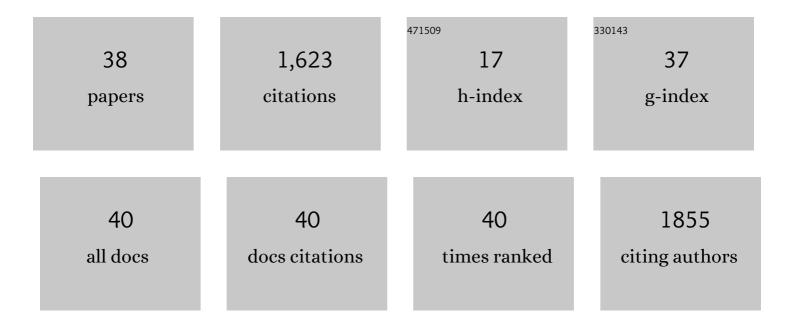
Martin Picard

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	How to best estimate the viscosity of lipid bilayers. Biophysical Chemistry, 2022, 281, 106732.	2.8	8
2	Structure, Assembly, and Function of Tripartite Efflux and Type 1 Secretion Systems in Gram-Negative Bacteria. Chemical Reviews, 2021, 121, 5479-5596.	47.7	103
3	Quantitative real-time analysis of the efflux by the MacAB-TolC tripartite efflux pump clarifies the role of ATP hydrolysis within mechanotransmission mechanism. Communications Biology, 2021, 4, 493.	4.4	7
4	Antibiotic export by MexB multidrug efflux transporter is allosterically controlled by a MexA-OprM chaperone-like complex. Nature Communications, 2020, 11, 4948.	12.8	45
5	Rationale for the Quantitative Reconstitution of Membrane Proteins into Proteoliposomes. Methods in Molecular Biology, 2020, 2168, 63-72.	0.9	1
6	LC–MS/MS-based quantification of efflux transporter proteins at the BBB. Journal of Pharmaceutical and Biomedical Analysis, 2019, 164, 496-508.	2.8	18
7	Biochemical Reconstitution and Characterization of Multicomponent Drug Efflux Transporters. Methods in Molecular Biology, 2018, 1700, 113-145.	0.9	10
8	Reconstitution of the activity of RND efflux pumps: a "bottom-up―approach. Research in Microbiology, 2018, 169, 442-449.	2.1	6
9	Quantification of Detergents Complexed with Membrane Proteins. Scientific Reports, 2017, 7, 41751.	3.3	66
10	Targeted unlabeled multiple reaction monitoring analysis of cell markers for the study of sample heterogeneity in isolated rat brain cortical microvessels. Journal of Neurochemistry, 2017, 142, 597-609.	3.9	14
11	Reconstitution of Membrane Proteins in Liposomes. Methods in Molecular Biology, 2017, 1635, 259-282.	0.9	14
12	Tripartite assembly of RND multidrug efflux pumps. Nature Communications, 2016, 7, 10731.	12.8	166
13	Focus on the Outer Membrane Factor OprM, the Forgotten Player from Efflux Pumps Assemblies. Antibiotics, 2015, 4, 544-566.	3.7	15
14	Catch me if you can: a biotinylated proteoliposome affinity assay for the investigation of assembly of the MexA-MexB-OprM efflux pump from Pseudomonas aeruginosa. Frontiers in Microbiology, 2015, 6, 541.	3.5	19
15	New OprM structure highlighting the nature of the N-terminal anchor. Frontiers in Microbiology, 2015, 6, 667.	3.5	15
16	In vitro transport activity of the fully assembled MexAB-OprM efflux pump from Pseudomonas aeruginosa. Nature Communications, 2015, 6, 6890.	12.8	47
17	Amphipol-Mediated Screening of Molecular Orthoses Specific for Membrane Protein Targets. Journal of Membrane Biology, 2014, 247, 925-940.	2.1	22
18	Solution Behavior and Crystallization of Cytochrome bc 1 in the Presence of Amphipols. Journal of Membrane Biology, 2014, 247, 981-996.	2.1	25

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19	In vitro Investigation of the MexAB Efflux Pump From Pseudomonas aeruginosa . Journal of Visualized Experiments, 2014, , e50894.	0.3	9
20	Hoechst likes to play hide and seek $\hat{a} \in \$ use it with caution!. Analytical Biochemistry, 2013, 440, 117-119.	2.4	5
21	Functional Investigation of the MexA-MexB-OprM Efflux Pump of Pseudomonas Aeruginosa. Biophysical Journal, 2013, 104, 286a.	0.5	3
22	Innovative Tools for the Structural and Functional Investigation of a Multidrug Efflux Pump from Pseudomonas Aeruginosa. Biophysical Journal, 2013, 104, 407a.	0.5	0
23	Photo-induced proton gradients for the in vitro investigation of bacterial efflux pumps. Scientific Reports, 2012, 2, 306.	3.3	25
24	Activity monitoring of functional OprM using a biomimetic microfluidic device. Analyst, The, 2012, 137, 847.	3.5	13
25	Stoichiometry of the <scp>M</scp> ex <scp>A</scp> â€ <scp>O</scp> pr <scp>M</scp> binding, as investigated by blue native gel electrophoresis. Electrophoresis, 2012, 33, 1282-1287.	2.4	14
26	Monitoring the active transport of efflux pumps after their reconstitution into proteoliposomes: Caveats and keys. Analytical Biochemistry, 2012, 420, 194-196.	2.4	8
27	Amphipols From A to Z. Annual Review of Biophysics, 2011, 40, 379-408.	10.0	226
28	Structural and Dynamical Insights into the Opening Mechanism of P. aeruginosa OprM Channel. Structure, 2010, 18, 507-517.	3.3	53
29	Surfactant Sponge Phase Is a Versatile, Tunable and Biologically Relevant Medium To Study Membrane Protein Interactions. Biophysical Journal, 2010, 98, 59a.	O.5	1
30	Ca2+ versus Mg2+ Coordination at the Nucleotide-binding site of the Sarcoplasmic Reticulum Ca2+-ATPase. Journal of Molecular Biology, 2007, 368, 1-7.	4.2	32
31	Inhibitors Bound to Ca ²⁺ -Free Sarcoplasmic Reticulum Ca ²⁺ â^'ATPase Lock Its Transmembrane Region but Not Necessarily Its Cytosolic Region, Revealing the Flexibility of the Loops Connecting Transmembrane and Cytosolic Domains. Biochemistry, 2007, 46, 15162-15174.	2.5	18
32	The structural basis of calcium transport by the calcium pump. Nature, 2007, 450, 1036-1042.	27.8	419
33	Protective and Inhibitory Effects of Various Types of Amphipols on the Ca2+-ATPase from Sarcoplasmic Reticulum: A Comparative Studyâ€. Biochemistry, 2006, 45, 1861-1869.	2.5	74
34	Conformational Changes in Sarcoplasmic Reticulum Ca2+-ATPase Mutants:Â Effect of Mutations either at Ca2+-Binding Site II or at Tryptophan 552 in the Cytosolic Domainâ€. Biochemistry, 2006, 45, 5261-5270.	2.5	13
35	Effects of Inhibitors on Luminal Opening of Ca2+ Binding Sites in an E2P-like Complex of Sarcoplasmic Reticulum Ca22+-ATPase with Be22+-fluoride. Journal of Biological Chemistry, 2006, 281, 3360-3369.	3.4	31
36	The Average Conformation at Micromolar [Ca2+] of Ca2+-ATPase with Bound Nucleotide Differs from That Adopted with the Transition State Analog ADP·AlFx or with AMPPCP under Crystallization Conditions at Millimolar [Ca2+]*. Journal of Biological Chemistry, 2005, 280, 18745-18754.	3.4	27

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37	Involvement of the L6–7 Loop in SERCA1a Ca2+-ATPase Activation by Ca2+ (or Sr2+) and ATP. Journal of Biological Chemistry, 2004, 279, 32125-32133.	3.4	15
38	Functional Properties of Sarcoplasmic Reticulum Ca2+-ATPase after Proteolytic Cleavage at Leu119-Lys120, Close to the A-domain. Journal of Biological Chemistry, 2004, 279, 9156-9166.	3.4	36