

The structure of a cytolytic \hat{I}_{\pm} -helical toxin pore reveals

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Helical Cytolysins: Molecular Tunnel-Boring Machines in Action. <i>ChemBioChem</i> , 2009, 10, 2305-2307.	1.3	2
2	Piercing insights. <i>Nature</i> , 2009, 459, 651-652.	13.7	60
3	NMR Characterization of Membrane Protein in Detergent Micelle Solutions by Use of Microcoil Equipment. <i>Journal of the American Chemical Society</i> , 2009, 131, 18450-18456.	6.6	27
4	Structures of membrane proteins. <i>Quarterly Reviews of Biophysics</i> , 2010, 43, 65-158.	2.4	157
5	Helix insertion into bilayers and the evolution of membrane proteins. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 1077-1088.	2.4	35
6	Formation of Very Large Conductance Channels by <i>Bacillus cereus</i> Nhe in Vero and CH4 Cells Identifies NheA as the Inherent Pore-Forming Structure. <i>Journal of Membrane Biology</i> , 2010, 237, 1-11.	1.0	21
7	A charge-switched nano-sized polymeric carrier for protein delivery. <i>International Journal of Pharmaceutics</i> , 2010, 392, 78-82.	2.6	26
8	Structure and assembly of pore-forming proteins. <i>Current Opinion in Structural Biology</i> , 2010, 20, 241-246.	2.6	162
9	Specific interactions of sticholysin I with model membranes: An NMR study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1959-1970.	1.5	36
10	Bacterial Nanofluidic Structures for Medicine and Engineering. <i>Small</i> , 2010, 6, 895-909.	5.2	2
11	New insights into protein export in malaria parasites. <i>Cellular Microbiology</i> , 2010, 12, 580-587.	1.1	40
12	The structure and function of mammalian membrane-attack complex/perforin-like proteins. <i>Tissue Antigens</i> , 2010, 76, 341-351.	1.0	63
13	Complete Genome Sequence and Comparative Metabolic Profiling of the Prototypical Enterohemorrhagic <i>Escherichia coli</i> Strain O42. <i>PLoS ONE</i> , 2010, 5, e8801.	1.1	165
14	Cytotoxicity of the <i>Bacillus cereus</i> Nhe Enterotoxin Requires Specific Binding Order of Its Three Exoprotein Components. <i>Infection and Immunity</i> , 2010, 78, 3813-3821.	1.0	62
15	Mutations Affecting Export and Activity of Cytolysin A from <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2010, 192, 4001-4011.	1.0	21
16	Enhanced Snapshot: Pore-Forming Toxins. <i>Cell</i> , 2010, 142, 334-334.e1.	13.5	10
17	Botulinum Neurotoxin: A Marvel of Protein Design. <i>Annual Review of Biochemistry</i> , 2010, 79, 591-617.	5.0	371
18	Hemolysin E (HlyE, ClyA, SheA) and Related Toxins. <i>Advances in Experimental Medicine and Biology</i> , 2010, 677, 116-126.	0.8	40

#	ARTICLE	IF	CITATIONS
19	A de novo peptide hexamer with a mutable channel. <i>Nature Chemical Biology</i> , 2011, 7, 935-941.	3.9	172
20	Crystal Structure of <i>Clostridium perfringens</i> Enterotoxin Displays Features of β -Pore-forming Toxins. <i>Journal of Biological Chemistry</i> , 2011, 286, 19549-19555.	1.6	88
22	Viral channel forming proteins – Modeling the target. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 561-571.	1.4	31
23	The behavior of sea anemone actinoporins at the water–membrane interface. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 2275-2288.	1.4	76
24	Characterization of a Dual-Function Domain That Mediates Membrane Insertion and Excision of Ff Filamentous Bacteriophage. <i>Journal of Molecular Biology</i> , 2011, 411, 972-985.	2.0	14
25	Structural Insights into the Oligomerization and Architecture of Eukaryotic Membrane Pore-Forming Toxins. <i>Structure</i> , 2011, 19, 181-191.	1.6	99
26	Molecular biology of Bax and Bak activation and action. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011, 1813, 521-531.	1.9	415
27	Oligomerization and Pore Formation by Equinatoxin II Inhibit Endocytosis and Lead to Plasma Membrane Reorganization. <i>Journal of Biological Chemistry</i> , 2011, 286, 37768-37777.	1.6	52
28	A glycine zipper motif mediates the formation of toxic β -amyloid oligomers in vitro and in vivo. <i>Molecular Neurodegeneration</i> , 2011, 6, 61.	4.4	37
29	Domains II and III of <i>Bacillus thuringiensis</i> Cry1Ab Toxin Remain Exposed to the Solvent after Insertion of Part of Domain I into the Membrane. <i>Journal of Biological Chemistry</i> , 2011, 286, 19109-19117.	1.6	23
30	Autotransporters and virulence of enteroaggregative <i>E. coli</i> . <i>Gut Microbes</i> , 2011, 2, 13-24.	4.3	52
31	Structural Characterization of an Early Fusion Intermediate of Influenza Virus Hemagglutinin. <i>Journal of Virology</i> , 2011, 85, 5172-5182.	1.5	113
32	The Mechanism of Toxicity in HET-S/HET-s Prion Incompatibility. <i>PLoS Biology</i> , 2012, 10, e1001451.	2.6	123
33	Biosynthesis, Localization, and Macromolecular Arrangement of the <i>Plasmodium falciparum</i> Translocon of Exported Proteins (PTEX). <i>Journal of Biological Chemistry</i> , 2012, 287, 7871-7884.	1.6	130
34	Infection strategies of enteric pathogenic <i>Escherichia coli</i> . <i>Gut Microbes</i> , 2012, 3, 71-87.	4.3	279
35	<i>Bacillus thuringiensis</i> Applications in Agriculture. , 2012, , 19-39.		28
36	Monoclonal Antibodies Neutralize <i>Bacillus cereus</i> Nhe Enterotoxin by Inhibiting Ordered Binding of Its Three Exoprotein Components. <i>Infection and Immunity</i> , 2012, 80, 832-838.	1.0	28
37	Crystallization and preliminary crystallographic analysis of the NheA component of the Nhe toxin from <i>Bacillus cereus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1073-1076.	0.7	8

#	ARTICLE	IF	CITATIONS
38	Enteroaggregative <i>Escherichia coli</i> pathotype: a genetically heterogeneous emerging foodborne enteropathogen. <i>FEMS Immunology and Medical Microbiology</i> , 2012, 66, 281-298.	2.7	113
39	5.9 Pore-Forming Toxins. , 2012, , 164-188.		4
40	Sequence Alignment of Viral Channel Proteins with Cellular Ion Channels. <i>Journal of Computational Biology</i> , 2012, 19, 1060-1072.	0.8	5
41	Inhibition of cytotoxicity by the Nhe cytotoxin of <i>Bacillus cereus</i> through the interaction of dodecyl maltoside with the NheB component. <i>FEMS Microbiology Letters</i> , 2012, 330, 98-104.	0.7	12
42	Prescriptive peptide design. <i>Amino Acids, Peptides and Proteins</i> , 2012, , 190-237.	0.7	0
43	Structures of Lysenin Reveal a Shared Evolutionary Origin for Pore-Forming Proteins And Its Mode of Sphingomyelin Recognition. <i>Structure</i> , 2012, 20, 1498-1507.	1.6	90
44	New currency for old rope: from coiled-coil assemblies to α -helical barrels. <i>Current Opinion in Structural Biology</i> , 2012, 22, 432-441.	2.6	130
45	An Engineered ClyA Nanopore Detects Folded Target Proteins by Selective External Association and Pore Entry. <i>Nano Letters</i> , 2012, 12, 4895-4900.	4.5	183
46	Mechanism of Function of Viral Channel Proteins and Implications for Drug Development. <i>International Review of Cell and Molecular Biology</i> , 2012, 294, 259-321.	1.6	30
47	Protein conducting channels' mechanisms, structures and applications. <i>Molecular BioSystems</i> , 2012, 8, 709.	2.9	5
48	In silico investigations of possible routes of assembly of ORF 3a from SARS-CoV. <i>Journal of Molecular Modeling</i> , 2012, 18, 501-514.	0.8	26
49	Microfluidic mixer designed for performing single-molecule kinetics with confocal detection on timescales from milliseconds to minutes. <i>Nature Protocols</i> , 2013, 8, 1459-1474.	5.5	76
50	Effects of MACPF/CDC proteins on lipid membranes. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 2083-2098.	2.4	71
51	Molecular assembly of the aerolysin pore reveals a swirling membrane-insertion mechanism. <i>Nature Chemical Biology</i> , 2013, 9, 623-629.	3.9	183
52	Tuning the Size and Properties of ClyA Nanopores Assisted by Directed Evolution. <i>Journal of the American Chemical Society</i> , 2013, 135, 13456-13463.	6.6	129
53	Role of Pore-Forming Toxins in Bacterial Infectious Diseases. <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 173-207.	2.9	339
54	<i>Escherichia coli</i> . , 2013, , 129-164.		7
55	A Non-classical Assembly Pathway of <i>Escherichia coli</i> Pore-forming Toxin Cytolysin A. <i>Journal of Biological Chemistry</i> , 2013, 288, 31042-31051.	1.6	33

#	ARTICLE	IF	CITATIONS
56	Membrane Damage by an Î±-Helical Pore-forming Protein, Equinatoxin II, Proceeds through a Succession of Ordered Steps. <i>Journal of Biological Chemistry</i> , 2013, 288, 23704-23715.	1.6	77
57	A cellular logic circuit for the detection of bacterial pore-forming toxins. <i>Chemical Communications</i> , 2013, 49, 5198.	2.2	10
58	Apoptosis are induced in J774 macrophages upon phagocytosis and killing of <i>Pseudomonas aeruginosa</i> . <i>Cellular Immunology</i> , 2013, 286, 11-15.	1.4	5
59	Three-dimensional structure of the actinoporin sticholysin I. Influence of long-distance effects on protein function. <i>Archives of Biochemistry and Biophysics</i> , 2013, 532, 39-45.	1.4	47
60	Bax Crystal Structures Reveal How BH3 Domains Activate Bax and Nucleate Its Oligomerization to Induce Apoptosis. <i>Cell</i> , 2013, 152, 519-531.	13.5	491
61	Prevalence of Hemolysin Genes and Comparison of <i>ehxA</i> Subtype Patterns in Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) and Non-STEC Strains from Clinical, Food, and Animal Sources. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6301-6311.	1.4	52
62	YaxAB, a <i>Yersinia enterocolitica</i> Pore-Forming Toxin Regulated by RovA. <i>Infection and Immunity</i> , 2013, 81, 4208-4219.	1.0	28
63	Structural and functional characterization of the N-terminal domain of the yeast Mg ²⁺ channel Mrs2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1653-1664.	2.5	16
64	Crystallization and preliminary X-ray analysis of monalysin, a novel Î²-pore-forming toxin from the entomopathogen <i>Pseudomonas entomophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 930-933.	0.7	7
65	A nanopore machine promotes the vectorial transport of DNA across membranes. <i>Nature Communications</i> , 2013, 4, 2415.	5.8	63
66	Physical understanding of pore formation on supported lipid bilayer by bacterial toxins. , 2013, , .		0
67	Cationic Polymers Inhibit the Conductance of Lysin Channels. <i>Scientific World Journal</i> , The, 2013, 2013, 1-8.	0.8	7
68	Complex Formation between NheB and NheC Is Necessary to Induce Cytotoxic Activity by the Three-Component <i>Bacillus cereus</i> Nhe Enterotoxin. <i>PLoS ONE</i> , 2013, 8, e63104.	1.1	38
69	Structure of the NheA Component of the Nhe Toxin from <i>Bacillus cereus</i> : Implications for Function. <i>PLoS ONE</i> , 2013, 8, e74748.	1.1	57
70	The <i>Bacillus cereus</i> Hbl and Nhe Tripartite Enterotoxin Components Assemble Sequentially on the Surface of Target Cells and Are Not Interchangeable. <i>PLoS ONE</i> , 2013, 8, e76955.	1.1	79
71	Role of Pore-Forming Toxins in Neonatal Sepsis. <i>Clinical and Developmental Immunology</i> , 2013, 2013, 1-13.	3.3	19
72	Detection of Two Isomeric Binding Configurations in a Proteinâ€‘Aptamer Complex with a Biological Nanopore. <i>ACS Nano</i> , 2014, 8, 12826-12835.	7.3	57
73	Transcriptional regulation of bacterial virulence gene expression by molecular oxygen and nitric oxide. <i>Virulence</i> , 2014, 5, 794-809.	1.8	90

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74	Inhibition of Pore Formation by Blocking the Assembly of Staphylococcus aureus α -Hemolysin Through a Novel Peptide Inhibitor: an In Silico Approach. International Journal of Peptide Research and Therapeutics, 2014, 20, 575-583.	0.9	11
75	Nanopore-based sensing devices and applications to genome sequencing: a brief history and the missing pieces. Science Bulletin, 2014, 59, 4918-4928.	1.7	14
76	The Role of Parasite Heat Shock Proteins in Protein Trafficking and Host Cell Remodeling. , 2014, , 99-117.		0
77	Lysis dynamics and membrane oligomerization pathways for Cytolysin A (ClyA) pore-forming toxin. RSC Advances, 2014, 4, 4930.	1.7	27
78	Heat Shock Proteins of Malaria. , 2014, , .		6
79	Bacterial Pathogen Manipulation of Host Membrane Trafficking. Annual Review of Cell and Developmental Biology, 2014, 30, 79-109.	4.0	132
80	Characterization of Variants of the Pore-Forming Toxin ClyA from <i>Escherichia coli</i> Controlled by a Redox Switch. Biochemistry, 2014, 53, 6357-6369.	1.2	13
81	Single molecule analysis by biological nanopore sensors. Analyst, The, 2014, 139, 3826-3835.	1.7	93
82	Photobleaching Reveals Heterogeneous Stoichiometry for Equinatoxin II Oligomers. ChemBioChem, 2014, 15, 2139-2145.	1.3	35
83	Multi-isotype antibody responses against the multimeric <i>Salmonella</i> Typhi recombinant hemolysin E antigen. Microbiology and Immunology, 2015, 59, 43-47.	0.7	6
84	Structural mapping of the C ₁ B ₁ ATPases of <i>Plasmodium falciparum</i> : Targeting protein folding and secretion for antimalarial drug design. Protein Science, 2015, 24, 1508-1520.	3.1	20
85	X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. Journal of Biological Chemistry, 2015, 290, 13191-13201.	1.6	33
86	Bak apoptotic pores involve a flexible C-terminal region and juxtaposition of the C-terminal transmembrane domains. Cell Death and Differentiation, 2015, 22, 1665-1675.	5.0	51
87	Basic mechanism of pore-forming toxins. , 2015, , 605-626.		0
88	How Lipid Membranes Affect Pore Forming Toxin Activity. Accounts of Chemical Research, 2015, 48, 3073-3079.	7.6	54
89	Structural basis for self-assembly of a cytolytic pore lined by protein and lipid. Nature Communications, 2015, 6, 6337.	5.8	185
90	Toxicity of an α -Pore-forming Toxin Depends on the Assembly Mechanism on the Target Membrane as Revealed by Single Molecule Imaging. Journal of Biological Chemistry, 2015, 290, 4856-4865.	1.6	48
91	More Than a Pore: The Interplay of Pore-Forming Proteins and Lipid Membranes. Journal of Membrane Biology, 2015, 248, 545-561.	1.0	66

#	ARTICLE	IF	CITATIONS
92	Current perspectives in pathogenesis and antimicrobial resistance of enteroaggregative <i>Escherichia coli</i> . <i>Microbial Pathogenesis</i> , 2015, 85, 44-49.	1.3	22
93	Functional characterization of Val60, a key residue involved in the membrane oligomerization of fragaceatoxin C, an actinoporin from <i>Actinia fragacea</i> . <i>FEBS Letters</i> , 2015, 589, 1840-1846.	1.3	20
94	Structural Symmetry in Membrane Proteins. <i>Annual Review of Biophysics</i> , 2015, 44, 311-337.	4.5	127
96	Amino acid residue Y196E substitution and C-terminal peptide synergistically alleviate the toxicity of <i>Clostridium perfringens</i> epsilon toxin. <i>Toxicon</i> , 2015, 100, 46-52.	0.8	8
97	Genotype-specific differences in structural features of hepatitis C virus (HCV) p7 membrane protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 1383-1392.	1.4	23
98	Single-Molecule Analyte Recognition with ClyA Nanopores Equipped with Internal Protein Adaptors. <i>Journal of the American Chemical Society</i> , 2015, 137, 5793-5797.	6.6	86
99	Perforins. <i>Springer Series in Biophysics</i> , 2015, , 289-312.	0.4	2
100	Electrophysiology of Unconventional Channels and Pores. <i>Springer Series in Biophysics</i> , 2015, , .	0.4	9
101	The assembly dynamics of the cytolytic pore toxin ClyA. <i>Nature Communications</i> , 2015, 6, 6198.	5.8	83
102	Using fluorescence for studies of biological membranes: a review. <i>Methods and Applications in Fluorescence</i> , 2015, 3, 042003.	1.1	33
103	Directly Observing the Lipid-Dependent Self-Assembly and Pore-Forming Mechanism of the Cytolytic Toxin Listeriolysin O. <i>Nano Letters</i> , 2015, 15, 6965-6973.	4.5	74
104	Crystal structure and solution characterization of the thioredoxin-2 from <i>Plasmodium falciparum</i> , a constituent of an essential parasitic protein export complex. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 403-409.	1.0	18
105	<i>Vibrio cholerae</i> Cytolysin: Structure-Function Mechanism of an Atypical Î²-Barrel Pore-Forming Toxin. <i>Advances in Experimental Medicine and Biology</i> , 2015, 842, 109-125.	0.8	16
106	Crystal structure of Cry6Aa: A novel nematocidal ClyA-type Î±-pore-forming toxin from <i>Bacillus thuringiensis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 307-313.	1.0	15
107	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 359-374.	1.1	29
108	Tuning the Selectivity and Sensitivity of an OmpG Nanopore Sensor by Adjusting Ligand Tether Length. <i>ACS Sensors</i> , 2016, 1, 614-622.	4.0	40
109	Necrosome core machinery: MLKL. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2153-2163.	2.4	135
110	The pesticidal Cry6Aa toxin from <i>Bacillus thuringiensis</i> is structurally similar to HlyE-family alpha pore-forming toxins. <i>BMC Biology</i> , 2016, 14, 71.	1.7	37

#	ARTICLE	IF	CITATIONS
111	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. <i>Journal of Biological Chemistry</i> , 2016, 291, 19210-19219.	1.6	23
112	Engineered transmembrane pores. <i>Current Opinion in Chemical Biology</i> , 2016, 34, 117-126.	2.8	95
113	The Solvent-Exposed C-Terminus of the Cytolysin A Pore-Forming Toxin Directs Pore Formation and Channel Function in Membranes. <i>Biochemistry</i> , 2016, 55, 5952-5961.	1.2	17
114	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 346-358.	1.1	31
115	Capturing the Membrane-Triggered Conformational Transition of an α -Helical Pore-Forming Toxin. <i>Journal of Physical Chemistry B</i> , 2016, 120, 12064-12078.	1.2	30
116	Inhibitory effect of liposome-entrapped lemongrass oil on the growth of <i>Listeria monocytogenes</i> in cheese. <i>Journal of Dairy Science</i> , 2016, 99, 6097-6104.	1.4	46
117	pH controlled gating of toxic protein pores by dendrimers. <i>Nanoscale</i> , 2016, 8, 13045-13058.	2.8	18
118	Functionally Relevant Specific Packing Can Determine Protein Folding Routes. <i>Journal of Molecular Biology</i> , 2016, 428, 509-521.	2.0	12
119	Pore-forming toxins: ancient, but never really out of fashion. <i>Nature Reviews Microbiology</i> , 2016, 14, 77-92.	13.6	600
120	Soluble Oligomers of the Pore-forming Toxin Cytolysin A from <i>Escherichia coli</i> Are Off-pathway Products of Pore Assembly. <i>Journal of Biological Chemistry</i> , 2016, 291, 5652-5663.	1.6	10
121	Protein-lipid interactions and non-lamellar lipidic structures in membrane pore formation and membrane fusion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 487-499.	1.4	53
122	Assembling the puzzle: Oligomerization of α -pore forming proteins in membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 457-466.	1.4	63
123	Quantifying kinetics from time series of single-molecule Förster resonance energy transfer efficiency histograms. <i>Nanotechnology</i> , 2017, 28, 114002.	1.3	11
124	Rapid Microfluidic Double-Jump Mixing Device for Single-Molecule Spectroscopy. <i>Journal of the American Chemical Society</i> , 2017, 139, 6062-6065.	6.6	18
125	Cry6Aa1, a <i>Bacillus thuringiensis</i> nematocidal and insecticidal toxin, forms pores in planar lipid bilayers at extremely low concentrations and without the need of proteolytic processing. <i>Journal of Biological Chemistry</i> , 2017, 292, 13122-13132.	1.6	10
126	Single-molecule nanopore enzymology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160230.	1.8	57
127	Computational studies of peptide-induced membrane pore formation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160219.	1.8	46
128	Metamorphic Proteins: Emergence of Dual Protein Folds from One Primary Sequence. <i>Biochemistry</i> , 2017, 56, 2971-2984.	1.2	52

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129	Label-Free and Real-Time Detection of Protein Ubiquitination with a Biological Nanopore. ACS Nano, 2017, 11, 4387-4394.	7.3	104
130	Disrupting a key hydrophobic pair in the oligomerization interface of the actinoporins impairs their pore-forming activity. Protein Science, 2017, 26, 550-565.	3.1	25
131	Expression and characterization of the Plasmodium translocon of the exported proteins component EXP2. Biochemical and Biophysical Research Communications, 2017, 482, 700-705.	1.0	23
132	Assessing the Structure and Stability of Transmembrane Oligomeric Intermediates of an α -Helical Toxin. Langmuir, 2017, 33, 11496-11510.	1.6	25
133	Analysis of Pore Formation and Protein Translocation Using Large Biological Nanopores. Analytical Chemistry, 2017, 89, 11269-11277.	3.2	43
134	Regulation of expression and trafficking of perforin-2 by LPS and TNF- α . Cellular Immunology, 2017, 320, 1-10.	1.4	15
136	Real-Time Conformational Changes and Controlled Orientation of Native Proteins Inside a Protein Nanoreactor. Journal of the American Chemical Society, 2017, 139, 18640-18646.	6.6	83
137	The Metamorphic Transformation of a Water-Soluble Monomeric Protein Into an Oligomeric Transmembrane Pore. Advances in Biomembranes and Lipid Self-Assembly, 2017, 26, 51-97.	0.3	12
138	Transmembrane oligomeric intermediates of pore forming toxin Cytolysin A determine leakage kinetics. RSC Advances, 2017, 7, 51750-51762.	1.7	15
139	Assembly mechanism of the α -pore-forming toxin cytolysin A from <i>Escherichia coli</i> . Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160211.	1.8	31
140	Building membrane nanopores. Nature Nanotechnology, 2017, 12, 619-630.	15.6	235
141	Delineation of B-cell Epitopes of Salmonella enterica serovar Typhi Hemolysin E: Potential antibody therapeutic target. Scientific Reports, 2017, 7, 2176.	1.6	12
142	Electron Cryo-microscopy as a Tool for Structure-Based Drug Development. Angewandte Chemie - International Edition, 2017, 56, 2846-2860.	7.2	36
143	Kryo-Elektronenmikroskopie als Methode für die strukturbasierte Wirkstoffentwicklung. Angewandte Chemie, 2017, 129, 2890-2905.	1.6	10
144	A monodisperse transmembrane α -helical peptide barrel. Nature Chemistry, 2017, 9, 411-419.	6.6	97
145	Anisotropic Self-Assembly of Organic-Inorganic Hybrid Microtoroids. Journal of the American Chemical Society, 2017, 139, 10232-10238.	6.6	18
146	Nanopore Sensing. Analytical Chemistry, 2017, 89, 157-188.	3.2	344
147	Comparison of coarse-grained (MARTINI) and atomistic molecular dynamics simulations of α and β toxin nanopores in lipid membranes. Journal of Chemical Sciences, 2017, 129, 1017-1030.	0.7	18

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148	<i>Vibrio cholerae</i> cytolysin: Multiple facets of the membrane interaction mechanism of a β -barrel pore-forming toxin. IUBMB Life, 2018, 70, 260-266.	1.5	21
149	Disruption of the open conductance in the β -tongue mutants of Cytolysin A. Scientific Reports, 2018, 8, 3796.	1.6	2
150	Determining the Physical Properties of Molecules with Nanometer-Scale Pores. ACS Sensors, 2018, 3, 251-263.	4.0	28
151	Pathways for creation and annihilation of nanoscale biomembrane domains reveal alpha and beta-toxin nanopore formation processes. Physical Chemistry Chemical Physics, 2018, 20, 29116-29130.	1.3	16
153	Structural Basis and Functional Implications of the Membrane Pore-Formation Mechanisms of Bacterial Pore-Forming Toxins. Advances in Experimental Medicine and Biology, 2018, 1112, 281-291.	0.8	16
154	Modular Pore-Forming Immunotoxins with Caged Cytotoxicity Tailored by Directed Evolution. ACS Chemical Biology, 2018, 13, 3153-3160.	1.6	23
155	Nanopore label-free detection of single-nucleotide deletion in <i>Bax</i> ^{1±} / <i>Bax</i> ^{1”2} . Electrophoresis, 2018, 39, 2410-2416.	1.3	9
156	Structural and Mechanistic Features of ClyA-Like β -Pore-Forming Toxins. Toxins, 2018, 10, 343.	1.5	11
157	Mapping an Equilibrium Folding Intermediate of the Cytolytic Pore Toxin ClyA with Single-Molecule FRET. Journal of Physical Chemistry B, 2018, 122, 11251-11261.	1.2	19
158	Advances in DNA Origami Nanopores: Fabrication, Characterization and Applications. Chinese Journal of Chemistry, 2018, 36, 875-885.	2.6	8
159	Flagella-mediated secretion of a novel <i>Vibrio cholerae</i> cytotoxin affecting both vertebrate and invertebrate hosts. Communications Biology, 2018, 1, 59.	2.0	43
160	Crystal structure of the <i>Streptococcus agalactiae</i> CAMP factor provides insights into its membrane-permeabilizing activity. Journal of Biological Chemistry, 2018, 293, 11867-11877.	1.6	14
161	Helix β -3 inter-molecular salt bridges and conformational changes are essential for toxicity of <i>Bacillus thuringiensis</i> 3D-Cry toxin family. Scientific Reports, 2018, 8, 10331.	1.6	13
162	Cholesterol promotes Cytolysin A activity by stabilizing the intermediates during pore formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7323-E7330.	3.3	48
163	Structure and mechanism of the two-component β -helical pore-forming toxin YaxAB. Nature Communications, 2018, 9, 1806.	5.8	46
164	Structural metamorphism and polymorphism in proteins on the brink of thermodynamic stability. Protein Science, 2018, 27, 1557-1567.	3.1	34
165	Cholesterol-dependent cytolysins: from water-soluble state to membrane pore. Biophysical Reviews, 2018, 10, 1337-1348.	1.5	32
166	Protein Motion and Configurations in a Form-Fitting Nanopore: Avidin in ClyA. Biophysical Journal, 2018, 115, 801-808.	0.2	14

#	ARTICLE	IF	CITATIONS
167	Engineering and Modeling the Electrophoretic Trapping of a Single Protein Inside a Nanopore. ACS Nano, 2019, 13, 9980-9992.	7.3	43
168	Identification and structural analysis of the tripartite β -pore forming toxin of <i>Aeromonas hydrophila</i> . Nature Communications, 2019, 10, 2900.	5.8	20
169	Structural and Biochemical Characterization of the YaxAB Pore-forming Toxin from <i>Yersinia Enterocolitica</i> . Springer Theses, 2019, , .	0.0	0
170	Cholesterol-Dependent Cytolysins: Membrane and Protein Structural Requirements for Pore Formation. Chemical Reviews, 2019, 119, 7721-7736.	23.0	35
171	ABC Toxins: Self-Assembling Nanomachines for the Targeted Cellular Delivery of Bioactive Proteins. , 2019, , 279-298.		0
172	Binding to The Target Cell Surface Is The Crucial Step in Pore Formation of Hemolysin BL from <i>Bacillus cereus</i> . Toxins, 2019, 11, 281.	1.5	24
173	The destructive spontaneous ingression of tunable silica nanosheets through cancer cell membranes. Chemical Science, 2019, 10, 6184-6192.	3.7	6
174	High-resolution cryo-EM structures of the <i>E. coli</i> hemolysin ClyA oligomers. PLoS ONE, 2019, 14, e0213423.	1.1	31
176	Nucleic Acid Amplification Strategy-Based Nanopore Sensors. , 2019, , 173-196.		0
177	Cryo-EM structures of <i>Helicobacter pylori</i> vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6800-6805.	3.3	33
178	Reversible fold-switching controls the functional cycle of the antitermination factor RfaH. Nature Communications, 2019, 10, 702.	5.8	50
179	Structural considerations of folded protein import through the chloroplast TOC / TIC translocons. FEBS Letters, 2019, 593, 565-572.	1.3	13
180	Rapid and Accurate Determination of Nanopore Ionic Current Using a Steric Exclusion Model. ACS Sensors, 2019, 4, 634-644.	4.0	53
181	A family of Type VI secretion system effector proteins that form ion-selective pores. Nature Communications, 2019, 10, 5484.	5.8	57
182	A large size-selective DNA nanopore with sensing applications. Nature Communications, 2019, 10, 5655.	5.8	126
183	Surface coatings for solid-state nanopores. Nanoscale, 2019, 11, 19636-19657.	2.8	75
184	Taking Toll on Membranes: Curious Cases of Bacterial β -Barrel Pore-Forming Toxins. Biochemistry, 2020, 59, 163-170.	1.2	20
185	Enteroaggregative <i>E. coli</i> Adherence to Human Heparan Sulfate Proteoglycans Drives Segment and Host Specific Responses to Infection. PLoS Pathogens, 2020, 16, e1008851.	2.1	24

#	ARTICLE	IF	CITATIONS
186	Accurate modeling of a biological nanopore with an extended continuum framework. <i>Nanoscale</i> , 2020, 12, 16775-16795.	2.8	26
187	Molecular Dynamics Study of Lipid and Cholesterol Reorganization Due to Membrane Binding and Pore Formation by Listeriolysin O. <i>Journal of Membrane Biology</i> , 2020, 253, 535-550.	1.0	20
188	Rearrangement of N-Terminal α -Helices of <i>Bacillus thuringiensis</i> Cry1Ab Toxin Essential for Oligomer Assembly and Toxicity. <i>Toxins</i> , 2020, 12, 647.	1.5	4
189	Sequence Diversity in the Pore-Forming Motifs of the Membrane-Damaging Protein Toxins. <i>Journal of Membrane Biology</i> , 2020, 253, 469-478.	1.0	10
190	FRET Dyes Significantly Affect SAXS Intensities of Proteins. <i>Israel Journal of Chemistry</i> , 2020, 60, 725-734.	1.0	3
191	The <i>Bacillus cereus</i> Food Infection as Multifactorial Process. <i>Toxins</i> , 2020, 12, 701.	1.5	88
192	Assessing the extent of the structural and dynamic modulation of membrane lipids due to pore forming toxins: insights from molecular dynamics simulations. <i>Soft Matter</i> , 2020, 16, 4840-4857.	1.2	13
193	Sequential CRISPR-Based Screens Identify LITAF and CDIP1 as the <i>Bacillus cereus</i> Hemolysin BL Toxin Host Receptors. <i>Cell Host and Microbe</i> , 2020, 28, 402-410.e5.	5.1	23
194	<i>Bacillus cereus</i> non-haemolytic enterotoxin activates the NLRP3 inflammasome. <i>Nature Communications</i> , 2020, 11, 760.	5.8	51
195	Opening of smaller toxin pores by lipid micelle formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5107-5108.	3.3	12
196	Reply to Desikan et al.: Micelle formation among various mechanisms of toxin pore formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5109-5110.	3.3	1
197	Pore-forming proteins: From defense factors to endogenous executors of cell death. <i>Chemistry and Physics of Lipids</i> , 2021, 234, 105026.	1.5	17
198	Predicting interfacial hot-spot residues that stabilize protein-protein interfaces in oligomeric membrane-toxin pores through hydrogen bonds and salt bridges. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 20-34.	2.0	6
199	Strategies for enzymological studies and measurements of biological molecules with the cytolysin A nanopore. <i>Methods in Enzymology</i> , 2021, 649, 567-585.	0.4	3
200	Electron microscopy as a critical tool in the determination of pore forming mechanisms in proteins. <i>Methods in Enzymology</i> , 2021, 649, 71-102.	0.4	7
201	The Food Poisoning Toxins of <i>Bacillus cereus</i> . <i>Toxins</i> , 2021, 13, 98.	1.5	124
202	Using multiscale molecular dynamics simulations to obtain insights into pore forming toxin mechanisms. <i>Methods in Enzymology</i> , 2021, 649, 461-502.	0.4	9
203	Biological Nanopores: Engineering on Demand. <i>Life</i> , 2021, 11, 27.	1.1	33

#	ARTICLE	IF	CITATIONS
204	Escherichia coli. , 2021, , 125-163.		0
205	A stable antimicrobial peptide with dual functions of treating and preventing citrus Huanglongbing. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	66
206	Structural Basis of the Pore-Forming Toxin/Membrane Interaction. Toxins, 2021, 13, 128.	1.5	21
207	Palmitoylated acyl protein thioesterase APT2 deforms membranes to extract substrate acyl chains. Nature Chemical Biology, 2021, 17, 438-447.	3.9	31
208	Pore-forming toxins of foodborne pathogens. Comprehensive Reviews in Food Science and Food Safety, 2021, 20, 2265-2285.	5.9	10
209	The Crystal Structure of Bacillus cereus HblL1. Toxins, 2021, 13, 253.	1.5	9
211	Cryo-EM structures of an insecticidal Bt toxin reveal its mechanism of action on the membrane. Nature Communications, 2021, 12, 2791.	5.8	28
212	Combining Rapid Microfluidic Mixing and Three-Color Single-Molecule FRET for Probing the Kinetics of Protein Conformational Changes. Journal of Physical Chemistry B, 2021, 125, 6617-6628.	1.2	4
213	Membrane-Suspended Nanopores in Microchip Arrays for Stochastic Transport Recording and Sensing. Frontiers in Nanotechnology, 2021, 3, .	2.4	2
215	Slow Escape from a Helical Misfolded State of the Pore-Forming Toxin Cytolysin A. JACS Au, 2021, 1, 1217-1230.	3.6	5
216	RBD-Modified Bacterial Vesicles Elicited Potential Protective Immunity against SARS-CoV-2. Nano Letters, 2021, 21, 5920-5930.	4.5	17
217	A New Contact Killing Toxin Permeabilizes Cells and Belongs to a Broadly Distributed Protein Family. MSphere, 2021, 6, e0031821.	1.3	5
218	Beyond pore formation: reorganization of the plasma membrane induced by pore-forming proteins. Cellular and Molecular Life Sciences, 2021, 78, 6229-6249.	2.4	13
219	Techniques for studying membrane pores. Current Opinion in Structural Biology, 2021, 69, 108-116.	2.6	4
220	Identification and characterization of metamorphic proteins: Current and future perspectives. Biopolymers, 2021, 112, e23473.	1.2	6
222	Pore Forming Protein Induced Biomembrane Reorganization and Dynamics: A Focused Review. Frontiers in Molecular Biosciences, 2021, 8, 737561.	1.6	9
223	A Novel Immunomodulator Delivery Platform Based on Bacterial Biomimetic Vesicles for Enhanced Antitumor Immunity. Advanced Materials, 2021, 33, e2103923.	11.1	19
224	Structural foundations of sticholysin functionality. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140696.	1.1	7

#	ARTICLE	IF	CITATIONS
225	Nanopore chip with self-aligned transverse tunneling junction for DNA detection. <i>Biosensors and Bioelectronics</i> , 2021, 193, 113552.	5.3	4
226	A generic force field for simulating native protein structures using dissipative particle dynamics. <i>Soft Matter</i> , 2021, 17, 9772-9785.	1.2	6
227	X-ray crystallography shines a light on pore-forming toxins. <i>Methods in Enzymology</i> , 2021, 649, 1-46.	0.4	8
228	Preparation of Cytolysin A (ClyA) Nanopores. <i>Methods in Molecular Biology</i> , 2021, 2186, 11-18.	0.4	5
229	Membrane Interactions and Cellular Effects of MACPF/CDC Proteins. <i>Sub-Cellular Biochemistry</i> , 2014, 80, 119-144.	1.0	7
230	Mechanistic Insights into Pore Formation by an $\hat{\pm}$ -Pore Forming Toxin: Protein and Lipid Bilayer Interactions of Cytolysin A. <i>Accounts of Chemical Research</i> , 2021, 54, 120-131.	7.6	14
231	Haemolysin E- and enterohaemolysin-derived haemolytic activity of O55/O157 strains and other <i>Escherichia coli</i> lineages. <i>Microbiology (United Kingdom)</i> , 2012, 158, 746-758.	0.7	14
234	Structure of the N-terminal domain of the effector protein LegC3 from <i>Legionella pneumophila</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 436-441.	2.5	10
235	The A component (SmhA) of a tripartite pore-forming toxin from <i>Serratia marcescens</i> : expression, purification and crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 577-582.	0.4	1
236	Functional Characterization of Sticholysin I and W111C Mutant Reveals the Sequence of the Actinoporin's Pore Assembly. <i>PLoS ONE</i> , 2014, 9, e110824.	1.1	37
237	The Deletion of Several Amino Acid Stretches of <i>Escherichia coli</i> Alpha-Hemolysin (HlyA) Suggests That the Channel-Forming Domain Contains Beta-Strands. <i>PLoS ONE</i> , 2014, 9, e112248.	1.1	17
238	Membrane-Targeted Self-Assembling Cyclic Peptide Nanotubes. <i>Current Topics in Medicinal Chemistry</i> , 2015, 14, 2647-2661.	1.0	33
239	Structural Basis of Pore Formation by Mosquito-larvicidal Proteins from <i>Bacillus thuringiensis</i> . <i>The Open Toxinology Journal</i> , 2013, 3, 119-125.	0.9	13
240	Composition of the Putative Prepore Complex of <i>Bacillus thuringiensis</i> ; Cry1Ab Toxin. <i>Advances in Biological Chemistry</i> , 2015, 05, 179-188.	0.2	1
241	Disordered clusters of Bak dimers rupture mitochondria during apoptosis. <i>ELife</i> , 2017, 6, .	2.8	60
242	Membrane insertion of $\hat{\pm}$ -xenorhabdolysin in near-atomic detail. <i>ELife</i> , 2018, 7, .	2.8	27
244	Chapter 13. Community- and Hospital-acquired Staphylococcal Infections. <i>RSC Nanoscience and Nanotechnology</i> , 2011, , 175-192.	0.2	0
245	Structural Biology of the Food Poisoning <i>Clostridium Perfringens</i> Enterotoxin. <i>Nihon Kessho Gakkaishi</i> , 2013, 55, 223-229.	0.0	0

#	ARTICLE	IF	CITATIONS
246	Microbial Toxins in Foods: The Importance of Escherichia coli, a Versatile Enemy. Springer Briefs in Molecular Science, 2015, , 79-101.	0.1	2
256	Nanopore sensors for viral particle quantification: current progress and future prospects. Bioengineered, 2021, 12, 9189-9215.	1.4	10
259	Evaluating cytotoxic effects of recombinant fragaceatoxin C pore forming toxin against AML cell lines. Iranian Journal of Basic Medical Sciences, 2018, 21, 878-883.	1.0	4
260	A tripartite cytolytic toxin formed by <i>Vibrio cholerae</i> proteins with flagellum-facilitated secretion. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
261	Effector-mediated membrane disruption controls cell death in CBASS antiphage defense. Molecular Cell, 2021, 81, 5039-5051.e5.	4.5	59
262	Reviewâ€”Single-Molecule Sensors Based on Protein Nanopores. Journal of the Electrochemical Society, 2021, 168, 126502.	1.3	5
263	Structures and functions of the membrane-damaging pore-forming proteins. Advances in Protein Chemistry and Structural Biology, 2022, 128, 241-288.	1.0	4
264	Pore formation by pore forming membrane proteins towards infections. Advances in Protein Chemistry and Structural Biology, 2022, 128, 79-111.	1.0	1
266	Cytolysin A (ClyA): A Bacterial Virulence Factor with Potential Applications in Nanopore Technology, Vaccine Development, and Tumor Therapy. Toxins, 2022, 14, 78.	1.5	7
267	Control of subunit stoichiometry in single-chain MspA nanopores. Biophysical Journal, 2022, 121, 742-754.	0.2	7
268	The Biology and the Evolutionary Dynamics of Diarrheagenic <i>Escherichia coli</i> Pathotypes. , 0, , .		2
269	Bacterial pore-forming toxins. Microbiology (United Kingdom), 2022, 168, .	0.7	16
270	Presence and function of Hbl Bâ€™™, the fourth protein component encoded by the <i>hbl</i> operon in <i>Bacillus cereus</i> . Virulence, 2022, 13, 483-501.	1.8	1
271	Review of the use of nanodevices to detect single molecules. Analytical Biochemistry, 2022, 654, 114645.	1.1	7
272	Rapid Surface Display of mRNA Antigens by Bacteriaâ€”Derived Outer Membrane Vesicles for a Personalized Tumor Vaccine. Advanced Materials, 2022, 34, e2109984.	11.1	82
275	The application of single molecule nanopore sensing for quantitative analysis. Chemical Society Reviews, 2022, 51, 3862-3885.	18.7	28
276	Phylogenetic and protein prediction analysis reveals the taxonomically diverse distribution of virulence factors in <i>Bacillus cereus</i> strains. PLoS ONE, 2022, 17, e0262974.	1.1	0
277	Dual role of CsrA in regulating the hemolytic activity of <i>Escherichia coli</i> O157:H7. Virulence, 2022, 13, 859-874.	1.8	3

#	ARTICLE	IF	CITATIONS
278	Polymerized porin as a novel delivery platform for coronavirus vaccine. <i>Journal of Nanobiotechnology</i> , 2022, 20, .	4.2	1
279	Structural and functional role of Domain I for the insecticidal activity of the <scp>Vip3Aa</scp> protein from <i>Bacillus thuringiensis</i>. <i>Microbial Biotechnology</i> , 2022, 15, 2607-2618.	2.0	8
280	Nanocarriers based on bacterial membrane materials for cancer vaccine delivery. <i>Nature Protocols</i> , 2022, 17, 2240-2274.	5.5	42
281	Cryo-EM elucidates mechanism of action of bacterial pore-forming toxins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022, 1864, 184013.	1.4	4
282	Function-based classification of hazardous biological sequences: Demonstration of a new paradigm for biohazard assessments. <i>Frontiers in Bioengineering and Biotechnology</i> , 0, 10, .	2.0	3
283	<i>V. cholerae</i> MakA is a cholesterol-binding pore-forming toxin that induces non-canonical autophagy. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	7
284	A major conformational change of Nâ€œterminal helices of <i>Bacillus thuringiensis</i> <scp>Cry1Ab</scp> insecticidal protein is necessary for membrane insertion and toxicity. <i>FEBS Journal</i> , 2023, 290, 2692-2705.	2.2	6
285	Conformational Flexibility Is a Key Determinant for the Lytic Activity of the Pore-Forming Protein, Cytolysin A. <i>Journal of Physical Chemistry B</i> , 2023, 127, 69-84.	1.2	2
286	Pore-Forming Proteins: From Pore Assembly to Structure by Quantitative Single-Molecule Imaging. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4528.	1.8	3
287	Recent Advances in DNA Origami-Engineered Nanomaterials and Applications. <i>Chemical Reviews</i> , 2023, 123, 3976-4050.	23.0	42
288	Minimal Out-of-Equilibrium Metabolism for Synthetic Cells: Aâ€œMembrane Perspective. <i>ACS Synthetic Biology</i> , 2023, 12, 922-946.	1.9	10
295	Story of Pore-Forming Proteins from Deadly Disease-Causing Agents to Modern Applications with Evolutionary Significance. <i>Molecular Biotechnology</i> , 0, , .	1.3	0