Gregor Anderluh

List of Publications by Year
in descending order

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	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
2	Cytolytic peptide and protein toxins from sea anemones (Anthozoa: Actiniaria). Toxicon, 2002, 40, 111-124.	1.6	340
3	DNA-guided assembly of biosynthetic pathways promotes improved catalytic efficiency. Nucleic Acids Research, 2012, 40, 1879-1889.	14.5	241
4	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
5	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
6	Surface plasmon resonance in proteinâ€"membrane interactions. Chemistry and Physics of Lipids, 2006, 141, 169-178.	3.2	201
7	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
8	Eudicot plant-specific sphingolipids determine host selectivity of microbial NLP cytolysins. Science, 2017, 358, 1431-1434.	12.6	167
9	Molecular Determinants of Sphingomyelin Specificity of a Eukaryotic Pore-forming Toxin. Journal of Biological Chemistry, 2008, 283, 18665-18677.	3.4	156
10	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
11	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
12	Membrane pore formation at proteinâ€"lipid interfaces. Trends in Biochemical Sciences, 2014, 39, 510-516.	7.5	140
13	Disparate proteins use similar architectures to damage membranes. Trends in Biochemical Sciences, 2008, 33, 482-490.	7.5	130
14	Molecular mechanism of pore formation by actinoporins. Toxicon, 2009, 54, 1125-1134.	1.6	129
15	Equinatoxin II Permeabilizing Activity Depends on the Presence of Sphingomyelin and Lipid Phase Coexistence. Biophysical Journal, 2008, 95, 691-698.	0.5	125
16	A Novel Mechanism of Pore Formation. Journal of Biological Chemistry, 2003, 278, 22678-22685.	3.4	121
17	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
18	Cloning, Sequencing, and Expression of Equinatoxin II. Biochemical and Biophysical Research Communications, 1996, 220, 437-442.	2.1	113

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19	Toxin Detection by Surface Plasmon Resonance. Sensors, 2009, 9, 1339-1354.	3.8	104
20	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
21	Pore formation by actinoporins, cytolysins from sea anemones. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 446-456.	2.6	100
22	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
23	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
24	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
25	Sterol and pH Interdependence in the Binding, Oligomerization, and Pore Formation of Listeriolysin O. Biochemistry, 2007, 46, 4425-4437.	2.5	87
26	pH dependence of listeriolysin O aggregation and poreâ€forming ability. FEBS Journal, 2012, 279, 126-141.	4.7	86
27	A global benchmark study using affinity-based biosensors. Analytical Biochemistry, 2009, 386, 194-216.	2.4	85
28	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
29	Human Perforin Employs Different Avenues to Damage Membranes. Journal of Biological Chemistry, 2011, 286, 2946-2955.	3.4	82
30	Structureâ€"function studies of tryptophan mutants of equinatoxin II, a sea anemone pore-forming protein. Biochemical Journal, 2000, 346, 223-232.	3.7	81
31	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
32	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
33	Visualization of the heterogeneous membrane distribution of sphingomyelin associated with cytokinesis, cell polarity, and sphingolipidosis. FASEB Journal, 2015, 29, 477-493.	0.5	76
34	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
35	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
36	Tracking Cholesterol/Sphingomyelin-Rich Membrane Domains with the Ostreolysin A-mCherry Protein. PLoS ONE, 2014, 9, e92783.	2.5	72

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37	Equinatoxins, pore-forming proteins from the sea anemone Actinia equina, belong to a multigene family. Toxicon, 1999, 37, 1391-1401.	1.6	71
38	Effects of MACPF/CDC proteins on lipid membranes. Cellular and Molecular Life Sciences, 2013, 70, 2083-2098.	5.4	71
39	Crystal structure of an invertebrate cytolysin pore reveals unique properties and mechanism of assembly. Nature Communications, 2016, 7, 11598.	12.8	71
40	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
41	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
42	Structure and mechanism of bactericidal mammalian perforin-2, an ancient agent of innate immunity. Science Advances, 2020, 6, eaax8286.	10.3	66
43	Plasticity of Listeriolysin O Pores and its Regulation by pH and Unique Histidine. Scientific Reports, 2015, 5, 9623.	3.3	65
44	Structural insight into LexAâ€“RecA* interaction. Nucleic Acids Research, 2013, 41, 9901-9910.	14.5	62
45	Interconversion between bound and free conformations of LexA orchestrates the bacterial SOS response. Nucleic Acids Research, 2011, 39, 6546-6557.	14.5	61
46	Structural basis for the multitasking nature of the potato virus Y coat protein. Science Advances, 2019, 5, eaaw3808.	10.3	61
47	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
48	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
49	Direct interaction of actin filaments with <scp>F</scp>â€‹<scp>BAR</scp> protein pacsin2. EMBO Reports, 2014, 15, 1154-1162.	4.5	56
50	A Toxin-based Probe Reveals Cytoplasmic Exposure of Golgi Sphingomyelin. Journal of Biological Chemistry, 2010, 285, 22186-22195.	3.4	55
51	How Lipid Membranes Affect Pore Forming Toxin Activity. Accounts of Chemical Research, 2015, 48, 3073-3079.	15.6	54
52	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
53	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
54	Structure and Activity of the N-Terminal Region of the Eukaryotic Cytolysin Equinatoxin IIâ€. Biochemistry, 2006, 45, 1818-1828.	2.5	53

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55	Sea anemone cytolysins as toxic components of immunotoxins. Toxicon, 2009, 54, 1206-1214.	1.6	52
56	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
57	SMN-primed ribosomes modulate the translation of transcripts related to spinal muscular atrophy. Nature Cell Biology, 2020, 22, 1239-1251.	10.3	52
58	High-Resolution Crystal Structures Elucidate the Molecular Basis of Cholera Blood Group Dependence. PLoS Pathogens, 2016, 12, e1005567.	4.7	51
59	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
60	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
61	Interaction of human stefinâ€ƒB in the prefibrillar oligomeric form with membranes. FEBS Journal, 2005, 272, 3042-3051.	4.7	48
62	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
63	Molecular Mechanism of Sphingomyelin-Specific Membrane Binding and Pore Formation by Actinoporins. Advances in Experimental Medicine and Biology, 2010, , 106-115.	1.6	45
64	Perforin Rapidly Induces Plasma Membrane Phospholipid Flip-Flop. PLoS ONE, 2011, 6, e24286.	2.5	45
65	Sphingomyelin-rich domains are sites of lysenin oligomerization: Implications for raft studies. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 471-481.	2.6	44
66	Characterization of the Lipid-Binding Site of Equinatoxin II by NMR and Molecular Dynamics Simulation. Biophysical Journal, 2015, 108, 1987-1996.	0.5	42
67	Molecular mechanism of pore formation by aerolysin-like proteins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160209.	4.0	42
68	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
69	What planar lipid membranes tell us about the pore-forming activity of cholesterol-dependent cytolysins. Biophysical Chemistry, 2013, 182, 64-70.	2.8	41
70	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
71	Subcellular localization of sphingomyelin revealed by two toxinâ€based probes in mammalian cells. Genes To Cells, 2012, 17, 720-727.	1.2	40
72	Structure and lipid-binding properties of the kindlin-3 pleckstrin homology domain. Biochemical Journal, 2017, 474, 539-556.	3.7	40

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73	Pore-forming toxins in Cnidaria. Seminars in Cell and Developmental Biology, 2017, 72, 133-141.	5.0	39
74	Molecular basis for functional diversity among microbial Nep1-like proteins. PLoS Pathogens, 2019, 15, e1007951.	4.7	39
75	Structureâ€'function studies of tryptophan mutants of equinatoxin II, a sea anemone pore-forming protein. Biochemical Journal, 2000, 346, 223.	3.7	38
76	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
77	Distribution of MACPF/CDC Proteins. Sub-Cellular Biochemistry, 2014, 80, 7-30.	2.4	38
78	Cytotoxic Activity of a Tumor Protease-Activated Pore-Forming Toxin. Bioconjugate Chemistry, 2005, 16, 369-376.	3.6	36
79	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
80	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
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	Photobleaching Reveals Heterogeneous Stoichiometry for Equinatoxin II Oligomers. ChemBioChem, 2014, 15, 2139-2145.	2.6	35
83	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
84	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
85	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
86	Human perforin permeabilizing activity, but not binding to lipid membranes, is affected by pH. Molecular Immunology, 2010, 47, 2492-2504.	2.2	33
87	Biological Nanopores: Engineering on Demand. Life, 2021, 11, 27.	2.4	33
88	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
89	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
90	The LexA regulated genes of the Clostridium difficile. BMC Microbiology, 2014, 14, 88.	3.3	32

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91	Structures of monomeric and oligomeric forms of the <i>Toxoplasma gondii</i> perforin-like protein 1. Science Advances, 2018, 4, eaaq0762.	10.3	32
92	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
93	Dissecting the Actinoporin Pore-Forming Mechanism. Structure, 2003, 11, 1312-1313.	3.3	30
94	Astrocyte Specific Remodeling of Plasmalemmal Cholesterol Composition by Ketamine Indicates a New Mechanism of Antidepressant Action. Scientific Reports, 2019, 9, 10957.	3.3	29
95	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
96	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
97	A Natively Unfolded Toxin Domain Uses Its Receptor as a Folding Template. Journal of Biological Chemistry, 2004, 279, 22002-22009.	3.4	27
98	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
99	Engineering a pH responsive pore forming protein. Scientific Reports, 2017, 7, 42231.	3.3	27
100	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
101	Fungal aegerolysin-like proteins: distribution, activities, and applications. Applied Microbiology and Biotechnology, 2015, 99, 601-610.	3.6	26
102	<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
103	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
104	Equinatoxin II Potentiates Temozolomide- and Etoposide-Induced Glioblastoma Cell Death. Current Topics in Medicinal Chemistry, 2012, 12, 2082-2093.	2.1	22
105	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
106	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
107	Capture of Intact Liposomes on Biacore Sensor Chips for Proteinâ€“Membrane Interaction Studies. Methods in Molecular Biology, 2010, 627, 201-211.	0.9	20
108	Surface Plasmon Resonance for Measuring Interactions of Proteins with Lipid Membranes. Methods in Molecular Biology, 2013, 974, 23-36.	0.9	20

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109	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
110	Archaeal aminoacyl-tRNA synthetases interact with the ribosome to recycle tRNAs. Nucleic Acids Research, 2014, 42, 5191-5201.	14.5	19
111	pH-triggered endosomal escape of pore-forming Listeriolysin O toxin-coated gold nanoparticles. Journal of Nanobiotechnology, 2019, 17, 108.	9.1	19
112	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
113	Development of Recombinant Lactococcus lactis Displaying Albumin-Binding Domain Variants against Shiga Toxin 1 B Subunit. PLoS ONE, 2016, 11, e0162625.	2.5	18
114	A Nanoscaffolded Spike-RBD Vaccine Provides Protection against SARS-CoV-2 with Minimal Anti-Scaffold Response. Vaccines, 2021, 9, 431.	4.4	18
115	How to Study Protein-protein Interactions. Acta Chimica Slovenica, 2016, 63, 424-439.	0.6	18
116	Electroformation of giant unilamellar vesicles from erythrocyte membranes under low-salt conditions. Analytical Biochemistry, 2013, 435, 174-180.	2.4	17
117	Surface plasmon resonance for monitoring the interaction of Potato virus Y with monoclonal antibodies. Analytical Biochemistry, 2014, 447, 74-81.	2.4	17
118	Ammodytoxin, a secretory phospholipase A2, inhibits G2 cell-cycle arrest in the yeast Saccharomyces cerevisiae. Biochemical Journal, 2005, 391, 383-388.	3.7	16
119	Inhibition of Pore-Forming Proteins. Toxins, 2019, 11, 545.	3.4	16
120	The molecular mechanisms of listeriolysin O-induced lipid membrane damage. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183604.	2.6	16
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	Protein disulphide isomerase binds ammodytoxin strongly: Possible implications for toxin trafficking. Biochemical and Biophysical Research Communications, 2005, 329, 733-737.	2.1	15
123	Salt-Induced Oligomerization of Partially Folded Intermediates of Equinatoxin II. Biochemistry, 2004, 43, 9536-9545.	2.5	14
124	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
125	Extracellular vesicles concentration is a promising and important parameter for industrial bioprocess monitoring. Biotechnology Journal, 2016, 11, 603-609.	3.5	14
126	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

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127	Regulation of cathepsin B activity by 2A2 monoclonal antibody. FEBS Journal, 2009, 276, 4739-4751.	4.7	13
128	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
129	The Pseudomonas aeruginosa RhlR-controlled aegerolysin RahU is a low-affinity rhamnolipid-binding protein. FEMS Microbiology Letters, 2015, 362, .	1.8	13
130	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
131	Selective inhibition of NLRP3 inflammasome by designed peptide originating from ASC. FASEB Journal, 2020, 34, 11068-11086.	0.5	13
132	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
133	Vesicle cholesterol controls exocytotic fusion pore. Cell Calcium, 2022, 101, 102503.	2.4	13
134	Immunochemical properties and pathological relevance of anti-Â2-glycoprotein I antibodies of different avidity. International Immunology, 2011, 23, 511-518.	4.0	12
135	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
136	Interactions of Archaeal Chromatin Proteins Alba1 and Alba2 with Nucleic Acids. PLoS ONE, 2013, 8, e58237.	2.5	12
137	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
138	Surface Plasmon Resonance for Measuring Interactions of Proteins with Lipids and Lipid Membranes. Methods in Molecular Biology, 2019, 2003, 53-70.	0.9	12
139	Acid- and base-induced conformational transitions of equinatoxin II. Biophysical Chemistry, 2001, 90, 103-121.	2.8	11
140	Intradomain LexA rotation is a prerequisite for DNA binding specificity. FEBS Letters, 2007, 581, 4816-4820.	2.8	11
141	A Neurotoxic Phospholipase A2 Impairs Yeast Amphiphysin Activity and Reduces Endocytosis. PLoS ONE, 2012, 7, e40931.	2.5	11
142	Development and Characterization of Peptide Ligands of Immunoglobulin G Fc Region. Bioconjugate Chemistry, 2018, 29, 2763-2775.	3.6	11
143	An oomycete NLP cytolysin forms transient small pores in lipid membranes. Science Advances, 2022, 8, eabj9406.	10.3	11
144	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

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145	Functional studies of aegerolysin and MACPFâ€like proteins in <i>Aspergillus niger</i>. Molecular Microbiology, 2019, 112, 1253-1269.	2.5	10
146	Design of Protein Logic Gate System Operating on Lipid Membranes. ACS Synthetic Biology, 2020, 9, 316-328.	3.8	10
147	<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
148	Nep1-like proteins as a target for plant pathogen control. PLoS Pathogens, 2021, 17, e1009477.	4.7	9
149	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
150	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
151	Targeted Lipid Analysis of Haemolytic Mycelial Extracts of Aspergillus niger. Molecules, 2014, 19, 9051-9069.	3.8	8
152	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
153	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
154	Phosphocholine Antagonizes Listeriolysin O-Induced Host Cell Responses of Listeria monocytogenes. Journal of Infectious Diseases, 2020, 222, 1505-1516.	4.0	8
155	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
156	Membrane Interactions and Cellular Effects of MACPF/CDC Proteins. Sub-Cellular Biochemistry, 2014, 80, 119-144.	2.4	7
157	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
158	The new COST Action European Venom Network (EUVEN)â€"synergy and future perspectives of modern venomics. GigaScience, 2021, 10, .	6.4	6
159	The use of giant unilamellar vesicles to study functional properties of pore-forming toxins. Methods in Enzymology, 2021, 649, 219-251.	1.0	6
160	Lipid-Binding Aegerolysin from Biocontrol Fungus Beauveria bassiana. Toxins, 2021, 13, 820.	3.4	6
161	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
162	Unconventional Secretion of Nigerolysins A from Aspergillus Species. Microorganisms, 2020, 8, 1973.	3.6	5

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163	An optimized protocol for expression and purification of murine perforin in insect cells. Journal of Immunological Methods, 2015, 426, 19-28.	1.4	4
164	In-line detection of monoclonal antibodies in the effluent of protein A chromatography with QCM sensor. Analytical Biochemistry, 2020, 608, 113899.	2.4	4
165	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
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