Gregor Anderluh

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7141396/publications.pdf

Version: 2024-02-01

179
papers

8,524
citations

38742
50
h-index

56724
83
g-index

188
all docs

188
docs citations

188
times ranked

8166
citing authors

#	Article	IF	Citations
1	Vesicle cholesterol controls exocytotic fusion pore. Cell Calcium, 2022, 101, 102503.	2.4	13
2	An oomycete NLP cytolysin forms transient small pores in lipid membranes. Science Advances, 2022, 8, eabj9406.	10.3	11
3	Binding of the transcription activator-like effector augments transcriptional regulation by another transcription factor. Nucleic Acids Research, 2022, 50, 6562-6574.	14.5	3
4	Biological Nanopores: Engineering on Demand. Life, 2021, 11, 27.	2.4	33
5	Crystal structure of RahU, an aegerolysin protein from the human pathogen Pseudomonas aeruginosa, and its interaction with membrane ceramide phosphorylethanolamine. Scientific Reports, 2021, 11, 6572.	3.3	6
6	The new COST Action European Venom Network (EUVEN)â€"synergy and future perspectives of modern venomics. GigaScience, 2021, 10, .	6.4	6
7	Cytotoxic Activity of LLO Y406A Is Targeted to the Plasma Membrane of Cancer Urothelial Cells. International Journal of Molecular Sciences, 2021, 22, 3305.	4.1	3
8	A Nanoscaffolded Spike-RBD Vaccine Provides Protection against SARS-CoV-2 with Minimal Anti-Scaffold Response. Vaccines, 2021, 9, 431.	4.4	18
9	Nep1-like proteins as a target for plant pathogen control. PLoS Pathogens, 2021, 17, e1009477.	4.7	9
10	The molecular mechanisms of listeriolysin O-induced lipid membrane damage. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183604.	2.6	16
11	Beyond pore formation: reorganization of the plasma membrane induced by pore-forming proteins. Cellular and Molecular Life Sciences, 2021, 78, 6229-6249.	5.4	13
12	The use of giant unilamellar vesicles to study functional properties of pore-forming toxins. Methods in Enzymology, 2021, 649, 219-251.	1.0	6
13	Lipid-Binding Aegerolysin from Biocontrol Fungus Beauveria bassiana. Toxins, 2021, 13, 820.	3.4	6
14	Design of Protein Logic Gate System Operating on Lipid Membranes. ACS Synthetic Biology, 2020, 9, 316-328.	3.8	10
15	Selective inhibition of NLRP3 inflammasome by designed peptide originating from ASC. FASEB Journal, 2020, 34, 11068-11086.	0.5	13
16	In-line detection of monoclonal antibodies in the effluent of protein A chromatography with QCM sensor. Analytical Biochemistry, 2020, 608, 113899.	2.4	4
17	SMN-primed ribosomes modulate the translation of transcripts related to spinal muscular atrophy. Nature Cell Biology, 2020, 22, 1239-1251.	10.3	52
18	Unconventional Secretion of Nigerolysins A from Aspergillus Species. Microorganisms, 2020, 8, 1973.	3.6	5

#	ARTICLE	IF	CITATIONS
19	Structure and mechanism of bactericidal mammalian perforin-2, an ancient agent of innate immunity. Science Advances, 2020, 6, eaax8286.	10.3	66
20	Phosphocholine Antagonizes Listeriolysin O-Induced Host Cell Responses of Listeria monocytogenes. Journal of Infectious Diseases, 2020, 222, 1505-1516.	4.0	8
21	More than one way to bind to cholesterol: atypical variants of membrane-binding domain of perfringolysin O selected by ribosome display. RSC Advances, 2020, 10, 38678-38682.	3.6	0
22	Functional studies of aegerolysin and MACPFâ€like proteins in <i>Aspergillus niger</i>. Molecular Microbiology, 2019, 112, 1253-1269.	2.5	10
23	Structural basis for the multitasking nature of the potato virus Y coat protein. Science Advances, 2019, 5, eaaw3808.	10.3	61
24	Astrocyte Specific Remodeling of Plasmalemmal Cholesterol Composition by Ketamine Indicates a New Mechanism of Antidepressant Action. Scientific Reports, 2019, 9, 10957.	3.3	29
25	Surface Plasmon Resonance for Measuring Interactions of Proteins with Lipids and Lipid Membranes. Methods in Molecular Biology, 2019, 2003, 53-70.	0.9	12
26	pH-triggered endosomal escape of pore-forming Listeriolysin O toxin-coated gold nanoparticles. Journal of Nanobiotechnology, 2019, 17, 108.	9.1	19
27	Crystal structures of cholera toxin in complex with fucosylated receptors point to importance of secondary binding site. Scientific Reports, 2019, 9, 12243.	3.3	32
28	Molecular basis for functional diversity among microbial Nep1-like proteins. PLoS Pathogens, 2019, 15, e1007951.	4.7	39
29	Inhibition of Pore-Forming Proteins. Toxins, 2019, 11, 545.	3.4	16
30	Specificity of Escherichia coli Heat-Labile Enterotoxin Investigated by Single-Site Mutagenesis and Crystallography. International Journal of Molecular Sciences, 2019, 20, 703.	4.1	7
31	<i>Arabidopsis</i> serylâ€<scp>tRNA</scp> synthetase: the first crystal structure and novel protein interactor of plant aminoacylâ€<scp>tRNA</scp> synthetase. FEBS Journal, 2019, 286, 536-554.	4.7	9
32	Membrane-Disrupting Proteins. , 2019, , 729-739.		0
33	Cholesterol Enriched Archaeosomes as a Molecular System for Studying Interactions of Cholesterol-Dependent Cytolysins with Membranes. Journal of Membrane Biology, 2018, 251, 491-505.	2.1	8
34	An archaeal aminoacyl-tRNA synthetase complex for improved substrate quality control. Biochimie, 2018, 147, 36-45.	2.6	3
35	19F NMR studies provide insights into lipid membrane interactions of listeriolysin O, a pore forming toxin from Listeria monocytogenes. Scientific Reports, 2018, 8, 6894.	3.3	13
36	Structures of monomeric and oligomeric forms of the <i>Toxoplasma gondii</i> perforin-like protein 1. Science Advances, 2018, 4, eaaq0762.	10.3	32

#	ARTICLE	IF	CITATIONS
37	Listeriolysinâ€...O Binding Affects Cholesterol and Phospholipid Acyl Chain Dynamics in Fluid Cholesterolâ€Rich Bilayers. Chemistry - A European Journal, 2018, 24, 14220-14225.	3.3	8
38	Development and Characterization of Peptide Ligands of Immunoglobulin G Fc Region. Bioconjugate Chemistry, 2018, 29, 2763-2775.	3.6	11
39	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	8.8	417
40	Engineering a pH responsive pore forming protein. Scientific Reports, 2017, 7, 42231.	3.3	27
41	Molecular mechanism of pore formation by aerolysin-like proteins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160209.	4.0	42
42	Role of the Tryptophan-Rich Motif of Listeriolysin O in Membrane Binding. Biophysical Journal, 2017, 112, 524a.	0.5	2
43	Structure and lipid-binding properties of the kindlin-3 pleckstrin homology domain. Biochemical Journal, 2017, 474, 539-556.	3.7	40
44	Pore-forming toxins in Cnidaria. Seminars in Cell and Developmental Biology, 2017, 72, 133-141.	5.0	39
45	Eudicot plant-specific sphingolipids determine host selectivity of microbial NLP cytolysins. Science, 2017, 358, 1431-1434.	12.6	167
46	Membrane pores: from structure and assembly, to medicine and technology. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160208.	4.0	12
47	A novel sphingomyelin/cholesterol domainâ€specific probe reveals the dynamics of the membrane domains during virus release and in Niemannâ€Pick type C. FASEB Journal, 2017, 31, 1301-1322.	0.5	34
48	A Cytolethal Distending Toxin Variant from Aggregatibacter actinomycetemcomitans with an Aberrant CdtB That Lacks the Conserved Catalytic Histidine 160. PLoS ONE, 2016, 11, e0159231.	2.5	5
49	Development of Recombinant Lactococcus lactis Displaying Albumin-Binding Domain Variants against Shiga Toxin 1 B Subunit. PLoS ONE, 2016, 11, e0162625.	2.5	18
50	Extracellular vesicles concentration is a promising and important parameter for industrial bioprocess monitoring. Biotechnology Journal, 2016, 11, 603-609.	3.5	14
51	Crystal structure of an invertebrate cytolysin pore reveals unique properties and mechanism of assembly. Nature Communications, 2016, 7, 11598.	12.8	71
52	Neutron reflection study of the interaction of the eukaryotic pore-forming actinoporin equinatoxin II with lipid membranes reveals intermediate states in pore formation. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 640-652.	2.6	38
53	Pore formation by actinoporins, cytolysins from sea anemones. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 446-456.	2.6	100
54	High-Resolution Crystal Structures Elucidate the Molecular Basis of Cholera Blood Group Dependence. PLoS Pathogens, 2016, 12, e1005567.	4.7	51

#	Article	IF	Citations
55	Listeriolysin O Membrane Damaging Activity Involves Arc Formation and Lineaction -- Implication for Listeria monocytogenes Escape from Phagocytic Vacuole. PLoS Pathogens, 2016, 12, e1005597.	4.7	74
56	How to Study Protein-protein Interactions. Acta Chimica Slovenica, 2016, 63, 424-439.	0.6	18
57	Membrane-Disrupting Proteins. , 2016, , 1-11.		0
58	Plasticity of Listeriolysin O Pores and its Regulation by pH and Unique Histidine. Scientific Reports, 2015, 5, 9623.	3.3	65
59	Listeriolysin O Affects the Permeability of Caco-2 Monolayer in a Pore-Dependent and Ca2+-Independent Manner. PLoS ONE, 2015, 10, e0130471.	2.5	21
60	The Pseudomonas aeruginosa RhlR-controlled aegerolysin RahU is a low-affinity rhamnolipid-binding protein. FEMS Microbiology Letters, 2015, 362, .	1.8	13
61	How Lipid Membranes Affect Pore Forming Toxin Activity. Accounts of Chemical Research, 2015, 48, 3073-3079.	15.6	54
62	Fungal aegerolysin-like proteins: distribution, activities, and applications. Applied Microbiology and Biotechnology, 2015, 99, 601-610.	3.6	26
63	An optimized protocol for expression and purification of murine perforin in insect cells. Journal of Immunological Methods, 2015, 426, 19-28.	1.4	4
64	Bacteriophage GIL01 gp7 interacts with host LexA repressor to enhance DNA binding and inhibit RecA-mediated auto-cleavage. Nucleic Acids Research, 2015, 43, 7315-7329.	14.5	27
65	Characterization of the Lipid-Binding Site of Equinatoxin II by NMR and Molecular Dynamics Simulation. Biophysical Journal, 2015, 108, 1987-1996.	0.5	42
66	Properties of Pores Formed by Cholesterol-Dependent Cytolysins and Actinoporins. Springer Series in Biophysics, 2015, , 267-286.	0.4	0
67	Visualization of the heterogeneous membrane distribution of sphingomyelin associated with cytokinesis, cell polarity, and sphingolipidosis. FASEB Journal, 2015, 29, 477-493.	0.5	76
68	Targeted Lipid Analysis of Haemolytic Mycelial Extracts of Aspergillus niger. Molecules, 2014, 19, 9051-9069.	3.8	8
69	Tracking Cholesterol/Sphingomyelin-Rich Membrane Domains with the Ostreolysin A-mCherry Protein. PLoS ONE, 2014, 9, e92783.	2.5	72
70	Archaeal aminoacyl-tRNA synthetases interact with the ribosome to recycle tRNAs. Nucleic Acids Research, 2014, 42, 5191-5201.	14.5	19
71	Surface plasmon resonance for monitoring the interaction of Potato virus Y with monoclonal antibodies. Analytical Biochemistry, 2014, 447, 74-81.	2.4	17
72	Direct interaction of actin filaments with <scp>F</scp>â€‹<scp>BAR</scp> protein pacsin2. EMBO Reports, 2014, 15, 1154-1162.	4.5	56

#	ARTICLE	IF	CITATIONS
73	Membrane pore formation at proteinâ€“lipid interfaces. Trends in Biochemical Sciences, 2014, 39, 510-516.	7.5	140
74	The LexA regulated genes of the Clostridium difficile. BMC Microbiology, 2014, 14, 88.	3.3	32
75	Photobleaching Reveals Heterogeneous Stoichiometry for Equinatoxin II Oligomers. ChemBioChem, 2014, 15, 2139-2145.	2.6	35
76	Distribution of MACPF/CDC Proteins. Sub-Cellular Biochemistry, 2014, 80, 7-30.	2.4	38
77	Membrane Interactions and Cellular Effects of MACPF/CDC Proteins. Sub-Cellular Biochemistry, 2014, 80, 119-144.	2.4	7
78	Membrane cholesterol and sphingomyelin, and ostreolysin A are obligatory for pore-formation by a MACPF/CDC-like pore-forming protein, pleurotolysin B. Biochimie, 2013, 95, 1855-1864.	2.6	68
79	Effects of MACPF/CDC proteins on lipid membranes. Cellular and Molecular Life Sciences, 2013, 70, 2083-2098.	5.4	71
80	What planar lipid membranes tell us about the pore-forming activity of cholesterol-dependent cytolysins. Biophysical Chemistry, 2013, 182, 64-70.	2.8	41
81	Novel toll-like receptor 4 (TLR4) antagonists identified by structure- and ligand-based virtual screening. European Journal of Medicinal Chemistry, 2013, 70, 393-399.	5.5	35
82	Electroformation of giant unilamellar vesicles from erythrocyte membranes under low-salt conditions. Analytical Biochemistry, 2013, 435, 174-180.	2.4	17
83	Membrane Damage by an Î±-Helical Pore-forming Protein, Equinatoxin II, Proceeds through a Succession of Ordered Steps. Journal of Biological Chemistry, 2013, 288, 23704-23715.	3.4	77
84	The Caco-2 cell culture model enables sensitive detection of enhanced protein permeability in the presence of N-decyl-Î²-d-maltopyranoside. New Biotechnology, 2013, 30, 507-515.	4.4	8
85	Surface Plasmon Resonance for Measuring Interactions of Proteins with Lipid Membranes. Methods in Molecular Biology, 2013, 974, 23-36.	0.9	20
86	Interactions of Archaeal Chromatin Proteins Alba1 and Alba2 with Nucleic Acids. PLoS ONE, 2013, 8, e58237.	2.5	12
87	<i>p</i>-Sulfonato-calix[<i>n</i>]arenes inhibit staphylococcal bicomponent leukotoxins by supramolecular interactions. Biochemical Journal, 2013, 450, 559-571.	3.7	24
88	Structural insight into LexAâ€“RecA* interaction. Nucleic Acids Research, 2013, 41, 9901-9910.	14.5	62
89	Equinatoxin II Potentiates Temozolomide- and Etoposide-Induced Glioblastoma Cell Death. Current Topics in Medicinal Chemistry, 2013, 12, 2082-2093.	2.1	1
90	DNA-guided assembly of biosynthetic pathways promotes improved catalytic efficiency. Nucleic Acids Research, 2012, 40, 1879-1889.	14.5	241

#	ARTICLE	IF	CITATIONS
91	Equinatoxin II Potentiates Temozolomide- and Etoposide-Induced Glioblastoma Cell Death. Current Topics in Medicinal Chemistry, 2012, 12, 2082-2093.	2.1	22
92	6-Arylpyrido[2,3-d]pyrimidines as Novel ATP-Competitive Inhibitors of Bacterial D-Alanine:D-Alanine Ligase. PLoS ONE, 2012, 7, e39922.	2.5	21
93	Influence of stearyl and trifluoromethylquinoline modifications of the cell penetrating peptide TP10 on its interaction with a lipid membrane. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 915-924.	2.6	36
94	Flexibility of the PDZ-binding motif in the micelle-bound form of Jagged-1 cytoplasmic tail. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1706-1716.	2.6	3
95	Structures of Lysenin Reveal a Shared Evolutionary Origin for Pore-Forming Proteins And Its Mode of Sphingomyelin Recognition. Structure, 2012, 20, 1498-1507.	3.3	90
96	Structure-Based Discovery of Substituted 4,5â€²-Bithiazoles as Novel DNA Gyrase Inhibitors. Journal of Medicinal Chemistry, 2012, 55, 6413-6426.	6.4	146
97	Coupling purification and on-column PEGylation of tumor necrosis factor alpha analogue. Analytical Biochemistry, 2012, 430, 105-107.	2.4	2
98	A Neurotoxic Phospholipase A2 Impairs Yeast Amphiphysin Activity and Reduces Endocytosis. PLoS ONE, 2012, 7, e40931.	2.5	11
99	Pore formation by human stefin B in its native and oligomeric states and the consequent amyloid induced toxicity. Frontiers in Molecular Neuroscience, 2012, 5, 85.	2.9	12
100	pH dependence of listeriolysin O aggregation and poreâ€•forming ability. FEBS Journal, 2012, 279, 126-141.	4.7	86
101	In silico discovery and biophysical evaluation of novel 5-(2-hydroxybenzylidene) rhodanine inhibitors of DNA gyrase B. Bioorganic and Medicinal Chemistry, 2012, 20, 2572-2580.	3.0	41
102	Subcellular localization of sphingomyelin revealed by two toxinâ€•based probes in mammalian cells. Genes To Cells, 2012, 17, 720-727.	1.2	40
103	Oligomerization and Pore Formation by Equinatoxin II Inhibit Endocytosis and Lead to Plasma Membrane Reorganization. Journal of Biological Chemistry, 2011, 286, 37768-37777.	3.4	52
104	The interaction of Jaggedâ€•1 cytoplasmic tail with afadin PDZ domain is local, foldingâ€•independent, and tuned by phosphorylation. Journal of Molecular Recognition, 2011, 24, 245-253.	2.1	13
105	Immunochemical properties and pathological relevance of anti-Â2-glycoprotein I antibodies of different avidity. International Immunology, 2011, 23, 511-518.	4.0	12
106	Human Perforin Employs Different Avenues to Damage Membranes. Journal of Biological Chemistry, 2011, 286, 2946-2955.	3.4	82
107	Perforin activity at membranes leads to invaginations and vesicle formation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21016-21021.	7.1	35
108	Interconversion between bound and free conformations of LexA orchestrates the bacterial SOS response. Nucleic Acids Research, 2011, 39, 6546-6557.	14.5	61

#	ARTICLE	IF	CITATIONS
109	Perforin Rapidly Induces Plasma Membrane Phospholipid Flip-Flop. PLoS ONE, 2011, 6, e24286.	2.5	45
110	Significance of K(L/V)WX(I/L/V)P Epitope of the B2Gpi in Its (Patho)Physiologic Function. Electronic Journal of the International Federation of Clinical Chemistry and Laboratory Medicine, 2011, 22, 118-24.	0.7	1
111	Repetitive domain of Clostridium difficile toxin B exhibits cytotoxic effects on human intestinal epithelial cells and decreases epithelial barrier function. Anaerobe, 2010, 16, 527-532.	2.1	14
112	Interaction between Oligomers of Stefin B and Amyloid-Î² in Vitro and in Cells. Journal of Biological Chemistry, 2010, 285, 3201-3210.	3.4	40
113	A Toxin-based Probe Reveals Cytoplasmic Exposure of Golgi Sphingomyelin. Journal of Biological Chemistry, 2010, 285, 22186-22195.	3.4	55
114	Human perforin permeabilizing activity, but not binding to lipid membranes, is affected by pH. Molecular Immunology, 2010, 47, 2492-2504.	2.2	33
115	Solid-state NMR study of membrane interactions of the pore-forming cytolysin, equinatoxin II. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 244-251.	2.6	23
116	Sphingomyelin-rich domains are sites of lysenin oligomerization: Implications for raft studies. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 471-481.	2.6	44
117	Preparation of Lipid Membrane Surfaces for Molecular Interaction Studies by Surface Plasmon Resonance Biosensors. Methods in Molecular Biology, 2010, 627, 191-200.	0.9	10
118	Capture of Intact Liposomes on Biacore Sensor Chips for Proteinâ€"Membrane Interaction Studies. Methods in Molecular Biology, 2010, 627, 201-211.	0.9	20
119	Molecular Mechanism of Sphingomyelin-Specific Membrane Binding and Pore Formation by Actinoporins. Advances in Experimental Medicine and Biology, 2010, , 106-115.	1.6	45
120	Proteins: membrane binding and pore formation. Preface. Advances in Experimental Medicine and Biology, 2010, 677, v-vi.	1.6	3
121	Molecular mechanism of sphingomyelin-specific membrane binding and pore formation by actinoporins. Advances in Experimental Medicine and Biology, 2010, 677, 106-15.	1.6	16
122	Probing HIV-1 Membrane Liquid Order by Laurdan Staining Reveals Producer Cell-dependent Differences. Journal of Biological Chemistry, 2009, 284, 22238-22247.	3.4	78
123	A common toxin fold mediates microbial attack and plant defense. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10359-10364.	7.1	224
124	Regulation of cathepsin B activity by 2A2 monoclonal antibody. FEBS Journal, 2009, 276, 4739-4751.	4.7	13
125	A global benchmark study using affinity-based biosensors. Analytical Biochemistry, 2009, 386, 194-216.	2.4	85
126	Sea anemone cytolysins as toxic components of immunotoxins. Toxicon, 2009, 54, 1206-1214.	1.6	52

#	Article	IF	Citations
127	Molecular mechanism of pore formation by actinoporins. Toxicon, 2009, 54, 1125-1134.	1.6	129
128	Toxin Detection by Surface Plasmon Resonance. Sensors, 2009, 9, 1339-1354.	3.8	104
129	Molecular Determinants of Sphingomyelin Specificity of a Eukaryotic Pore-forming Toxin. Journal of Biological Chemistry, 2008, 283, 18665-18677.	3.4	156
130	Interaction with model membranes and pore formation by human stefinâ€ƒB â€“ studying the native and prefibrillar states. FEBS Journal, 2008, 275, 2455-2466.	4.7	28
131	Disparate proteins use similar architectures to damage membranes. Trends in Biochemical Sciences, 2008, 33, 482-490.	7.5	130
132	Equinatoxin II Permeabilizing Activity Depends on the Presence of Sphingomyelin and Lipid Phase Coexistence. Biophysical Journal, 2008, 95, 691-698.	0.5	125
133	Kinetics of cholesterol extraction from lipid membranes by methyl-Î²-cyclodextrinâ€”A surface plasmon resonance approach. Biochimica Et Biophysica Acta - Biomembranes, 2008, 1778, 175-184.	2.6	74
134	The effects of lipids on the structure of the eukaryotic cytolysin equinatoxin II: A synchrotron radiation circular dichroism spectroscopic study. Biochimica Et Biophysica Acta - Biomembranes, 2008, 1778, 2091-2096.	2.6	26
135	Granzyme B translocates across the lipid membrane only in the presence of lytic agents. Biochemical and Biophysical Research Communications, 2008, 371, 391-394.	2.1	13
136	Size and morphology of toxic oligomers of amyloidogenic proteins: a case study of human stefin B. Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis, 2008, 15, 147-159.	3.0	34
137	Potentiation of anticancer-drug cytotoxicity by sea anemone pore-forming proteins in human glioblastoma cells. Anti-Cancer Drugs, 2008, 19, 517-525.	1.4	49
138	Intradomain LexA rotation is a prerequisite for DNA binding specificity. FEBS Letters, 2007, 581, 4816-4820.	2.8	11
139	Sterol and pH Interdependence in the Binding, Oligomerization, and Pore Formation of Listeriolysin O. Biochemistry, 2007, 46, 4425-4437.	2.5	87
140	The equinatoxin N-terminus is transferred across planar lipid membranes and helps to stabilize the transmembrane pore. FEBS Journal, 2007, 274, 539-550.	4.7	46
141	Structure and Activity of the N-Terminal Region of the Eukaryotic Cytolysin Equinatoxin IIâ€. Biochemistry, 2006, 45, 1818-1828.	2.5	53
142	Lipid Interactions of Î±-Helical Protein Toxins. , 2006, , 139-162.		1
143	Membrane binding of zebrafish actinoporin-like protein: AF domains, a novel superfamily of cell membrane binding domains. Biochemical Journal, 2006, 398, 381-392.	3.7	33
144	Surface plasmon resonance in proteinâ€“membrane interactions. Chemistry and Physics of Lipids, 2006, 141, 169-178.	3.2	201

#	ARTICLE	IF	CITATIONS
145	Ammodytoxin, a secretory phospholipase A2, inhibits G2 cell-cycle arrest in the yeast Saccharomyces cerevisiae. Biochemical Journal, 2005, 391, 383-388.	3.7	16
146	Properties of nonfused liposomes immobilized on an L1 Biacore chip and their permeabilization by a eukaryotic pore-forming toxin. Analytical Biochemistry, 2005, 344, 43-52.	2.4	83
147	Interaction of human stefinâ€ƒB in the prefibrillar oligomeric form with membranes. FEBS Journal, 2005, 272, 3042-3051.	4.7	48
148	Cytotoxic Activity of a Tumor Protease-Activated Pore-Forming Toxin. Bioconjugate Chemistry, 2005, 16, 369-376.	3.6	36
149	Effect of pH on the Pore Forming Activity and Conformational Stability of Ostreolysin, a Lipid Raft-Binding Protein from the Edible MushroomPleurotus ostreatusâ€‚â€¡. Biochemistry, 2005, 44, 11137-11147.	2.5	56
150	Interaction of the Eukaryotic Pore-forming Cytolysin Equinatoxin II with Model Membranes: 19F NMR Studies. Journal of Molecular Biology, 2005, 347, 27-39.	4.2	87
151	Protein disulphide isomerase binds ammodytoxin strongly: Possible implications for toxin trafficking. Biochemical and Biophysical Research Communications, 2005, 329, 733-737.	2.1	15
152	Single Peptide Bonds Exhibit Poly(Pro)II (â€œRandom Coilâ€) Circular Dichroism Spectra. Journal of the American Chemical Society, 2005, 127, 9700-9701.	13.7	59
153	A Natively Unfolded Toxin Domain Uses Its Receptor as a Folding Template. Journal of Biological Chemistry, 2004, 279, 22002-22009.	3.4	27
154	Pore Formation by Equinatoxin, a Eukaryotic Pore-forming Toxin, Requires a Flexible N-terminal Region and a Stable Î²-Sandwich. Journal of Biological Chemistry, 2004, 279, 46509-46517.	3.4	102
155	Salt-Induced Oligomerization of Partially Folded Intermediates of Equinatoxin II. Biochemistry, 2004, 43, 9536-9545.	2.5	14
156	Membrane insertion of the N-terminal Î±-helix of equinatoxin II, a sea anemone cytolytic toxin. Biochemical Journal, 2004, 384, 421-428.	3.7	50
157	Dissecting the Actinoporin Pore-Forming Mechanism. Structure, 2003, 11, 1312-1313.	3.3	30
158	Peeking into a secret world of pore-forming toxins: membrane binding processes studied by surface plasmon resonance. Toxicon, 2003, 42, 225-228.	1.6	19
159	Effects of the Eukaryotic Pore-Forming Cytolysin Equinatoxin II on Lipid Membranes and the Role of Sphingomyelin. Biophysical Journal, 2003, 84, 2382-2392.	0.5	67
160	Expression of proteins using the third domain of the Escherichia coli periplasmic-protein TolA as a fusion partner. Protein Expression and Purification, 2003, 28, 173-181.	1.3	32
161	Pore Formation by Equinatoxin II, a Eukaryotic Protein Toxin, Occurs by Induction of Nonlamellar Lipid Structures. Journal of Biological Chemistry, 2003, 278, 45216-45223.	3.4	116
162	Concerted Folding and Binding of a Flexible Colicin Domain to Its Periplasmic Receptor TolA. Journal of Biological Chemistry, 2003, 278, 21860-21868.	3.4	27

#	ARTICLE	IF	CITATIONS
163	A Novel Mechanism of Pore Formation. Journal of Biological Chemistry, 2003, 278, 22678-22685.	3.4	121
164	Two-step Membrane Binding by Equinatoxin II, a Pore-forming Toxin from the Sea Anemone, Involves an Exposed Aromatic Cluster and a Flexible Helix. Journal of Biological Chemistry, 2002, 277, 41916-41924.	3.4	185
165	Solution structure of the eukaryotic pore-forming cytolysin equinatoxin II: implications for pore formation. Journal of Molecular Biology, 2002, 315, 1219-1229.	4.2	140
166	Cytolytic peptide and protein toxins from sea anemones (Anthozoa: Actiniaria). Toxicon, 2002, 40, 111-124.	1.6	340
167	Acid- and base-induced conformational transitions of equinatoxin II. Biophysical Chemistry, 2001, 90, 103-121.	2.8	11
168	Crystal Structure of the Soluble Form of Equinatoxin II, a Pore-Forming Toxin from the Sea Anemone Actinia equina. Structure, 2001, 9, 341-346.	3.3	202
169	Structureâ€’function studies of tryptophan mutants of equinatoxin II, a sea anemone pore-forming protein. Biochemical Journal, 2000, 346, 223.	3.7	38
170	Mechanism of Action of Equinatoxin II, a Fore-Forming Protein From the Sea Anemone <i>Actinia equina</i>. Biochemical Society Transactions, 2000, 28, A453-A453.	3.4	0
171	Structureâ€“function studies of tryptophan mutants of equinatoxin II, a sea anemone pore-forming protein. Biochemical Journal, 2000, 346, 223-232.	3.7	81
172	A common motif in proparts of Cnidarian toxins and nematocyst collagens and its putative role. BBA - Proteins and Proteomics, 2000, 1476, 372-376.	2.1	53
173	Letter to the editor: Sequence-specific resonance assignments of the potent cytolysin equinatoxin II. Journal of Biomolecular NMR, 2000, 18, 281-282.	2.8	8
174	Cysteine-scanning mutagenesis of an eukaryotic pore-forming toxin from sea anemone. Topology in lipid membranes. FEBS Journal, 1999, 263, 128-136.	0.2	87
175	Equinatoxins, pore-forming proteins from the sea anemone Actinia equina, belong to a multigene family. Toxicon, 1999, 37, 1391-1401.	1.6	71
176	Antiparasite activity of sea-anemone cytolysins onGiardia duodenalis and specific targeting withanti-Giardia antibodies. International Journal for Parasitology, 1999, 29, 489-498.	3.1	53
177	Avidinâ€“FITC Topological Studies with Three Cysteine Mutants of Equinatoxin II, a Sea Anemone Pore-Forming Protein. Biochemical and Biophysical Research Communications, 1998, 242, 187-190.	2.1	18
178	Sequence analysis of the cDNA encoding the precursor of equinatoxin V, a newly discovered hemolysin from the sea anemone Actinia equina. BBA - Proteins and Proteomics, 1997, 1341, 105-107.	2.1	32
179	Cloning, Sequencing, and Expression of Equinatoxin II. Biochemical and Biophysical Research Communications, 1996, 220, 437-442.	2.1	113