2003, 25, 259-260.	2.8	1
285	Switching Off the Switch. <i>Structure</i> , 2003, 11, 131-132.	3.3	1
286	New NMR Assignment ^1H , ^{13}C , and ^{15}N Assignment of the Second PH Domain of Human Pleckstrin (234-350). <i>Journal of Biomolecular NMR</i> , 2006, 36, 21-21.	2.8	1
287	^1H , ^{13}C , and ^{15}N chemical shift assignments for the Eps15-EH2-stonin α 2 complex. <i>Biomolecular NMR Assignments</i> , 2008, 2, 55-58.	0.8	1
288	Repeat Recognition. <i>Structure</i> , 2010, 18, 1228-1229.	3.3	1

#	ARTICLE	IF	CITATIONS
289	Alternative Splicing Regulation: Structural and Biophysical Studies. , 2013, , 53-57.		1
290	Ultrashort Broadband Cooperative Pulses for Multidimensional Biomolecular NMR Experiments. <i>Angewandte Chemie</i> , 2018, 130, 14706-14710.	2.0	1
291	Capturing dynamic conformational shifts in protein-ligand recognition using integrative structural biology in solution. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 107-119.	2.6	1
292	Highly Accurate Filters to Flag Frequent Hitters in AlphaScreen Assays by Suggesting their Mechanism. <i>Molecular Informatics</i> , 2021, , 2100151.	2.5	1
293	Computer-Aided Design and Synthesis of a New Class of PEX14 Inhibitors: Substituted 2,3,4,5-Tetrahydrobenzo[F][1,4]oxazepines as Potential New Trypanocidal Agents. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5256-5268.	5.4	1
294	¹⁹ F-NMR Unveils the Ligand-Induced Conformation of a Catalytically Inactive Twisted Homodimer of tRNA-Guanine Transglycosylase. <i>ACS Chemical Biology</i> , 2022, 17, 1745-1755.	3.4	1
295	Speeding Up Biomolecular NMR Spectroscopy. <i>ChemInform</i> , 2004, 35, no.	0.0	0
296	Structural Basis of Single-Stranded RNA Recognition. <i>ChemInform</i> , 2004, 35, no.	0.0	0
297	Chemical Shift Backbone Assignments of TAP-N, the 31 kDa Cargo-binding Region of the Protein TAP. <i>Journal of Biomolecular NMR</i> , 2006, 36, 23-23.	2.8	0
298	Structure And Dynamics Of Protein-RNA Recognition In The Regulation Of Gene Expression. <i>Biophysical Journal</i> , 2009, 96, 373a.	0.5	0
299	Conformational Dynamics During Spliceosome Assembly Investigated by Single-Pair FRET. <i>Biophysical Journal</i> , 2014, 106, 465a.	0.5	0
300	Dynamic RNA world. <i>Rna</i> , 2015, 21, 727-728.	3.5	0
301	Conformational Selection of Dimethylarginine Recognition by the Survival Motor Neuron Tudor Domain. <i>Angewandte Chemie</i> , 2018, 130, 495-499.	2.0	0
302	Ultrashort Broadband Cooperative Pulses for Multidimensional Biomolecular NMR Experiments (<i>Angew. Chem.</i> 44/2018). <i>Angewandte Chemie</i> , 2018, 130, 14868-14868.	2.0	0
303	When Less Is More: Combining Site-Specific Isotope Labeling and NMR Unravels Structural Details of Huntingtin Repeats. <i>Structure</i> , 2020, 28, 730-732.	3.3	0
304	New Frontiers in Drug Discovery: Academia Meets Industry at the International Helmholtz Drug Discovery Conference (HDDC). <i>ChemMedChem</i> , 2020, 15, 468-470.	3.2	0
305	Structural studies of a dual ligand binding SH3 domain in Pex13. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2002, 58, c286-c286.	0.3	0
306	Receptor recognition by the flexible peroxisomal targeting signal type 1 of sterol carrier protein 2. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, s175-s175.	0.3	0

#	ARTICLE	IF	CITATIONS
307	Structure of Bcl-XL, a dominant inhibitor of programmed cell death. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C172-C172.	0.3	0
308	Alternative Splicing Regulation: Structural and Biophysical Studies. , 2019, , 1-7.		0