FrÃ©dÃ©ric Poitevin

List of Publications by Year
in descending order

31 papers	1,672 citations	516710 16 h-index	434195 31 g-index
35 all docs	35 docs citations	35 times ranked	1840 citing authors

#	Article	IF	Citations
1	X-ray structure of the mouse serotonin 5-HT3 receptor. Nature, 2014, 512, 276-281.	27.8	358
2	Structure and Pharmacology of Pentameric Receptor Channels: From Bacteria to Brain. Structure, 2012, 20, 941-956.	3.3	202
3	Crystal structures of a pentameric ligand-gated ion channel provide a mechanism for activation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 966-971.	7.1	175
4	One-microsecond molecular dynamics simulation of channel gating in a nicotinic receptor homologue. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6275-6280.	7.1	159
5	Structural basis for ion permeation mechanism in pentameric ligand-gated ion channels. EMBO Journal, 2013, 32, 728-741.	7.8	140
6	A locally closed conformation of a bacterial pentameric proton-gated ion channel. Nature Structural and Molecular Biology, 2012, 19, 642-649.	8.2	135
7	AquaSAXS: a web server for computation and fitting of SAXS profiles with non-uniformally hydrated atomic models. Nucleic Acids Research, 2011, 39, W184-W189.	14.5	91
8	String method solution of the gating pathways for a pentameric ligand-gated ion channel. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4158-E4167.	7.1	60
9	Nutrient transport suggests an evolutionary basis for charged archaeal surface layer proteins. ISME Journal, 2018, 12, 2389-2402.	9.8	51
10	Computational Assembly of Polymorphic Amyloid Fibrils Reveals Stable Aggregates. Biophysical Journal, 2013, 104, 683-693.	0.5	36
11	Chemical crystallography by serial femtosecond X-ray diffraction. Nature, 2022, 601, 360-365.	27.8	33
12	Near-physiological-temperature serial crystallography reveals conformations of SARS-CoV-2 main protease active site for improved drug repurposing. Structure, 2021, 29, 1382-1396.e6.	3.3	28
13	Intermolecular correlations are necessary to explain diffuse scattering from protein crystals. IUCrJ, 2018, 5, 211-222.	2.2	24
14	Structural basis for a novel mechanism of <scp>DNA</scp> bridging and alignment in eukaryotic <scp>DSB DNA</scp> repair. EMBO Journal, 2015, 34, 1126-1142.	7.8	21
15	Structure of the Visual Signaling Complex between Transducin and Phosphodiesterase 6. Molecular Cell, 2020, 80, 237-245.e4.	9.7	21
16	Structural Heterogeneities of the Ribosome: New Frontiers and Opportunities for Cryo-EM. Molecules, 2020, 25, 4262.	3.8	20
17	The Renormalization Group and Its Applications to Generating Coarse-Grained Models of Large Biological Molecular Systems. Journal of Chemical Theory and Computation, 2017, 13, 1424-1438.	5.3	16
18	Aminoglycoside ribosome interactions reveal novel conformational states at ambient temperature. Nucleic Acids Research, 2018, 46, 9793-9804.	14.5	15

#	Article	IF	Citations
19	Modified Poissonâ€“Boltzmann equations for characterizing biomolecular solvation. Journal of Theoretical and Computational Chemistry, 2014, 13, 1440001.	1.8	13
20	Structure of the 30S ribosomal decoding complex at ambient temperature. Rna, 2018, 24, 1667-1676.	3.5	12
21	Comparative Normal Mode Analysis of the Dynamics of DENV and ZIKV Capsids. Frontiers in Molecular Biosciences, 2016, 3, 85.	3.5	11
22	Protocol for structure determination of SARS-CoV-2 main protease at near-physiological-temperature by serial femtosecond crystallography. STAR Protocols, 2022, 3, 101158.	1.2	11
23	Case Study of High-Throughput Drug Screening and Remote Data Collection for SARS-CoV-2 Main Protease by Using Serial Femtosecond X-ray Crystallography. Crystals, 2021, 11, 1579.	2.2	9
24	Cooperative allostery and structural dynamics of streptavidin at cryogenic- and ambient-temperature. Communications Biology, 2022, 5, 73.	4.4	6
25	Derivation of the Crickâ€“Wyman Equation for Allosteric Proteins Defining the Difference between the Number of Binding Sites and the Hill Coefficient. Journal of Molecular Biology, 2013, 425, 1497-1499.	4.2	5
26	Reproducibility of protein x-ray diffuse scattering and potential utility for modeling atomic displacement parameters. Structural Dynamics, 2021, 8, 044701.	2.3	5
27	Conformational Dynamics in a Nicotinic Receptor Homologue Probed by Simulations. Biophysical Journal, 2011, 100, 272a.	0.5	3
28	Beyond Poissonâ€“Boltzmann: Numerical Sampling of Charge Density Fluctuations. Journal of Physical Chemistry B, 2016, 120, 6270-6277.	2.6	3
29	Application of transport-based metric for continuous interpolation between cryo-EM density maps. AIMS Mathematics, 2021, 7, 986-999.	1.6	2
30	Gating Pathways for a Pentameric Ligand-Gated Ion Channel Solved by Atomistic String Method Simulations. Biophysical Journal, 2017, 112, 475a.	0.5	1
31	Reduction of small-angle scattering profiles to finite sets of structural invariants. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, 317-332.	0.1	0