

Michael Sattler

List of Publications by Year in descending order

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308
papers

21,641
citations

12330

69
h-index

12272

133
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361
all docs

361
docs citations

361
times ranked

23710
citing authors

#	ARTICLE	IF	CITATIONS
1	Multifaceted N-Degron Recognition and Ubiquitylation by GID/CTLH E3 Ligases. <i>Journal of Molecular Biology</i> , 2022, 434, 167347.	4.2	15
2	Locus-Conserved Circular RNA cZNF292 Controls Endothelial Cell Flow Responses. <i>Circulation Research</i> , 2022, 130, 67-79.	4.5	23
3	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
4	NudC guides client transfer between the Hsp40/70 and Hsp90 chaperone systems. <i>Molecular Cell</i> , 2022, 82, 555-569.e7.	9.7	20
5	What Features of Ligands Are Relevant to the Opening of Cryptic Pockets in Drug Targets?. <i>Informatics</i> , 2022, 9, 8.	3.9	2
6	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
7	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
8	Extended conformational states dominate the Hsp90 chaperone dynamics. <i>Journal of Biological Chemistry</i> , 2022, 298, 102101.	3.4	2
9	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
10	The Charged Linker Modulates the Conformations and Molecular Interactions of Hsp90. <i>ChemBioChem</i> , 2021, 22, 1084-1092.	2.6	22
11	Albumin-binding domain extends half-life of glucagon-like peptide-1. <i>European Journal of Pharmacology</i> , 2021, 890, 173650.	3.5	17
12	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. <i>Nature Chemical Biology</i> , 2021, 17, 272-279.	8.0	26
13	Proteolysis of Rab32 by Salmonella GtgE induces an inactive GTPase conformation. <i>IScience</i> , 2021, 24, 101940.	4.1	12
14	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
15	FARS1-related disorders caused by allelic mutations in cytosolic phenylalanyl-tRNA synthetase genes: Look beyond the lungs!. <i>Clinical Genetics</i> , 2021, 99, 789-801.	2.0	16
16	Competitive Microtubule Binding of PEX14 Coordinates Peroxisomal Protein Import and Motility. <i>Journal of Molecular Biology</i> , 2021, 433, 166765.	4.2	10
17	Thymosin β 4 protects against aortic aneurysm via endocytic regulation of growth factor signaling. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	15
18	Facile Synthesis of a Croconaine-Based Nanoformulation for Optoacoustic Imaging and Photothermal Therapy. <i>Advanced Healthcare Materials</i> , 2021, 10, e2002115.	7.6	34

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19	Membrane Interactions of the Peroxisomal Proteins PEX5 and PEX14. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 651449.	3.7	18
20	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
21	Interferon-induced degradation of the persistent hepatitis B virus cccDNA form depends on ISG20. <i>EMBO Reports</i> , 2021, 22, e49568.	4.5	38
22	Orphan GPR116 mediates the insulin sensitizing effects of the hepatokine FNDC4 in adipose tissue. <i>Nature Communications</i> , 2021, 12, 2999.	12.8	22
23	Croconaine-based nanoparticles enable efficient optoacoustic imaging of murine brain tumors. <i>Photoacoustics</i> , 2021, 22, 100263.	7.8	19
24	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
25	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. <i>Communications Biology</i> , 2021, 4, 949.	4.4	2
26	Molecular insights on CALX-CBD12 interdomain dynamics from MD simulations, RDCs, and SAXS. <i>Biophysical Journal</i> , 2021, 120, 3664-3675.	0.5	4
27	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
28	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , 2021, 22, e53007.	4.5	5
29	Highly Accurate Filters to Flag Frequent Hitters in AlphaScreen Assays by Suggesting their Mechanism. <i>Molecular Informatics</i> , 2021, , 2100151.	2.5	1
30	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
31	A modular toolbox to generate complex polymeric ubiquitin architectures using orthogonal sortase enzymes. <i>Nature Communications</i> , 2021, 12, 6515.	12.8	35
32	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
33	Client binding shifts the populations of dynamic Hsp90 conformations through an allosteric network. <i>Science Advances</i> , 2021, 7, eabl7295.	10.3	25
34	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
35	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
36	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

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37	Autophagy unleashes noncanonical microRNA functions. <i>Autophagy</i> , 2020, 16, 2294-2296.	9.1	6
38	Active coacervate droplets as a model for membraneless organelles and protocells. <i>Nature Communications</i> , 2020, 11, 5167.	12.8	135
39	The dynamics of linear polyubiquitin. <i>Science Advances</i> , 2020, 6, .	10.3	38
40	DNA Structure-Specific Cleavage of DNA-Protein Crosslinks by the SPRTN Protease. <i>Molecular Cell</i> , 2020, 80, 102-113.e6.	9.7	39
41	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
42	Identification of phenothiazine derivatives as UHM-binding inhibitors of early spliceosome assembly. <i>Nature Communications</i> , 2020, 11, 5621.	12.8	20
43	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
44	Paramagnetic NMR in drug discovery. <i>Journal of Biomolecular NMR</i> , 2020, 74, 287-309.	2.8	40
45	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
46	Conformational dynamics modulate the catalytic activity of the molecular chaperone Hsp90. <i>Nature Communications</i> , 2020, 11, 1410.	12.8	50
47	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
48	Detection and quantification of the anti-obesity drug celastrol in murine liver and brain. <i>Neurochemistry International</i> , 2020, 136, 104713.	3.8	10
49	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
50	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
51	Ferritin-Displayed GLP-1 with Improved Pharmacological Activities and Pharmacokinetics. <i>Molecular Pharmaceutics</i> , 2020, 17, 1663-1673.	4.6	7
52	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
53	Structural Insight into IAPP-Derived Amyloid Inhibitors and Their Mechanism of Action. <i>Angewandte Chemie</i> , 2020, 132, 5820-5830.	2.0	3
54	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

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55	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
56	The Photocatalyzed Thiol-ene reaction: A New Tag to Yield Fast, Selective and reversible Paramagnetic Tagging of Proteins. <i>ChemPhysChem</i> , 2020, 21, 863-869.	2.1	11
57	Structure and Molecular Recognition Mechanism of IMP-13 Metallo- β -Lactamase. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	8
58	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
59	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
60	Machine learning a model for RNA structure prediction. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa090.	3.2	19
61	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
62	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
63	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
64	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
65	FSP1 is a glutathione-independent ferroptosis suppressor. <i>Nature</i> , 2019, 575, 693-698.	27.8	1,624
66	The molecular basis of chaperone-mediated interleukin 23 assembly control. <i>Nature Communications</i> , 2019, 10, 4121.	12.8	18
67	Combinatorial recognition of clustered RNA elements by the multidomain RNA-binding protein IMP3. <i>Nature Communications</i> , 2019, 10, 2266.	12.8	53
68	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
69	Selective Inhibitors of FKBP51 Employ Conformational Selection of Dynamic Invisible States. <i>Angewandte Chemie</i> , 2019, 131, 9529-9533.	2.0	5
70	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
71	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
72	Selective Inhibitors of FKBP51 Employ Conformational Selection of Dynamic Invisible States. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 9429-9433.	13.8	18

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73	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
74	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
75	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
76	Staufen2-mediated RNA recognition and localization requires combinatorial action of multiple domains. <i>Nature Communications</i> , 2019, 10, 1659.	12.8	18
77	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
78	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
79	Inhibition of CPAP tubulin interaction prevents proliferation of centrosome-amplified cancer cells. <i>EMBO Journal</i> , 2019, 38, .	7.8	24
80	Recent Advances in Half-life Extension Strategies for Therapeutic Peptides and Proteins. <i>Current Pharmaceutical Design</i> , 2019, 24, 4932-4946.	1.9	29
81	Alternative Splicing Regulation: Structural and Biophysical Studies. , 2019, , 1-7.		0
82	Ultrashort Broadband Cooperative Pulses for Multidimensional Biomolecular NMR Experiments. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 14498-14502.	13.8	12
83	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
84	A switch point in the molecular chaperone Hsp90 responding to client interaction. <i>Nature Communications</i> , 2018, 9, 1472.	12.8	30
85	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
86	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
87	Ultrashort Broadband Cooperative Pulses for Multidimensional Biomolecular NMR Experiments. <i>Angewandte Chemie</i> , 2018, 130, 14706-14710.	2.0	1
88	Identification of small-molecule inhibitors of USP2a. <i>European Journal of Medicinal Chemistry</i> , 2018, 150, 261-267.	5.5	24
89	Conformational Selection of Dimethylarginine Recognition by the Survival Motor Neuron Tudor Domain. <i>Angewandte Chemie</i> , 2018, 130, 495-499.	2.0	0
90	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

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91	Rücktitelbild: Ultrashort Broadband Cooperative Pulses for Multidimensional Biomolecular NMR Experiments (Angew. Chem. 44/2018). Angewandte Chemie, 2018, 130, 14868-14868.	2.0	0
92	Come, sweet death: targeting glycosomal protein import for antitrypanosomal drug development. Current Opinion in Microbiology, 2018, 46, 116-122.	5.1	14
93	Celastrol Promotes Weight Loss in Diet-Induced Obesity by Inhibiting the Protein Tyrosine Phosphatases PTP1B and TCPTP in the Hypothalamus. Journal of Medicinal Chemistry, 2018, 61, 11144-11157.	6.4	45
94	Roquin targets mRNAs in a 3' UTR-specific manner by different modes of regulation. Nature Communications, 2018, 9, 3810.	12.8	40
95	Capturing dynamic conformational shifts in protein-ligand recognition using integrative structural biology in solution. Emerging Topics in Life Sciences, 2018, 2, 107-119.	2.6	1
96	Celastrol-Induced Weight Loss Is Driven by Hypophagia and Independent From UCP1. Diabetes, 2018, 67, 2456-2465.	0.6	39
97	Structural basis for terminal loop recognition and stimulation of pri-miRNA-18a processing by hnRNP A1. Nature Communications, 2018, 9, 2479.	12.8	80
98	Targeting TRAF6 E3 ligase activity with a small-molecule inhibitor combats autoimmunity. Journal of Biological Chemistry, 2018, 293, 13191-13203.	3.4	52
99	Molecular architecture and dynamics of ASH1 mRNA recognition by its mRNA-transport complex. Nature Structural and Molecular Biology, 2017, 24, 152-161.	8.2	40
100	Structure-function analysis of the DNA-binding domain of a transmembrane transcriptional activator. Scientific Reports, 2017, 7, 1051.	3.3	46
101	Segmental, Domain-Selective perdeuteration and Small-Angle Neutron Scattering for Structural Analysis of Multi-Domain Proteins. Angewandte Chemie - International Edition, 2017, 56, 9322-9325.	13.8	52
102	Allosteric modulation of peroxisomal membrane protein recognition by farnesylation of the peroxisomal import receptor PEX19. Nature Communications, 2017, 8, 14635.	12.8	47
103	Inhibitors of PEX14 disrupt protein import into glycosomes and kill <i>Trypanosoma</i> parasites. Science, 2017, 355, 1416-1420.	12.6	59
104	Integrated structural biology to unravel molecular mechanisms of protein-RNA recognition. Methods, 2017, 118-119, 119-136.	3.8	49
105	Molecular basis for asymmetry sensing of siRNAs by the Drosophila Loqs-PD/Dcr-2 complex in RNA interference. Nucleic Acids Research, 2017, 45, 12536-12550.	14.5	27
106	A chemical compound inhibiting the Aha1-Hsp90 chaperone complex. Journal of Biological Chemistry, 2017, 292, 17073-17083.	3.4	37
107	Structural insights into the interaction of the nuclear exosome helicase Mtr4 with the preribosomal protein Nop53. Rna, 2017, 23, 1780-1787.	3.5	42
108	RNA structure refinement using NMR solvent accessibility data. Scientific Reports, 2017, 7, 5393.	3.3	26

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109	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
110	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
111	Expression and purification of a difficult sarcomeric protein: Telethonin. <i>Protein Expression and Purification</i> , 2017, 140, 74-80.	1.3	3
112	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
113	Inhibitors of glycosomal protein import provide new leads against trypanosomiasis. <i>Microbial Cell</i> , 2017, 4, 229-232.	3.2	7
114	Structural basis for the recognition of spliceosomal SmN/B/B TM proteins by the RBM5 OCRE domain in splicing regulation. <i>ELife</i> , 2016, 5, .	6.0	28
115	Investigating the Role of Large-Scale Domain Dynamics in Protein-Protein Interactions. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 54.	3.5	23
116	Novel small molecules targeting ciliary transport of Smoothed and oncogenic Hedgehog pathway activation. <i>Scientific Reports</i> , 2016, 6, 22540.	3.3	16
117	Roquin recognizes a non-canonical hexaloop structure in the 3 ^{UTR} of Ox40. <i>Nature Communications</i> , 2016, 7, 11032.	12.8	38
118	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
119	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
120	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
121	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
122	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
123	Molecular basis for CPAP-tubulin interaction in controlling centriolar and ciliary length. <i>Nature Communications</i> , 2016, 7, 11874.	12.8	66
124	DNA annealing by Red β 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
125	Recognition of the 3 ^{UTR} 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
126	<scp>RNA</scp> recognition by Roquin in posttranscriptional gene regulation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 455-469.	6.4	15

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127	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
128	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
129	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
130	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
131	Pitchfork and Gprasp2 Target Smoothed to the Primary Cilium for Hedgehog Pathway Activation. <i>PLoS ONE</i> , 2016, 11, e0149477.	2.5	21
132	Selective activators of protein phosphatase 5 target the auto-inhibitory mechanism. <i>Bioscience Reports</i> , 2015, 35, .	2.4	18
133	Structural basis for cpSRP43 chromodomain selectivity and dynamics in Alb3 insertase interaction. <i>Nature Communications</i> , 2015, 6, 8875.	12.8	24
134	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
135	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
136	Deciphering the protein-RNA recognition code: Combining large-scale quantitative methods with structural biology. <i>BioEssays</i> , 2015, 37, 899-908.	2.5	26
137	Hsp90-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
138	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
139	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
140	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
141	Structural Characterization of LRRK2 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 3751-3756.	6.4	34
142	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
143	Differential inhibition of Arabidopsis superoxide dismutases by peroxynitrite-mediated tyrosine nitration. <i>Journal of Experimental Botany</i> , 2015, 66, 989-999.	4.8	116
144	Efficient segmental isotope labeling of multi-domain proteins using Sortase A. <i>Journal of Biomolecular NMR</i> , 2015, 63, 1-8.	2.8	79

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145	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
146	Dynamic RNA world. <i>Rna</i> , 2015, 21, 727-728.	3.5	0
147	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
148	Breaking the protein-RNA recognition code. <i>Cell Cycle</i> , 2014, 13, 3619-3620.	2.6	14
149	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
150	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
151	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
152	Conformational Dynamics During Spliceosome Assembly Investigated by Single-Pair FRET. <i>Biophysical Journal</i> , 2014, 106, 465a.	0.5	0
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154	Modulation of the Hsp90 Chaperone Cycle by a Stringent Client Protein. <i>Molecular Cell</i> , 2014, 53, 941-953.	9.7	129
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