

# RÃ©gis PomÃ©s

## List of Publications by Year in descending order

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53  
papers

3,234  
citations

159358

30  
h-index

189595

50  
g-index

66  
all docs

66  
docs citations

66  
times ranked

4541  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defluorination Capability of Haloacid Dehalogenases in the HAD-Like Hydrolase Superfamily Correlates with Active Site Compactness. <i>ChemBioChem</i> , 2022, 23, .	1.3	12
2	Structural basis of Plasmodium vivax inhibition by antibodies binding to the circumsporozoite protein repeats. <i>ELife</i> , 2022, 11, .	2.8	5
3	NMR Structure and Dynamics Studies of Yeast Respiratory Supercomplex Factor 2. <i>Structure</i> , 2021, 29, 275-283.e4.	1.6	10
4	Structural basis for voltage-sensor trapping of the cardiac sodium channel by a deathstalker scorpion toxin. <i>Nature Communications</i> , 2021, 12, 128.	5.8	54
5	Identification of binding sites for ivacaftor on the cystic fibrosis transmembrane conductance regulator. <i>IScience</i> , 2021, 24, 102542.	1.9	29
6	Open-state structure and pore gating mechanism of the cardiac sodium channel. <i>Cell</i> , 2021, 184, 5151-5162.e11.	13.5	56
7	The evolutionary background and functional consequences of the rs2071307 polymorphism in human tropoelastin. <i>Biopolymers</i> , 2021, 112, e23414.	1.2	4
8	The basic residues in the Orai1 channel inner pore promote opening of the outer hydrophobic gate. <i>Journal of General Physiology</i> , 2020, 152, .	0.9	21
9	Structural ordering of the Plasmodium berghei circumsporozoite protein repeats by inhibitory antibody 3D11. <i>ELife</i> , 2020, 9, .	2.8	15
10	A sulfur-aromatic gate latch is essential for opening of the Orai1 channel pore. <i>ELife</i> , 2020, 9, .	2.8	13
11	Lysosomal integral membrane protein-2 (LIMP-2/SCARB2) is involved in lysosomal cholesterol export. <i>Nature Communications</i> , 2019, 10, 3521.	5.8	99
12	Substrate-Based Allosteric Regulation of a Homodimeric Enzyme. <i>Journal of the American Chemical Society</i> , 2019, 141, 11540-11556.	6.6	26
13	Hydrophobic gasket mutation produces gating pore currents in closed human voltage-gated proton channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18951-18961.	3.3	35
14	Solution NMR structure of yeast Rcf1, a protein involved in respiratory supercomplex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3048-3053.	3.3	21
15	Mechanistic insights into allosteric regulation of the A2A adenosine G protein-coupled receptor by physiological cations. <i>Nature Communications</i> , 2018, 9, 1372.	5.8	126
16	Structural basis for gating pore current in periodic paralysis. <i>Nature</i> , 2018, 557, 590-594.	13.7	55
17	Mapping the functional anatomy of Orai1 transmembrane domains for CRAC channel gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5193-E5202.	3.3	52
18	Role of Liquid-Liquid Phase Separation in Assembly of Elastin and Other Extracellular Matrix Proteins. <i>Journal of Molecular Biology</i> , 2018, 430, 4741-4753.	2.0	86

#	ARTICLE	IF	CITATIONS
19	The role of dimer asymmetry and protomer dynamics in enzyme catalysis. <i>Science</i> , 2017, 355, .	6.0	155
20	STIM1 activates CRAC channels through rotation of the pore helix to open a hydrophobic gate. <i>Nature Communications</i> , 2017, 8, 14512.	5.8	87
21	Structures of closed and open states of a voltage-gated sodium channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3051-E3060.	3.3	139
22	<sc>O</sc>rkambiÂ® and amplifier coâ€therapy improves function from a rare <i><sc>CFTR</sc></i> mutation in geneâ€edited cells and patient tissue. <i>EMBO Molecular Medicine</i> , 2017, 9, 1224-1243.	3.3	94
23	Molecular recognition and packing frustration in a helical protein. <i>PLoS Computational Biology</i> , 2017, 13, e1005909.	1.5	5
24	The liquid structure of elastin. <i>ELife</i> , 2017, 6, .	2.8	137
25	Somatostatin binds to the human amyloid Î² peptide and favors the formation of distinct oligomers. <i>ELife</i> , 2017, 6, .	2.8	37
26	Structure and Dynamics of Extracellular Loops in Human Aquaporin-1 from Solid-State NMR and Molecular Dynamics. <i>Journal of Physical Chemistry B</i> , 2016, 120, 9887-9902.	1.2	24
27	Structure of Human Acid Sphingomyelinase Reveals the Role of the Saposin Domain in Activating Substrate Hydrolysis. <i>Journal of Molecular Biology</i> , 2016, 428, 3026-3042.	2.0	46
28	Mechanism of Amyloidogenesis of a Bacterial AAA+ Chaperone. <i>Structure</i> , 2016, 24, 1095-1109.	1.6	12
29	Sampling errors in free energy simulations of small molecules in lipid bilayers. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 2539-2548.	1.4	83
30	Peptide Bond Isomerization in High-Temperature Simulations. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 1989-1999.	2.3	18
31	Atomistic picture of conformational exchange in a T4 lysozyme cavity mutant: an experiment-guided molecular dynamics study. <i>Chemical Science</i> , 2016, 7, 3602-3613.	3.7	34
32	Hydrophobic Gating of Ion Permeation in Magnesium Channel CorA. <i>PLoS Computational Biology</i> , 2015, 11, e1004303.	1.5	48
33	Can Specific Protein-Lipid Interactions Stabilize an Active State of the Beta 2 Adrenergic Receptor?. <i>Biophysical Journal</i> , 2015, 109, 1652-1662.	0.2	58
34	The molecular mechanism of Zinc acquisition by the neisserial outer-membrane transporter ZnuD. <i>Nature Communications</i> , 2015, 6, 7996.	5.8	58
35	Indolicidin Binding Induces Thinning of a Lipid Bilayer. <i>Biophysical Journal</i> , 2014, 106, L29-L31.	0.2	81
36	Modification and periplasmic translocation of the biofilm exopolysaccharide poly-Î²-1,6- <i>N</i>-acetyl- <sc>d</sc>-glucosamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11013-11018.	3.3	48

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37	Modulated growth, stability and interactions of liquid-like coacervate assemblies of elastin. <i>Matrix Biology</i> , 2014, 36, 39-50.	1.5	39
38	Catalysis of Na <sup>+</sup> permeation in the bacterial sodium channel Na <sup>v</sup> Ab. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11331-11336.	3.3	113
39	Accelerating Convergence in Molecular Dynamics Simulations of Solutes in Lipid Membranes by Conducting a Random Walk along the Bilayer Normal. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 3686-3703.	2.3	83
40	Structure of saposin A lipoprotein discs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2908-2912.	3.3	77
41	Structural Disorder and Protein Elasticity. <i>Advances in Experimental Medicine and Biology</i> , 2012, 725, 159-183.	0.8	72
42	Statistical Convergence of Equilibrium Properties in Simulations of Molecular Solutes Embedded in Lipid Bilayers. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 4175-4188.	2.3	175
43	Simulated tempering distributed replica sampling: A practical guide to enhanced conformational sampling. <i>Journal of Physics: Conference Series</i> , 2010, 256, 012011.	0.3	2
44	Molecular simulations of protein disorder This paper is one of a selection of papers published in this special issue entitled "Canadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting - Protein Folding: Principles and Diseases" and has undergone the Journal's usual peer review process. <i>Biochemistry and Cell Biology</i> , 2010, 88, 269-290.	0.9	68
45	Systematic design of unimolecular star copolymer micelles using molecular dynamics simulations. <i>Soft Matter</i> , 2010, 6, 5491.	1.2	30
46	Simulated Tempering Distributed Replica Sampling, Virtual Replica Exchange, and Other Generalized-Ensemble Methods for Conformational Sampling. <i>Journal of Chemical Theory and Computation</i> , 2009, 5, 2640-2662.	2.3	50
47	Distributed Replica Sampling. <i>Journal of Chemical Theory and Computation</i> , 2006, 2, 725-731.	2.3	26
48	Proline and Glycine Control Protein Self-Organization into Elastomeric or Amyloid Fibrils. <i>Structure</i> , 2006, 14, 1667-1676.	1.6	320
49	A Scalable FPGA-based Multiprocessor. , 2006, , .		33
50	Proton Relay in Membrane Proteins. <i>ACS Symposium Series</i> , 2004, , 159-173.	0.5	0
51	Relay and blockage of protons in water chains. <i>Frontiers in Bioscience - Landmark</i> , 2003, 8, d1288-1297.	3.0	8
52	Molecular Mechanism of H <sup>+</sup> Conduction in the Single-File Water Chain of the Gramicidin Channel. <i>Biophysical Journal</i> , 2002, 82, 2304-2316.	0.2	250
53	Molecular mechanism of biological proton transport. , 1999, , .		0