Alexander Grishaev

List of Publications by Year
in descending order

29	1,629	394421 19	454955 30
papers	citations	h-index	g-index

32	32	32	1978
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Conformational heterogeneity of UCAAUC RNA oligonucleotide from molecular dynamics simulations, SAXS, and NMR experiments. Rna, 2022, 28, 937-946.	3.5	11
2	Chemical shifts-based similarity restraints improve accuracy of RNA structures determined via NMR. Rna, 2020, 26, 2051-2061.	3.5	4
3	Accuracy of MD solvent models in RNA structure refinement assessed via liquid-crystal NMR and spin relaxation data. Journal of Structural Biology, 2019, 207, 250-259.	2.8	7
4	Maximizing accuracy of RNA structure in refinement against residual dipolar couplings. Journal of Biomolecular NMR, 2019, 73, 117-139.	2.8	7
5	Prediction of nearest neighbor effects on backbone torsion angles and NMR scalar coupling constants in disordered proteins. Protein Science, 2018, 27, 146-158.	7.6	24
6	Comment on â€œInnovative scattering analysis shows that hydrophobic disordered proteins are expanded in waterâ€. Science, 2018, 361, .	12.6	36
7	PAGE4 and Conformational Switching: Insights from Molecular Dynamics Simulations and Implications for Prostate Cancer. Journal of Molecular Biology, 2018, 430, 2422-2438.	4.2	36
8	Phosphorylation-induced conformational dynamics in an intrinsically disordered protein and potential role in phenotypic heterogeneity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2644-E2653.	7.1	72
9	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. Journal of the American Chemical Society, 2016, 138, 11702-11713.	13.7	121
10	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. Journal of the American Chemical Society, 2016, 138, 11714-11726.	13.7	171
11	Quantitative Characterization of Configurational Space Sampled by HIVâ€1 Nucleocapsid Using Solution NMR, Xâ€ray Scattering and Protein Engineering. ChemPhysChem, 2016, 17, 1548-1552.	2.1	16
12	Dissociation of glucocerebrosidase dimer in solution by its co-factor, saposin C. Biochemical and Biophysical Research Communications, 2015, 457, 561-566.	2.1	19
13	Large interdomain rearrangement triggered by suppression of micro- to millisecond dynamics in bacterial Enzyme I. Nature Communications, 2015, 6, 5960.	12.8	33
14	Dynamic equilibrium between closed and partially closed states of the bacterial Enzyme I unveiled by solution NMR and X-ray scattering. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11565-11570.	7.1	28
15	Structural Basis of hAT Transposon End Recognition by Hermes, an Octameric DNA Transposase from Musca domestica. Cell, 2014, 158, 353-367.	28.9	63
16	Imino Hydrogen Positions in Nucleic Acids from Density Functional Theory Validated by NMR Residual Dipolar Couplings. Journal of the American Chemical Society, 2012, 134, 6956-6959.	13.7	2
17	Contrast-Matched Small-Angle X-ray Scattering from a Heavy-Atom-Labeled Protein in Structure Determination: Application to a Lead-Substituted Calmodulinâ€“Peptide Complex. Journal of the American Chemical Society, 2012, 134, 14686-14689.	13.7	38
18	Sample Preparation, Data Collection, and Preliminary Data Analysis in Biomolecular Solution Xâ€Ray Scattering. Current Protocols in Protein Science, 2012, 70, Unit17.14.	2.8	27

#	Article	IF	Citations
19	Improved Fitting of Solution X-ray Scattering Data to Macromolecular Structures and Structural Ensembles by Explicit Water Modeling. Journal of the American Chemical Society, 2010, 132, 15484-15486.	13.7	120
20	Chemical Shift Anisotropy of Imino ¹⁵N Nuclei in Watsonâ^'Crick Base Pairs from Magic Angle Spinning Liquid Crystal NMR and Nuclear Spin Relaxation. Journal of the American Chemical Society, 2009, 131, 9490-9491.	13.7	24
21	Solution structure of tRNAVal from refinement of homology model against residual dipolar coupling and SAXS data. Journal of Biomolecular NMR, 2008, 42, 99-109.	2.8	74
22	Magnetic field induced residual dipolar couplings of imino groups in nucleic acids from measurements at a single magnetic field. Journal of Biomolecular NMR, 2007, 39, 91-96.	2.8	18
23	Pseudo-CSA Restraints for NMR Refinement of Nucleic Acid Structure. Journal of the American Chemical Society, 2006, 128, 10010-10011.	13.7	15
24	Chemical Shift Tensors of Protonated Base Carbons in Helical RNA and DNA from NMR Relaxation and Liquid Crystal Measurements. Journal of the American Chemical Society, 2006, 128, 11443-11454.	13.7	42
25	Carbon-13 chemical shift anisotropy in DNA bases from field dependence of solution NMR relaxation rates. Magnetic Resonance in Chemistry, 2006, 44, 302-310.	1.9	16
26	Weak alignment NMR: a hawk-eyed view of biomolecular structure. Current Opinion in Structural Biology, 2005, 15, 563-570.	5.7	246
27	Refinement of Multidomain Protein Structures by Combination of Solution Small-Angle X-ray Scattering and NMR Data. Journal of the American Chemical Society, 2005, 127, 16621-16628.	13.7	208
28	Measurement of Ribose Carbon Chemical Shift Tensors for A-form RNA by Liquid Crystal NMR Spectroscopy. Journal of the American Chemical Society, 2005, 127, 7387-7396.	13.7	29
29	An Empirical Backboneâ^'Backbone Hydrogen-Bonding Potential in Proteins and Its Applications to NMR Structure Refinement and Validation. Journal of the American Chemical Society, 2004, 126, 7281-7292.	13.7	115