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	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
2	Inhibition of insulin fibrillation by osmolytes: Mechanistic Insights. Scientific Reports, 2015, 5, 17599.	3.3	79
3	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
4	Conformation of Biological Molecules. Nmr, 1982, , .	0.5	60
5	Dynamin Interacts with Members of the Sumoylation Machinery. Journal of Biological Chemistry, 2004, 279, 31445-31454.	3.4	40
6	Folding Regulates Autoprocessing of HIV-1 Protease Precursor. Journal of Biological Chemistry, 2005, 280, 11369-11378.	3.4	36
7	pH driven conformational dynamics and dimer-to-monomer transition in DLC8. Protein Science, 2006, 15, 335-342.	7.6	36
8	Molecular conformation of gonadoliberin using two-dimensional NMR spectroscopy. FEBS Journal, 1986, 158, 323-332.	0.2	34
9	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
10	Natural compound safranal driven inhibition and dis-aggregation of Î±-synuclein fibrils. International Journal of Biological Macromolecules, 2019, 141, 585-595.	7.5	32
11	NMR Elucidation of Early Folding Hierarchy in HIV-1 Protease. Journal of Biological Chemistry, 2003, 278, 19980-19985.	3.4	31
12	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
13	Native and nonnative conformational preferences in the urea-unfolded state of barstar. Protein Science, 2009, 13, 3085-3091.	7.6	28
14	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
15	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
16	Nonâ€Uniformâ€Sampling Ultrahigh Resolution TOCSY NMR: Analysis of Complex Mixtures at Microgram Levels. ChemPhysChem, 2016, 17, 2304-2308.	2.1	26
17	Equilibrium unfolding of DLC8 monomer by urea and guanidine hydrochloride: Distinctive global and residue level features. Biochimie, 2007, 89, 117-134.	2.6	25
18	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

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19	Structural characterization of the large soluble oligomers of the GTPase effector domain of dynamin. FEBS Journal, 2006, 273, 388-397.	4.7	22
20	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
21	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
22	Synergistic Inhibition of Protein Fibrillation by Proline and Sorbitol: Biophysical Investigations. PLoS ONE, 2016, 11, e0166487.	2.5	21
23	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
24	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
25	NMR comparison of the native energy landscapes of DLC8 dimer and monomer. Biophysical Chemistry, 2008, 134, 10-19.	2.8	19
26	Alanine check points in HNN and HN(C)N spectra. Journal of Magnetic Resonance, 2006, 181, 21-28.	2.1	18
27	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
28	Tuning the HNN experiment: generation of serineâ€“threonine check points. Journal of Biomolecular NMR, 2008, 40, 145-152.	2.8	17
29	BEST-HNN and 2D-(HN)NH experiments for rapid backbone assignment in proteins. Journal of Magnetic Resonance, 2010, 204, 111-117.	2.1	17
30	Parallel acquisition of 3D-HA(CA)NH and 3D-HACACO spectra. Journal of Biomolecular NMR, 2013, 56, 77-84.	2.8	17
31	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
32	Aqueous extract of Triphala inhibits cancer cell proliferation through perturbation of microtubule assembly dynamics. Biomedicine and Pharmacotherapy, 2018, 98, 76-81.	5.6	17
33	NMR of unfolded proteins. Journal of Chemical Sciences, 2005, 117, 3-21.	1.5	15
34	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
35	NMR insights into a megadaltonâ€size protein selfâ€assembly. Protein Science, 2008, 17, 1319-1325.	7.6	15
36	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

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37	NMR Insights into Folding and Self-Association of Plasmodium falciparum P2. PLoS ONE, 2012, 7, e36279.	2.5	13
38	NMR insights into dynamics regulated target binding of DLC8 dimer. Biochemical and Biophysical Research Communications, 2007, 355, 950-955.	2.1	12
39	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
40	Sequence effects in structures of the dinucleotides d-pApT AND d-pTpA. Journal of Molecular Structure, 1981, 72, 261-267.	3.6	11
41	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
42	Hadamard Homonuclear Broadband Decoupled TOCSY NMR: Improved Efficacy in Detecting Longâ€range Chemical Shift Correlations. ChemPhysChem, 2016, 17, 4037-4042.	2.1	11
43	Targeting disorders in unstructured and structured proteins in various diseases. Biophysical Chemistry, 2022, 281, 106742.	2.8	11
44	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
45	Generation of serine/threonine check points in HN(C)N spectra. Journal of Chemical Sciences, 2009, 121, 955-964.	1.5	10
46	Residueâ€wise conformational stability of DLC8 dimer from nativeâ€state hydrogen exchange. Proteins: Structure, Function and Bioinformatics, 2009, 75, 40-52.	2.6	10
47	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
48	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
49	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
50	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
51	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
52	Visualization of Early Events in Acetic Acid Denaturation of HIV-1 Protease: A Molecular Dynamics Study. PLoS ONE, 2011, 6, e19830.	2.5	9
53	Organization of phospholipids in biological membranes. International Journal of Quantum Chemistry, 1979, 16, 19-29.	2.0	8
54	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

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55	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
56	AUTOBA: Automation of backbone assignment from HN(C)N suite of experiments. Journal of Biomolecular NMR, 2011, 50, 285-297.	2.8	8
57	Ultra-high resolution in low field tabletop NMR spectrometers. RSC Advances, 2017, 7, 49102-49104.	3.6	8
58	Quantum-mechanical theory for transport across biological membranes. International Journal of Quantum Chemistry, 1978, 13, 411-428.	2.0	7
59	Protein-Nucleic acid interactions: Investigations on the peptide backbone interaction with polynucleotides. International Journal of Quantum Chemistry, 1981, 20, 23-32.	2.0	7
60	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
61	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
62	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
63	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
64	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
65	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
66	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
67	Following autolysis in proteases by NMR: Insights into multiple unfolding pathways and mutational plasticities. Biophysical Chemistry, 2006, 123, 1-10.	2.8	6
68	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
69	Hierarchy in guanidine unfolding of DLC8 dimer: Regulatory functional implications. Biochimie, 2009, 91, 401-407.	2.6	6
70	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
71	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
72	Residual structure and dynamics in DMSO-d6 denatured Dynein Light Chain protein. Biochimie, 2012, 94, 231-241.	2.6	6

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73	Residue level description of In vivo self-association ofPlasmodium falciparumP2. Journal of Biomolecular Structure and Dynamics, 2014, 32, 602-612.	3.5	6
74	Unfolding of CPR3 Gets Initiated at the Active Site and Proceeds via Two Intermediates. Biophysical Journal, 2017, 112, 605-619.	0.5	6
75	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
76	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
77	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
78	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
79	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
80	Carbon-13T1 measurements on glyceryl trivalerate. Magnetic Resonance in Chemistry, 1981, 17, 71-73.	0.7	4
81	NMRâ€derived solution structure of SUMO from Drosophila melanogaster (dSmt3). Proteins: Structure, Function and Bioinformatics, 2009, 75, 1046-1050.	2.6	4
82	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
83	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
84	Reduced dimensionality 3D HNCAN for unambiguous HN, CA and N assignment in proteins. Journal of Magnetic Resonance, 2012, 216, 161-168.	2.1	4
85	Molten globule nature of Plasmodium falciparum P2 homo-tetramer. Biochemistry and Biophysics Reports, 2015, 1, 97-107.	1.3	4
86	Ribosomal Protein P2 from apicomplexan parasite Toxoplasma gondii is intrinsically a molten globule. Biophysical Chemistry, 2015, 200-201, 27-33.	2.8	4
87	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
88	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
89	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
90	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

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91	Molecular study of binding of Plasmodium ribosomal protein P2 to erythrocytes. Biochimie, 2020, 176, 181-191.	2.6	3
92	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
93	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
94	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
95	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
96	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
97	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
98	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
99	NMR assignments of mitochondrial cyclophilin Cpr3 from Saccharomyces cerevisiae. Biomolecular NMR Assignments, 2016, 10, 203-206.	0.8	1
100	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
101	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
102	NMR Derived Model of GTPase Effector Domain (GED) Self Association: Relevance to Dynamin Assembly. PLoS ONE, 2012, 7, e30109.	2.5	1
103	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
104	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
105	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
106	Ultraclean Pure Shift NMR Spectroscopy with Adiabatic Composite Refocusing Pulses: Application to Metabolite Samples. ChemistrySelect, 2019, 4, 9893-9896.	1.5	0
107	Backbone and side-chain resonance assignments of centromeric protein Scm3 from Saccharomyces cerevisiae. Biomolecular NMR Assignments, 2019, 13, 267-273.	0.8	0