

Ramasubbu Sankararamakrishnan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6476142/publications.pdf>

Version: 2024-02-01

64
papers

2,035
citations

293460

24
h-index

274796

44
g-index

69
all docs

69
docs citations

69
times ranked

2621
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Water in channel-like cavities: structure and dynamics. <i>Biophysical Journal</i> , 1996, 70, 693-702.	0.2	128
3	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
4	Lone pair \cdots 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
5	Molecular dynamics simulations of water within models of ion channels. <i>Biophysical Journal</i> , 1996, 70, 1643-1661.	0.2	97
6	Close Contacts between Carbonyl Oxygen Atoms and Aromatic Centers in Protein Structures: \cdots or Lone-Pair \cdots Interactions?. <i>Journal of Physical Chemistry B</i> , 2007, 111, 8680-8683.	1.2	97
7	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
8	Geometry of proline-containing α -helices in proteins. <i>International Journal of Peptide and Protein Research</i> , 1992, 39, 356-363.	0.1	82
9	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
10	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
11	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
12	Anti-apoptotic Bcl-2 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
13	Seven-helix bundles: molecular modeling via restrained molecular dynamics. <i>Biophysical Journal</i> , 1995, 68, 1295-1310.	0.2	39
14	New subfamilies of major intrinsic proteins in fungi suggest novel transport properties in fungal channels: implications for the host-fungal interactions. <i>BMC Evolutionary Biology</i> , 2014, 14, 173.	3.2	38
15	Unconventional N-H \cdots N Hydrogen Bonds Involving Proline Backbone Nitrogen in Protein Structures. <i>Biophysical Journal</i> , 2016, 110, 1967-1979.	0.2	38
16	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
17	N \cdots H \cdots N Hydrogen Bonds Involving Histidine Imidazole Nitrogen Atoms: A New Structural Role for Histidine Residues in Proteins. <i>Biochemistry</i> , 2016, 55, 3774-3783.	1.2	36
18	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

#	ARTICLE	IF	CITATIONS
19	Modelling membrane proteins using structural restraints. <i>Nature Structural Biology</i> , 1995, 2, 624-631.	9.7	35
20	MIPModDB: a central resource for the superfamily of major intrinsic proteins. <i>Nucleic Acids Research</i> , 2012, 40, D362-D369.	6.5	33
21	Quantum Chemical Investigations on Intraresidue Carbonyl~Carbonyl Contacts in Aspartates of High-Resolution Protein Structures. <i>Journal of Physical Chemistry B</i> , 2010, 114, 1038-1049.	1.2	30
22	Controlling in Vitro Insulin Amyloidosis with Stable Peptide Conjugates: A Combined Experimental and Computational Study. <i>Journal of Physical Chemistry B</i> , 2015, 119, 15395-15406.	1.2	30
23	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
24	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
25	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
26	Hidden coding potential of eukaryotic genomes: nonAUG started ORFs. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 103-114.	2.0	25
27	Major Intrinsic Protein Superfamily. <i>Methods in Enzymology</i> , 2015, 557, 485-520.	0.4	25
28	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
29	Anion-selective Formate/nitrite transporters: taxonomic distribution, phylogenetic analysis and subfamily-specific conservation pattern in prokaryotes. <i>BMC Genomics</i> , 2017, 18, 560.	1.2	24
30	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
31	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
32	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
33	Cooperativity in Plant Plasma Membrane Intrinsic Proteins (PIPs): Mechanism of Increased Water Transport in Maize PIP1 Channels in Hetero-tetramers. <i>Scientific Reports</i> , 2018, 8, 12055.	1.6	22
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Comparison of metal-binding strength between methionine and cysteine residues: Implications for the design of metal-binding motifs in proteins. <i>Biophysical Chemistry</i> , 2017, 224, 32-39.	1.5	16
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	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. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1436-1449.	1.4	13
41	Imidazole Nitrogens of Two Histidine Residues Participating in N-H...N Hydrogen Bonds in Protein Structures: Structural Bioinformatics Approach Combined with Quantum Chemical Calculations. <i>Journal of Physical Chemistry B</i> , 2018, 122, 1205-1212.	1.2	13
42	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
43	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
44	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. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 73, 115-128.	1.3	10
45	Characterization of proline-containing right-handed β -helix by molecular dynamics studies. <i>Biophysical Chemistry</i> , 1991, 40, 97-108.	1.5	9
46	Dynamics of Noncovalent Interactions in All- β and All- β^2 Class Proteins: Implications for the Stability of Amyloid Aggregates. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 3208-3216.	2.5	8
47	Computational Design of BH3-Mimetic Peptide Inhibitors That Can Bind Specifically to Mcl-1 or Bcl-X _L : Role of Non-Hot Spot Residues. <i>Biochemistry</i> , 2020, 59, 4379-4394.	1.2	8
48	Designing BH3-Mimetic Peptide Inhibitors for the Viral Bcl-2 Homologues A179L and BHRF1: Importance of Long-Range Electrostatic Interactions. <i>ACS Omega</i> , 2021, 6, 26976-26989.	1.6	8
49	dbSWEET: An Integrated Resource for SWEET Superfamily to Understand, Analyze and Predict the Function of Sugar Transporters in Prokaryotes and Eukaryotes. <i>Journal of Molecular Biology</i> , 2018, 430, 2203-2211.	2.0	7
50	Antiapoptotic Bcl-2 homolog CED-9 in <i>Caenorhabditis elegans</i> : Dynamics of BH3 and CED-4 binding regions and comparison with mammalian antiapoptotic Bcl-2 proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1035-1047.	1.5	6
51	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
52	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
53	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. <i>Journal of Membrane Biology</i> , 2019, 252, 17-29.	1.0	4
54	Simplified Models of the Pore Domain of the Nicotinic Acetylcholine Receptor. <i>Biochemical Society Transactions</i> , 1994, 22, 158S-158S.	1.6	3

#	ARTICLE	IF	CITATIONS
55	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
56	The Structures of Bacteriorhodopsin With Different Retinal-Schiff Base Orientations - Computer Modeling And Energy Minimization Studies. Journal of Biomolecular Structure and Dynamics, 1992, 9, 1073-1095.	2.0	2
57	Molecular Dynamics Studies of M2 Helices of Nicotinic Acetylcholine Receptors. Biochemical Society Transactions, 1994, 22, 156S-156S.	1.6	2
58	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. Protein and Peptide Letters, 2007, 14, 590-596.	0.4	2
59	Distinguishing Features of Aquaglyceroporin in Plasmodium Falciparum: Comparative Molecular Dynamics Simulations of Three Aquaporins. Biophysical Journal, 2012, 102, 452a.	0.2	1
60	PLASTICITY OF BH3 DOMAIN-BINDING HYDROPHOBIC GROOVES IN THE ANTI-APOPTOTIC MCL-1 AND A1 PROTEINS. , 2013, , 468-481.		1
61	Non-Covalent Interactions Involving Aromatic Residues in Protein Structures: Stability and Dynamics in Membrane and Globular Proteins using Molecular Dynamics Simulations. Biophysical Journal, 2010, 98, 635a-636a.	0.2	0
62	Differential Binding Affinities of Anti-Apoptotic MCL-1 and A1 Proteins for the Pro-Apoptotic BH3 Peptides: Understanding the Molecular Basis using MD Simulations. Biophysical Journal, 2011, 100, 396a.	0.2	0
63	Affinities of Selective-Serotonin Reuptake Inhibitor (SSRI) for Human Transporters: Molecular Modeling and Quantum Chemical Studies. Biophysical Journal, 2014, 106, 255a.	0.2	0
64	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