RÃ©gis PomÃ¨s

List of Publications by Year
in descending order

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53	3,234	159358	189595
papers	citations	30 h-index	50 g-index

66	66	66	4541
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Proline and Glycine Control Protein Self-Organization into Elastomeric or Amyloid Fibrils. Structure, 2006, 14, 1667-1676.	1.6	320
2	Molecular Mechanism of H+ Conduction in the Single-File Water Chain of the Gramicidin Channel. Biophysical Journal, 2002, 82, 2304-2316.	0.2	250
3	Statistical Convergence of Equilibrium Properties in Simulations of Molecular Solutes Embedded in Lipid Bilayers. Journal of Chemical Theory and Computation, 2011, 7, 4175-4188.	2.3	175
4	The role of dimer asymmetry and protomer dynamics in enzyme catalysis. Science, 2017, 355, .	6.0	155
5	Structures of closed and open states of a voltage-gated sodium channel. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3051-E3060.	3.3	139
6	The liquid structure of elastin. ELife, 2017, 6, .	2.8	137
7	Mechanistic insights into allosteric regulation of the A2A adenosine G protein-coupled receptor by physiological cations. Nature Communications, 2018, 9, 1372.	5.8	126
8	Catalysis of Na ⁺ permeation in the bacterial sodium channel Na _V Ab. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11331-11336.	3.3	113
9	Lysosomal integral membrane protein-2 (LIMP-2/SCARB2) is involved in lysosomal cholesterol export. Nature Communications, 2019, 10, 3521.	5.8	99
10	<scp>O</scp>rkambiÂ® and amplifier coâ€therapy improves function from a rare <scp>CFTR</scp> mutation in geneâ€edited cells and patient tissue. EMBO Molecular Medicine, 2017, 9, 1224-1243.	3.3	94
11	STIM1 activates CRAC channels through rotation of the pore helix to open a hydrophobic gate. Nature Communications, 2017, 8, 14512.	5.8	87
12	Role of Liquidâ€“Liquid Phase Separation in Assembly of Elastin and Other Extracellular Matrix Proteins. Journal of Molecular Biology, 2018, 430, 4741-4753.	2.0	86
13	Accelerating Convergence in Molecular Dynamics Simulations of Solutes in Lipid Membranes by Conducting a Random Walk along the Bilayer Normal. Journal of Chemical Theory and Computation, 2013, 9, 3686-3703.	2.3	83
14	Sampling errors in free energy simulations of small molecules in lipid bilayers. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 2539-2548.	1.4	83
15	Indolicidin Binding Induces Thinning of a Lipid Bilayer. Biophysical Journal, 2014, 106, L29-L31.	0.2	81
16	Structure of saposin A lipoprotein discs. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2908-2912.	3.3	77
17	Structural Disorder and Protein Elasticity. Advances in Experimental Medicine and Biology, 2012, 725, 159-183.	0.8	72
18	Molecular simulations of protein disorderThis paper is one of a selection of papers published in this special issue entitled â€œCanadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting â€" Protein Folding: Principles and Diseasesâ€•and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2010, 88, 269-290.	0.9	68

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19	Can Specific Protein-Lipid Interactions Stabilize an Active State of the Beta 2 Adrenergic Receptor?. Biophysical Journal, 2015, 109, 1652-1662.	0.2	58
20	The molecular mechanism of Zinc acquisition by the neisserial outer-membrane transporter ZnuD. Nature Communications, 2015, 6, 7996.	5.8	58
21	Open-state structure and pore gating mechanism of the cardiac sodium channel. Cell, 2021, 184, 5151-5162.e11.	13.5	56
22	Structural basis for gating pore current in periodic paralysis. Nature, 2018, 557, 590-594.	13.7	55
23	Structural basis for voltage-sensor trapping of the cardiac sodium channel by a deathstalker scorpion toxin. Nature Communications, 2021, 12, 128.	5.8	54
24	Mapping the functional anatomy of Orai1 transmembrane domains for CRAC channel gating. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5193-E5202.	3.3	52
25	Simulated Tempering Distributed Replica Sampling, Virtual Replica Exchange, and Other Generalized-Ensemble Methods for Conformational Sampling. Journal of Chemical Theory and Computation, 2009, 5, 2640-2662.	2.3	50
26	Modification and periplasmic translocation of the biofilm exopolysaccharide poly-Î²-1,6- N -acetyl- <scp>d</scp> -glucosamine. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11013-11018.	3.3	48
27	Hydrophobic Gating of Ion Permeation in Magnesium Channel CorA. PLoS Computational Biology, 2015, 11, e1004303.	1.5	48
28	Structure of Human Acid Sphingomyelinase Reveals the Role of the Saposin Domain in Activating Substrate Hydrolysis. Journal of Molecular Biology, 2016, 428, 3026-3042.	2.0	46
29	Modulated growth, stability and interactions of liquid-like coacervate assemblies of elastin. Matrix Biology, 2014, 36, 39-50.	1.5	39
30	Somatostatin binds to the human amyloid Î² peptide and favors the formation of distinct oligomers. ELife, 2017, 6, .	2.8	37
31	Hydrophobic gasket mutation produces gating pore currents in closed human voltage-gated proton channels. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18951-18961.	3.3	35
32	Atomistic picture of conformational exchange in a T4 lysozyme cavity mutant: an experiment-guided molecular dynamics study. Chemical Science, 2016, 7, 3602-3613.	3.7	34
33	A Scalable FPGA-based Multiprocessor. , 2006, , .		33
34	Systematic design of unimolecular star copolymer micelles using molecular dynamics simulations. Soft Matter, 2010, 6, 5491.	1.2	30
35	Identification of binding sites for ivacaftor on the cystic fibrosis transmembrane conductance regulator. IScience, 2021, 24, 102542.	1.9	29
36	Distributed Replica Sampling. Journal of Chemical Theory and Computation, 2006, 2, 725-731.	2.3	26

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37	Substrate-Based Allosteric Regulation of a Homodimeric Enzyme. Journal of the American Chemical Society, 2019, 141, 11540-11556.	6.6	26
38	Structure and Dynamics of Extracellular Loops in Human Aquaporin-1 from Solid-State NMR and Molecular Dynamics. Journal of Physical Chemistry B, 2016, 120, 9887-9902.	1.2	24
39	Solution NMR structure of yeast Rcf1, a protein involved in respiratory supercomplex formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3048-3053.	3.3	21
40	The basic residues in the Orai1 channel inner pore promote opening of the outer hydrophobic gate. Journal of General Physiology, 2020, 152, .	0.9	21
41	Peptide Bond Isomerization in High-Temperature Simulations. Journal of Chemical Theory and Computation, 2016, 12, 1989-1999.	2.3	18
42	Structural ordering of the Plasmodium berghei circumsporozoite protein repeats by inhibitory antibody 3D11. ELife, 2020, 9, .	2.8	15
43	A sulfur-aromatic gate latch is essential for opening of the Orai1 channel pore. ELife, 2020, 9, .	2.8	13
44	Mechanism of Amyloidogenesis of a Bacterial AAA+ Chaperone. Structure, 2016, 24, 1095-1109.	1.6	12
45	Defluorination Capability of <scp>I</scp>â€2â€Haloacid Dehalogenases in the HADâ€Like Hydrolase Superfamily Correlates with Active Site Compactness. ChemBioChem, 2022, 23, .	1.3	12
46	NMR Structure and Dynamics Studies of Yeast Respiratory Supercomplex Factor 2. Structure, 2021, 29, 275-283.e4.	1.6	10
47	Relay and blockage of protons in water chains. Frontiers in Bioscience - Landmark, 2003, 8, d1288-1297.	3.0	8
48	Molecular recognition and packing frustration in a helical protein. PLoS Computational Biology, 2017, 13, e1005909.	1.5	5
49	Structural basis of Plasmodium vivax inhibition by antibodies binding to the circumsporozoite protein repeats. ELife, 2022, 11, .	2.8	5
50	The evolutionary background and functional consequences of the rs2071307 polymorphism in human tropoelastin. Biopolymers, 2021, 112, e23414.	1.2	4
51	Simulated tempering distributed replica sampling: A practical guide to enhanced conformational sampling. Journal of Physics: Conference Series, 2010, 256, 012011.	0.3	2
52	Molecular mechanism of biological proton transport. , 1999, , .		0
53	Proton Relay in Membrane Proteins. ACS Symposium Series, 2004, , 159-173.	0.5	0