Rajiv Kumar Kar

List of Publications by Year
in descending order

59 papers	1,322 citations	361045 20 h-index	395343 33 g-index
62 all docs	62 docs citations	62 times ranked	2313 citing authors

#	Article	IF	Citations
1	Femtosecond-to-millisecond structural changes in a light-driven sodium pump. Nature, 2020, 583, 314-318.	13.7	115
2	A Peptide-Nanoparticle System with Improved Efficacy against Multidrug Resistant Bacteria. Scientific Reports, 2019, 9, 4485.	1.6	80
3	Indolicidin Targets Duplex DNA: Structural and Mechanistic Insight through a Combination of Spectroscopy and Microscopy. ChemMedChem, 2014, 9, 2052-2058.	1.6	75
4	Use of a Small Peptide Fragment as an Inhibitor of Insulin Fibrillation Process: A Study by High and Low Resolution Spectroscopy. PLoS ONE, 2013, 8, e72318.	1.1	64
5	Structural and sequential context of p53: A review of experimental and theoretical evidence. Progress in Biophysics and Molecular Biology, 2015, 117, 250-263.	1.4	48
6	Accelerated molecular dynamics simulation analysis of MSI-594 in a lipid bilayer. Physical Chemistry Chemical Physics, 2017, 19, 19289-19299.	1.3	46
7	Membrane disruptive antimicrobial activities of human Î²-defensin-3 analogs. European Journal of Medicinal Chemistry, 2015, 91, 91-99.	2.6	44
8	Mode of Action of a Designed Antimicrobial Peptide: High Potency against Cryptococcus neoformans. Biophysical Journal, 2016, 111, 1724-1737.	0.2	37
9	Structural and biochemical investigation of MARK4 inhibitory potential of cholic acid: Towards therapeutic implications in neurodegenerative diseases. International Journal of Biological Macromolecules, 2020, 161, 596-604.	3.6	37
10	Evidence for Inhibition of Lysozyme Amyloid Fibrillization by Peptide Fragments from Human Lysozyme: A Combined Spectroscopy, Microscopy, and Docking Study. Biomacromolecules, 2016, 17, 1998-2009.	2.6	35
11	Computational Elucidation of Structural Basis for Ligand Binding withLeishmania donovaniAdenosine Kinase. BioMed Research International, 2013, 2013, 1-14.	0.9	32
12	Sequence context induced antimicrobial activity: insight into lipopolysaccharide permeabilization. Molecular BioSystems, 2014, 10, 1596-1612.	2.9	30
13	Quercetin loaded folate targeted plasmonic silver nanoparticles for light activated chemo-photothermal therapy of DMBA induced breast cancer in Sprague Dawley rats. RSC Advances, 2020, 10, 31961-31978.	1.7	30
14	Acetylation of Gly1 and Lys2 Promotes Aggregation of Human Î³D-Crystallin. Biochemistry, 2014, 53, 7269-7282.	1.2	26
15	Frontiers in Multiscale Modeling of Photoreceptor Proteins. Photochemistry and Photobiology, 2021, 97, 243-269.	1.3	26
16	Human cathelicidin peptide LL37 binds telomeric G-quadruplex. Molecular BioSystems, 2013, 9, 1833.	2.9	25
17	Structural Elucidation of the Cell-Penetrating Penetratin Peptide in Model Membranes at the Atomic Level: Probing Hydrophobic Interactions in the Bloodâ€“Brain Barrier. Biochemistry, 2016, 55, 4982-4996.	1.2	24
18	Solution Structures, Dynamics, and Ice Growth Inhibitory Activity of Peptide Fragments Derived from an Antarctic Yeast Protein. PLoS ONE, 2012, 7, e49788.	1.1	21

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19	Convergent Synthesis and Conformational Analysis of the Hexasaccharide Repeating Unit of the Oâ€Antigen of Shigella flexneri Serotype 1d. European Journal of Organic Chemistry, 2014, 2014, 4577-4584.	1.2	20
20	Structure and Dynamics of Antifreeze Proteinâ€“Model Membrane Interactions: A Combined Spectroscopic and Molecular Dynamics Study. Journal of Physical Chemistry B, 2016, 120, 902-914.	1.2	20
21	Understanding flavin electronic structure and spectra. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1541.	6.2	19
22	Interaction between Nbp35 and Cfd1 Proteins of Cytosolic Fe-S Cluster Assembly Reveals a Stable Complex Formation in Entamoeba histolytica. PLoS ONE, 2014, 9, e108971.	1.1	19
23	Deciphering the role of the AT-rich interaction domain and the HMG-box domain of ARID-HMG proteins of Arabidopsis thaliana. Plant Molecular Biology, 2016, 92, 371-388.	2.0	16
24	Biophysical insights into the membrane interaction of the core amyloid-forming Aî²₄₀fragment K16â€“K28 and its role in the pathogenesis of Alzheimer's disease. Physical Chemistry Chemical Physics, 2016, 18, 16890-16901.	1.3	16
25	Effect of pH on the structure and function of pyruvate dehydrogenase kinase 3: Combined spectroscopic and MD simulation studies. International Journal of Biological Macromolecules, 2020, 147, 768-777.	3.6	16
26	LC-MS characterized methanolic extract of zanthoxylum armatum possess anti-breast cancer activity through Nrf2-Keap1 pathway: An in-silico, in-vitro and in-vivo evaluation. Journal of Ethnopharmacology, 2021, 269, 113758.	2.0	16
27	Novel G-quadruplex stabilizing agents: in-silico approach and dynamics. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1497-1518.	2.0	15
28	Biophysical and biochemical aspects of antifreeze proteins: Using computational tools to extract atomistic information. Progress in Biophysics and Molecular Biology, 2015, 119, 194-204.	1.4	15
29	Spectroscopic Properties of Lumiflavin: A Quantum Chemical Study. Photochemistry and Photobiology, 2019, 95, 662-674.	1.3	15
30	Double GC:GC Mismatch in dsDNA Enhances Local Dynamics Retaining the DNA Footprint: A Highâ€Resolution NMR Study. ChemMedChem, 2014, 9, 2059-2064.	1.6	14
31	C -cinnamoyl glycosides as a new class of anti-filarial agents. European Journal of Medicinal Chemistry, 2016, 114, 308-317.	2.6	14
32	Nuclear spin-hyperpolarization generated in a flavoprotein under illumination: experimental field-dependence and theoretical level crossing analysis. Scientific Reports, 2019, 9, 18436.	1.6	14
33	Interaction of ATP with a Small Heat Shock Protein from Mycobacterium leprae: Effect on Its Structure and Function. PLoS Neglected Tropical Diseases, 2015, 9, e0003661.	1.3	13
34	Sequence specificity of amylin-insulin interaction: a fragment-based insulin fibrillation inhibition study. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 405-415.	1.1	13
35	Highâ€resolution structure of a partially folded insulin aggregation intermediate. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1648-1659.	1.5	13
36	Will It Be Beneficial To Simulate the Antifreeze Proteins at Ice Freezing Condition or at Lower Temperature?. Journal of Physical Chemistry B, 2015, 119, 11485-11495.	1.2	12

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37	Synthesis of novel muramic acid derivatives and their interaction with lysozyme: Action of lysozyme revisited. Journal of Colloid and Interface Science, 2017, 498, 395-404.	5.0	12
38	Nonproductive Binding Modes as a Prominent Feature of AÎ²₄₀ Fiber Elongation: Insights from Molecular Dynamics Simulation. Journal of Chemical Information and Modeling, 2018, 58, 1576-1586.	2.5	11
39	Gram-Scale Synthesis of 1,8-Naphthyridines in Water: The Friedlander Reaction Revisited. ACS Omega, 2021, 6, 19304-19313.	1.6	11
40	Molecular Details of a Salt Bridge and Its Role in Insulin Fibrillation by NMR and Raman Spectroscopic Analysis. Journal of Physical Chemistry B, 2020, 124, 1125-1136.	1.2	10
41	Biophysical Characterization of Essential Phosphorylation at the Flexible C-Terminal Region of C-Raf with 14-3-3Î¶ Protein. PLoS ONE, 2015, 10, e0135976.	1.1	9
42	Transient Near-UV Absorption of the Light-Driven Sodium Pump Krokinobacter eikastus Rhodopsin 2: A Spectroscopic Marker for Retinal Configuration. Journal of Physical Chemistry Letters, 2021, 12, 6284-6291.	2.1	9
43	Two-photon conversion of a bacterial phytochrome. Biophysical Journal, 2021, 120, 964-974.	0.2	8
44	Solvent Relaxation NMR: A Tool for Real-Time Monitoring Water Dynamics in Protein Aggregation Landscape. ACS Chemical Neuroscience, 2021, 12, 2903-2916.	1.7	8
45	Structural Dynamics of RNA in the Presence of Choline Amino Acid Based Ionic Liquid: A Spectroscopic and Computational Outlook. ACS Central Science, 2021, 7, 1688-1697.	5.3	8
46	Insight into the isomerization mechanism of retinal proteins from hybrid quantum mechanics/molecular mechanics simulations. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1562.	6.2	7
47	Tuning the Quantum Chemical Properties of Flavins via Modification at C8. Journal of Physical Chemistry B, 2021, 125, 12654-12669.	1.2	7
48	Evidences for zinc (II) and copper (II) ion interactions with Mycobacterium leprae HSP18: Effect on its structure and chaperone function. Journal of Inorganic Biochemistry, 2018, 188, 62-75.	1.5	6
49	Doubling FÃ¶rster Resonance Energy Transfer Efficiency in Proteins with Extrinsic Thioamide Probes: Implications for Thiomodified Nucleobases. Chemistry - A European Journal, 2021, 27, 4373-4383.	1.7	6
50	Quantifying the Structural Requirements for Designing Newer FLT3 Inhibitors. Medicinal Chemistry, 2012, 8, 913-927.	0.7	5
51	Expedient synthesis of the pentasaccharide repeating unit of the O-antigen of Escherichia coli O86 and its conformational analysis. Glycoconjugate Journal, 2016, 33, 887-896.	1.4	5
52	Atomistic Insight into the Role of Threonine 127 in the Functional Mechanism of Channelrhodopsin-2. Applied Sciences (Switzerland), 2019, 9, 4905.	1.3	4
53	Linear synthesis and conformational analysis of the pentasaccharide repeating unit of the cell wall O-antigen of Escherichia coli O13. Carbohydrate Research, 2014, 391, 9-15.	1.1	3
54	Synthesis of the tetrasaccharide repeating unit of the O-antigen of the Escherichia coli O69 strain and its conformational analysis. RSC Advances, 2014, 4, 37079-37084.	1.7	3

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55	Activity of a novel sulfonamide compound 2-nitro-N-(pyridin-2-ylmethyl)benzenesulfonamide against Leishmania donovani. Drug Design, Development and Therapy, 2016, 10, 1753.	2.0	3
56	Synthesis of the pentasaccharide repeating unit of the O-antigen of Escherichia coli O175 using one-pot glycosylations and its conformational analysis. Tetrahedron, 2014, 70, 9262-9267.	1.0	2
57	Characterization of Antimicrobial Peptideâ€“Membrane Interaction Using All-Atom Molecular Dynamic Simulation. Springer Protocols, 2020, , 163-176.	0.1	2
58	Computational Resources for Bioscience Education. Applied Biochemistry and Biotechnology, 2021, 193, 3418-3424.	1.4	0
59	Cover Image, Volume 12, Issue 2. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, .	6.2	0