

Alexander Grishaev

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6867995/publications.pdf>

Version: 2024-02-01

29
papers

1,629
citations

394421

19
h-index

454955

30
g-index

32
all docs

32
docs citations

32
times ranked

1978
citing authors

#	ARTICLE	IF	CITATIONS
1	Weak alignment NMR: a hawk-eyed view of biomolecular structure. <i>Current Opinion in Structural Biology</i> , 2005, 15, 563-570.	5.7	246
2	Refinement of Multidomain Protein Structures by Combination of Solution Small-Angle X-ray Scattering and NMR Data. <i>Journal of the American Chemical Society</i> , 2005, 127, 16621-16628.	13.7	208
3	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. <i>Journal of the American Chemical Society</i> , 2016, 138, 11714-11726.	13.7	171
4	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. <i>Journal of the American Chemical Society</i> , 2016, 138, 11702-11713.	13.7	121
5	Improved Fitting of Solution X-ray Scattering Data to Macromolecular Structures and Structural Ensembles by Explicit Water Modeling. <i>Journal of the American Chemical Society</i> , 2010, 132, 15484-15486.	13.7	120
6	An Empirical Backbone ¹⁵ N Backbone Hydrogen-Bonding Potential in Proteins and Its Applications to NMR Structure Refinement and Validation. <i>Journal of the American Chemical Society</i> , 2004, 126, 7281-7292.	13.7	115
7	Solution structure of tRNA ^{Val} from refinement of homology model against residual dipolar coupling and SAXS data. <i>Journal of Biomolecular NMR</i> , 2008, 42, 99-109.	2.8	74
8	Phosphorylation-induced conformational dynamics in an intrinsically disordered protein and potential role in phenotypic heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2644-E2653.	7.1	72
9	Structural Basis of hAT Transposon End Recognition by Hermes, an Octameric DNA Transposase from <i>Musca domestica</i> . <i>Cell</i> , 2014, 158, 353-367.	28.9	63
10	Chemical Shift Tensors of Protonated Base Carbons in Helical RNA and DNA from NMR Relaxation and Liquid Crystal Measurements. <i>Journal of the American Chemical Society</i> , 2006, 128, 11443-11454.	13.7	42
11	Contrast-Matched Small-Angle X-ray Scattering from a Heavy-Atom-Labeled Protein in Structure Determination: Application to a Lead-Substituted Calmodulin ¹⁵ N Peptide Complex. <i>Journal of the American Chemical Society</i> , 2012, 134, 14686-14689.	13.7	38
12	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , 2018, 361, .	12.6	36
13	PAGE4 and Conformational Switching: Insights from Molecular Dynamics Simulations and Implications for Prostate Cancer. <i>Journal of Molecular Biology</i> , 2018, 430, 2422-2438.	4.2	36
14	Large interdomain rearrangement triggered by suppression of micro- to millisecond dynamics in bacterial Enzyme I. <i>Nature Communications</i> , 2015, 6, 5960.	12.8	33
15	Measurement of Ribose Carbon Chemical Shift Tensors for A-form RNA by Liquid Crystal NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2005, 127, 7387-7396.	13.7	29
16	Dynamic equilibrium between closed and partially closed states of the bacterial Enzyme I unveiled by solution NMR and X-ray scattering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11565-11570.	7.1	28
17	Sample Preparation, Data Collection, and Preliminary Data Analysis in Biomolecular Solution X-ray Scattering. <i>Current Protocols in Protein Science</i> , 2012, 70, Unit17.14.	2.8	27
18	Chemical Shift Anisotropy of Imino ¹⁵ N Nuclei in Watson ³ Crick Base Pairs from Magic Angle Spinning Liquid Crystal NMR and Nuclear Spin Relaxation. <i>Journal of the American Chemical Society</i> , 2009, 131, 9490-9491.	13.7	24

#	ARTICLE	IF	CITATIONS
19	Prediction of nearest neighbor effects on backbone torsion angles and NMR scalar coupling constants in disordered proteins. <i>Protein Science</i> , 2018, 27, 146-158.	7.6	24
20	Dissociation of glucocerebrosidase dimer in solution by its co-factor, saposin C. <i>Biochemical and Biophysical Research Communications</i> , 2015, 457, 561-566.	2.1	19
21	Magnetic field induced residual dipolar couplings of imino groups in nucleic acids from measurements at a single magnetic field. <i>Journal of Biomolecular NMR</i> , 2007, 39, 91-96.	2.8	18
22	Carbon-13 chemical shift anisotropy in DNA bases from field dependence of solution NMR relaxation rates. <i>Magnetic Resonance in Chemistry</i> , 2006, 44, 302-310.	1.9	16
23	Quantitative Characterization of Configurational Space Sampled by HIV-1 Nucleocapsid Using Solution NMR, X-ray Scattering and Protein Engineering. <i>ChemPhysChem</i> , 2016, 17, 1548-1552.	2.1	16
24	Pseudo-CSA Restraints for NMR Refinement of Nucleic Acid Structure. <i>Journal of the American Chemical Society</i> , 2006, 128, 10010-10011.	13.7	15
25	Conformational heterogeneity of UCAAUC RNA oligonucleotide from molecular dynamics simulations, SAXS, and NMR experiments. <i>Rna</i> , 2022, 28, 937-946.	3.5	11
26	Accuracy of MD solvent models in RNA structure refinement assessed via liquid-crystal NMR and spin relaxation data. <i>Journal of Structural Biology</i> , 2019, 207, 250-259.	2.8	7
27	Maximizing accuracy of RNA structure in refinement against residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2019, 73, 117-139.	2.8	7
28	Chemical shifts-based similarity restraints improve accuracy of RNA structures determined via NMR. <i>Rna</i> , 2020, 26, 2051-2061.	3.5	4
29	Imino Hydrogen Positions in Nucleic Acids from Density Functional Theory Validated by NMR Residual Dipolar Couplings. <i>Journal of the American Chemical Society</i> , 2012, 134, 6956-6959.	13.7	2