RamakrishnaÂ V Hosur

List of Publications by Year
in descending order

107 papers	1,546 citations	361413 20 h-index	395702 33 g-index
110 all docs	110 docs citations	110 times ranked	1316 citing authors

#	Article	IF	Citations
1	Targeting disorders in unstructured and structured proteins in various diseases. Biophysical Chemistry, 2022, 281, 106742.	2.8	11
2	Mahalanobis distance correlation: A novel approach for quantitating changes in multidimensional NMR spectra in biological applications. Journal of Magnetic Resonance, 2022, 337, 107165.	2.1	2
3	Ashwagandha-polyphenols-functionalized gold nanoparticles facilitate apoptosis by perturbing microtubule assembly dynamics in breast cancer cells. Journal of Drug Delivery Science and Technology, 2022, 70, 103225.	3.0	1
4	Triphala polyphenols-functionalized gold nanoparticles impair cancer cell survival through induction of tubulin dysfunction. Journal of Drug Delivery Science and Technology, 2021, 61, 102167.	3.0	7
5	Modulation of Î±-synuclein fibrillation by plant metabolites, daidzein, fisetin and scopoletin under physiological conditions. International Journal of Biological Macromolecules, 2021, 182, 1278-1291.	7.5	21
6	Title of the manuscript: Mechanistic insights into chalcone butein-induced inhibition of Î±-synuclein fibrillation: Biophysical and insilico studies. Journal of Molecular Liquids, 2021, 334, 116105.	4.9	10
7	Replica exchange molecular dynamics simulations reveal self-association sites in M-crystallin caused by mutations provide insights of cataract. Scientific Reports, 2021, 11, 23270.	3.3	4
8	Molecular study of binding of Plasmodium ribosomal protein P2 to erythrocytes. Biochimie, 2020, 176, 181-191.	2.6	3
9	All-in-one NMR spectroscopy of small organic molecules: complete chemical shift assignment from a single NMR experiment. RSC Advances, 2020, 10, 21174-21179.	3.6	7
10	Ultraclean Pure Shift NMR Spectroscopy with Adiabatic Composite Refocusing Pulses: Application to Metabolite Samples. ChemistrySelect, 2019, 4, 9893-9896.	1.5	0
11	Natural compound safranal driven inhibition and dis-aggregation of Î±-synuclein fibrils. International Journal of Biological Macromolecules, 2019, 141, 585-595.	7.5	32
12	Triphala inhibits alpha-synuclein fibrillization and their interaction study by NMR provides insights into the self-association of the protein. RSC Advances, 2019, 9, 28470-28477.	3.6	7
13	Mechanistic Insights from Replica Exchange Molecular Dynamics Simulations into Mutation Induced Disordered-to-Ordered Transition in Hahellin, a Î²Î³-Crystallin. Journal of Physical Chemistry B, 2019, 123, 5086-5098.	2.6	7
14	Gâ€SERF Editing in Twoâ€Dimensional Pureâ€Shift Total Correlation Spectroscopy: Scalar Coupling Measurements for a Group of Spins in Organic Molecules. ChemPhysChem, 2019, 20, 1559-1566.	2.1	2
15	Backbone and side-chain resonance assignments of centromeric protein Scm3 from Saccharomyces cerevisiae. Biomolecular NMR Assignments, 2019, 13, 267-273.	0.8	0
16	Fast and simultaneous determination of ¹Hâ€“¹H and ¹Hâ€“¹⁹F scalar couplings in complex spin systems: Application of PSYCHE homonuclear broadband decoupling. Magnetic Resonance in Chemistry, 2018, 56, 1043-1046.	1.9	7
17	Aqueous extract of Triphala inhibits cancer cell proliferation through perturbation of microtubule assembly dynamics. Biomedicine and Pharmacotherapy, 2018, 98, 76-81.	5.6	17
18	Multiple homonuclear bandâ€selective decoupling <scp>NMR</scp>: Fast and unambiguous determination of diastereomeric excess. Magnetic Resonance in Chemistry, 2018, 56, 1037-1042.	1.9	5

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19	Real-time J-upscaling in two-dimensional pure shift diagonal NMR: Simultaneous resolution enhancement in chemical shifts and scalar couplings. Journal of Magnetic Resonance, 2018, 296, 176-180.	2.1	1
20	NMR supersequences with real-time homonuclear broadband decoupling: Sequential acquisition of protein and small molecule spectra in a single experiment. Journal of Magnetic Resonance, 2018, 297, 108-112.	2.1	6
21	An efficient combination of BEST and NUS methods in multidimensional NMR spectroscopy for high throughput analysis of proteins. RSC Advances, 2018, 8, 17616-17621.	3.6	10
22	Rapid elucidation of chemical shift correlations in complex NMR spectra of organic molecules: Two-dimensional Hadamard pure shift NMR spectroscopy. Journal of Magnetic Resonance, 2018, 293, 77-81.	2.1	6
23	Unfolding of CPR3 Gets Initiated at the Active Site and Proceeds via Two Intermediates. Biophysical Journal, 2017, 112, 605-619.	0.5	6
24	Ultra-high resolution in low field tabletop NMR spectrometers. RSC Advances, 2017, 7, 49102-49104.	3.6	8
25	Hadamard Homonuclear Broadband Decoupled TOCSY NMR: Improved Efficacy in Detecting Longâ€range Chemical Shift Correlations. ChemPhysChem, 2016, 17, 4037-4042.	2.1	11
26	Nonâ€Uniformâ€Sampling Ultrahigh Resolution TOCSY NMR: Analysis of Complex Mixtures at Microgram Levels. ChemPhysChem, 2016, 17, 2304-2308.	2.1	26
27	NMR assignments of mitochondrial cyclophilin Cpr3 from Saccharomyces cerevisiae. Biomolecular NMR Assignments, 2016, 10, 203-206.	0.8	1
28	Synergistic Inhibition of Protein Fibrillation by Proline and Sorbitol: Biophysical Investigations. PLoS ONE, 2016, 11, e0166487.	2.5	21
29	Inhibition of insulin fibrillation by osmolytes: Mechanistic Insights. Scientific Reports, 2015, 5, 17599.	3.3	79
30	Molten globule nature of Plasmodium falciparum P2 homo-tetramer. Biochemistry and Biophysics Reports, 2015, 1, 97-107.	1.3	4
31	Ribosomal Protein P2 from apicomplexan parasite Toxoplasma gondii is intrinsically a molten globule. Biophysical Chemistry, 2015, 200-201, 27-33.	2.8	4
32	Reduced dimensionality (3,2)D NMR experiments and their automated analysis: implications to highâ€throughput structural studies on proteins. Magnetic Resonance in Chemistry, 2015, 53, 79-87.	1.9	0
33	The C-terminal Domain of Eukaryotic Acidic Ribosomal P2 Proteins is Intrinsically Disordered with Conserved Structural Propensities. Protein and Peptide Letters, 2015, 22, 212-218.	0.9	4
34	Urea Dependent ¹⁵N NMR-Relaxation Studies on PfP2 Multimers Reveal that the C-Terminal Behaves like an Independent Intrinsically Disordered Peptide. Protein and Peptide Letters, 2015, 22, 425-431.	0.9	1
35	Residue level description of In vivo self-association ofPlasmodium falciparumP2. Journal of Biomolecular Structure and Dynamics, 2014, 32, 602-612.	3.5	6
36	Complete backbone and DENQ side chain NMR assignments in proteins from a single experiment: implications to structureâ€“function studies. Journal of Structural and Functional Genomics, 2014, 15, 25-32.	1.2	5

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37	A reduced dimensionality NMR pulse sequence and an efficient protocol for unambiguous assignment in intrinsically disordered proteins. Journal of Biomolecular NMR, 2014, 59, 199-210.	2.8	17
38	Curcumin and kaempferol prevent lysozyme fibril formation by modulating aggregation kinetic parameters. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 670-680.	2.3	74
39	Parallel acquisition of 3D-HA(CA)NH and 3D-HACACO spectra. Journal of Biomolecular NMR, 2013, 56, 77-84.	2.8	17
40	Single point mutation induced alterations in the equilibrium structural transitions on the folding landscape of HIV-1 protease. Journal of Biomolecular Structure and Dynamics, 2013, 31, 684-693.	3.5	1
41	Intrinsic vs Environment Driven Equilibrium Folding Transitions in GTPase Effector Domain of Dynamin: NMR Insights. Protein and Peptide Letters, 2012, 19, 1297-1301.	0.9	0
42	A unified NMR strategy for high-throughput determination of backbone fold of small proteins. Journal of Structural and Functional Genomics, 2012, 13, 201-212.	1.2	3
43	Denaturation of HIV-1 Protease (PR) Monomer by Acetic Acid: Mechanistic and Trajectory Insights from Molecular Dynamics Simulations and NMR. Journal of Biomolecular Structure and Dynamics, 2012, 29, 893-903.	3.5	4
44	Reduced Dimensionality (4,3)D-<u>HN</u>(C)NH for Rapid Assignment of ¹H^Nâ€“¹⁵N HSQC Peaks in Proteins: An Analytical Tool for Protein Folding, Proteomics, and Drug Discovery Programs. Analytical Chemistry, 2012, 84, 10404-10410.	6.5	6
45	Residual structure and dynamics in DMSO-d6 denatured Dynein Light Chain protein. Biochimie, 2012, 94, 231-241.	2.6	6
46	NMR Insights into Folding and Self-Association of Plasmodium falciparum P2. PLoS ONE, 2012, 7, e36279.	2.5	13
47	Facile backbone (¹H, ¹⁵N, ¹³Ca, and ¹³Câ€²) assignment of ¹³C/¹⁵Nâ€labeled proteins using orthogonal projection planes of HNN and HN(C)N experiments and its automation. Magnetic Resonance in Chemistry, 2012, 50, 357-363.	1.9	4
48	Reduced dimensionality 3D HNCAN for unambiguous HN, CA and N assignment in proteins. Journal of Magnetic Resonance, 2012, 216, 161-168.	2.1	4
49	Simultaneous acquisition of 13CÎ±â€“15N and 1Hâ€“15Nâ€“15N sequential correlations in proteins: application of dual receivers in 3D HNN. Journal of Biomolecular NMR, 2012, 52, 5-10.	2.8	26
50	NMR Derived Model of GTPase Effector Domain (GED) Self Association: Relevance to Dynamin Assembly. PLoS ONE, 2012, 7, e30109.	2.5	1
51	NMR Insights into the Core of GED Assembly by H/D Exchange Coupled with DMSO Dissociation and Analysis of the Denatured State. Journal of Molecular Biology, 2011, 405, 1202-1214.	4.2	11
52	AUTOBA: Automation of backbone assignment from HN(C)N suite of experiments. Journal of Biomolecular NMR, 2011, 50, 285-297.	2.8	8
53	Resonance assignments of GTPase effector domain of dynamin in the aprotic solvent deuterated dimethyl sulfoxide. Biomolecular NMR Assignments, 2011, 5, 59-61.	0.8	2
54	hNCOcanH pulse sequence and a robust protocol for rapid and unambiguous assignment of backbone (¹H^N, ¹⁵N and ¹³Câ€²) resonances in ¹⁵N/¹³Câ€labeled proteins. Magnetic Resonance in Chemistry, 2011, 49, 575-583.	1.9	7

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55	Visualization of Early Events in Acetic Acid Denaturation of HIV-1 Protease: A Molecular Dynamics Study. PLoS ONE, 2011, 6, e19830.	2.5	9
56	BEST-HNN and 2D-(HN)NH experiments for rapid backbone assignment in proteins. Journal of Magnetic Resonance, 2010, 204, 111-117.	2.1	17
57	hnCOcaNH and hncoCANH pulse sequences for rapid and unambiguous backbone assignment in (13C,15N) labeled proteins. Journal of Magnetic Resonance, 2010, 206, 134-138.	2.1	9
58	Hierarchy of local structural and dynamics perturbations due to subdenaturing urea in the native state ensemble of DLC8 dimer. Biophysical Chemistry, 2010, 153, 17-26.	2.8	8
59	NMR investigations on residue level unfolding thermodynamics in DLC8 dimer by temperature dependent native state hydrogen exchange. Journal of Biomolecular NMR, 2009, 44, 1-11.	2.8	10
60	Structure-function-folding relationships and native energy landscape of dynein light chain protein: nuclear magnetic resonance insights. Journal of Biosciences, 2009, 34, 465-479.	1.1	20
61	Generation of serine/threonine check points in HN(C)N spectra. Journal of Chemical Sciences, 2009, 121, 955-964.	1.5	10
62	1H, 15N, 13C resonance assignment of 9.7ÂM urea-denatured state of the GTPase effector domain (GED) of dynamin. Biomolecular NMR Assignments, 2009, 3, 13-16.	0.8	3
63	Residueâ€wise conformational stability of DLC8 dimer from nativeâ€state hydrogen exchange. Proteins: Structure, Function and Bioinformatics, 2009, 75, 40-52.	2.6	10
64	Conserved structural and dynamics features in the denatured states of drosophila SUMO, human SUMO and ubiquitin proteins: Implications to sequenceâ€folding paradigm. Proteins: Structure, Function and Bioinformatics, 2009, 76, 387-402.	2.6	8
65	NMRâ€derived solution structure of SUMO from Drosophila melanogaster (dSmt3). Proteins: Structure, Function and Bioinformatics, 2009, 75, 1046-1050.	2.6	4
66	Hierarchy in guanidine unfolding of DLC8 dimer: Regulatory functional implications. Biochimie, 2009, 91, 401-407.	2.6	6
67	Comparison of NMR structural and dynamics features of the urea and guanidine-denatured states of GED. Archives of Biochemistry and Biophysics, 2009, 481, 169-176.	3.0	6
68	Fluctuating partially native-like topologies in the acid denatured ensemble of autolysis resistant HIV-1 protease. Archives of Biochemistry and Biophysics, 2009, 482, 33-41.	3.0	7
69	Native and nonnative conformational preferences in the urea-unfolded state of barstar. Protein Science, 2009, 13, 3085-3091.	7.6	28
70	Tuning the HNN experiment: generation of serineâ€“threonine check points. Journal of Biomolecular NMR, 2008, 40, 145-152.	2.8	17
71	1H, 15N, 13C resonance assignment of folded and 8ÂM urea-denatured state of SUMO from Drosophila melanogaster. Biomolecular NMR Assignments, 2008, 2, 13-15.	0.8	9
72	Spectroscopic labeling of A, S/T in the 1Hâ€“15N HSQC spectrum of uniformly (15Nâ€“13C) labeled proteins. Journal of Magnetic Resonance, 2008, 194, 289-294.	2.1	6

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73	pH dependent unfolding characteristics of DLC8 dimer: Residue level details from NMR. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1795-1803.	2.3	9
74	NMR comparison of the native energy landscapes of DLC8 dimer and monomer. Biophysical Chemistry, 2008, 134, 10-19.	2.8	19
75	Effect of a single point mutation on the stability, residual structure and dynamics in the denatured state of GED: Relevance to self-assembly. Biophysical Chemistry, 2008, 137, 13-18.	2.8	2
76	Equilibrium Refolding Transitions Driven by Trifluoroethanol and by Guanidine Hydrochloride Dilution Are Similar in GTPase Effector Domain: Implications to Sequenceâ˜Self-Association Paradigm. Biochemistry, 2008, 47, 12945-12953.	2.5	2
77	NMR insights into a megadaltonâ€size protein selfâ€assembly. Protein Science, 2008, 17, 1319-1325.	7.6	15
78	NMR Characterization of Structural and Dynamics Perturbations Due to a Single Point Mutation in Drosophila DLC8 Dimer: Functional Implications. Biochemistry, 2008, 47, 6251-6259.	2.5	12
79	NMR insights into dynamics regulated target binding of DLC8 dimer. Biochemical and Biophysical Research Communications, 2007, 355, 950-955.	2.1	12
80	Equilibrium unfolding of DLC8 monomer by urea and guanidine hydrochloride: Distinctive global and residue level features. Biochimie, 2007, 89, 117-134.	2.6	25
81	NMR Characterization of the Energy Landscape of SUMO-1 in the Native-state Ensemble. Journal of Molecular Biology, 2007, 367, 1480-1493.	4.2	21
82	Pockets of Short-Range Transient Order and Restricted Topological Heterogeneity in the Guanidine-Denatured State Ensemble of GED of Dynamin. Biochemistry, 2007, 46, 11819-11832.	2.5	20
83	Local Structural Preferences and Dynamics Restrictions in the Urea-Denatured State of SUMO-1: NMR Characterization. Biophysical Journal, 2006, 90, 2498-2509.	0.5	15
84	pH driven conformational dynamics and dimer-to-monomer transition in DLC8. Protein Science, 2006, 15, 335-342.	7.6	36
85	Residue-level NMR View of the Urea-driven Equilibrium Folding Transition of SUMO-1 (1-97): Native Preferences Do Not Increase Monotonously. Journal of Molecular Biology, 2006, 361, 180-194.	4.2	13
86	Structural characterization of the large soluble oligomers of the GTPase effector domain of dynamin. FEBS Journal, 2006, 273, 388-397.	4.7	22
87	Following autolysis in proteases by NMR: Insights into multiple unfolding pathways and mutational plasticities. Biophysical Chemistry, 2006, 123, 1-10.	2.8	6
88	Alanine check points in HNN and HN(C)N spectra. Journal of Magnetic Resonance, 2006, 181, 21-28.	2.1	18
89	NMR of unfolded proteins. Journal of Chemical Sciences, 2005, 117, 3-21.	1.5	15
90	Folding Regulates Autoprocessing of HIV-1 Protease Precursor. Journal of Biological Chemistry, 2005, 280, 11369-11378.	3.4	36

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91	Dynamin Interacts with Members of the Sumoylation Machinery. Journal of Biological Chemistry, 2004, 279, 31445-31454.	3.4	40
92	Application of HN(C)N to rapid estimation of 1J(Nâ€“CÎ±) coupling constants correlated to Ï˜ torsion angles in proteins: implication to structural genomics. Biochemical and Biophysical Research Communications, 2003, 311, 678-684.	2.1	5
93	NMR Elucidation of Early Folding Hierarchy in HIV-1 Protease. Journal of Biological Chemistry, 2003, 278, 19980-19985.	3.4	31
94	NMR Identification and Characterization of the Flexible Regions in the 160 kDa Molten Globule-Like Aggregate of Barstar at Low pHâ€. Biochemistry, 2002, 41, 9885-9899.	2.5	29
95	A novel protocol based on HN(C)N for rapid resonance assignment in (15N, 13C) labeled proteins: implications to structural genomics. Biochemical and Biophysical Research Communications, 2002, 293, 427-432.	2.1	32
96	NMR identification of local structural preferences in HIV-1 protease tethered heterodimer in 6 M guanidine hydrochloride. FEBS Letters, 2001, 509, 218-224.	2.8	27
97	Improved 3D triple resonance experiments, HNN and HN(C)N, for HN and 15N sequential correlations in (13C, 15N) labeled proteins: application to unfolded proteins. Journal of Biomolecular NMR, 2001, 20, 135-147.	2.8	179
98	CD and NMR investigations on trifluoroethanol-induced step-wise folding of helical segment from scorpion neurotoxin. FEBS Journal, 1999, 264, 468-478.	0.2	22
99	Molecular conformation of gonadoliberin using two-dimensional NMR spectroscopy. FEBS Journal, 1986, 158, 323-332.	0.2	34
100	Conformation of Biological Molecules. Nmr, 1982, , .	0.5	60
101	Carbon-13T1 measurements on glyceryl trivalerate. Magnetic Resonance in Chemistry, 1981, 17, 71-73.	0.7	4
102	Protein-Nucleic acid interactions: Investigations on the peptide backbone interaction with polynucleotides. International Journal of Quantum Chemistry, 1981, 20, 23-32.	2.0	7
103	Sequence effects in structures of the dinucleotides d-pApT AND d-pTpA. Journal of Molecular Structure, 1981, 72, 261-267.	3.6	11
104	Theoretical description of fluidity in biological membranes: Rotational motion in lipid hydrocarbon chains. International Journal of Quantum Chemistry, 1980, 17, 983-993.	2.0	1
105	Organization of phospholipids in biological membranes. International Journal of Quantum Chemistry, 1979, 16, 19-29.	2.0	8
106	Quantum-mechanical theory for transport across biological membranes. International Journal of Quantum Chemistry, 1978, 13, 411-428.	2.0	7
107	Conformational structure of glycerol trivalerate and its relation to phospholipids: Studies by NMR and potential energy calculations. Chemistry and Physics of Lipids, 1978, 21, 77-96.	3.2	17