

Robert Schneider

List of Publications by Year in descending order

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32
papers

1,740
citations

304368

22
h-index

476904

29
g-index

32
all docs

32
docs citations

32
times ranked

2303
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	6.6	128
2	Binding Mechanisms of Intrinsically Disordered Proteins: Theory, Simulation, and Experiment. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 52.	1.6	118
3	A structural link between inactivation and block of a K ⁺ channel. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 605-612.	3.6	117
4	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.	6.6	113
5	Î²-Barrel Mobility Underlies Closure of the Voltage-Dependent Anion Channel. <i>Structure</i> , 2012, 20, 1540-1549.	1.6	104
6	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.	6.6	103
7	Towards a robust description of intrinsic protein disorder using nuclear magnetic resonance spectroscopy. <i>Molecular BioSystems</i> , 2012, 8, 58-68.	2.9	95
8	Coupling of activation and inactivation gate in a K ⁺ -channel: potassium and ligand sensitivity. <i>EMBO Journal</i> , 2009, 28, 2825-2834.	3.5	94
9	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.	1.8	92
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.	6.6	90
11	Structural Characterization of Polyglutamine Fibrils by Solid-State NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2011, 412, 121-136.	2.0	88
12	Elucidating binding mechanisms and dynamics of intrinsically disordered protein complexes using NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2019, 54, 10-18.	2.6	78
13	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.	6.6	70
14	Atomic Resolution Description of the Interaction between the Nucleoprotein and Phosphoprotein of Hendra Virus. <i>PLoS Pathogens</i> , 2013, 9, e1003631.	2.1	68
15	The Native Conformation of the Human VDAC1 N-terminus. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 1882-1885.	7.2	67
16	The Molecular Mechanism of Toxin-Induced Conformational Changes in a Potassium Channel: Relation to C-Type Inactivation. <i>Structure</i> , 2008, 16, 747-754.	1.6	52
17	Ensemble Structure of the Modular and Flexible Full-Length Vesicular Stomatitis Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2012, 423, 182-197.	2.0	37
18	Comparative analysis of NMR chemical shift predictions for proteins in the solid phase. <i>Solid State Nuclear Magnetic Resonance</i> , 2009, 35, 235-242.	1.5	35

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19	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.	6.6	34
20	High-Resolution 3D Structure Determination of Kaliotoxin by Solid-State NMR Spectroscopy. <i>PLoS ONE</i> , 2008, 3, e2359.	1.1	32
21	Insights into the Structure and Dynamics of Measles Virus Nucleocapsids by 1H-detected Solid-state NMR. <i>Biophysical Journal</i> , 2014, 107, 941-946.	0.2	30
22	Solid-state NMR, electrophysiology and molecular dynamics characterization of human VDACC2. <i>Journal of Biomolecular NMR</i> , 2015, 61, 311-320.	1.6	26
23	Nuclear Magnetic Resonance Spectroscopy for the Identification of Multiple Phosphorylations of Intrinsically Disordered Proteins. <i>Journal of Visualized Experiments</i> , 2016, . .	0.2	17
24	Studying Intrinsically Disordered Proteins under True In Vivo Conditions by Combined Cross-Polarization and Carbonyl-Detection NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 7418-7422.	7.2	17
25	Structural Characterization of the SMRT Corepressor Interacting with Histone Deacetylase 7. <i>Scientific Reports</i> , 2017, 7, 3678.	1.6	14
26	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.	1.6	7
27	Studying Intrinsically Disordered Proteins under True In Vivo Conditions by Combined Cross-Polarization and Carbonyl-Detection NMR Spectroscopy. <i>Angewandte Chemie</i> , 2016, 128, 7544-7548.	1.6	6
28	Experimental studies of binding of intrinsically disordered proteins to their partners. , 2019, , 139-187.		3
29	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.	2.0	3
30	Peakr: simulating solid-state NMR spectra of proteins. <i>Bioinformatics</i> , 2013, 29, 1134-1140.	1.8	2
31	Computational Electrophysiology on Vdac-1 reveals Mechanism of Anion Flux. <i>Biophysical Journal</i> , 2011, 100, 267a.	0.2	0
32	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.	0.5	0