FrÃ©dÃ©ric Poitevin

List of Publications by Year
in descending order

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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	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
2	Chemical crystallography by serial femtosecond X-ray diffraction. Nature, 2022, 601, 360-365.	27.8	33
3	Cooperative allostery and structural dynamics of streptavidin at cryogenic- and ambient-temperature. Communications Biology, 2022, 5, 73.	4.4	6
4	Reproducibility of protein x-ray diffuse scattering and potential utility for modeling atomic displacement parameters. Structural Dynamics, 2021, 8, 044701.	2.3	5
5	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
6	Application of transport-based metric for continuous interpolation between cryo-EM density maps. AIMS Mathematics, 2021, 7, 986-999.	1.6	2
7	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
8	Structure of the Visual Signaling Complex between Transducin and Phosphodiesterase 6. Molecular Cell, 2020, 80, 237-245.e4.	9.7	21
9	Structural Heterogeneities of the Ribosome: New Frontiers and Opportunities for Cryo-EM. Molecules, 2020, 25, 4262.	3.8	20
10	Structure of the 30S ribosomal decoding complex at ambient temperature. Rna, 2018, 24, 1667-1676.	3.5	12
11	Aminoglycoside ribosome interactions reveal novel conformational states at ambient temperature. Nucleic Acids Research, 2018, 46, 9793-9804.	14.5	15
12	Nutrient transport suggests an evolutionary basis for charged archaeal surface layer proteins. ISME Journal, 2018, 12, 2389-2402.	9.8	51
13	Intermolecular correlations are necessary to explain diffuse scattering from protein crystals. IUCrJ, 2018, 5, 211-222.	2.2	24
14	Gating Pathways for a Pentameric Ligand-Gated Ion Channel Solved by Atomistic String Method Simulations. Biophysical Journal, 2017, 112, 475a.	0.5	1
15	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
16	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
17	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
18	Comparative Normal Mode Analysis of the Dynamics of DENV and ZIKV Capsids. Frontiers in Molecular Biosciences, 2016, 3, 85.	3.5	11

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19	Beyond Poissonâ€“Boltzmann: Numerical Sampling of Charge Density Fluctuations. Journal of Physical Chemistry B, 2016, 120, 6270-6277.	2.6	3
20	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
21	Modified Poissonâ€“Boltzmann equations for characterizing biomolecular solvation. Journal of Theoretical and Computational Chemistry, 2014, 13, 1440001.	1.8	13
22	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
23	X-ray structure of the mouse serotonin 5-HT3 receptor. Nature, 2014, 512, 276-281.	27.8	358
24	Structural basis for ion permeation mechanism in pentameric ligand-gated ion channels. EMBO Journal, 2013, 32, 728-741.	7.8	140
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	Computational Assembly of Polymorphic Amyloid Fibrils Reveals Stable Aggregates. Biophysical Journal, 2013, 104, 683-693.	0.5	36
27	A locally closed conformation of a bacterial pentameric proton-gated ion channel. Nature Structural and Molecular Biology, 2012, 19, 642-649.	8.2	135
28	Structure and Pharmacology of Pentameric Receptor Channels: From Bacteria to Brain. Structure, 2012, 20, 941-956.	3.3	202
29	Conformational Dynamics in a Nicotinic Receptor Homologue Probed by Simulations. Biophysical Journal, 2011, 100, 272a.	0.5	3
30	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
31	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