

Ramasubbu Sankararamakrishnan

List of Publications by Year in descending order

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citing authors

#	ARTICLE	IF	CITATIONS
1	Designing BH3-Mimetic Peptide Inhibitors for the Viral Bcl-2 Homologues A179L and BHRF1: Importance of Long-Range Electrostatic Interactions. ACS Omega, 2021, 6, 26976-26989.	1.6	8
2	Is the E.Âcoli Homolog of the Formate/Nitrite Transporter Family an Anion Channel? A Computational Study. Biophysical Journal, 2020, 118, 846-860.	0.2	3
3	Computational Design of BH3-Mimetic Peptide Inhibitors That Can Bind Specifically to Mcl-1 or Bcl-X_L: Role of Non-Hot Spot Residues. Biochemistry, 2020, 59, 4379-4394.	1.2	8
4	Presence of Intra-helical Salt-Bridge in Loop E Half-Helix Can Influence the Transport Properties of AQP1 and GlpF Channels: Molecular Dynamics Simulations of In Silico Mutants. Journal of Membrane Biology, 2019, 252, 17-29.	1.0	4
5	dbSWEET: An Integrated Resource for SWEET Superfamily to Understand, Analyze and Predict the Function of Sugar Transporters in Prokaryotes and Eukaryotes. Journal of Molecular Biology, 2018, 430, 2203-2211.	2.0	7
6	Imidazole Nitrogens of Two Histidine Residues Participating in Nâ€“Hâ€“N Hydrogen Bonds in Protein Structures: Structural Bioinformatics Approach Combined with Quantum Chemical Calculations. Journal of Physical Chemistry B, 2018, 122, 1205-1212.	1.2	13
7	Cooperativity in Plant Plasma Membrane Intrinsic Proteins (PIPs): Mechanism of Increased Water Transport in Maize PIP1 Channels in Hetero-tetramers. Scientific Reports, 2018, 8, 12055.	1.6	22
8	Binding affinity of pro-apoptotic BH3 peptides for the anti-apoptotic Mcl-1 and A1 proteins: Molecular dynamics simulations of Mcl-1 and A1 in complex with six different BH3 peptides. Journal of Molecular Graphics and Modelling, 2017, 73, 115-128.	1.3	10
9	Comparison of metal-binding strength between methionine and cysteine residues: Implications for the design of metal-binding motifs in proteins. Biophysical Chemistry, 2017, 224, 32-39.	1.5	16
10	Anion-selective Formate/nitrite transporters: taxonomic distribution, phylogenetic analysis and subfamily-specific conservation pattern in prokaryotes. BMC Genomics, 2017, 18, 560.	1.2	24
11	Unconventional N-Hâ€“N Hydrogen Bonds Involving Proline Backbone Nitrogen in Protein Structures. Biophysical Journal, 2016, 110, 1967-1979.	0.2	38
12	Nâ€“Hâ€“N Hydrogen Bonds Involving Histidine Imidazole Nitrogen Atoms: A New Structural Role for Histidine Residues in Proteins. Biochemistry, 2016, 55, 3774-3783.	1.2	36
13	Molecular Dynamics Simulations of Wild-Type and Mutant AQP6 Channels: Investigation of Anion Transport in Human AQP6. Biophysical Journal, 2015, 108, 373a-374a.	0.2	0
14	Controlling in Vitro Insulin Amyloidosis with Stable Peptide Conjugates: A Combined Experimental and Computational Study. Journal of Physical Chemistry B, 2015, 119, 15395-15406.	1.2	30
15	Intra-helical salt-bridge and helix destabilizing residues within the same helical turn: Role of functionally important loop E half-helix in channel regulation of major intrinsic proteins. Biochimica Et Biophysica Acta - Biomembranes, 2015, 1848, 1436-1449.	1.4	13
16	Major Intrinsic Protein Superfamily. Methods in Enzymology, 2015, 557, 485-520.	0.4	25
17	New subfamilies of major intrinsic proteins in fungi suggest novel transport properties in fungal channels: implications for the host-fungal interactions. BMC Evolutionary Biology, 2014, 14, 173.	3.2	38
18	Antiapoptotic Bclâ€“2 homolog CEDâ€“9 in <i>Caenorhabditis elegans</i>: Dynamics of BH3 and CEDâ€“4 binding regions and comparison with mammalian antiapoptotic Bclâ€“2 proteins. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1035-1047.	1.5	6

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19	Oxygen π -aromatic contacts in intra-strand base pairs: Analysis of high-resolution DNA crystal structures and quantum chemical calculations. <i>Journal of Structural Biology</i> , 2014, 187, 49-57.	1.3	6
20	Affinities of Selective-Serotonin Reuptake Inhibitor (SSRI) for Human Transporters: Molecular Modeling and Quantum Chemical Studies. <i>Biophysical Journal</i> , 2014, 106, 255a.	0.2	0
21	Relationship between helix stability and binding affinities: molecular dynamics simulations of Bfl-1/A1-binding pro-apoptotic BH3 peptide helices in explicit solvent. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 65-77.	2.0	16
22	Hidden coding potential of eukaryotic genomes: nonAUG started ORFs. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 103-114.	2.0	25
23	PLASTICITY OF BH3 DOMAIN-BINDING HYDROPHOBIC GROOVES IN THE ANTI-APOPTOTIC MCL-1 AND A1 PROTEINS. , 2013, , 468-481.		1
24	Behavior of Solvent-Exposed Hydrophobic Groove in the Anti-Apoptotic Bcl-XL Protein: Clues for Its Ability to Bind Diverse BH3 Ligands from MD Simulations. <i>PLoS ONE</i> , 2013, 8, e54397.	1.1	10
25	MIPModDB: a central resource for the superfamily of major intrinsic proteins. <i>Nucleic Acids Research</i> , 2012, 40, D362-D369.	6.5	33
26	Distinguishing Features of Aquaglyceroporin in Plasmodium Falciparum: Comparative Molecular Dynamics Simulations of Three Aquaporins. <i>Biophysical Journal</i> , 2012, 102, 452a.	0.2	1
27	Dynamics of Noncovalent Interactions in All- β and All- α Class Proteins: Implications for the Stability of Amyloid Aggregates. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 3208-3216.	2.5	8
28	Differential Binding Affinities of Anti-Apoptotic MCL-1 and A1 Proteins for the Pro-Apoptotic BH3 Peptides: Understanding the Molecular Basis using MD Simulations. <i>Biophysical Journal</i> , 2011, 100, 396a.	0.2	0
29	Molecular dynamics simulations of pro-apoptotic BH3 peptide helices in aqueous medium: relationship between helix stability and their binding affinities to the anti-apoptotic protein Bcl-XL. <i>Journal of Computer-Aided Molecular Design</i> , 2011, 25, 413-426.	1.3	25
30	Force field dependence of phospholipid headgroup and acyl chain properties: Comparative molecular dynamics simulations of DMPC bilayers. <i>Journal of Computational Chemistry</i> , 2010, 31, 266-277.	1.5	20
31	Non-Covalent Interactions Involving Aromatic Residues in Protein Structures: Stability and Dynamics in Membrane and Globular Proteins using Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2010, 98, 635a-636a.	0.2	0
32	Quantum Chemical Investigations on Intraresidue Carbonyl π -Carbonyl Contacts in Aspartates of High-Resolution Protein Structures. <i>Journal of Physical Chemistry B</i> , 2010, 114, 1038-1049.	1.2	30
33	Identification of Core Structural Residues in the Sequentially Diverse and Structurally Homologous Bcl-2 Family of Proteins. <i>Biochemistry</i> , 2010, 49, 2574-2584.	1.2	24
34	Genome-wide analysis of major intrinsic proteins in the tree plant <i>Populus trichocarpa</i> : Characterization of XIP subfamily of aquaporins from evolutionary perspective. <i>BMC Plant Biology</i> , 2009, 9, 134.	1.6	225
35	Lone pair π - π interactions between water oxygens and aromatic residues: Quantum chemical studies based on high-resolution protein structures and model compounds. <i>Protein Science</i> , 2009, 18, 595-605.	3.1	111
36	End-to-end and end-to-middle interhelical interactions: new classes of interacting helix pairs in protein structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1032-1041.	2.5	4

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37	Anti-apoptotic Bcl _L protein in complex with BH3 peptides of pro-apoptotic Bak, Bad, and Bim proteins: Comparative molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 492-514.	1.5	44
38	Self-contacts in Asx and Glx residues of high-resolution protein structures: Role of local environment and tertiary interactions. <i>Journal of Molecular Graphics and Modelling</i> , 2008, 27, 20-33.	1.3	12
39	Prediction of translation initiation sites in human mRNA sequences with AUG start codon in weak Kozak context: A neural network approach. <i>Biochemical and Biophysical Research Communications</i> , 2008, 369, 1166-1168.	1.0	15
40	Molecular Dynamics Simulations of C-Terminal Decapeptide of Gastrin-Releasing Peptide in DMPC Bilayers: Structure, Stability and Orientation of the Peptide Hormone Within the Bilayers. <i>Protein and Peptide Letters</i> , 2007, 14, 590-596.	0.4	2
41	Homology modeling of major intrinsic proteins in rice, maize and Arabidopsis: comparative analysis of transmembrane helix association and aromatic/arginine selectivity filters. <i>BMC Structural Biology</i> , 2007, 7, 27.	2.3	94
42	Close Contacts between Carbonyl Oxygen Atoms and Aromatic Centers in Protein Structures: Lone-Pair or Lone-Pair Interactions?. <i>Journal of Physical Chemistry B</i> , 2007, 111, 8680-8683.	1.2	97
43	A Survey of mRNA Sequences with a Non-AUG Start Codon in RefSeq Database. <i>Journal of Biomolecular Structure and Dynamics</i> , 2006, 24, 33-41.	2.0	37
44	Recognition of GPCRs by Peptide Ligands and Membrane Compartments theory: Structural Studies of Endogenous Peptide Hormones in Membrane Environment. <i>Bioscience Reports</i> , 2006, 26, 131-158.	1.1	29
45	ATCUN-like metal-binding motifs in proteins: Identification and characterization by crystal structure and sequence analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 211-221.	1.5	62
46	Surface Tension Parameterization in Molecular Dynamics Simulations of a Phospholipid-bilayer Membrane: Calibration and Effects. <i>Journal of Physical Chemistry B</i> , 2004, 108, 11802-11811.	1.2	21
47	Positioning and Stabilization of Dynorphin Peptides in Membrane Bilayers: the Mechanistic Role of Aromatic and Basic Residues Revealed from Comparative MD Simulations. <i>Journal of Physical Chemistry B</i> , 2002, 106, 209-218.	1.2	23
48	Solvation in simulated annealing and high-temperature molecular dynamics of proteins: A restrained water droplet model. <i>International Journal of Quantum Chemistry</i> , 2000, 77, 174-186.	1.0	25
49	Molecular Dynamics Simulations Predict a Tilted Orientation for the Helical Region of Dynorphin A(1-17) in Dimyristoylphosphatidylcholine Bilayers. <i>Biophysical Journal</i> , 2000, 79, 2331-2344.	0.2	47
50	The pore domain of the nicotinic acetylcholine receptor: molecular modeling, pore dimensions, and electrostatics. <i>Biophysical Journal</i> , 1996, 71, 1659-1671.	0.2	72
51	Solvation, water permeation, and ionic selectivity of a putative model for the pore region of the voltage-gated sodium channel. <i>Biophysical Journal</i> , 1996, 71, 2276-2288.	0.2	23
52	Water in channel-like cavities: structure and dynamics. <i>Biophysical Journal</i> , 1996, 70, 693-702.	0.2	128
53	Molecular dynamics simulations of water within models of ion channels. <i>Biophysical Journal</i> , 1996, 70, 1643-1661.	0.2	97
54	Molecular modelling of Staphylococcal β -toxin ion channels by restrained molecular dynamics. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 161-171.	1.0	22

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55	Modelling membrane proteins using structural restraints. <i>Nature Structural Biology</i> , 1995, 2, 624-631.	9.7	35
56	Structural features of isolated M2 helices of nicotinic receptors. Simulated annealing via molecular dynamics studies. <i>Biophysical Chemistry</i> , 1995, 55, 215-230.	1.5	21
57	Seven-helix bundles: molecular modeling via restrained molecular dynamics. <i>Biophysical Journal</i> , 1995, 68, 1295-1310.	0.2	39
58	Parallel helix bundles and ion channels: molecular modeling via simulated annealing and restrained molecular dynamics. <i>Biophysical Journal</i> , 1994, 67, 1501-1515.	0.2	115
59	Simplified Models of the Pore Domain of the Nicotinic Acetylcholine Receptor. <i>Biochemical Society Transactions</i> , 1994, 22, 158S-158S.	1.6	3
60	Molecular Dynamics Studies of M2 Helices of Nicotinic Acetylcholine Receptors. <i>Biochemical Society Transactions</i> , 1994, 22, 156S-156S.	1.6	2
61	Characterization of proline-containing $\hat{\pm}$ -helix (helix F model of bacteriorhodopsin) by molecular dynamics studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 26-41.	1.5	35
62	The Structures of Bacteriorhodopsin With Different Retinal-Schiff Base Orientations - Computer Modeling And Energy Minimization Studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 1992, 9, 1073-1095.	2.0	2
63	Geometry of proline-containing α -helices in proteins. <i>International Journal of Peptide and Protein Research</i> , 1992, 39, 356-363.	0.1	82
64	Characterization of proline-containing right-handed $\hat{\pm}$ -helix by molecular dynamics studies. <i>Biophysical Chemistry</i> , 1991, 40, 97-108.	1.5	9