Nico Tjandra

List of Publications by Year
in descending order

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89 papers	10,162 citations	126907 33 h-index	54911 84 g-index
92 all docs	92 docs citations	92 times ranked	8847 citing authors

#	Article	IF	Citations
1	Tsg101/ESCRT-I recruitment regulated by the dual binding modes of K63-linked diubiquitin. Structure, 2022, 30, 289-299.e6.	3.3	5
2	The fluorescent aptamer Squash extensively repurposes the adenine riboswitch fold. Nature Chemical Biology, 2022, 18, 191-198.	8.0	12
3	Incorporation of residual chemical shift anisotropy into the treatment of 15N pseudocontact shifts for structural refinement. Journal of Magnetic Resonance, 2022, 340, 107213.	2.1	1
4	Simultaneous measurement of 1HC/N-R2â€²s for rapid acquisition of backbone and sidechain paramagnetic relaxation enhancements (PREs) in proteins. Journal of Biomolecular NMR, 2021, 75, 109-118.	2.8	0
5	Inducible foldâ€switching as a mechanism to fibrillate proâ€apoptotic BCL â€2 proteins. Biopolymers, 2021, 112, e23424.	2.4	2
6	Novel Tsg101 Binding Partners Regulate Viral L Domain Trafficking. Viruses, 2021, 13, 1147.	3.3	7
7	Prazoles Targeting Tsg101 Inhibit Release of Epstein-Barr Virus following Reactivation from Latency. Journal of Virology, 2021, 95, e0246620.	3.4	9
8	Structural Basis for the Interaction of Fibrin with the Very Low-Density Lipoprotein Receptor Revealed by NMR and Site-Directed Mutagenesis. Biochemistry, 2021, 60, 2537-2548.	2.5	2
9	Bax expression is optimal at low oxygen tension and constant agitation. Protein Expression and Purification, 2020, 165, 105501.	1.3	7
10	Structural basis for polyglutamate chain initiation and elongation by TTLL family enzymes. Nature Structural and Molecular Biology, 2020, 27, 802-813.	8.2	35
11	Humanin selectively prevents the activation of pro-apoptotic protein BID by sequestering it into fibers. Journal of Biological Chemistry, 2020, 295, 18226-18238.	3.4	16
12	Selective Targeting of Virus Replication by Proton Pump Inhibitors. Scientific Reports, 2020, 10, 4003.	3.3	31
13	Squeezing lipids: NMR characterization of lipoprotein particles under pressure. Chemistry and Physics of Lipids, 2020, 228, 104874.	3.2	3
14	RNA Binding Suppresses Tsg101 Recognition of Ub-Modified Gag and Facilitates Recruitment to the Plasma Membrane. Viruses, 2020, 12, 447.	3.3	6
15	The Kindlin Outside Connection. Structure, 2019, 27, 1615-1616.	3.3	0
16	Comparison of Solution Properties of Polymethylated DOTA-like Lanthanide Complexes with Opposite Chirality of the Pendant Arms. Inorganic Chemistry, 2019, 58, 15788-15800.	4.0	7
17	NMR Analysis of Apo Glutamineâ€Binding Protein Exposes Challenges in the Study of Interdomain Dynamics. Angewandte Chemie - International Edition, 2019, 58, 16899-16902.	13.8	10
18	Potential Regulatory Role of Competitive Encounter Complexes in Paralogous Phosphotransferase Systems. Journal of Molecular Biology, 2019, 431, 2331-2342.	4.2	8

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19	Model of a Kinetically Driven Crosstalk between Paralogous Protein Encounter Complexes. Biophysical Journal, 2019, 117, 1655-1665.	0.5	6
20	Humanin induces conformational changes in the apoptosis regulator BAX and sequesters it into fibers, preventing mitochondrial outer-membrane permeabilization. Journal of Biological Chemistry, 2019, 294, 19055-19065.	3.4	27
21	NMR Analysis of Apo Glutamineâ€Binding Protein Exposes Challenges in the Study of Interdomain Dynamics. Angewandte Chemie, 2019, 131, 17055-17058.	2.0	0
22	Long-Range RNA Structural Information via a Paramagnetically Tagged Reporter Protein. Journal of the American Chemical Society, 2019, 141, 1430-1434.	13.7	16
23	Solvent saturation transfer to proteins (SSTP) for structural and functional characterization of proteins. Journal of Biomolecular NMR, 2018, 70, 11-20.	2.8	3
24	The Structure of Melanoregulin Reveals a Role for Cholesterol Recognition in the Protein's Ability to Promote Dynein Function. Structure, 2018, 26, 1373-1383.e4.	3.3	6
25	Nuclear Magnetic Resonance Solution Structure of the Recombinant Fragment Containing Three Fibrin-Binding Cysteine-Rich Domains of the Very Low Density Lipoprotein Receptor. Biochemistry, 2018, 57, 4395-4403.	2.5	7
26	Conformational Ensemble of Disordered Proteins Probed by Solvent Paramagnetic Relaxation Enhancement (sPRE). Angewandte Chemie, 2018, 130, 13707-13710.	2.0	5
27	Conformational Ensemble of Disordered Proteins Probed by Solvent Paramagnetic Relaxation Enhancement (sPRE). Angewandte Chemie - International Edition, 2018, 57, 13519-13522.	13.8	28
28	Residual Dipolar Coupling for Conformational and Dynamic Studies. , 2018, , 419-434.		0
29	Sirt1 carboxyl-domain is an ATP-repressible domain that is transferrable to other proteins. Nature Communications, 2017, 8, 15560.	12.8	24
30	Flexible IgE epitope-containing domains of Phl p 5 cause high allergenic activity. Journal of Allergy and Clinical Immunology, 2017, 140, 1187-1191.	2.9	19
31	Conformational Heterogeneity in the Activation Mechanism of Bax. Structure, 2017, 25, 1310-1316.e3.	3.3	7
32	Tsg101 chaperone function revealed by HIV-1 assembly inhibitors. Nature Communications, 2017, 8, 1391.	12.8	37
33	Residual Dipolar Coupling for Conformational and Dynamic Studies. , 2017, , 1-16.		0
34	Structure of the NPr:EINNtr Complex: Mechanism for Specificity in Paralogous Phosphotransferase Systems. Structure, 2016, 24, 2127-2137.	3.3	16
35	Characterizing the magnetic susceptibility tensor of lanthanide-containing polymethylated-DOTA complexes. Journal of Biomolecular NMR, 2016, 66, 125-139.	2.8	23
36	Increasing the Chemicalâ€Shift Dispersion of Unstructured Proteins with a Covalent Lanthanide Shift Reagent. Angewandte Chemie - International Edition, 2016, 55, 14847-14851.	13.8	29

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37	Bcl-2 proteins bid and bax form a network to permeabilize the mitochondria at the onset of apoptosis. Cell Death and Disease, 2016, 7, e2424-e2424.	6.3	49
38	Verbesserung der Dispersion der chemischen Verschiebungen von unstrukturierten Proteinen durch einen kovalent gebundenen Lanthanoidkomplex. Angewandte Chemie, 2016, 128, 15069-15073.	2.0	1
39	Analysis of the isomer ratios of polymethylated-DOTA complexes and the implications on protein structural studies. Dalton Transactions, 2016, 45, 4673-4687.	3.3	38
40	Characterization of the membrane-inserted C-terminus of cytoprotective BCL-XL. Protein Expression and Purification, 2016, 122, 56-63.	1.3	22
41	Acquiring snapshots of the orientation of transâ€membrane protein domains using a hybrid FRET pair. FEBS Letters, 2015, 589, 885-889.	2.8	4
42	Exploiting image registration for automated resonance assignment in NMR. Journal of Biomolecular NMR, 2015, 62, 143-156.	2.8	1
43	Structure of Transmembrane Domain of Lysosome-associated Membrane Protein Type 2a (LAMP-2A) Reveals Key Features for Substrate Specificity in Chaperone-mediated Autophagy. Journal of Biological Chemistry, 2014, 289, 35111-35123.	3.4	63
44	Conformational Rearrangements in the Pro-apoptotic Protein, Bax, as It Inserts into Mitochondria. Journal of Biological Chemistry, 2014, 289, 32871-32882.	3.4	61
45	Decoding the components of dynamics in threeâ€domain proteins. Journal of Computational Chemistry, 2014, 35, 518-525.	3.3	2
46	Single color FRET based measurements of conformational changes of proteins resulting from translocation inside cells. Methods, 2014, 66, 180-187.	3.8	9
47	Structural Insights of tBid, the Caspase-8-activated Bid, and Its BH3 Domain. Journal of Biological Chemistry, 2013, 288, 35840-35851.	3.4	59
48	Structural mechanism of Bax inhibition by cytomegalovirus protein vMIA. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20901-20906.	7.1	53
49	Parameterization of solventâ€“protein interaction and its use on NMR protein structure determination. Journal of Magnetic Resonance, 2012, 221, 76-84.	2.1	31
50	Application of Solution NMR Spectroscopy to Study Protein Dynamics. Entropy, 2012, 14, 581-598.	2.2	20
51	Estimation of Interdomain Flexibility of N-Terminus of Factor H Using Residual Dipolar Couplings. Biochemistry, 2011, 50, 8138-8149.	2.5	26
52	Bcl-xL Retrotranslocates Bax from the Mitochondria into the Cytosol. Cell, 2011, 145, 104-116.	28.9	512
53	The Use of Residual Dipolar Coupling in Studying Proteins by NMR. Topics in Current Chemistry, 2011, 326, 47-67.	4.0	100
54	A practical implementation of cross-spectrum in protein backbone resonance assignment. Journal of Magnetic Resonance, 2010, 203, 208-212.	2.1	8

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55	Determination of the Solution-Bound Conformation of an Amino Acid Binding Protein by NMR Paramagnetic Relaxation Enhancement: Use of a Single Flexible Paramagnetic Probe with Improved Estimation of Its Sampling Space. Journal of the American Chemical Society, 2009, 131, 9532-9537.	13.7	32
56	BAX activation is initiated at a novel interaction site. Nature, 2008, 455, 1076-1081.	27.8	617
57	Extended Model Free Approach To Analyze Correlation Functions of Multidomain Proteins in the Presence of Motional Coupling. Journal of the American Chemical Society, 2008, 130, 12745-12751.	13.7	24
58	Residue-Specific13Câ€˜ CSA Tensor Principal Components for Ubiquitin:Â Correlation between Tensor Components and Hydrogen Bonding. Journal of the American Chemical Society, 2007, 129, 1321-1326.	13.7	20
59	Refinement of protein structure against non-redundant carbonyl 13C NMR relaxation. Journal of Biomolecular NMR, 2007, 38, 243-253.	2.8	4
60	Top-down approach in protein RDC data analysis: de novo estimation of the alignment tensor. Journal of Biomolecular NMR, 2007, 38, 303-313.	2.8	6
61	Determination of the residue-specific 15N CSA tensor principal components using multiple alignment media. Journal of Biomolecular NMR, 2006, 35, 249-259.	2.8	14
62	Residual Dipolar Couplings in NMR Structure Analysis. Annual Review of Biophysics and Biomolecular Structure, 2004, 33, 387-413.	18.3	193
63	Backbone15N relaxation analysis of the N-terminal domain of the HTLV-I capsid protein and comparison with the capsid protein of HIV-1. Protein Science, 2003, 12, 973-981.	7.6	7
64	The Xplor-NIH NMR molecular structure determination package. Journal of Magnetic Resonance, 2003, 160, 65-73.	2.1	2,165
65	15N chemical shift anisotropy in protein structure refinement and comparison with NH residual dipolar couplings. Journal of Magnetic Resonance, 2003, 164, 171-176.	2.1	41
66	Temperature Dependence of Domain Motions of Calmodulin Probed by NMR Relaxation at Multiple Fields. Journal of the American Chemical Society, 2003, 125, 11379-11384.	13.7	68
67	NMR dipolar couplings for the structure determination of biopolymers in solution. Progress in Nuclear Magnetic Resonance Spectroscopy, 2002, 40, 175-197.	7.5	145
68	Dipolar Couplings in Macromolecular Structure Determination. Methods in Enzymology, 2001, 339, 127-174.	1.0	388
69	Analysis of Slow Interdomain Motion of Macromolecules Using NMR Relaxation Data. Journal of the American Chemical Society, 2001, 123, 3953-3959.	13.7	130
70	Analysis of NMR Relaxation Data of Biomolecules with Slow Domain Motions Using Wobble-in-a-Cone Approximation. Journal of the American Chemical Society, 2001, 123, 11484-11485.	13.7	22
71	Carbonyl CSA Restraints from Solution NMR for Protein Structure Refinement. Journal of the American Chemical Society, 2001, 123, 11065-11066.	13.7	44
72	Simple multidimensional NMR experiments to obtain different types of one-bond dipolar couplings simultaneously. Journal of Biomolecular NMR, 2001, 19, 63-67.	2.8	19

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73	Structure of Bax. Cell, 2000, 103, 645-654.	28.9	1,008
74	An Approach to Direct Determination of Protein Dynamics from15N NMR Relaxation at Multiple Fields, Independent of Variable15N Chemical Shift Anisotropy and Chemical Exchange Contributions. Journal of the American Chemical Society, 1999, 121, 8577-8582.	13.7	84
75	The use of dipolar couplings for determining the solution structure of rat apoâ€S100B(Î²Î²). Protein Science, 1999, 8, 800-809.	7.6	77
76	Determining the Magnitude of the Fully Asymmetric Diffusion Tensor from Heteronuclear Relaxation Data in the Absence of Structural Information. Journal of the American Chemical Society, 1998, 120, 4889-4890.	13.7	59
77	Direct Measurement of15N Chemical Shift Anisotropy in Solution. Journal of the American Chemical Society, 1998, 120, 10947-10952.	13.7	154
78	Solution NMR Measurement of Amide Proton Chemical Shift Anisotropy in 15N-Enriched Proteins. Correlation with Hydrogen Bond Length. Journal of the American Chemical Society, 1997, 119, 8076-8082.	13.7	134
79	Are proteins even floppier than we thought?. Nature Structural Biology, 1997, 4, 254-256.	9.7	43
80	Defining long range order in NMR structure determination from the dependence of heteronuclear relaxation times on rotational diffusion anisotropy. Nature Structural Biology, 1997, 4, 443-449.	9.7	174
81	Use of dipolar 1Hâ€“15N and 1Hâ€“13C couplings in the structure determination of magnetically oriented macromolecules in solution. Nature Structural Biology, 1997, 4, 732-738.	9.7	456
82	High-resolution heteronuclear NMR of human ubiquitin in an aqueous liquid crystalline medium. Journal of Biomolecular NMR, 1997, 10, 289-292.	2.8	176
83	Refined solution structure and backbone dynamics of HIVâ€1 Nef. Protein Science, 1997, 6, 1248-1263.	7.6	146
84	Magnetic Field Dependence of Nitrogenâ^'ProtonJSplittings in15N-Enriched Human Ubiquitin Resulting from Relaxation Interference and Residual Dipolar Coupling. Journal of the American Chemical Society, 1996, 118, 6264-6272.	13.7	318
85	Protein Backbone Dynamics and15N Chemical Shift Anisotropy from Quantitative Measurement of Relaxation Interference Effects. Journal of the American Chemical Society, 1996, 118, 6986-6991.	13.7	317
86	Anisotropic rotational diffusion of perdeuterated HIV protease from 15N NMR relaxation measurements at two magnetic fields. Journal of Biomolecular NMR, 1996, 8, 273-284.	2.8	236
87	Solution structure of calcium-free calmodulin. Nature Structural and Molecular Biology, 1995, 2, 768-776.	8.2	677
88	Rotational diffusion anisotropy of human ubiquitin from 15N NMR relaxation. Journal of the American Chemical Society, 1995, 117, 12562-12566.	13.7	678
89	Rotational Dynamics of Calciumâ€Free Calmodulin Studied by ¹⁵Nâ€NMR Relaxation Measurements. FEBS Journal, 1995, 230, 1014-1024.	0.2	8