

# Ashok Sekhar

## List of Publications by Year in descending order

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39  
papers

1,861  
citations

331670

21  
h-index

302126

39  
g-index

42  
all docs

42  
docs citations

42  
times ranked

1976  
citing authors

#	ARTICLE	IF	CITATIONS
1	Elucidating the mechanisms underlying protein conformational switching using NMR spectroscopy. <i>Journal of Magnetic Resonance Open</i> , 2022, 10-11, 100034.	1.1	2
2	Structure and Carbohydrate Recognition by the Nonmitogenic Lectin Horcolin. <i>Biochemistry</i> , 2022, 61, 464-478.	2.5	2
3	Quantification of Entropic Excluded Volume Effects Driving Crowding-Induced Collapse and Folding of a Disordered Protein. <i>Journal of Physical Chemistry Letters</i> , 2022, 13, 3112-3120.	4.6	4
4	Metamorphic proteins: the Janus proteins of structural biology. <i>Open Biology</i> , 2021, 11, 210012.	3.6	11
5	Measuring radiofrequency fields in NMR spectroscopy using offset-dependent nutation profiles. <i>Journal of Magnetic Resonance</i> , 2021, 330, 107032.	2.1	2
6	Characterizing Post-Translational Modifications and Their Effects on Protein Conformation Using NMR Spectroscopy. <i>Biochemistry</i> , 2020, 59, 57-73.	2.5	29
7	Engineering Order and Cooperativity in a Disordered Protein. <i>Biochemistry</i> , 2019, 58, 2389-2397.	2.5	10
8	An NMR View of Protein Dynamics in Health and Disease. <i>Annual Review of Biophysics</i> , 2019, 48, 297-319.	10.0	113
9	Effects of maturation on the conformational free-energy landscape of SOD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2546-E2555.	7.1	48
10	Measuring Diffusion Constants of Invisible Protein Conformers by Triple-Quantum <sup>1</sup> H CPMG Relaxation Dispersion. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16777-16780.	13.8	17
11	Measuring Diffusion Constants of Invisible Protein Conformers by Triple-Quantum <sup>1</sup> H CPMG Relaxation Dispersion. <i>Angewandte Chemie</i> , 2018, 130, 17019-17022.	2.0	5
12	Conserved conformational selection mechanism of Hsp70 chaperone-substrate interactions. <i>ELife</i> , 2018, 7, .	6.0	71
13	Self-Assembly of Human Profilin-1 Detected by Carr-Purcell-Meiboom-Gill Nuclear Magnetic Resonance (CPMG NMR) Spectroscopy. <i>Biochemistry</i> , 2017, 56, 692-703.	2.5	23
14	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. <i>Journal of Biomolecular NMR</i> , 2017, 67, 243-271.	2.8	123
15	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in <sup>1</sup> H-CEST. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 6122-6125.	13.8	35
16	Conformational heterogeneity in the Hsp70 chaperone-substrate ensemble identified from analysis of NMR-detected titration data. <i>Protein Science</i> , 2017, 26, 2207-2220.	7.6	19
17	A Universal Pattern in the Percolation and Dissipation of Protein Structural Perturbations. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 4779-4784.	4.6	39
18	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8194-E8203.	7.1	381

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19	An enhanced sensitivity methyl <sup>1</sup> H triple-quantum pulse scheme for measuring diffusion constants of macromolecules. <i>Journal of Biomolecular NMR</i> , 2017, 68, 249-255.	2.8	9
20	Separating Dipolar and Chemical Exchange Magnetization Transfer Processes in <sup>1</sup> H-CEST. <i>Angewandte Chemie</i> , 2017, 129, 6218-6221.	2.0	2
21	Promiscuous binding by Hsp70 results in conformational heterogeneity and fuzzy chaperone-substrate ensembles. <i>ELife</i> , 2017, 6, .	6.0	72
22	Hsp70 biases the folding pathways of client proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2794-801.	7.1	84
23	Evaluating the influence of initial magnetization conditions on extracted exchange parameters in NMR relaxation experiments: applications to CPMG and CEST. <i>Journal of Biomolecular NMR</i> , 2016, 65, 143-156.	2.8	6
24	Probing the free energy landscapes of ALS disease mutants of SOD1 by NMR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6939-E6945.	7.1	47
25	Evolution of magnetization due to asymmetric dimerization: theoretical considerations and application to aberrant oligomers formed by apoSOD1 <sup>2SH</sup> . <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 5720-5728.	2.8	8
26	Probing Invisible, Excited Protein States by Non-Uniformly Sampled Pseudo-4D CEST Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 10507-10511.	13.8	25
27	Mapping the conformation of a client protein through the Hsp70 functional cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10395-10400.	7.1	85
28	Heterogeneous binding of the SH3 client protein to the DnaK molecular chaperone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4206-15.	7.1	49
29	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. <i>ELife</i> , 2015, 4, e07296.	6.0	91
30	Triple resonance-based <sup>13</sup> C <sup>±</sup> and <sup>13</sup> C <sup>2</sup> CEST experiments for studies of ms timescale dynamics in proteins. <i>Journal of Biomolecular NMR</i> , 2014, 60, 203-208.	2.8	28
31	Understanding the mechanism of proteasome 20S core particle gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5532-5537.	7.1	46
32	Viscosity-Dependent Kinetics of Protein Conformational Exchange: Microviscosity Effects and the Need for a Small Viscogen. <i>Journal of Physical Chemistry B</i> , 2014, 118, 4546-4551.	2.6	24
33	Defining a length scale for millisecond-timescale protein conformational exchange. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11391-11396.	7.1	29
34	NMR paves the way for atomic level descriptions of sparsely populated, transiently formed biomolecular conformers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12867-12874.	7.1	230
35	Folding of the four-helix bundle FF domain from a compact on-pathway intermediate state is governed predominantly by water motion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19268-19273.	7.1	17
36	Protein folding rates and thermodynamic stability are key determinants for interaction with the Hsp70 chaperone system. <i>Protein Science</i> , 2012, 21, 1489-1502.	7.6	18

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37	Transient interactions of a slowâ€folding protein with the Hsp70 chaperone machinery. <i>Protein Science</i> , 2012, 21, 1042-1055.	7.6	20
38	EPIC- and CHANCE-HSQC: Two <sup>15</sup> N-photo-CIDNP-enhanced pulse sequences for the sensitive detection of solvent-exposed tryptophan. <i>Journal of Magnetic Resonance</i> , 2009, 200, 207-213.	2.1	16
39	<sup>1</sup> H Photo-CIDNP Enhancements in Heteronuclear Correlation NMR Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2009, 113, 8310-8318.	2.6	13