Nikolai R Skrynnikov

List of Publications by Year
in descending order

62	3,609	147566	149479
papers	citations	31 h-index	56 g-index

64	64	64	2838
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2001, 123, 11341-11352.	6.6	454
2	Measurement of Slow (Î¼sâ^'ms) Time Scale Dynamics in Protein Side Chains by15N Relaxation Dispersion NMR Spectroscopy:Â Application to Asn and Gln Residues in a Cavity Mutant of T4 Lysozyme. Journal of the American Chemical Society, 2001, 123, 967-975.	6.6	298
3	Orienting domains in proteins using dipolar couplings measured by liquid-state NMR: differences in solution and crystal forms of maltodextrin binding protein loaded with Î²-cyclodextrin. Journal of Molecular Biology, 2000, 295, 1265-1273.	2.0	197
4	Deuterium Spin Probes of Side-Chain Dynamics in Proteins. 1. Measurement of Five Relaxation Rates per Deuteron in 13C-Labeled and Fractionally 2H-Enriched Proteins in Solution. Journal of the American Chemical Society, 2002, 124, 6439-6448.	6.6	180
5	Probing Slow Time Scale Dynamics at Methyl-Containing Side Chains in Proteins by Relaxation Dispersion NMR Measurements:Â Application to Methionine Residues in a Cavity Mutant of T4 Lysozyme. Journal of the American Chemical Society, 2001, 123, 4556-4566.	6.6	170
6	Reconstructing NMR Spectra of â€œInvisibleâ€•Excited Protein States Using HSQC and HMQC Experiments. Journal of the American Chemical Society, 2002, 124, 12352-12360.	6.6	169
7	Structural Characterization of Proteins with an Attached ATCUN Motif by Paramagnetic Relaxation Enhancement NMR Spectroscopy. Journal of the American Chemical Society, 2001, 123, 9843-9847.	6.6	162
8	An NMR Experiment for the Accurate Measurement of Heteronuclear Spin-Lock Relaxation Rates. Journal of the American Chemical Society, 2002, 124, 10743-10753.	6.6	130
9	Deuterium Spin Probes of Side-Chain Dynamics in Proteins. 2. Spectral Density Mapping and Identification of Nanosecond Time-Scale Side-Chain Motions. Journal of the American Chemical Society, 2002, 124, 6449-6460.	6.6	129
10	Ligand-induced structural changes to maltodextrin-binding protein as studied by solution NMR spectroscopy. Journal of Molecular Biology, 2001, 309, 961-974.	2.0	126
11	High Resolution1H Detected1H,13C Correlation Spectra in MAS Solid-State NMR using Deuterated Proteins with Selective1H,2H Isotopic Labeling of Methyl Groups. Journal of the American Chemical Society, 2006, 128, 12620-12621.	6.6	107
12	Protein Side-Chain Dynamics As Observed by Solution- and Solid-State NMR Spectroscopy: A Similarity Revealed. Journal of the American Chemical Society, 2008, 130, 16611-16621.	6.6	102
13	What is the average conformation of bacteriophage T4 lysozyme in solution? a domain orientation study using dipolar couplings measured by solution NMR 1 1Edited by P. E. Wright. Journal of Molecular Biology, 2001, 308, 745-764.	2.0	90
14	Slow conformational exchange and overall rocking motion in ubiquitin protein crystals. Nature Communications, 2017, 8, 145.	5.8	78
15	Structural Determinants for High-Affinity Binding in a Nedd4 WW3â^— Domain-Comm PY Motif Complex. Structure, 2006, 14, 543-553.	1.6	77
16	Methyl Rotation Barriers in Proteins from2H Relaxation Data. Implications for Protein Structure. Journal of the American Chemical Society, 2007, 129, 6827-6838.	6.6	73
17	Observing the overall rocking motion of a protein in a crystal. Nature Communications, 2015, 6, 8361.	5.8	67
18	Microsecond Time-Scale Conformational Exchange in Proteins: Using Long Molecular Dynamics Trajectory To Simulate NMR Relaxation Dispersion Data. Journal of the American Chemical Society, 2012, 134, 2555-2562.	6.6	64

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19	Protein Side-Chain Dynamics Observed by Solution- and Solid-State NMR:Â Comparative Analysis of Methyl2H Relaxation Data. Journal of the American Chemical Society, 2006, 128, 12354-12355.	6.6	60
20	Comparison of 13CH3, 13CH2D, and 13CHD2 methyl labeling strategies in proteins. Journal of Biomolecular NMR, 2005, 33, 25-41.	1.6	59
21	Combined Analysis of15N Relaxation Data from Solid- and Solution-State NMR Spectroscopy. Journal of the American Chemical Society, 2007, 129, 12594-12595.	6.6	58
22	15NH/D-SOLEXSY experiment for accurate measurement of amide solvent exchange rates: application to denatured drkN SH3. Journal of Biomolecular NMR, 2010, 46, 227-244.	1.6	57
23	Comparison of Solid-State Dipolar Couplings and Solution Relaxation Data Provides Insight into Protein Backbone Dynamics. Journal of the American Chemical Society, 2010, 132, 5015-5017.	6.6	57
24	Motion of a Disordered Polypeptide Chain as Studied by Paramagnetic Relaxation Enhancements,¹⁵N Relaxation, and Molecular Dynamics Simulations: How Fast Is Segmental Diffusion in Denatured Ubiquitin?. Journal of the American Chemical Society, 2011, 133, 14614-14628.	6.6	53
25	Paramagnetic relaxation enhancements in unfolded proteins: Theory and application to drkN SH3 domain. Protein Science, 2009, 18, 1401-1424.	3.1	50
26	A New Amide Proton R1Ï•Experiment Permits Accurate Characterization of Microsecond Time-scale Conformational Exchange. Journal of Biomolecular NMR, 2005, 32, 281-293.	1.6	47
27	Role of Electrostatic Interactions in Binding of Peptides and Intrinsically Disordered Proteins to Their Folded Targets. 1. NMR and MD Characterization of the Complex between the c-Crk N-SH3 Domain and the Peptide Sos. Biochemistry, 2014, 53, 6473-6495.	1.2	46
28	Domain orientation in beta-cyclodextrin-loaded maltose binding protein: diffusion anisotropy measurements confirm the results of a dipolar coupling study. Journal of Biomolecular NMR, 2001, 20, 83-88.	1.6	40
29	Assessment of molecular structure using frame-independent orientational restraints derived from residual dipolar couplings. Journal of Biomolecular NMR, 2000, 18, 239-252.	1.6	37
30	Observation ofÂÎ¼s time-scale protein dynamics in the presence of Ln3+ ions: application to the N-terminal domain of cardiac troponin C. Journal of Biomolecular NMR, 2007, 37, 79-95.	1.6	34
31	CP-HISQC: a better version of HSQC experiment for intrinsically disordered proteins under physiological conditions. Journal of Biomolecular NMR, 2014, 58, 175-192.	1.6	34
32	Onset of disorder and protein aggregation due to oxidation-induced intermolecular disulfide bonds: case study of RRM2 domain from TDP-43. Scientific Reports, 2017, 7, 11161.	1.6	31
33	What Drives 15N Spin Relaxation in Disordered Proteins? Combined NMR/MD Study of the H4 Histone Tail. Biophysical Journal, 2018, 115, 2348-2367.	0.2	26
34	Histone H4 Tails in Nucleosomes: a Fuzzy Interaction with DNA. Angewandte Chemie - International Edition, 2021, 60, 6480-6487.	7.2	24
35	Ensemble MD simulations restrained via crystallographic data: Accurate structure leads to accurate dynamics. Protein Science, 2014, 23, 488-507.	3.1	22
36	Relative Orientation of Peptide Planes in Proteins Is Reflected in Carbonylâ^'Carbonyl Chemical Shift Anisotropy Cross-Correlated Spin Relaxation. Journal of the American Chemical Society, 2000, 122, 7059-7071.	6.6	21

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37	Proton-decoupled CPMG: A better experiment for measuring 15N R2 relaxation in disordered proteins. Journal of Magnetic Resonance, 2014, 241, 155-169.	1.2	21
38	Domain cooperativity in multidomain proteins: what can we learn from molecular alignment in anisotropic media?. Journal of Biomolecular NMR, 2011, 51, 131-150.	1.6	19
39	Role of Electrostatic Interactions in Binding of Peptides and Intrinsically Disordered Proteins to Their Folded Targets: 2. The Model of Encounter Complex Involving the Double Mutant of the c-Crk N-SH3 Domain and Peptide Sos. Biochemistry, 2016, 55, 1784-1800.	1.2	16
40	A method for incorporating dipolar couplings into structure calculations in cases of (near) axial symmetry of alignment. Journal of Biomolecular NMR, 2000, 18, 183-188.	1.6	15
41	Estimating the Accuracy of Protein Structures using Residual Dipolar Couplings. Journal of Biomolecular NMR, 2005, 33, 83-93.	1.6	15
42	Calculations of the Contribution of Ring Currents to the Chemical Shielding Anisotropy. Journal of the American Chemical Society, 2002, 124, 1832-1833.	6.6	12
43	A New Spin Probe of Protein Dynamics:Â Nitrogen Relaxation in15Nâ˜'2H Amide Groups. Journal of the American Chemical Society, 2005, 127, 3220-3229.	6.6	12
44	Detection of nanosecond time scale side-chain jumps in a protein dissolved in water/glycerol solvent. Journal of Biomolecular NMR, 2009, 45, 57-72.	1.6	11
45	Microsecond time-scale dynamics from relaxation in the rotating frame: experiments using spin lock with alternating phase. Journal of Magnetic Resonance, 2004, 169, 164-173.	1.2	10
46	A new structural arrangement in proteins involving lysine NH3 + group and carbonyl. Scientific Reports, 2017, 7, 16402.	1.6	10
47	Simple MD-based model for oxidative folding of peptides and proteins. Scientific Reports, 2017, 7, 9293.	1.6	7
48	Very large residual dipolar couplings from deuterated ubiquitin. Journal of Biomolecular NMR, 2012, 54, 53-67.	1.6	6
49	Structural and dynamic origins of ESR lineshapes in spin-labeled GB1 domain: the insights from spin dynamics simulations based on long MD trajectories. Scientific Reports, 2020, 10, 957.	1.6	6
50	Insights into Ubiquitin Product Release in Hydrolysis Catalyzed by the Bacterial Deubiquitinase SdeA. Biochemistry, 2021, 60, 584-596.	1.2	4
51	Modeling a unit cell: crystallographic refinement procedure using the biomolecular MD simulation platform Amber. IUCrJ, 2022, 9, 114-133.	1.0	4
52	Molecular Dynamics model of peptide-protein conjugation: case study of covalent complex between Sos1 peptide and N-terminal SH3 domain from Grb2. Scientific Reports, 2019, 9, 20219.	1.6	3
53	The Role of Rotational Motion in Diffusion NMR Experiments on Supramolecular Assemblies: Application to Sup35NM Fibrils. Angewandte Chemie - International Edition, 2021, 60, 15445-15451.	7.2	3
54	Introducing color into stacking gels makes sample loading easy. Analytical Biochemistry, 2007, 366, 111-112.	1.1	2

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55	Histone H4 Tails in Nucleosomes: a Fuzzy Interaction with DNA. Angewandte Chemie, 2021, 133, 6554-6561.	1.6	1
56	Selective On-Resonance N.M.R. Irradiation of a Dipolar Double.. Australian Journal of Chemistry, 2000, 53, 355.	0.5	1
57	Interview with Robert Tycko: On amyloids, Alzheimer disease, and solid-state NMR. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2015, 44, 182-189.	0.2	0
58	Interview with David A. Case: On force fields, biomolecular modeling, and NMR. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2016, 45A, e21403.	0.2	0
59	How Accurate are Pre-Derived Distances? Combined MD and Experimental Study of Spin-Labeled GB1 Domain. Biophysical Journal, 2021, 120, 76a-77a.	0.2	0
60	How Effective are Retro-Inverso Peptides? Insights from MD Supported by Paramagnetic NMR Data. Biophysical Journal, 2021, 120, 81a.	0.2	0
61	The Role of Rotational Motion in Diffusion NMR Experiments on Supramolecular Assemblies: Application to Sup35NM Fibrils. Angewandte Chemie, 2021, 133, 15573-15579.	1.6	0
62	Toward a proper interpretation of hydrogen exchange data in disordered proteins. Biophysical Journal, 2021, 120, 3855-3856.	0.2	0