isabelle Broutin

List of Publications by Year in descending order

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ISARELLE REQUITIN

#	Article	IF	CITATIONS
1	How to best estimate the viscosity of lipid bilayers. Biophysical Chemistry, 2022, 281, 106732.	2.8	8
2	Molecular Determinants for OMF Selectivity in Tripartite RND Multidrug Efflux Systems. Antibiotics, 2022, 11, 126.	3.7	6
3	The Structural and Functional Study of Efflux Pumps Belonging to the RND Transporters Family from Gram-Negative Bacteria. Antibiotics, 2022, 11, 429.	3.7	2
4	Studying dynamics without explicit dynamics: A structureâ€based study of the export mechanism by <scp>AcrB</scp> . Proteins: Structure, Function and Bioinformatics, 2021, 89, 259-275.	2.6	9
5	MexAB-OprM Efflux Pump Interaction with the Peptidoglycan of Escherichia coli and Pseudomonas aeruginosa. International Journal of Molecular Sciences, 2021, 22, 5328.	4.1	10
6	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
7	Minimal nanodisc without exogenous lipids for stabilizing membrane proteins in detergent-free buffer. Biochimica Et Biophysica Acta - Biomembranes, 2019, 1861, 852-860.	2.6	3
8	The Peptide ERα17p Is a GPER Inverse Agonist that Exerts Antiproliferative Effects in Breast Cancer Cells. Cells, 2019, 8, 590.	4.1	17
9	VEGF (Vascular Endothelial Growth Factor) Functionalized Magnetic Beads in a Microfluidic Device to Improve the Angiogenic Balance in Preeclampsia. Hypertension, 2019, 74, 145-153.	2.7	20
10	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
11	Constitutive Activation of MexT by Amino Acid Substitutions Results in MexEF-OprN Overproduction in Clinical Isolates of Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	23
12	Biochemical Reconstitution and Characterization of Multicomponent Drug Efflux Transporters. Methods in Molecular Biology, 2018, 1700, 113-145.	0.9	10
13	Lysine Succinylation and Acetylation in <i>Pseudomonas aeruginosa</i> . Journal of Proteome Research, 2018, 17, 2449-2459.	3.7	81
14	Functional Mechanism of the Efflux Pumps Transcription Regulators From Pseudomonas aeruginosa Based on 3D Structures. Frontiers in Molecular Biosciences, 2018, 5, 57.	3.5	51
15	From Vascular Smooth Muscle Cells to Folliculogenesis: What About Vasorin?. Frontiers in Medicine, 2018, 5, 335.	2.6	16
16	Quantification of Detergents Complexed with Membrane Proteins. Scientific Reports, 2017, 7, 41751.	3.3	66
17	VEGFR1 domain 2 covalent labeling with horseradish peroxidase: Development of a displacement assay on VEGF. Analytical Biochemistry, 2017, 530, 107-112.	2.4	3
18	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

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19	Reconstitution of Membrane Proteins in Liposomes. Methods in Molecular Biology, 2017, 1635, 259-282.	0.9	14
20	Xenon for tunnelling analysis of the efflux pump component OprN. PLoS ONE, 2017, 12, e0184045.	2.5	5
21	Germline Prolactin Receptor Mutation Is Not a Major Cause of Sporadic Prolactinoma in Humans. Neuroendocrinology, 2016, 103, 738-745.	2.5	17
22	Tripartite assembly of RND multidrug efflux pumps. Nature Communications, 2016, 7, 10731.	12.8	166
23	Biophysical Studies of the Induced Dimerization of Human VEGF Receptor 1 Binding Domain by Divalent Metals Competing with VEGF-A. PLoS ONE, 2016, 11, e0167755.	2.5	10
24	Focus on the Outer Membrane Factor OprM, the Forgotten Player from Efflux Pumps Assemblies. Antibiotics, 2015, 4, 544-566.	3.7	15
25	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
26	New OprM structure highlighting the nature of the N-terminal anchor. Frontiers in Microbiology, 2015, 6, 667.	3.5	15
27	Natural paniceins from mediterranean sponge inhibit the multidrug resistance activity of Patched and increase chemotherapy efficiency on melanoma cells. Oncotarget, 2015, 6, 22282-22297.	1.8	24
28	Residue 146 regulates prolactin receptor folding, basal activity and ligand-responsiveness: Potential implications in breast tumorigenesis. Molecular and Cellular Endocrinology, 2015, 401, 173-188.	3.2	14
29	Mutations in β-Lactamase AmpC Increase Resistance of Pseudomonas aeruginosa Isolates to Antipseudomonal Cephalosporins. Antimicrobial Agents and Chemotherapy, 2015, 59, 6248-6255.	3.2	187
30	In vitro transport activity of the fully assembled MexAB-OprM efflux pump from Pseudomonas aeruginosa. Nature Communications, 2015, 6, 6890.	12.8	47
31	A Residue Quartet in the Extracellular Domain of the Prolactin Receptor Selectively Controls Mitogen-activated Protein Kinase Signaling. Journal of Biological Chemistry, 2015, 290, 11890-11904.	3.4	4
32	Carbapenem resistance in cystic fibrosis strains of Pseudomonas aeruginosa as a result of amino acid substitutions in porin OprD. International Journal of Antimicrobial Agents, 2015, 45, 529-532.	2.5	39
33	Vascular Endothelial Growth Factor Peptide Ligands Explored by Competition Assay and Isothermal Titration Calorimetry. Biochemistry, 2015, 54, 5147-5156.	2.5	15
34	Multiple Mutations Lead to MexXY-OprM-Dependent Aminoglycoside Resistance in Clinical Strains of Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2014, 58, 221-228.	3.2	93
35	Amphipol-Mediated Screening of Molecular Orthoses Specific for Membrane Protein Targets. Journal of Membrane Biology, 2014, 247, 925-940.	2.1	22
36	<pre>In vitro Investigation of the MexAB Efflux Pump From Pseudomonas aeruginosa. Journal of Visualized Experiments, 2014, , e50894.</pre>	0.3	9

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37	Unusual binding of Grb2 protein to a bivalent polyproline-ligand immobilized on a SPR sensor: Intermolecular bivalent binding. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 524-535.	2.3	1
38	Hoechst likes to play hide and seek $\hat{a} \in \mid$ use it with caution!. Analytical Biochemistry, 2013, 440, 117-119.	2.4	5
39	Contribution of asparagine 346 residue to the carbapenemase activity of CMY-2 β-lactamase. FEMS Microbiology Letters, 2013, 345, 147-153.	1.8	14
40	Identification of Polyproline II Regions Derived From the Prolineâ€Rich Nuclear Receptor Coactivators PNRC and PNRC2: New Insights for ERα Coactivator Interactions. Chirality, 2013, 25, 628-642.	2.6	6
41	Photo-induced proton gradients for the in vitro investigation of bacterial efflux pumps. Scientific Reports, 2012, 2, 306.	3.3	25
42	Activity monitoring of functional OprM using a biomimetic microfluidic device. Analyst, The, 2012, 137, 847.	3.5	13
43	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
44	Monitoring the active transport of efflux pumps after their reconstitution into proteoliposomes: Caveats and keys. Analytical Biochemistry, 2012, 420, 194-196.	2.4	8
45	<i>INF2</i> Mutations in Charcot–Marie–Tooth Disease with Glomerulopathy. New England Journal of Medicine, 2011, 365, 2377-2388.	27.0	235
46	Targeting the Proangiogenic VEGF-VEGFR Protein-Protein Interface with Drug-like Compounds by In Silico and InÂVitro Screening. Chemistry and Biology, 2011, 18, 1631-1639.	6.0	38
47	Novel NOBOX loss-of-function mutations account for 6.2% of cases in a large primary ovarian insufficiency cohort. Human Mutation, 2011, 32, 1108-1113.	2.5	94
48	Mutations in INF2 Are a Major Cause of Autosomal Dominant Focal Segmental Glomerulosclerosis. Journal of the American Society of Nephrology: JASN, 2011, 22, 239-245.	6.1	138
49	Structural and Dynamical Insights into the Opening Mechanism of P. aeruginosa OprM Channel. Structure, 2010, 18, 507-517.	3.3	53
50	<i>NKX2-1</i> mutations leading to surfactant protein promoter dysregulation cause interstitial lung disease in "Brain-Lung-Thyroid Syndrome― Human Mutation, 2010, 31, E1146-E1162.	2.5	108
51	Crystal Structure of an Affinity-matured Prolactin Complexed to Its Dimerized Receptor Reveals the Topology of Hormone Binding Site 2. Journal of Biological Chemistry, 2010, 285, 8422-8433.	3.4	59
52	Structural Characterization of the Stem–Stem Dimerization Interface between Prolactin Receptor Chains Complexed with the Natural Hormone. Journal of Molecular Biology, 2010, 404, 112-126.	4.2	45
53	Molecular Determinants of Grb14-Mediated Inhibition of Insulin Signaling. Molecular Endocrinology, 2009, 23, 1043-1051.	3.7	28
54	Five new TTF1/NKX2.1 mutations in brain-lung-thyroid syndrome: rescue by PAX8 synergism in one case. Human Molecular Genetics, 2009, 18, 2266-2276.	2.9	187

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55	Enzyme structural plasticity and the emergence of broadâ€spectrum antibiotic resistance. EMBO Reports, 2008, 9, 344-349.	4.5	63
56	Structural and Thermodynamic Bases for the Design of Pure Prolactin Receptor Antagonists. Journal of Biological Chemistry, 2007, 282, 33118-33131.	3.4	66
57	High affinity Grb2-SH3 domain ligand incorporating Cl²-substituted prolines in a Sos-derived decapeptide. Bioorganic and Medicinal Chemistry, 2007, 15, 1439-1447.	3.0	24
58	A non-canonical Grb2–PLC-γ1–Sos cascade triggered by lipovitellin 1, an apolipoprotein B homologue. Cellular Signalling, 2007, 19, 2540-2548.	3.6	7
59	Expression, purification, crystallization and preliminary X-ray studies of the outer membrane efflux proteins OprM and OprN fromPseudomonas aeruginosa. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 315-318.	0.7	14
60	Solution NMR structure of the SH3 domain of human nephrocystin and analysis of a mutation-causing juvenile nephronophthisis. Proteins: Structure, Function and Bioinformatics, 2005, 59, 347-355.	2.6	10
61	Surface Plasmon Resonance Thermodynamic and Kinetic Analysis as a Strategic Tool in Drug Design. Distinct Ways for Phosphopeptides to Plug into Src- and Grb2 SH2 Domains. Journal of Medicinal Chemistry, 2005, 48, 753-763.	6.4	42
62	Changes in structural dynamics of the Grb2 adaptor protein upon binding of phosphotyrosine ligand to its SH2 domain. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1700, 53-64.	2.3	22
63	SAXS Study of the PIR Domain from the Grb14 Molecular Adaptor: A Natively Unfolded Protein with a Transient Structure Primer?. Biophysical Journal, 2004, 87, 4056-4064.	0.5	48
64	The PIR domain of Grb14 is an intrinsically unstructured protein: implication in insulin signaling. FEBS Letters, 2003, 554, 240-246.	2.8	26
65	Crystal structures of the SH2 domain of grb2: highlight on the binding of a new high-affinity inhibitor. Journal of Molecular Biology, 2002, 315, 1167-1177.	4.2	87
66	Structural effects of monovalent anions on polymorphic lysozyme crystals. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 929-940.	2.5	71
67	Grb2 promotes reinitiation of meiosis in Xenopus oocytes. Cellular Signalling, 2001, 13, 51-55.	3.6	13
68	1.7 Ã X-ray structure of space-grown collagenase crystals. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 376-378.	2.5	8
69	GRB2 Links Signaling to Actin Assembly by Enhancing Interaction of Neural Wiskott-Aldrich Syndrome Protein (N-WASp) with Actin-related Protein (ARP2/3) Complex. Journal of Biological Chemistry, 2000, 275, 21946-21952.	3.4	186
70	Structures of cellular retinoic acid binding proteins I and II in complex with synthetic retinoids. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1850-1857.	2.5	11
71	Crystallogenesis studies in microgravity with the Advanced Protein Crystallization Facility on SpaceHab-01. Journal of Crystal Growth, 1997, 181, 79-96.	1.5	32
72	Crystallographic analyses of lysozyme and collagenase microgravity grown crystals versus ground controls. Journal of Crystal Growth, 1997, 181, 97-108.	1.5	18

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73	1.8 Ã Structure of Hypoderma lineatum Collagenase: a Member of the Serine Proteinase Family. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 380-392.	2.5	13
74	Lysozyme solubility in H2O and D2O solutions as a function of sodium chloride concentration. Journal of Applied Crystallography, 1995, 28, 614-617.	4.5	32
75	The catalytic site of serine proteinases as a specific binding cavity for xenon. Structure, 1995, 3, 309-316.	3.3	56