

Bernd Simon

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

2,149
citations

331259

21
h-index

301761

39
g-index

43
all docs

43
docs citations

43
times ranked

3490
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and dynamics of the quaternary hunchback mRNA translation repression complex. <i>Nucleic Acids Research</i> , 2021, 49, 8866-8885.	6.5	4
2	Structural basis of PETISCO complex assembly during piRNA biogenesis in <i>C. elegans</i> . <i>Genes and Development</i> , 2021, 35, 1304-1323.	2.7	14
3	Titin kinase ubiquitination aligns autophagy receptors with mechanical signals in the sarcomere. <i>EMBO Reports</i> , 2021, 22, e48018.	2.0	22
4	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	13.7	159
5	Pseudo-RNA-Binding Domains Mediate RNA Structure Specificity in Upstream of N-Ras. <i>Cell Reports</i> , 2020, 32, 107930.	2.9	18
6	Macrocyclic Peptides Uncover a Novel Binding Mode for Reversible Inhibitors of LSD1. <i>ACS Omega</i> , 2020, 5, 3979-3995.	1.6	21
7	Structural Basis of an Asymmetric Condensin ATPase Cycle. <i>Molecular Cell</i> , 2019, 74, 1175-1188.e9.	4.5	68
8	Improving the sensitivity of FT-NMR spectroscopy by apodization weighted sampling. <i>Journal of Biomolecular NMR</i> , 2019, 73, 155-165.	1.6	29
9	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of <i>Drosophila</i> helicase Maleless. <i>Nucleic Acids Research</i> , 2019, 47, 4319-4333.	6.5	17
10	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. <i>Blood</i> , 2019, 133, 366-376.	0.6	22
11	Structural basis for terminal loop recognition and stimulation of pri-miRNA-18a processing by hnRNP A1. <i>Nature Communications</i> , 2018, 9, 2479.	5.8	80
12	DENR-MCTS1 heterodimerization and tRNA recruitment are required for translation reinitiation. <i>PLoS Biology</i> , 2018, 16, e2005160.	2.6	33
13	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.	7.2	52
14	Fe65-PTB2 Dimerization Mimics Fe65-APP Interaction. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 140.	1.4	10
15	Synthesis of Highly Selective Submicromolar Microcystin-Based Inhibitors of Protein Phosphatase (PP)2A over PP1. <i>Angewandte Chemie</i> , 2016, 128, 14191-14195.	1.6	3
16	A bromodomain-DNA interaction facilitates acetylation-dependent bivalent nucleosome recognition by the BET protein BRDT. <i>Nature Communications</i> , 2016, 7, 13855.	5.8	103
17	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , 2016, 13, 515-520.	9.0	49
18	Synthesis of Highly Selective Submicromolar Microcystin-Based Inhibitors of Protein Phosphatase (PP)2A over PP1. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 13985-13989.	7.2	20

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19	Exploration of pathomechanisms triggered by a single-nucleotide polymorphism in titin's I-band: the cardiomyopathy-linked mutation T2580I. <i>Open Biology</i> , 2016, 6, 160114.	1.5	17
20	Resolving the β -glycosidic linkage of arginine-rhamnosylated translation elongation factor P triggers generation of the first Arg ^{>} Rha ^{</sup> specific antibody. <i>Chemical Science</i>, 2016, 7, 6995-7001.}	3.7	30
21	RNA structure determination by solid-state NMR spectroscopy. <i>Nature Communications</i> , 2015, 6, 7024.	5.8	76
22	Structural Analysis of Protein-RNA Complexes in Solution Using NMR Paramagnetic Relaxation Enhancements. <i>Methods in Enzymology</i> , 2015, 558, 333-362.	0.4	16
23	The structure of the SOLE element of <i>oskar</i> mRNA. <i>Rna</i> , 2015, 21, 1444-1453.	1.6	20
24	¹ H, ¹³ C, and ¹⁵ N chemical shift assignments of the phosphotyrosine binding domain 2 (PTB2) of human FE65. <i>Biomolecular NMR Assignments</i> , 2014, 8, 93-95.	0.4	1
25	NMR approaches for structural analysis of multidomain proteins and complexes in solution. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 80, 26-63.	3.9	164
26	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.	7.2	25
27	The structure of the box C/D enzyme reveals regulation of RNA methylation. <i>Nature</i> , 2013, 502, 519-523.	13.7	154
28	Multi-domain conformational selection underlies pre-mRNA splicing regulation by U2AF. <i>Nature</i> , 2011, 475, 408-411.	13.7	202
29	Recognition of 2'-O-Methylated 3'-End of piRNA by the PAZ Domain of a Piwi Protein. <i>Structure</i> , 2011, 19, 172-180.	1.6	98
30	Genetic Variation in Titin in Arrhythmogenic Right Ventricular Cardiomyopathy-Overlap Syndromes. <i>Circulation</i> , 2011, 124, 876-885.	1.6	263
31	An Efficient Protocol for NMR-Spectroscopy-Based Structure Determination of Protein Complexes in Solution. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 1967-1970.	7.2	104
32	Structure of the K-turn U4 RNA: a combined NMR and SANS study. <i>Nucleic Acids Research</i> , 2010, 38, 6274-6285.	6.5	49
33	Structure of the intracellular domain of the amyloid precursor protein in complex with Fe65-PTB2. <i>EMBO Reports</i> , 2008, 9, 1134-1140.	2.0	78
34	Speeding Up Biomolecular NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 782-786.	7.2	11
35	De Novo Structure Determination from Residual Dipolar Couplings by NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2002, 41, 437-440.	7.2	28
36	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.	1.6	32

#	ARTICLE	IF	CITATIONS
37	Title is missing!. Journal of Biomolecular NMR, 1997, 10, 95-106.	1.6	50