Ranajeet Ghose

List of Publications by Year
in descending order

67	1,354	304602 22	377752 34
papers	citations	h-index	g-index

74	74	74	1336
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural basis for the recognition of the bacterial tyrosine kinase Wzc by its cognate tyrosine phosphatase Wzb. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4
2	NMR solution structures of Runella slithyformis RNA 2â€²-phosphotransferase Tpt1 provide insights into NAD+ binding and specificity. Nucleic Acids Research, 2021, 49, 9607-9624.	6.5	2
3	Structural dynamics of the complex of calmodulin with a minimal functional construct of eukaryotic elongation factor 2 kinase and the role of Thr348 autophosphorylation. Protein Science, 2021, 30, 1221-1234.	3.1	8
4	An ATPase with a twist: A unique mechanism underlies the activity of the bacterial tyrosine kinase, Wzc. Science Advances, 2021, 7, eabj5836.	4.7	5
5	A Conserved Structural Role for the Walker-A Lysine in P-Loop Containing Kinases. Frontiers in Molecular Biosciences, 2021, 8, 747206.	1.6	1
6	The Cold-Unfolded State Is Expanded but Contains Long- and Medium-Range Contacts and Is Poorly Described by Homopolymer Models. Biochemistry, 2020, 59, 3290-3299.	1.2	8
7	Long-range dynamic correlations regulate the catalytic activity of the bacterial tyrosine kinase Wzc. Science Advances, 2020, 6, .	4.7	10
8	Keep a lid on it: A troika in kinase allostery. Journal of Biological Chemistry, 2020, 295, 8492-8493.	1.6	0
9	The role of calcium in the interaction between calmodulin and a minimal functional construct of eukaryotic elongation factor 2 kinase. Protein Science, 2019, 28, 2089-2098.	3.1	8
10	Targeting ERK beyond the boundaries of the kinase active site in melanoma. Molecular Carcinogenesis, 2019, 58, 1551-1570.	1.3	26
11	Solution Structure of the Carboxy-Terminal Tandem Repeat Domain of Eukaryotic Elongation Factor 2 Kinase and Its Role in Substrate Recognition. Journal of Molecular Biology, 2019, 431, 2700-2717.	2.0	8
12	A Novel Class of Common Docking Domain Inhibitors That Prevent ERK2 Activation and Substrate Phosphorylation. ACS Chemical Biology, 2019, 14, 1183-1194.	1.6	25
13	Modulating multi-functional ERK complexes by covalent targeting of a recruitment site in vivo. Nature Communications, 2019, 10, 5232.	5.8	17
14	Cover Image, Volume 58, Issue 9. Molecular Carcinogenesis, 2019, 58, i.	1.3	0
15	Nature of the Pre-Chemistry Ensemble in Mitogen-Activated Protein Kinases. Journal of Molecular Biology, 2019, 431, 145-157.	2.0	12
16	Sequential Protein Expression and Capsid Assembly in Cell: Toward the Study of Multiprotein Viral Capsids Using Solid-State Nuclear Magnetic Resonance Techniques. Biochemistry, 2018, 57, 1568-1571.	1.2	1
17	Structural Dynamics of the Activation of Elongation Factor 2 Kinase by Ca2+-Calmodulin. Journal of Molecular Biology, 2018, 430, 2802-2821.	2.0	15
18	Methyl NMR spectroscopy: Measurement of dynamics in viral RNA-directed RNA polymerases. Methods, 2018, 148, 100-114.	1.9	8

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19	Characterization of DNA Binding by the Isolated N-Terminal Domain of Vaccinia Virus DNA Topoisomerase IB. Biochemistry, 2017, 56, 3307-3317.	1.2	4
20	Cystoviral RNA-directed RNA polymerases: Regulation of RNA synthesis on multiple time and length scales. Virus Research, 2017, 234, 135-152.	1.1	6
21	Signal Integration at Elongation Factor 2 Kinase. Journal of Biological Chemistry, 2017, 292, 2032-2045.	1.6	15
22	Local destabilization, rigid body, and fuzzy docking facilitate the phosphorylation of the transcription factor Ets-1 by the mitogen-activated protein kinase ERK2. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6287-E6296.	3.3	22
23	Structure of the C-Terminal Helical Repeat Domain of Eukaryotic Elongation Factor 2 Kinase. Biochemistry, 2016, 55, 5377-5386.	1.2	4
24	Structural Basis for the Recognition of Eukaryotic Elongation Factor 2 Kinase by Calmodulin. Structure, 2016, 24, 1441-1451.	1.6	19
25	Structural and Dynamic Features of F-recruitment Site Driven Substrate Phosphorylation by ERK2. Scientific Reports, 2015, 5, 11127.	1.6	19
26	Methyl Relaxation Measurements Reveal Patterns of Fast Dynamics in a Viral RNA-Directed RNA Polymerase. Biochemistry, 2015, 54, 5828-5838.	1.2	5
27	Sequence-specific backbone 1H, 13C and 15N assignments of the catalytic domain of the Escherichia coli protein tyrosine kinase, Wzc. Biomolecular NMR Assignments, 2014, 8, 37-41.	0.4	4
28	Cystoviral Polymerase Complex Protein P7 Uses Its Acidic C-Terminal Tail to Regulate the RNA-Directed RNA Polymerase P2. Journal of Molecular Biology, 2014, 426, 2580-2593.	2.0	7
29	A Measured Approach: Determining the PLCÎ³1 Docking Site on Itk Using a Biochemical Ruler. Journal of Molecular Biology, 2013, 425, 679-682.	2.0	1
30	Structure of the RNAâ€directed RNA Polymerase from the cystovirus Ï•12. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1479-1484.	1.5	8
31	Regulatory Interactions between a Bacterial Tyrosine Kinase and Its Cognate Phosphatase. Journal of Biological Chemistry, 2013, 288, 15212-15228.	1.6	26
32	Multiple-Quantum NMR Spectroscopy: Detection of Slow Dynamics. , 2013, , 1646-1655.		0
33	Solution structure and DNA-binding properties of the phosphoesterase domain of DNA ligase D. Nucleic Acids Research, 2012, 40, 2076-2088.	6.5	7
34	Docking Interactions of Hematopoietic Tyrosine Phosphatase with MAP Kinases ERK2 and p38Î±. Biochemistry, 2012, 51, 8047-8049.	1.2	20
35	Assignment of Backbone Resonances in a Eukaryotic Protein Kinase â€“ ERK2 as a Representative Example. Methods in Molecular Biology, 2012, 831, 359-368.	0.4	10
36	Expression and Purification of Src-family Kinases for Solution NMR Studies. Methods in Molecular Biology, 2012, 831, 111-131.	0.4	8

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37	Slow Conformational Dynamics in the Cystoviral RNA-Directed RNA Polymerase P2: Influence of Substrate Nucleotides and Template RNA. Biochemistry, 2011, 50, 1875-1884.	1.2	14
38	Solution NMR Insights into Docking Interactions Involving Inactive ERK2. Biochemistry, 2011, 50, 3660-3672.	1.2	39
39	Sequence-specific 1H, 13C and 15N assignments of the phosphoesterase (PE) domain of Pseudomonas aeruginosa DNA ligase D (LigD). Biomolecular NMR Assignments, 2011, 5, 151-155.	0.4	2
40	A Model of a MAPKâ€¢Substrate Complex in an Active Conformation: A Computational and Experimental Approach. PLoS ONE, 2011, 6, e18594.	1.1	20
41	Nuclear spin relaxation in isotropic and anisotropic media. Progress in Nuclear Magnetic Resonance Spectroscopy, 2010, 57, 111-158.	3.9	57
42	On the measurement of 15Nâ€“{1H} nuclear Overhauser effects. 2. Effects of the saturation scheme and water signal suppression. Journal of Magnetic Resonance, 2010, 207, 294-303.	1.2	40
43	Dynamics on multiple timescales in the RNA-directed RNA polymerase from the cystovirus Ï•6. Nucleic Acids Research, 2010, 38, 5105-5118.	6.5	18
44	Solution NMR Studies of Chlorella Virus DNA Ligase-adenylate. Journal of Molecular Biology, 2010, 395, 291-308.	2.0	11
45	Optimized bacterial expression and purification of the c-Src catalytic domain for solution NMR studies. Journal of Biomolecular NMR, 2009, 44, 87-93.	1.6	14
46	Sequence-specific 1HN, 13C, and 15N backbone resonance assignments of the 34ÂkDa Paramecium bursaria Chlorella virus 1 (PBCV1) DNA ligase. Biomolecular NMR Assignments, 2009, 3, 77-80.	0.4	2
47	Accurate Sampling of High-Frequency Motions in Proteins by Steady-State ‹sup›15‹/sup›Nâ“{‹sup›1‹/sup›H} Nuclear Overhauser Effect Measurements in the Presence of Cross-Correlated Relaxation. Journal of the American Chemical Society, 2009, 131, 6048-6049.	6.6	57
48	On the measurement of 15Nâ€“{1H} nuclear Overhauser effects. Journal of Magnetic Resonance, 2008, 192, 302-313.	1.2	37
49	Structure and Dynamics of the P7 Protein from the Bacteriophage Ï•12. Journal of Molecular Biology, 2008, 382, 402-422.	2.0	19
50	Detection of correlated dynamics on multiple timescales by measurement of the differential relaxation of zero- and double-quantum coherences involving sidechain methyl groups in proteins. Journal of Magnetic Resonance, 2006, 180, 1-17.	1.2	8
51	Structure and Dynamics of ASC2, a Pyrin Domain-only Protein That Regulates Inflammatory Signaling. Journal of Biological Chemistry, 2006, 281, 31863-31875.	1.6	48
52	Structure and Dynamics of ASC2, a Pyrin Domain-only Protein That Regulates Inflammatory Signaling. Journal of Biological Chemistry, 2006, 281, 31863-31875.	1.6	20
53	Probing Slow Backbone Dynamics in Proteins Using TROSY-Based Experiments to Detect Cross-Correlated Time-Modulation of Isotropic Chemical Shifts. Journal of Biomolecular NMR, 2004, 28, 213-227.	1.6	24
54	Dynamic Influences on a High-Affinity, High-Specificity Interaction Involving the C-Terminal SH3 Domain of p67phox. Biochemistry, 2004, 43, 8094-8106.	1.2	21

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55	NMR structure determination and investigation using a reduced proton (REDPRO) labeling strategy for proteins. FEBS Letters, 2002, 524, 177-182.	1.3	44
56	Determination of the Rotational Diffusion Tensor of Macromolecules in Solution from NMR Relaxation Data with a Combination of Exact and Approximate Methodsâ€"Application to the Determination of Interdomain Orientation in Multidomain Proteins. Journal of Magnetic Resonance, 2001, 149, 204-217.	1.2	66
57	Average Liouvillian theory in nuclear magnetic resonance?Principles, properties, and applications. Concepts in Magnetic Resonance, 2000, 12, 152-172.	1.3	33
58	The Effect of Finite Sampling on the Determination of Orientational Properties:Â A Theoretical Treatment with Application to Interatomic Vectors in Proteins. Journal of the American Chemical Society, 2000, 122, 10640-10649.	6.6	35
59	Relative Orientation of CÎ±HÎ±-Bond Vectors of Successive Residues in Proteins through Cross-Correlated Relaxation in NMR. Journal of the American Chemical Society, 2000, 122, 1758-1761.	6.6	37
60	Title is missing!. Journal of Biomolecular NMR, 1999, 14, 277-280.	1.6	42
61	Efficient determination of angles subtended by C(alpha)-H(alpha) and N-H(N) vectors in proteins via dipole-dipole cross-correlation. Journal of Biomolecular NMR, 1999, 13, 375-380.	1.6	42
62	Relaxation of Two-Spin Coherence Due to Cross-Correlated Fluctuations of Dipoleâ^'Dipole Couplings and Anisotropic Shifts in NMR of 15N,13C-Labeled Biomolecules. Journal of the American Chemical Society, 1999, 121, 6876-6883.	6.6	68
63	Backbone Dynamics of the N-Terminal Domain inE. ColiDnaJ Determined by15N- and13CO-Relaxation Measurementsâ€. Biochemistry, 1999, 38, 10567-10577.	1.2	29
64	Electron Spinâ€"Nuclear Spin Cross-Correlation Effects on Multiplet Splittings in Paramagnetic Proteins. Journal of Magnetic Resonance, 1997, 128, 138-143.	1.2	59
65	NMR Studies of a13C,15N-Labeled GM4-Lactam Glycolipid at an Oriented Model-Membrane Interface. Journal of the American Chemical Society, 1996, 118, 4001-4008.	6.6	35
66	NMR investigations of the structural properties of the nodulation protein, NodF, fromRhizobium leguminosarumand its homology withEscherichia coliacyl carrier protein. FEBS Letters, 1996, 388, 66-72.	1.3	22
67	Dependence of 13C Chemical Shifts on Glycosidic Torsional Angles in Ribonucleic Acids. Journal of the American Chemical Society, 1994, 116, 8827-8828.	6.6	47