

Robert Schneider

List of Publications by Year in descending order

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32
papers

1,740
citations

304743

22
h-index

477307

29
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32
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docs citations

32
times ranked

2303
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Dynamics of the C-terminal X Domain of Nipah and Hendra Viruses Controls the Attachment to the C-terminal Tail of the Nucleocapsid Protein. <i>Journal of Molecular Biology</i> , 2022, 434, 167551.	4.2	3
2	Experimental studies of binding of intrinsically disordered proteins to their partners. , 2019, , 139-187.		3
3	Elucidating binding mechanisms and dynamics of intrinsically disordered protein complexes using NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2019, 54, 10-18.	5.7	78
4	NMR and circular dichroism data for domain 2 of the HCV NS5A protein phosphorylated by the Casein Kinase II. <i>Data in Brief</i> , 2018, 17, 325-333.	1.0	0
5	NMR reveals the intrinsically disordered domain 2 of NS5A protein as an allosteric regulator of the hepatitis C virus RNA polymerase NS5B. <i>Journal of Biological Chemistry</i> , 2017, 292, 18024-18043.	3.4	7
6	Structural Characterization of the SMRT Corepressor Interacting with Histone Deacetylase 7. <i>Scientific Reports</i> , 2017, 7, 3678.	3.3	14
7	Two-Partner Secretion: Combining Efficiency and Simplicity in the Secretion of Large Proteins for Bacteria-Host and Bacteria-Bacteria Interactions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 148.	3.9	92
8	Binding Mechanisms of Intrinsically Disordered Proteins: Theory, Simulation, and Experiment. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 52.	3.5	118
9	Studying Intrinsically Disordered Proteins under True Inâ€¦Vivo Conditions by Combined Crossâ€¦Polarization and Carbonylâ€¦Detection NMR Spectroscopy. <i>Angewandte Chemie</i> , 2016, 128, 7544-7548.	2.0	6
10	Identification of Dynamic Modes in an Intrinsically Disordered Protein Using Temperature-Dependent NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2016, 138, 6240-6251.	13.7	90
11	Nuclear Magnetic Resonance Spectroscopy for the Identification of Multiple Phosphorylations of Intrinsically Disordered Proteins. <i>Journal of Visualized Experiments</i> , 2016, , .	0.3	17
12	Studying Intrinsically Disordered Proteins under True Inâ€¦Vivo Conditions by Combined Crossâ€¦Polarization and Carbonylâ€¦Detection NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 7418-7422.	13.8	17
13	Solid-state NMR, electrophysiology and molecular dynamics characterization of human VDAC2. <i>Journal of Biomolecular NMR</i> , 2015, 61, 311-320.	2.8	26
14	Visualizing the Molecular Recognition Trajectory of an Intrinsically Disordered Protein Using Multinuclear Relaxation Dispersion NMR. <i>Journal of the American Chemical Society</i> , 2015, 137, 1220-1229.	13.7	128
15	Insights into the Structure and Dynamics of Measles Virus Nucleocapsids by 1H-detected Solid-state NMR. <i>Biophysical Journal</i> , 2014, 107, 941-946.	0.5	30
16	Peakr: simulating solid-state NMR spectra of proteins. <i>Bioinformatics</i> , 2013, 29, 1134-1140.	4.1	2
17	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	4.7	68
18	Mapping the Potential Energy Landscape of Intrinsically Disordered Proteins at Amino Acid Resolution. <i>Journal of the American Chemical Society</i> , 2012, 134, 15138-15148.	13.7	113

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19	β -Barrel Mobility Underlies Closure of the Voltage-Dependent Anion Channel. <i>Structure</i> , 2012, 20, 1540-1549.	3.3	104
20	Ensemble Structure of the Modular and Flexible Full-Length Vesicular Stomatitis Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2012, 423, 182-197.	4.2	37
21	Towards a robust description of intrinsic protein disorder using nuclear magnetic resonance spectroscopy. <i>Molecular BioSystems</i> , 2012, 8, 58-68.	2.9	95
22	Computational Electrophysiology on Vdac-1 reveals Mechanism of Anion Flux. <i>Biophysical Journal</i> , 2011, 100, 267a.	0.5	0
23	Structural Characterization of Polyglutamine Fibrils by Solid-State NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2011, 412, 121-136.	4.2	88
24	The Native Conformation of the Human VDAC1 N-terminus. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 1882-1885.	13.8	67
25	Probing Molecular Motion by Double-Quantum (^{13}C , ^{13}C) Solid-State NMR Spectroscopy: Application to Ubiquitin. <i>Journal of the American Chemical Society</i> , 2010, 132, 223-233.	13.7	34
26	Comparative analysis of NMR chemical shift predictions for proteins in the solid phase. <i>Solid State Nuclear Magnetic Resonance</i> , 2009, 35, 235-242.	2.3	35
27	Coupling of activation and inactivation gate in a K ⁺ -channel: potassium and ligand sensitivity. <i>EMBO Journal</i> , 2009, 28, 2825-2834.	7.8	94
28	Structural Rearrangements of Membrane Proteins Probed by Water-Edited Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2009, 131, 170-176.	13.7	103
29	A structural link between inactivation and block of a K ⁺ channel. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 605-612.	8.2	117
30	The Molecular Mechanism of Toxin-Induced Conformational Changes in a Potassium Channel: Relation to C-Type Inactivation. <i>Structure</i> , 2008, 16, 747-754.	3.3	52
31	Solid-State NMR Spectroscopy Applied to a Chimeric Potassium Channel in Lipid Bilayers. <i>Journal of the American Chemical Society</i> , 2008, 130, 7427-7435.	13.7	70
32	High-Resolution 3D Structure Determination of Kaliotoxin by Solid-State NMR Spectroscopy. <i>PLoS ONE</i> , 2008, 3, e2359.	2.5	32