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	Modeling a unit cell: crystallographic refinement procedure using the biomolecular MD simulation platform Amber. IUCrJ, 2022, 9, 114-133.	1.0	4
2	Histone H4 Tails in Nucleosomes: a Fuzzy Interaction with DNA. Angewandte Chemie, 2021, 133, 6554-6561.	1.6	1
3	Histone H4 Tails in Nucleosomes: a Fuzzy Interaction with DNA. Angewandte Chemie - International Edition, 2021, 60, 6480-6487.	7.2	24
4	Insights into Ubiquitin Product Release in Hydrolysis Catalyzed by the Bacterial Deubiquitinase SdeA. Biochemistry, 2021, 60, 584-596.	1.2	4
5	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
6	How Effective are Retro-Inverso Peptides? Insights from MD Supported by Paramagnetic NMR Data. Biophysical Journal, 2021, 120, 81a.	0.2	0
7	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
8	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
9	Toward a proper interpretation of hydrogen exchange data in disordered proteins. Biophysical Journal, 2021, 120, 3855-3856.	0.2	0
10	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
11	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
12	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
13	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
14	Simple MD-based model for oxidative folding of peptides and proteins. Scientific Reports, 2017, 7, 9293.	1.6	7
15	Slow conformational exchange and overall rocking motion in ubiquitin protein crystals. Nature Communications, 2017, 8, 145.	5.8	78
16	A new structural arrangement in proteins involving lysine NH3 + group and carbonyl. Scientific Reports, 2017, 7, 16402.	1.6	10
17	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
18	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

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19	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
20	Observing the overall rocking motion of a protein in a crystal. Nature Communications, 2015, 6, 8361.	5.8	67
21	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
22	Ensemble MD simulations restrained via crystallographic data: Accurate structure leads to accurate dynamics. Protein Science, 2014, 23, 488-507.	3.1	22
23	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
24	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
25	Very large residual dipolar couplings from deuterated ubiquitin. Journal of Biomolecular NMR, 2012, 54, 53-67.	1.6	6
26	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
27	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
28	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
29	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
30	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
31	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
32	Paramagnetic relaxation enhancements in unfolded proteins: Theory and application to drkN SH3 domain. Protein Science, 2009, 18, 1401-1424.	3.1	50
33	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
34	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
35	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
36	Introducing color into stacking gels makes sample loading easy. Analytical Biochemistry, 2007, 366, 111-112.	1.1	2

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37	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
38	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
39	Structural Determinants for High-Affinity Binding in a Nedd4 WW3â^— Domain-Comm PY Motif Complex. Structure, 2006, 14, 543-553.	1.6	77
40	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
41	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
42	Estimating the Accuracy of Protein Structures using Residual Dipolar Couplings. Journal of Biomolecular NMR, 2005, 33, 83-93.	1.6	15
43	Comparison of 13CH3, 13CH2D, and 13CHD2 methyl labeling strategies in proteins. Journal of Biomolecular NMR, 2005, 33, 25-41.	1.6	59
44	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
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	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
47	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
48	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
49	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
50	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
51	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
52	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
53	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
54	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

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55	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
56	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
57	Slow Dynamics in Folded and Unfolded States of an SH3 Domain. Journal of the American Chemical Society, 2001, 123, 11341-11352.	6.6	454
58	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
59	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
60	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
61	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
62	Selective On-Resonance N.M.R. Irradiation of a Dipolar Double.. Australian Journal of Chemistry, 2000, 53, 355.	0.5	1