

# Bernd Simon

## List of Publications by Citations

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40  
papers

1,524  
citations

19  
h-index

39  
g-index

43  
ext. papers

1,889  
ext. citations

13.3  
avg, IF

4.34  
L-index

#	Paper	IF	Citations
40	Genetic variation in titin in arrhythmogenic right ventricular cardiomyopathy-overlap syndromes. <i>Circulation</i> , <b>2011</b> , 124, 876-85	16.7	225
39	Multi-domain conformational selection underlies pre-mRNA splicing regulation by U2AF. <i>Nature</i> , <b>2011</b> , 475, 408-11	50.4	156
38	NMR approaches for structural analysis of multidomain proteins and complexes in solution. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , <b>2014</b> , 80, 26-63	10.4	130
37	The structure of the box C/D enzyme reveals regulation of RNA methylation. <i>Nature</i> , <b>2013</b> , 502, 519-23	50.4	127
36	An efficient protocol for NMR-spectroscopy-based structure determination of protein complexes in solution. <i>Angewandte Chemie - International Edition</i> , <b>2010</b> , 49, 1967-70	16.4	88
35	Recognition of 2'-O-methylated 3' end of piRNA by the PAZ domain of a Piwi protein. <i>Structure</i> , <b>2011</b> , 19, 172-80	5.2	82
34	A bromodomain-DNA interaction facilitates acetylation-dependent bivalent nucleosome recognition by the BET protein BRDT. <i>Nature Communications</i> , <b>2016</b> , 7, 13855	17.4	66
33	Structure of the intracellular domain of the amyloid precursor protein in complex with Fe65-PTB2. <i>EMBO Reports</i> , <b>2008</b> , 9, 1134-40	6.5	65
32	RNA structure determination by solid-state NMR spectroscopy. <i>Nature Communications</i> , <b>2015</b> , 6, 7024	17.4	58
31	Towards structural investigations on isotope labelled native bacteriorhodopsin in detergent micelles by solution-state NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , <b>1997</b> , 10, 95-106	3	47
30	Structure of the K-turn U4 RNA: a combined NMR and SANS study. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 6274-85	17.4	45
29	Automated structure modeling of large protein assemblies using crosslinks as distance restraints. <i>Nature Methods</i> , <b>2016</b> , 13, 515-20	21.6	44
28	Structural Basis of an Asymmetric Condensin ATPase Cycle. <i>Molecular Cell</i> , <b>2019</b> , 74, 1175-1188.e9	17.6	41
27	Structural basis for terminal loop recognition and stimulation of pri-miRNA-18a processing by hnRNP A1. <i>Nature Communications</i> , <b>2018</b> , 9, 2479	17.4	41
26	Segmental, Domain-Selective Perdeuteration and Small-Angle Neutron Scattering for Structural Analysis of Multi-Domain Proteins. <i>Angewandte Chemie - International Edition</i> , <b>2017</b> , 56, 9322-9325	16.4	39
25	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , <b>2021</b> , 597, 533-538	50.4	29
24	A TROSY relayed HCCH-COSY experiment for correlating adenine H2/H8 resonances in uniformly <sup>13</sup> C-labeled RNA molecules. <i>Journal of Biomolecular NMR</i> , <b>2001</b> , 20, 173-6	3	28

23	De novo structure determination from residual dipolar couplings by NMR spectroscopy. <i>Angewandte Chemie - International Edition</i> , <b>2002</b> , 41, 437-40	16.4	25
22	Efficient detection of hydrogen bonds in dynamic regions of RNA by sensitivity-optimized NMR pulse sequences. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 10487-90	16.4	20
21	Resolving the N-glycosidic linkage of arginine-rhamnosylated translation elongation factor P triggers generation of the first Arg specific antibody. <i>Chemical Science</i> , <b>2016</b> , 7, 6995-7001	9.4	17
20	DENR-MCTS1 heterodimerization and tRNA recruitment are required for translation reinitiation. <i>PLoS Biology</i> , <b>2018</b> , 16, e2005160	9.7	16
19	Synthesis of Highly Selective Submicromolar Microcystin-Based Inhibitors of Protein Phosphatase (PP)2A over PP1. <i>Angewandte Chemie - International Edition</i> , <b>2016</b> , 55, 13985-13989	16.4	16
18	Structural Analysis of Protein-RNA Complexes in Solution Using NMR Paramagnetic Relaxation Enhancements. <i>Methods in Enzymology</i> , <b>2015</b> , 558, 333-362	1.7	15
17	Macrocyclic Peptides Uncover a Novel Binding Mode for Reversible Inhibitors of LSD1. <i>ACS Omega</i> , <b>2020</b> , 5, 3979-3995	3.9	14
16	Improving the sensitivity of FT-NMR spectroscopy by apodization weighted sampling. <i>Journal of Biomolecular NMR</i> , <b>2019</b> , 73, 155-165	3	13
15	The structure of the SOLE element of oskar mRNA. <i>Rna</i> , <b>2015</b> , 21, 1444-53	5.8	13
14	Pseudo-RNA-Binding Domains Mediate RNA Structure Specificity in Upstream of N-Ras. <i>Cell Reports</i> , <b>2020</b> , 32, 107930	10.6	10
13	Speeding up biomolecular NMR spectroscopy. <i>Angewandte Chemie - International Edition</i> , <b>2004</b> , 43, 782-66.4	6.4	9
12	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. <i>Blood</i> , <b>2019</b> , 133, 366-376	2.2	9
11	Exploration of pathomechanisms triggered by a single-nucleotide polymorphism in titin N1-band: the cardiomyopathy-linked mutation T2580I. <i>Open Biology</i> , <b>2016</b> , 6,	7	8
10	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of Drosophila helicase Maleless. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 4319-4333	20.1	7
9	Fe65-PTB2 Dimerization Mimics Fe65-APP Interaction. <i>Frontiers in Molecular Neuroscience</i> , <b>2017</b> , 10, 1406.1	6.1	6
8	An Efficient Protocol for NMR-Spectroscopy-Based Structure Determination of Protein Complexes in Solution. <i>Angewandte Chemie</i> , <b>2010</b> , 122, 2011-2014	3.6	5
7	Titin kinase ubiquitination aligns autophagy receptors with mechanical signals in the sarcomere. <i>EMBO Reports</i> , <b>2021</b> , 22, e48018	6.5	4
6	Synthesis of Highly Selective Submicromolar Microcystin-Based Inhibitors of Protein Phosphatase (PP)2A over PP1. <i>Angewandte Chemie</i> , <b>2016</b> , 128, 14191-14195	3.6	3

5	$^1\text{H}$ , $^{13}\text{C}$ , and $^{15}\text{N}$ chemical shift assignments of the phosphotyrosine binding domain 2 (PTB2) of human FE65. <i>Biomolecular NMR Assignments</i> , <b>2014</b> , 8, 93-5	0.7	1
4	Efficient Detection of Hydrogen Bonds in Dynamic Regions of RNA by Sensitivity-Optimized NMR Pulse Sequences. <i>Angewandte Chemie</i> , <b>2013</b> , 125, 10681-10684	3.6	1
3	Structural basis for terminal loop recognition and processing of pri-miRNA-18a by hnRNP A1		1
2	Structure and dynamics of the quaternary hunchback mRNA translation repression complex. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 8866-8885	20.1	0
1	Structural basis of PETISCO complex assembly during piRNA biogenesis in. <i>Genes and Development</i> , <b>2021</b> , 35, 1304-1323	12.6	0